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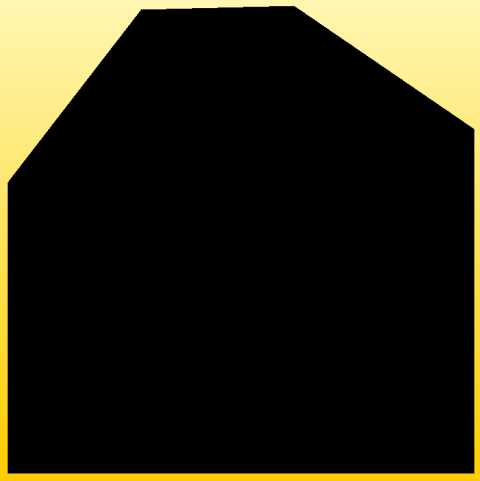

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RESEARCH JOURNAL

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Research Notes

PKV Res. J. Vol. 39 (1&2), January & July 2015

Floral Bud Distortion: Insights of Peculiar Disorder Prevailing in Soybean

P. V. Jadhav[1], P. B. Kale[2], R. S. Wakekar[3], M. P. Moharil[4], R. S. Nandanwar[5], S. S.Mane[6], M. S. Dudhave[7], A. G. Deshmukh[8], J. G. Manjaya[9] and R. G. Dani[10]

ABSTRACT

Siphonogamy is a key event in the reproductive course of plants which has been extensively studied in past years. However, we describe a peculiar and often harmful disorder in soybean leading to significant yield loss in India. To determine the prevalence of floral bud distortion, extensive random survey was undertaken in soybean growing areas of central India during two succeeding seasons, kharif-2010 and 2011. The average rate of the disorder obtained from 41 locations of Madhya Pradesh, Maharashtra and Karnataka ranged from 8.0 to 14.6per cent and severity from 2.0 to 90.0per cent under field condition. The affected plants were found to have either no or deformed pods and distorted flowers, and they remained green after maturity. All the genotypes grown in surveyed regions (JS-335, JS-93-05, JS 73-23, JS 95-60, AMS-MB-5-19, Co-2, Bragg, JS 10-44, Samrat) were affected by the disorder. Diagnosis of symptomatic plants revealed presence of *Tobacco streak virus* (TSV), *Groundnut bud necrosis virus* (GBNV) and phytoplasma. Cytological studies showed significantly reduced number of pollen grains with high sterility in symptomatic plants. However, stigma of both the sources found receptive. Biochemical analysis showed significant increase in carbohydrate, protein along with chlorophyll content index in symptomatic plant. Molecular characterization based on cDNA-decamere profiling of symptomatic and asymptomatic plant tissues (Leaf bud and node) was developed. Homology analysis revealed alterations in expression of various genes associated with floral bud distortion *viz*., Auxin Response Factor 9 (ARF9), Forkhead-associated (FHA) domain, isoaspartyl peptidase/L-asparaginase protein (L-ASNase) and pentatricopeptide repeat-containing protein (PPR), which are directly or indirectly involved in plant development. .

Area under soybean [*Glycine max* (L.) Merrill] cultivation is rapidly expanding partly due to its high nutritional value as food for both humans and livestock and as an important industrial crop. It is considered as a 'Golden bean' due to its dual qualities *viz.,* high protein (40per cent) and oil (18–20per cent) content. India with an area of 12.03 million ha and a production of 12.98 million tonnes, during 2013–2014 is among top four soybean producing countries (Anonymous 2013).

In recent years soybean has been devastated by an unknown floral bud distortion. The symptoms produced did not resemble any of the documented disorders of soybean and were inconsistent in their distribution across locations. The research community has no information about its cause or control. Therefore, cytological examination of plant reproductive organs (*viz.* anther, pollen and stigma) needs to be done to understand their factual structural and functional disability associated with the disorder.

Recently, cDNA-RAPD technique has been successfully used for determining differentially expressed TDFs in sugarcane (Pagaria *et al.*, 2010), chickpea (Nimbalkar et al., 2006) and *Phalaenopsis orchids* (Chen et al. 2005). It proved a cost-effective technique that provides information on complex phenotype reûecting changes in the abundance of hundreds of RNAs under various conditions and does not require specialized expertise to handle as in the other sophisticated technical activities. Accordingly, the objective of this study was to assess the cytological behavior of floral reproductive organs and molecular alterations associated with the disorder to identify the key genes that were differentially expressed in symptomatic soybean plants using cDNA-RAPD technique. Similarly, the differentially expressed-transcript derived fragments (TDFs) were characterized using *in-silico* tools.

MATERIAL AND METHODS

Survey, symptomatology and diagnosis

The comprehensive random roving survey was conducted to estimate the incidence of floral bud distortion in the major soybean growing areas of Madhya Pradesh, Maharashtra and adjoining parts of Karnataka state. The

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survey was done at R7-R8th crop stage, 65-70 days after sowing. Based on symptomatology, representative samples were tested for four suspected causal agents *viz*., *Tobacco streak virus* (TSV), *Groundnut bud necrosis virus* (GBNV), *Tobacco Ring spot Virus* (TRSV) and phytoplasma using ELISA and PCR respectively (Bhat *et al.,* 2002).

Reproductive Biology

Cytological study was carried out to determine pollen germination, viability and stigma receptivity of symptomatic and asymptomatic plant. Pollen viability test was done by using 3 different dyes *viz*., acetocarmine (Alexander, 1969; Kaur et al., 2005; Ling *et al.*, 2012), potassium iodide (I/KI) as reported by Djanaguiraman et al., (2013) and vital dye solution (Johri and Vasil, 1961).

Further, pollen anatomy was studied by scanning electron microscopy (SEM) as per the standard procedure given by Kaur *et al.* (2005) using JSM 1100 JEOL. Pollen germination percentage was estimated using an artificial medium refined in this crop as per the procedure given by Thomas (2000) and Jayaprakash and Sabesan (2013). The stigma receptivity was evaluated and change in color with the presence of peroxidases was recorded according to Dafni and Motte-Moause in 1998.

Biochemical profiling

The biochemical characterization was carried out to identify differential levels of metabolites in leaf, node and root tissues of symptomatic and asymptomatic plants. Standard methods were followed for estimation of various components *viz*, carbohydrate (Anthron method), nitrogen (per cent), chlorophyll, proline (mg), total protein content (mg) and reagents were prepared as described by Zenoni *et al*., (2011). High Performance Liquid Chromatography (HPLC) and Fourier transmission infrared (FTIR) analysis was carried out by using standard methods given by Cesar *et al.* (2006) and Zenoni *et al*., (2011), respectively.

Molecular Attributes

cDNA synthesis and decamer profiling

Total RNA was isolated from the frozen bud, node and leaf tissues of symptomatic and asymptomatic plants at R5 stage using TriZol® (InVitrogen). Further, the first strand DNA was synthesized by using kit (Thermo Scientific, USA). Noemalization of synthesized cDNA was done prior to PCR profiling PCR amplification of cDNA from each tissue was achieved using decamer primers. Amplicon generated were scored and data was analyzed based on the consensus results of three independent runs. Clearly resolved polymorphic bands (TDFs) of both plants were scored manually considering the presence/absence or differences in intensity derived values (IDV).

BLAST homology and Placement of TDFs in coding regions

The differentially expressed TDFs were eluted individually from the agaros gel (QIAEX II gel extraction kit, Qiagen) (Eurofins MWG/Operon Inc., Banglore). The sequences were analyzed using ChromasLite 2.01 software for editing. The sequence homology was searched against publically available database using BLAST algorithms (http://www.ncbi.nlm.nih.gov/Blast.cgi) (Altschul *et al.,* 1997). Gene specific relatedness was established with the FBD symptoms and published reports to annotate pathways involved in development of floral abnormality. The placement of TDFs in CDS regions of predicted gene structure was done using FGENESH (http://linux1.softberry.com/berry.phtml) an *in-silico* tool.

In silico protein Interaction and sub cellular localization

The available soybean databases (Phytozome, SoyBase and NCBI) were used to anchor identified TDF sequences generated on chromosomes of *G. max*. This was done to identify their distribution, relative position and abundance in the genome. The exact locations of TDFs were determined using MegaBLAST tool producing at least 80per cent identity (Soares-Cavalcanti *et al.,* 2012).

RESULTS AND DISCUSSION

Survey, symptomatology and diagnosis

The floral bud distortion (FBD) is a peculiar disorder occurring in soybean growing regions. The symptoms of FBD does not resemble with any of the documented soybean disease, pest or disorder. The principal symptoms exhibited by symptomatic plant were the normally growing plant without pod and prolonged vegetative phase. Secondly these plants were found randomly distributed in the field. The FBD exhibited decreasing apical dominance and distorted floral organs *i.e.* petals, stamens, carpel and ovary, leading to failure of pod development on affected plants (Jadhav *et al.*, 2013).

The average incidence was varied from 8.0 to 14.6per cent with severity of 2.0-90.0 per cent in different parts of the states surveyed. During *Kharif*-2010, the highest incidence of 80per cent was recorded in fields of the village of Simriya and Karakbail located in Narsimhapur

district of Madhya Pradesh. However, during *Kharif*-2011, the entire field was severely affected in the village of Hadgaon (>80%) in Akola district of Maharashtra, followed by the village Borgaon Bujrug (>50%) of Pandana Tahasil (MP). In adjoining parts of Karnataka, average incidence was found in both the seasons. The incidence was observed irrespective of soybean genotype grown under surveyed regions.

Individual as well as mixed presence of TSV and GBNV was found in symptomatic plants. However, two samples were found positive for the presence of phytoplasma in nested PCR reaction. Mixed infections leads to more severe symptoms in the field samples (Balogun *et al.* 2002). Further observations were clustered according to the titer of virus (es) and PCR results were correlated with the symptomatology. The symptomatic plants were categorized in to four different group on the basis of diagnosis as follows:

SN	Presence of pathogen	Major symptoms recorded
1	TSV	Reduced plant height and less number of necrotic pods along with typical FBD symptoms
2	GBNV	Thick green stem, plant height along with typical FBD symptoms
3	TSV and GBNV	Thick green stem, plant height along with typical FBD symptoms
4	Phytoplasma	Virescence, abnormal pods, thickening and green stem appearance

Reproductive Biology

Floral reproductive organs, pollen and stigma of symptomatic and asymptomatic plants were evaluated for their morphology, pollen count, vigor, viability, germinability and receptivity. A significant difference was observed in all the parameters studied. Pollen count per microscopic field was significantly reduced in symptomatic plants as compared to asymptomatic plant. Interestingly, the pollen grains were structurally distorted in symptomatic plants. Whilst in asymptomatic plants relatively high number of spherical round pollens were recorded. The pollen grains of symptomatic plants were found structurally distorted as compare to asymptomatic plants. It indicates pollen dysfunction is a prime cause associated with the disorder in soybean, hindering pollination and fertilization in symptomatic plants.

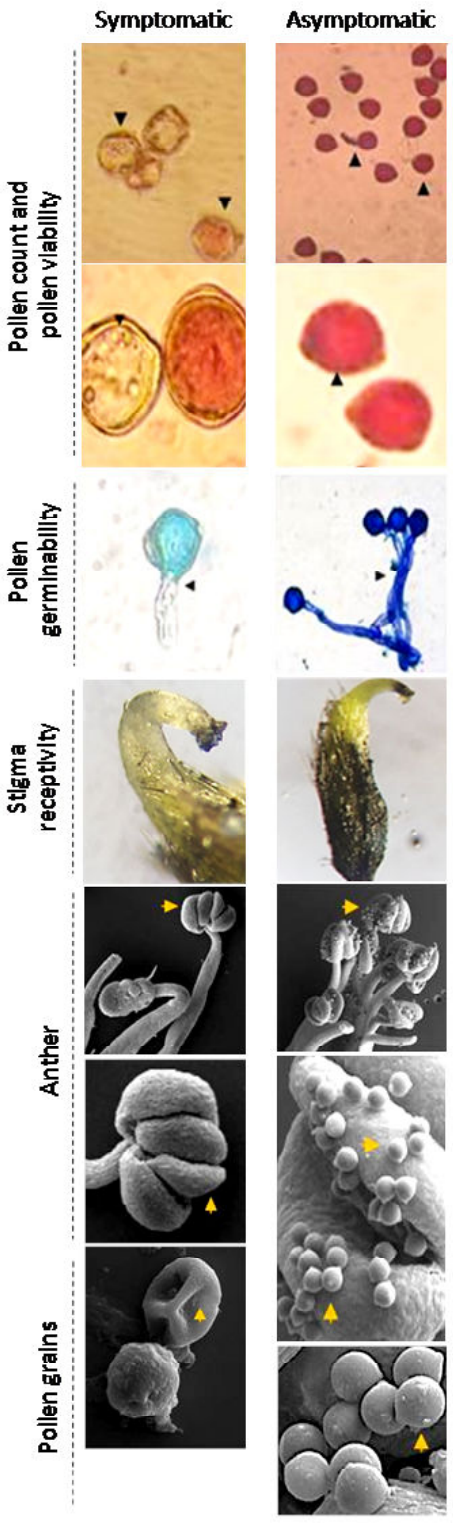

Fig. 1. Cytological behavior of FBD in symptomatic and asymptomatic plant

Table 1. Biochemical contents in symptomatic and asymptomatic plants

Biochemical component	TSS/ Carbohydrate		Protein		Proline		Total chlorophyll	
Genotype	**TAMS 98-21**	**JS 335**	**TAMS 98-21**	**JS 335**	**TAMS 98-21**	**JS 335**	**TAMS 98-21**	**JS 335**
Asymptomatic	1.06	1.11	6.13	6.71	0.298	0.297	1.59	1.46
Symptomatic	2.31	1.80	14.98	14.59	0.306	0.302	3.41	3.15
Fold increase	**2.19**	**1.61**	**2.23**	**2.38**	**1.025**	**1.014**	**2.14**	**2.15**

Note: *Experimental valued are mean of three replications*

Similarly, reduced pollen viability (<34%) and germinability (15.75%) along with abnormal exine was found in symptomatic plant. However, stigmas were knob-shaped and found receptive in both symptomatic and asymptomatic plants (Figure 1).

Biochemical profiling

Two soybean genotypes, JS-335 and TAMS-38 were analyzed for biochemical profiling. Significant differences were observed in estimates of carbohydrate, protein, proline and chlorophyll in symptomatic and asymptomatic plants of both the genotypes. The levels of the biochemical parameters were found progressively increased in symptomatic plants as compare to asymptomatic (Table 1). Excess protein, carbohydrate content and total chlorophill pigments in symptomatic plants may be due to one of three possible reasons i.e. i) extended vegetative phase; ii) altered source: sink relation (where no sink available to deposit); iii) and presence of virus titer and / or combination of all of these factors.

Further, HPLC analysis revealed two prominent peaks at 3.42 and 3.66 minutes in symptomatic tissue. Whereas, FTIR produced additional spectra at 2973.98 cm^{-1} and 1654.71 cm^{-1} in case of symptomatic sample. This represents differences in metabolites and hence, differentially expressed molecules in the samples.

Molecular Attributes

cDNA synthesis and decamer profiling

The quantified cDNA of three tissues (leaf bud and node) from symptomatic and asymptomatic plants was profiled using 60 decamere primers. Altogether, 47 primers produced reproducible and scorable profiles yielding 197 scorable amplicons. Only 26 TDFs were found differentially regulated, amongst them 15 were found completely polymorphic and 11 showed differences in their intensity derived values (IDV). Using Jaccards Coefficient, tissues were distributed in 2 major groups (A and B) as showed in dendrogram. Group 'A' represents all 3 tissues (leaf, pod and node) of the asymptomatic plant along with transcripts generated in leaf tissues of symptomatic tissue. While group 'B' is made up of remaining symptomatic tissues (pod and node) (Fig. 2).

Sequencing and BLAST homology

Sequenced data of 9 differentially expressed TDFs (leaf, pod and node) generated was analyzed using *in silico* tool for structural and functional characterization (Table 2). The possible role of TDFs is discussed in relation to FBD comparing with regulatory transcriptomes available in database. Amongst nine, 4 sequences showed homology with annotated proteins (Figure 3) and 5 were found as uncharacterized proteins.

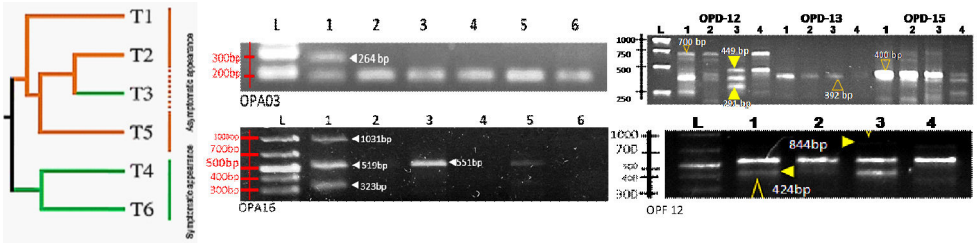

Fig. 2. Tissue wise hierarchical clustering and distribution of TDFs

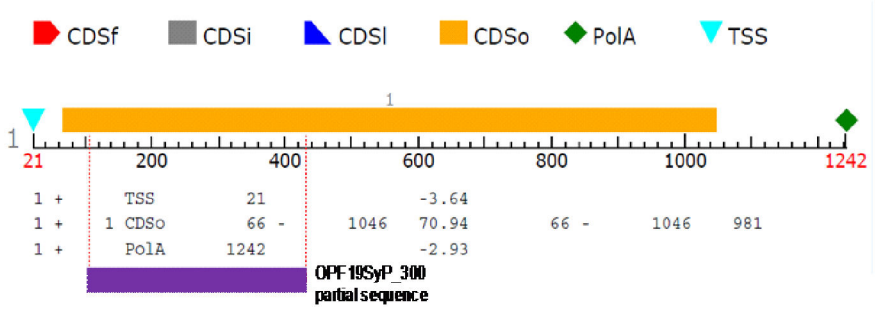

Fig. 3 : Prediction of location OPF19SyP_300 partial sequence on L-ASNase gene in Glycine max.In silico protein interaction

In silico protein interaction

Deciphering the interaction links between proteins is needed to understand their comprehensive role in cellular mechanisms. Here, four characterized hits listed involved in plant developmental processes are mentioned in table Table 2, Figure 4 (Sr. No. 1, 3, 4, 7). i) The ARF9 (*Auxin response factor 9;* LOC 100799088) is a transcriptional factor that binds specifically to the DNA sequence at 5'-TGTCTC-3' located in the auxin-responsive promoter elements (AuxREs). It is involved in overall plant development, phase transition from vegetative to reproductive and environmental signaling pathways. *In silico* interactome studies explored its interaction with other transcription factors like ARF6 (*Auxin response factor 6*), TIR1 (*Transport inhibitor response 1*) and MP (*Monopteros*).

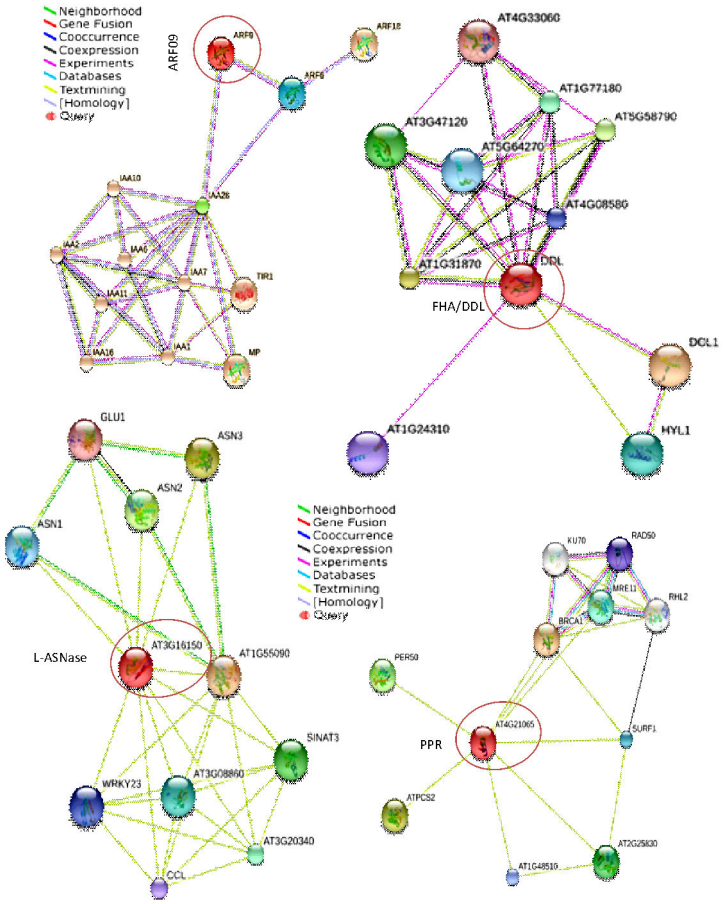

Fig. 4. Network of Protein interaction between ARF09 with other plant proteins

Table 2 : BLAST sequences homology NCBI database

SN	Name assigned	Regulation	Sequence	Tissue	Length (bp)	Homology	Organism	*E* value	Function
1.	OPA-03-SyP 475 partial	Up	TTCGACACAGGAACAAGTGGGAAATTGTCTTCACTGATGATGAAGGGGATATGATGCTTGTTCGACACAGGAACAAGTGGGAAATTGTCTTCACTGATGAAAGAATCTTCATTTGTTCAAGCCAGGATGTGCACAAATTGAGCTCAGGGAGCAAACTACCTATCTCTTCTATGGGAGAGATTGTAATAAGCTTAAACACAACCGAGACCTGAAACTTTTACATTCTTGTTCTTACTATTTTGTTGGTTTTTTTCTTTTATTTTTCTGTTGCTTTTATTTTGCTTATTCAAGGTAAGAATGTTAGTTTGTTTTTGGCTAGGCAAG	Symp - node	325	PREDICTED: Auxin response factor 9-like	*G. max*	2e-4	Auxin response factors (ARFs) are transcription factors that bind to TGTCTC
2.	OPA-16-AllAs Partial	Down	CTAATCAAAGTCATGAGCAAAAACTCAATGGGAAAGGAGGGGTTAATGAAATCACTCCAAATTATTTGTTTATTCTCTAAATTTAAATTTTAAAAAATCTTGGTCCAAAATTATCAGTAATTGTTTTTTAAATGATGGAGGTGATTATCTTCCGTTACTAGCTAGAGTTTACTTTTCTTTCCTTTTCTCTTTTGATAAATTTTTTATATATAAAAGTTATGTCATTGTTTTATTTATCATTTTCAGATCTCTGTTTCTGGTCAAATTCAGTTTGAGCCTCGAAAAACCTATGTCTACATTTATCCA	All Asymp - tissues	304	PREDICTED: Uncharacterized transcript variant X1, mRNA	*G. max*	3e-32	-
3.	OPD12_700B-partial	Down	ACGAGAGCAGGAACTAGGGGAAGGAAGAAATTGCAGAATGAGCCACCATTGGATAGCAGTACAGTTATCATAATTGGAACATATTGAAAACGTCGAGGAGAAGAGCTTAAGGAGGAAATAAACCTGTTGACGTGGGAGAAGGTAAGAAAAATGCTAATTTTGACGAAAGATGCAGTGGGTCGAGCCCTCAAGAGGTTTGTGATCGAGATGAAAACCAAGATGGTGTATCATTTCAGAAGGTTGCGAAGAGGTTGCTGATGGGGCGAGCTTCACATGATGAGGACTTCCTTTGTAAGCTGAGAAGGCGCCGGATTTGAAGAAGATGACACTTGGAGATTGGTTTGATTATTTGGAGACTCATTTGCCTAGACAAATTATTGATGCAACCGAAGAGGTAATTTCTGGCATGAAAATTAAATCTAAACAAGTACAGGAGTATGTTGTTCAGCAGAAGATTGAGAATTGCCAAGGAGATTAG	Asymp - node	477	PREDICTED: FHA domain-containing protein	*G. max*	7e-15	Involved in signaling, cell cycle, transcription, DNA repair & protein degradation
4.	OPF-19SyC - 300_Partial	Up	ATTTTGAACCACTCCCCGATATAATCTAACATTACATTTGATATTTACTTATATATATATTTAAAAATATATTATACATTAAATTAGTTCTATTTAATCGGTATCTTCTAGTTCTAGTCTGCGACATGGATAATAACTAGGATACTCGAGGGAGGCTGCGGTCAATTTTACCGTTGAAAGAATGAAAGTTATGTCTCTTTTTTTGTATATATGAAAGTTATGTCTTTTGCTTCCATGAAAGTTCACATATGACATGCCAATGATCAGAATCAGATGCTCCCTGATCGGTCTAGAGG	Symp - node	296	PREDICTED: Probable isoaspartyl peptidase/L-asparaginase 2-like	*C. arietinum*	1.4	Nitrogen supply to sink tissue in legume developing seeds
5.	OPF-19-400-B_Partial	Up	CCGAAAACCACCCCGATAAAAAATGCTCCACTAAAATTGATATTTACTTATATCTATATTTACCCCATCTTATACAGTTAACTTCTTTTTTATACTCGGCTCTTCAAATTCTAGCCTGCGATATGGATAATAAATAGGATACTCGAGGGAGGCTGCGGTCAATTTTACCGTTGAAAGAATGAAAGTTATGCTCTCTTTTTTTGTATATATGAAAGTTATGTCTTTTGCTTCCATGAAAGTTCACATATGACATGCCAATGATCAGAATCAGATGCTCCCTGATCCGTCTAGAGGC	Symp - node	294	Hypothetical protein	*M. truncatula*	0.19	-
6.	OPD15-400-A_Partial	Down	TCAGATCTTATTTTTTGAAAATTGAAACGAGCGAAAAGGTAAATCGCGTTGTTTGGATGTTCAACGGGCAATCGGTTCTATGGGGTTTTTTAGTCAGAAAGGCTAGACAAGTCGGGTGAGTGCTGTGGTGCCATAGATAAAGATTGATCCCCATAAAAAAGAAATCAGGCTCTTCTGCGAACCGTAAGAAGATTAATTATTTAAGCCACCTCGTCCGTGTCTAGATGTTTGAAGACCGCATTAAACTCCTGAGTTGTACAAGTACTAATGGCCGCGACGGTTACACGTCCACCCCCCCTTCATACTGTTCTACCATG	Asymp - node	317	Hypothetical protein	*P. vulgaris*	1.6	-
7.	OPF12-400-A_S_Partial	Up	CCCCGGATACCGGATAATTGTGCACCGTGGGGAAAAGGAAACGGCTTGCTTGGGTGTTGAAGGGGGAATTGGTGACTTTAAACACTCTACCAAGCTACCGCACAGCGCTTGCGGGGGGATGTTGGGGAGCCCGATGGCAAGGGTTGGACCTTATGCAAACGAATTCCAGACCATCCTGCGCACTCTGCGAAGATTATCGACATTATGCTACCACGCGGGCTTCTGCAATTTTCACACGGCGTAACCCCCCGAGGTACCCCAAGACTAAAATGCCTGTCGATTTCACTTCCTCACCCCCCTCCCACCCTTTGAACCCA	All Symp - tissues	315	PREDICTED: Pentatricopeptide repeat-containing protein	*G. max*	0.033	Restores fertility to cytoplasmic male-sterile plants
8.	OPD12-A_250_Partial	Down	TCGGCAAATCCCTTAATAGAGGAGTGCAAGTACATGTGATCGGCTTATATTGGTGTTTTACAGAGCATCTGTTCTACGCGGCAAAAAGCACAGTGACTCAGAATAAGGTAACCGAACCCCAAACCCTTCTGATTTACCCACCCTACAAATCTCATGCGCACAACCTC	Asymp - node	167	Hypothetical protein	*P. vulgaris*	0.78	-
9.	OPD13 A_Partial	Down	ACGGGCCGACGCTTAACAAAGGAGCGCTCGGGACACTTAAACCGCCTTGTCTGCCGTCGTTCCAGACTCACTTTGCTGACAGCTAGTTTTTTTGCACTTAGGCCAAACGGATCATGTAAACAGGGTCATCCCAGACACCCAAGGTAGACACCCTATAAAAAAAAAATCGAGGACCCCCCTTCCGCCTCGCAATGAATTTTCTCGGTTTTGCAGACCTCGCGGTCCTGAAGCGGTTTTAACCCCGCGTTTGAAGCACCTTTGTAGTTAGTAATCATTAGGCCCCGACGATTCGACGCCGTCCCCACCTTCCTACT	Asymp - node	311	PREDICTED: Uncharacterized protein	*G. max*	1.6	-

In silico interactome studies showed interaction of DDL with "Dicer-Like 1" protein which is expressed in flowers, seeds, ovule integuments, inflorescence and floral meristems, stigma of flowers and embryo. Other interacting protein "Hyponastic Leaves 1" (HYL1) is characterized by shorter plant height, delayed flowering, leaf hyponasty, reduced fertility, decreased rate of root growth, and an altered root gravitropic response.

It also exhibits less sensitivity to auxin and cytokinin. Amongst other interacting proteins, some are with unknown functions but majority are having known functions *viz.,* DNA/RNA/protein/ion binding, splicing or mRNA maturation, PTGS in circadian clock and flowering time genes, protein folding and pathogen response.

L-Asparaginase type 2-like enzymes are important for nitrogen remobilization and seed production. Asparaginase has been shown to be important for stress response in soybeans. *In silico interactome* of "L-ASNase" protein revealed interactions with ubiquitin-protein ligase activity, protein binding, zinc ion binding; ubiquitin-dependent protein catabolic process and located in nucleus. Few very recent articles described that, PPR proteins act directly or indirectly on RNA. Most proteins of this family localized in either mitochondria or plastids (Lurin *et al.,* 2004). Bentolila *et al.,* (2002) reported PPR containing gene restores fertility to cytoplasmic male-sterile plants.

In *Petunia* fertility restorer gene product is composed of 14 repeats of the 35-aa penta-tricopeptide repeat motif. *In silico interactome* analysis of PPR with other plant proteins revealed its role in DNA repair and in cell-cycle control, heavy-metal-binding, stress response and ion binding ability. Alterations in above said gene expressions may leads to cause major morphological alterations similar to that observed in FBD.

Sub cellular protein localization

Uncharacterized sequences from Table 2, Sr. No. 2, 5, 6, 8 and 9 were submitted to *in silico* tool for sub-cellular localization and possible functional understanding (Table 3).

- Amongst TDFs, OPA-16-AllAs Partial (down regulated) derived un-annotated protein showed most relevant hit with Glucose-6-phosphate isomerase. It is involved in various pathways *viz*., Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose. Also found in defense response to fungus, incompatible interaction (Mukherjee, 2010). This may correlate with the increased carbohydrate content in the symptomatic plant found during biochemical investigation.
- The representative of "OPF-19-400-B-Partial" (up-regulated) an un-annotated protein revealed its possible localization in nuclear region. Most relevant hit revealed its identity with ID: SPI7_SOLTU found as a serine protease inhibitor-7 of *Solanum tuberosum* (Potato). It acts as trypsin inhibitor (serine protease). This protects the plant by inhibiting proteases of invading organisms (Maganja, *et al.,* 1992). Another relevant ID GAS2_ARATH was found to be identical with Gibberellin-regulated protein that have possible role in signaling as well as hormone controlled developmental processes such as seed germination, flowering and seed maturation (Herzog *et al.,* 1995).
- Protein representative of "OPD15-400-A-Partial" (down regulated) found at nuclear region. This showed relatedness with transcriptional repressor subunit LEUNIG in *Arabidopsis thaliana***.** This transcriptional repressor is a subunit of the SEU-LUG is a transcriptional co-repressor of the 'C' class floral homeotic gene AGAMOUS act during the early stages of floral meristem development. Also interact together with APETALA2 and SEUSS to repress AGAMOUS expression. It plays a role in ovule and pollen development. Subunits interact with AGL24-AP1 and SVP-AP1 dimers, and possibly with SEP3, especially when composited with SEU. It also interacts with MED14, HDA19 and CDKE-1 (Sridhar *et al.,* 2004). This is associated with symptoms like abnormal floral, pollen and no ovule development in case of FBD.
- The "OPD12-A-250-Partial" and "OPD13 A-Partial" TDF was found to be down regulated in the present investigation. The *in silico* studies showed it's localization in Cytosol region. Most relevant hit was found with ID: ALF_ORYSA reported as a Fructose-bisphosphatealdolase cytoplasmic isozyme *Oryza sativa* subsp. japonica (Rice). The isozyme is involved in carbohydrate degradation; glycolysis; D-glyceraldehyde 3-phosphate and glycerone phosphate from D-glucose. Another candidate ID: FER_SOLAB revealed relatedness with ferredoxins in *Solanum abutiloides* which are iron-sulfur proteins that transfer electrons in a wide variety of metabolic reactions (Mino *et al.,* 2003). In case of FBD plants, this links with increased carbohydrate content than the asymptomatic plant.

Table 3. Predicted functions and localization of un-annotated sequences subjected to sub-cellular localization tool

SN	TDF	Regulation	Homology	*In silico* prediction- function/relevant hit	Sub-cellular localization
1	OPA-16-All As Partial	Down	Uncharacterized transcript	Glucose-6-phosphate isomerase and Carbohydrate degradation	Cytosol
2	OPF-19-400-B-Partial	Up	Hypothetical protein	serine protease inhibitor-7and Gibberellin-regulated protein	Nuclear
3	OPD15-400-A-Partial	Down	Hypothetical protein	SEU-LUG a transcriptional co-repressor of the 'C' class floral homeotic gene and reproductive development	Nuclear
4	OPD12-A-250-Partial	Down	Hypothetical protein	Fructose-bisphosphatealdolase cytoplasmic isozyme and Carbohydrate degradation	Cytosol
5	OPD13 A-Partial	Down	Uncharacterized protein	Ferredoxins which are iron-sulfur proteins that transfer electrons	Cytosol

Virtual Karyotyping of TDFs

Identified TDF sequences generated were anchored on *G. max* virtual chromosomes revealed their distribution, relative position, and abundance (Soares-Cavalcanti *et al.,* 2012). The generated virtual karyotype of TDFs sequence in 20 chromosomes is as depicted in Figure 5 and Table 4.

Table 4. Details of Virtual Karyotyping of TDFs

SN	Name assigned	Alleles found	Chromosome no.
1	OPA-03-SyP_475_partial	3	1,7,18
2	OPA-16-AllAs_Partial	1	2
3	OPD-12_700B_partial	2	7,13
4	OPF-19SyC -300_Partial	2	4,6
5	OPF-19-400-B_Partial	2	4,6
6	OPD-15-400-A_Partial	5	2,5,10,15,18
7	OPF-12-400-A_S_Partial	3	6,11,13
8	OPD-12-A_250_Partial	11	3,4,5,6,7,8,10,12,13,17,19,20
9	OPD-13 A_Partial	6	1,2,6,10,11,14

CONCLUSION

Pollen grains in FBD were found reduced in number, viability and germination ability along with abnormal exine and wrinkled pollen shapes. Diagnosis showed presence of TSV and GBNV and phytoplasma in FBD plants. All biochemical tested (TSS, chlorophyll, protein, proline) revealed increase their content in symptomatic plants as compared to asymptomatic. Fourier transform infrared spectroscopy (FTIR) analysis revealed two prominent spectra at 2973.98 cm^{-1} and 1654.71 cm^{-1} in symptomatic sample. Differential expression study revealed five uncharacterized and four annotated sequences. Annotated sequence (ARF9, FHA, L-ASNase and PPR) were further analyzed for their interactions with other plant proteins. These are involved in regulation of overall plant development (ARF9), plant height, delayed flowering, leaf hyponasty and reduced fertility (FHA), Nitrogen remobilization and seed production, stress

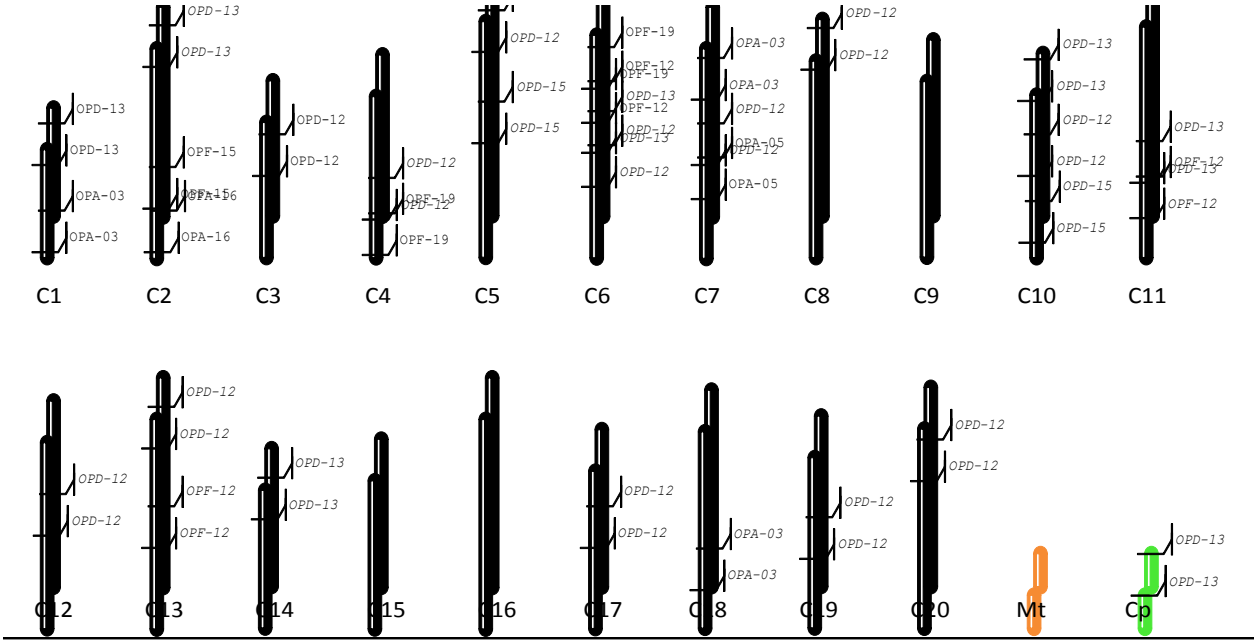

Fig. 5. In-silico karyotype of sequences (TDFs) on soybean chromosomes

response (L-ASNase) and fertility (PPR) in soybean. Un-annotated proteins also showed most relevant hit with proteins involved in carbohydrate degradation and defense response, reproductive development etc. These findings successfully generated insights on morpho-cytological, physiological, biochemical and molecular basis of FBD. In this study, although limited numbers of TDFs were obtained, interesting and relevant genes were derived which showed their association with Floral Bud Distortion. This information could provide a baseline for future studies towards determination of functionally important genes involved in floral development.

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Genetic Studies of Half Sib Families in Random Mating Population of Safflower

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ABSTRACT

The present study was undertaken to determine the expected genetic gain for seed yield and its components from half-sib selection method, to assess the effect of intermating on genetic correlation and to assess the frequency of half-sib families significantly superior over Bhima, A1, AKS-207 and AKS-68. The 105 half-sib families were evaluated in *rabi* 2011 along with four check varieties. Expected genetic advance was 42.48 per cent and 48.23 per cent at 10 per cent selection intensity over population mean and Bhima respectively for the seed yield plant^{-1}. Days to 50 per cent flowering and maturity exhibited negative correlation with seed yield plant^{-1} indicating breaking of positive correlation to negative correlation. Therefore, selection of high yielding families with early maturity is possible. Number of primary branches plant^{-1}, number of capitula plant^{-1} and number of seed capitulum^{-1} were positive and significantly correlated with seed yield plant^{-1}. This indicate that the half-sib recurrent selection is effective for increasing population mean and extraction of superior recombinant lines better than check varieties. Fifteen half-sib families i.e. (HS-14, HS-25, HS-48, HS-62, HS-63, HS-73, HS-76, HS-81, HS-82, HS-83, HS-85, HS-96, HS-97, HS-101 and HS-102) were identified as significantly superior half-sibs over Bhima, A1, AKS-207 and AKS-68 based on seed yield plant^{-1} and number of capitula plant^{-1}.

Safflower (*Carthamus tinctorius* L.) is usually considered to be a self-pollinated crop. Classen (1950), however, reported cross pollination ranging from zero to 100 per cent although in most of the plants he used, the detectable crossing ranged from 5 to 40 per cent. Safflower is traditionally grown for its flowers which were used for colouring, flavuoring and making dyes. The medicinal use of flower in China has become known to the rest of the world in last five years. Safflower has been gaining importance in recent years, in several parts of the country, because of its superior adaptability under drought conditions. Besides, it contains 30per cent oil in Indian varieties. Safflower oil is preliminary used for cooking. The oil contain high amount of linoleic acid (76%), which is very useful for patients suffering from heart diseases. The unsaturated fatty acids of safflower lower the serum cholesterol (Nimbkar, 2002)

India is one of the major safflower producers in the world, contributing to as much as 68 and 60per cent of the world's acreage and production, respectively. However, the average productivity of 579 kg ha^{-1} and oil content of 30-32 per cent could be considered quite low as compared to the 1300 kg ha^{-1} seed yield and 40 per cent seed oil obtained elsewhere. Safflower acreage and production around the world has been witnessing wide fluctuations since last two decades. The crop is grown in an area of 6.91 lakh ha, with a production of about 6.15 lakh tonnes in more than 60 countries worldwide. The safflower improvement programme in India was started in 1931 and N-630, the first variety was released in 1940. In India 25 varieties and five safflower hybrids were released in last four decades viz. DSH-129, MKH-11, NARINH-1, MRSA-521 and NARI-H-15. These varieties have the genetic potential to give yield of 15-20 q ha^{-1} with oil content of about 30 per cent under optimal condition. However attempts to further improve the yield and oil content were not successful for the last four decades. Similarly there is no breakthrough in the improvement of oil content in the last seven decades. This is mainly due to the use of pedigree selection technique in population derived from two line crosses, negative correlation between seed yield and oil content. The conventional breeding methods have been very useful only for recombining simple inherited characters. Therefore, these conventional breeding methods have not been very efficient for improving quantitatively inherited characters like seed yield, oil content, tolerance to stresses and horizontal resistance to diseases and insects. Moreover, the crossing and record keeping procedure are often both money and time consuming for the rate of progress attained. Conventional method have several limitations such as limited use of available genetic variability resulting in the development of varieties with a narrow genetic base, successive loss of genes in the segregating generation with no chance of recombination for genes linked for yield and oil content (Jensen, 1970). These limitations can be over come by

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application of recurrent selection method in self pollinating crops including Safflower. Considering the above facts this study was taken with the objectives, to determine the expected genetic gain for seed yield and its components from half-sib selection method t o assess the effect of intermating on genetic correlation and to asses frequency of half-sib families significantly superior over check Bhima, A1, AKS-207 and AKS-68.

MATERIAL AND METHODS

The experimental material consisted of Safflower population developed by crossing HUS-MS-305 and 62 male parents out of which 25 crosses were developed at AICRP, Akola, 25 crosses at AICRP, Solapur and 12 crosses were developed at Botany Section, College of Agriculture, Nagpur during 2008.The F_1s were raised in 2009 in respective research stations and equal amount of F_1s seeds were mixed and base population was constructed. The base population was raised in 2010 and composited to form random mating population. Half sib seed were harvested from individual male sterile plants. 105 families were developed from random mating population. These 105 half-sib families developed were grown in *Rabi* 2011 along with check viz. Bhima, A1, AKS-207 and AKS-68 for evaluation in augmented block design with five blocks. Each block consisted of 21 half-sibs and 4 checks. Row to row and plant to plant spacing was maintained as 45 x 20 cm. The recommended packages of practices were followed to raise good crop. The data were recorded on five competitive fertile plants from each family on seven characters viz., plant height (cm), number of primary branches plant^{-1}, number of capitula plant^{-1}, number of seeds capitulum^{-1}, 100 seed weight (g), oil content (per cent) and seed yield plant^{-1} (g) except days to 50per cent flowering and days to maturity for which data was recorded on plot basis. The mean data of five observational plants from each family were used for following statistical analysis analysis of variance for experimental design as suggested by Federer (1961) and estimation of family components, estimation of heritability in narrow sense, estimation of expected genetic advance and estimation of simple correlation as suggested by Hallauer and Miranda (1989).

RESULTS AND DISCUSSION

Analysis of variance and mean performance of half-sib families: The analysis of variance for the half-sib families were estimated for nine character viz. days to 50 per cent flowering, plant height, days to maturity, number of primary branches plant^{-1}, number of capitula plant^{-1}, number of seed capitulum^{-1}, 100 seed weight, oil content and seed yield plant^{-1} and presented in Table 1. The mean squares due to half-sib families were significant for all the characters except days to maturity, number of primary branches plant^{-1} and 100 seed weight indicating existence of substantial genetic variability among half-sib families for six characters i.e. days to 50per cent flowering, plant height, number of capitula plant^{-1}, number of seed capitulum^{-1}, oil content and seed yield plant^{-1} after one cycle of recurrent selection. The basic objective of all recurrent selection method is to increase the frequency of favorable genes in a population so that the opportunities to extract superior genotypes are enhanced.

Maximum, minimum, range and mean values of agronomic characters were measured on 105 half-sib families and presented in Table 2. In the present study, the days to 50 per cent flowering ranged from 91 to 109 days with mean value of 96.60 days. Plant height ranged from 88.8 to 144 cm with mean height of 113.37 cm. Number of capitula plant^{-1} ranged from 17.8 to 80.2 with mean of 39.22. Number of seeds capitulum^{-1} ranged from 20.0 to 57.8 with 38.86 mean. Seed yield plant^{-1} ranged from 15.62 to 78.90 g with mean seed yield of 50.80 g. Oil content ranged from 24.7 to 31.63 per cent with 28.33 per cent mean oil content. The maximum range was recorded by seed yield plant^{-1} (63.28 g) followed by number of capitula plant^{-1} (62.4), plant height (55.2 cm), days to maturity (41), number of seeds capitulum^{-1}(37.8), days to 50per cent flowering (18), number of primary branches plant^{-1} (10.4), oil content (6.93 per cent) and 100 seed weight (3.72 g) indicating considerable amount of genetic variance in random mating population which will facilitate selection of superior families. These results revealed that characters like seed yield plant^{-1}, number of capitula plant^{-1} and plant height showing maximum range in the 105 half-sib families studied can be considered as traits for selecting superior families. In accordance to these results Deshmukh (2009), Gawande (2010) and Awchar (2011) also reported the importance of seed yield plant^{-1} and number of capitula plant^{-1} for selecting superior families based on means and range. Mean values of half-sib families when compared with check varieties, upper limit values of half-sib families for all the nine characters studies were found to be higher than the best check variety for the respective characters. This indicates the availability of promising half-sib families superior than check. Hence

Table 1. Analysis of variance for half-sib families

Source of variances	DF	Mean Squares								
		Days to 50 % flowering	Plant height (cm)	Days to maturity	No. of primary branches Plant^{-1}	No. of capitula plant^{-1}	No. of seed capitulum^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Oil content (%)
Block (ignoring treatments)	4	30.10**	426.29**	64.50*	7.90*	107.44*	62.30	0.38	102.75	9.28**
Treatments (eliminating block)	108	15.04**	82.45**	40.72	4.54*	138.46**	66.29*	0.90	313.80*	1.84**
Checks	3	16.33*	42.68*	20.40	1.40	28.97	83.53*	1.84*	46.49	0.22**
Checks+Var vs.Var.	105	15.01**	83.59**	41.30	4.63*	141.59**	65.79*	0.87	321.44*	1.89**
Error	12	3.37	10.32	18.73	1.64	26.15	21.55	0.38	101.66	0.01
Block (eliminating check+Var.)	4	8.57	12.37	14.28	1.71	73.92	10.73	0.32	156.32	0.004
Entries (ignoring Blocks)	108	15.84**	97.78**	42.58	4.77*	139.70**	68.20*	0.90	311.82*	2.18**
Checks	3	16.33*	42.68*	20.40	1.40	28.97	83.53*	1.84*	46.49	0.22**
Half-sib	104	14.97**	92.69**	41.58	4.67	140.52**	62.82*	0.88	321.61*	2.23**
Checks vs. Varieties	1	105.00**	792.52**	213.14**	25.03**	386.76**	580.85**	0.26	89.72	3.12**
Error	12	3.37	10.32	18.73	1.64	26.15	21.55	0.38	101.66	0.01

* Significance level at 5% and ** Significance level at 1%

Table 2. Mean values of agronomic characters measured on selected half-sib families.

Charecters	Days to 50 % flowering	Plant height (cm)	Days to maturity	No. of primary branches Plant^{-1}	No. of capitula plant^{-1}	No. of seed capitulum^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Oil content (%)
Maximum	109	144	167	15.8	80.2	57.8	6.9	78.90	31.63
Minimum	91	88.8	126	5.4	17.8	20.0	3.18	15.62	24.7
Range	18	55.2	41	10.4	62.4	37.8	3.72	63.28	6.93
Mean(H.S.)*	96.60	113.37	136.76	8.91	39.22	38.86	5.31	50.80	28.33
Check Varieties**									
Bhima	95.20	108.72	136.20	9.54	43.00	35.72	4.56	44.74	29.06
A1	94.80	106.96	132.40	10.52	41.28	37.20	5.62	50.32	28.64
AKS-207	91.40	102.26	131.80	10.64	44.96	30.04	5.94	51.52	28.79
AKS-68	95.00	108.08	132.40	9.84	46.84	28.96	5.64	47.37	28.57

* Mean performance of 105 half- sib families ** Mean performance of 4 lines of check from five blocks

the half-sib families can be subjected to selection of superior families for the above mentioned characters i.e. seed yield plant^{-1}, number of capitula plant^{-1} and plant height if these traits also record a good extent of heritability and genetic advance.

Half- sib family components of variance and heritability: The estimates of half- sib family components of variance and heritability for each agronomic trait were calculated and presented in Table 3. For recurrent selection programme, significant and large genetic variation among half-sib families is prerequisite. The genetic variance among half- sib families (σ^2_A) and additive variance (σ^2_A) was high for seed yield plant^{-1} (219.95 and 879.80) followed by number of capitula plant^{-1} (114.37 and 457.48), plant height (82.37 and 329.48), number of seeds capitulum^{-1} (41.27 and 165.08), days to maturity (22.85 and 91.40), days to 50 per cent flowering (11.60 and 46.40), number of primary branches plant^{-1} (3.03 and 12.12), oil content (2.23 and 8.92) and 100 seed weight (0.50 and 2.00) respectively. The high genetic variance among half-sib families were also reported by Reddii (2002), Mummaneni (2003), Naole (2004), Panchbhai (2004), Goyal (2006), Metker (2008), Gawande (2010), Chapade (2010) and Awchar (2011) in random mating population of safflower. Estimates of heritability in safflower populations segregating for genetic male sterility are useful in determining the best method of selection to improve the population for specific traits. The most important function of heritability in determining the best method of selection to improve population for specific traits and the genetic study of quantitative traits in its predictive role, expressing the reliability of the phenotypic value as a guide to the breeding value. In the present study the narrow sense heritability estimates on family mean basis were high for oil content (0.99) followed by plant height (0.88), number of capitula plant^{-1} (0.81), days to 50 per cent flowering (0.77), seed yield plant^{-1} (0.68), number of seed capitulum^{-1} (0.65), number of primary branches plant^{-1} (0.64), 100 seed weight (0.56) and days to maturity (0.54) respectively. High estimates of heritability were also reported in random mating population of safflower for several agronomic traits like days to 50 per cent flowering, plant height, days to maturity, number of primary branches plant^{-1}, number capitula plant^{-1}, number of seed capitulum^{-1} , 100 seed weight and seed yield plant^{-1} by Reddii (2002), Mummaneni (2003), Naole (2004), Goyal (2006), Pavithran (2007), Metker (2008), Gawande (2010) Chapade (2010) and Awchar (2011).

Expected genetic advance with half-sib selection: The expected genetic advance per cycle from single trait selection using half-sib family selection and expected genetic advance expressed as per cent of population mean are presented in Table 4. Genetic advance is a measure of expected progress under selection and it depends on the magnitude of genetic variance, heritability and selection intensity. The information about magnitude of genetic variance and heritability can be used in ascertaining the possibility of extracting superior progenies for use in the development of superior safflower varieties. The expected genetic advance from single trait selection at 5 and 10 per cent of half-sib families was high for seed yield plant^{-1} (25.26 and 21.58 respectively), followed by number of capitula plant^{-1} (19.87 and 16.98), plant height (17.62 and 15.05), number of seeds capitulum^{-1} (10.72 and 9.16), days to maturity (7.29 and 6.23), days to 50 per cent flowering (6.17 and 5.27), oil content (3.07 and 2.62), number of primary branches plant^{-1} (2.88 and 2.46) and 100 seed weight (1.09 and 0.93). The expected genetic advance expressed as per cent of population mean at 5 and 10 per cent was highest for number of capitula plant^{-1} (50.66 and 43.29) followed by seed yield plant^{-1} (49.72 and 42.48), number of primary branches plant^{-1} (32.32 and 27.60), number of seeds capitulum^{-1} (27.58 and 23.57), 100 seed weight (20.52 and 17.51), plant height (15.54 and 13.27), oil content (10.83 and 9.24), days to 50per cent flowering (6.38 and 5.45) and days to maturity (5.33 and 4.55).

The expected genetic advance expressed as per cent over Bhima at 5 and 10 per cent selection intensity was highest for seed yield plant^{-1} (56.45 and 48.23) followed by number of capitula plant^{-1} (46.20 and 39.48), number of primary branches plant^{-1} (30.18 and 25.78), number of seed capitulum^{-1}(30.01 and 25.64), 100 seed weight (23.90 and 20.39), plant height (16.20 and 13.84), oil content (10.56 and 9.01), days to 50 per cent flowering (6.48 and 5.53) and days to maturity (5.35 and 4.57) respectively. The expected genetic advance from single trait selection, expressed as per cent of population mean and over check Bhima revealed the importance of seed yield plant^{-1} and number of capitula plant^{-1} as they exhibited maximum genetic advance. The heritability in narrow sense for these two characters was 68 per cent and 81 per cent, respectively. Hence, selection of

Table 3. Estimation of half-sib family components of variance and heritability for different agronomic traits.

Half-sib family component	Days to 50% flowering	Plant height(cm)	Days to maturity	No. of primary branches plant^{-1}	No. of capitula plant^{-1}	No. of seed capitulum^{-1}	100 seed weight (g)	Seed yield Plant^{-1} (g)	Oil (%)
	11.60	82.37	22.85	3.03	114.37	41.27	0.50	219.95	2.23
	46.40	329.48	91.40	12.12	457.48	165.08	2.00	879.80	8.92
	14.97	92.69	41.58	4.67	140.52	62.82	0.88	321.61	2.23
	0.77	0.88	0.54	0.64	0.81	0.65	0.56	0.68	0.99

Table 4. Expected genetic advance per cycle from single trait selection using half-sib family selectio n system.

Unit of evaluation and selection	Generation cycle	(#) selection intensity	Days to 50% flowering	Plant height (cm)	Daysto maturity	No. of primary branches plant^{-1}	No. of capitula plant^{-1}	No. of seed capitulum^{-1}	100seed weight (g)	Seedyield Plant^{-1} (g)	Oil (%)
Half-sib	2	5	6.17	17.62	7.29	2.88	19.87	10.72	1.09	25.26	3.07
		10	5.27	15.05	6.23	2.46	16.98	9.16	0.93	21.58	2.62
Expected genetic advance as per cent mean of population											
Half-sib	2	5	6.38	15.54	5.33	32.32	50.66	27.58	20.52	49.72	10.83
		10	5.45	13.27	4.55	27.60	43.29	23.57	17.51	42.48	9.24
Expected genetic advance as per cent mean over Bhima											
Half-sib	2	5	6.48	16.20	5.35	30.18	46.20	30.01	23.90	56.45	10.56
		10	5.53	13.84	4.57	25.78	39.48	25.64	20.39	48.23	9.01

 # Response to selection of top 5 per cent (K=2.06), 10 per cent (K=1.76) of large number of families where K is standardized selection differential

5 per cent or 10 per cent superior half-sibs based on seed yield plant^{-1} and number of capitula plant^{-1} will definitely result in improved performance in the next cycle.

In accordance to this study in safflower, Reddii (2002) reported 11.51, 9.48 and 7.82 per cent genetic advance in seed yield plant^{-1} and 13.45, 11.49 and 11.31 per cent genetic advance in number of capitula plant^{-1} at 5, 10 and 20 per cent selection intensity in random mating population of safflower after one cycle of recurrent selection. The expected genetic advance obtained from second cycle of recurrent selection was 28.8, 23.99 and 19.08 per cent in seed yield plant^{-1} and 29.19, 24.94 and 19.83 in number of capitula plant^{-1} at 5, 10 and 20 per cent selection intensity as reported by Naole (2004). In third cycle Goyal (2006) reported 49.49, 42.29 and 33.64 per cent genetic advance in seed yield plant^{-1} and 30.67, 26.20 and 20.84 in number of seed capitulum^{-1} from 5, 10 and 20 per cent selection intensity. Deshmukh (2009) reported expected genetic advance as 39.68 per cent and 45.68 per cent at 10 per cent selection intensity over population mean and Bhima respectively for seed yield plant^{-1} and 27.52 per cent and 28.02 per cent for capitula plant^{-1} after one cycle of recurrent selection. Gawande (2010) reported that expected genetic advance was 28.88 per cent and 22.78 per cent at 10 per cent selection intensity over population mean and Bhima respectively for seed yield plant^{-1} and 8.86 per cent and 8.37 per cent for number of capitula plant^{-1} after third cycle of recurrent selection. Awchar (2011) reported 60.95, 52.10 and 41.40 per cent genetic advance in seed yield plant^{-1} and 16.65, 14.24 and 11.33 per cent in number of capitula plant^{-1} at 5, 10 and 20 per cent selection intensity for mean population. The genetic advance over Bhima at 5, 10 and 20 per cent selection intensity was 46.22, 39.51 and 31.40 respectively and for number of capitula plant^{-1} was 15.78, 13.51 and 10.74 respectively after third cycle of recurrent selection. This clearly indicates the accumulation of favourable genes for yield and important yield component number of capitula plant^{-1}. The present study on recurrent selection in safflower population segregating for genetic male sterility also indicated that the improvement in seed yield and its components can be obtained by adopting half-sib family testing and selection.

Simple correlations: The recurrent selection experiments are mainly designed and conducted for improving seed yield plant^{-1}. However, this does not mean that other traits are unimportant. The simple correlations among different traits were estimated and presented in Table 5. In the present study, days to 50 per cent flowering exhibited significant and negative correlation with number of capitula plant^{-1} (-0.26**), 100 seed weight (-0.21*) and seed yield plant^{-1}(-0.25**) and also exhibited significant and positive correlation with plant height (0.30**). Plant height exhibited significant and positive correlation with days to maturity (0.22*) and oil content (0.26**). The number of primary branches plant^{-1} exhibited significant and positive correlation with number of capitula plant^{-1} (0.72**) and seed yield plant^{-1} (0.60**). Number of capitula plant^{-1} exhibited significant and positive correlation with seed yield plant^{-1} (0.78**). Number of seed capitulum^{-1} showed that significant and negative correlation with 100 seed weight (-0.40**) and exhibited significant and positive correlation with seed yield plant^{-1} (0.23*). 100 seed weight exhibited significant and negative correlation with oil content (-0.28**). Days to maturity (-0.17) and oil content (0.14) showed non significant correlation with seed yield plant^{-1}.

In the present study, days to 50 per cent flowering and days to maturity exhibited negative correlation with seed yield plant^{-1} indicating breaking of positive correlation to negative correlation. Therefore, selection of high yielding families with early maturity is possible.

Mummaneni (2003) reported positive and significant correlation for days to 50 per cent flowering (0.875**), plant height (0.865**), days to maturity (0.879**), number of primary branches plant^{-1} (0.672**) and number of capitula plant^{-1} (0.802**). Naole (2004) also reported significant and negative correlation between seed yield plant^{-1} and days to maturity (-0.377**) showing that unfavorable gene combination can be broken by recurrent selection. Goyal (2006) reported in random-mating population of safflower that seed yield plant^{-1} exhibited positive and significant correlation with days to maturity (0.316**). Deshmukh (2009) reported that days to 50 per cent flowering (-0.21**) and days to maturity (-0.07) had negative correlation with seed yield plant^{-1} indicating breaking of positive correlation to negative correlation. This study on correlation and reports mentioned above will facilitates selection of recombinant lines with high yield and earliness.

Identification of promising half-sib families:- The objective of any recurrent selection method is to increase the frequency of desirable genes thereby increase the

Table 5. Simple correlation among nine quantitative characters for half- sib family selection.

Characters	Plant height (cm)	Days to maturity	No. of primary branches plant^{-1}	No. of capitula plant^{-1}	No. of seed capitulum^{-1}	100 seed weight	Oil %	Seed yield plant^{-1}
Days to 50% flowering	0.30**	0.71**	-0.16	-0.26**	0.04	-0.21*	0.03	-0.25**
Plant height(cm)		0.22*	0.06	0.09	0.07	-0.08	0.26**	0.08
Days to maturity			-0.07	-0.08	-0.02	-0.14	-0.01	-0.17
No. of primarybranches plant^{-1}			0.72**	0.05	0.10	0.16	0.60**	
No. of capitula plant^{-1}					-0.01	0.17	0.08	0.78**
No. of seed capitulum^{-1}						-0.40**	0.19	0.23*
100 seed weight (g)							-0.28**	0.10
Oil content (%)								0.14

* Significance level at 5% ** Significance level at 1%

frequency of lines than check varieties. In the present study out of 105 half sib families eight half-sib families (HS-14, HS-25, HS-40, HS-73, HS-81, HS-83, HS-96 and HS-97) were significantly superior over check Bhima, A1, AKS-207 and AKS-68 for seed yield plant^{-1} and ten half-sib families (HS-62, HS-63, HS-73, HS-76, HS-81, HS-82, HS-85, HS-96, HS-101, and HS-102) were significantly superior over checks for number of capitula plant^{-1}and are presented in Table 6. Half-sib HS-96, HS-73 and HS-81 were observed to be significantly superior over check for both the important character. The half-sibs which were superior for number of capitula plant^{-1} alone also reported seed yield plant^{-1} higher than the check though not significant. Hence, the remnant seeds of all the fifteen selected half-sib families will be used for recombination cycle in next season.

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Heterosis for Yield and Yield Contributing Characters in Maize

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ABSTRACT

Thirty two F_1 crosses obtained by crossing four females and eight males in a line x tester fashion were used to assess the possibility of estimating the amount of heterosis for yield and yield components. Thirty two crosses and twelve parents along with check Rajarshi were raised in *Kharif* 2013-14 and observations on days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height, lenght of internode, cob length, cob girth, number of grains cob^{-1},100 grain weight, grain yield plant^{-1}, grain yield plot^{-1} and fodder yield plot^{-1} were recorded. Heterosis was recorded for all the characters studied. Among the crosses NM-32-1-1 x NM-62-4-1 and NM-32-1-1 x NM-60-4 were identified as best crosses on the basis of high *per se* performance, high significant useful heterosis and high significant sca effect in the desirable direction. Hence, these two crosses identified could be directly used for heterosis breeding in maize.

Maize (*Zea mays* L.) is the third most important cereal grain in the world after wheat and rice. Maize is of American origin, particularly Mexico. Maize belongs to family Poaceae also called as Graminae and subfamily Panicoideae. Wild species of maize are *Zea mexicana* (2n = 20), *Zea perennis* (2n = 40), *Zea luxurians* (2n = 20), *Zea diploperennis* (2n = 20). Maize is monoecious plant, highly cross pollinated species. It is also one of the first plant species identified to photosynthesize by C_4 path way with high yield potential. (Dass *et al.,* 2010) Maize kernel contains about 77 per cent starch, 2 per cent sugar, 5 per cent protein, 2 per cent ash on a water free basis, 5 per cent pentosan and 5 per cent oil. It has more than 1000 industrial uses and mainly used for production of starch due to its high starch content (77 per cent). Maize is not only used as food, feed and fodder but also used for some five hundred different industrial purposes for manufacturing *viz.* starch, alcohol, acetic acid, glucose, paper, furfural, rayon, dyes, synthetic rubber and resin etc.

Maize being a cross-pollinated crop there is wide scope for the development of single cross hybrids and varieties.The invention of heterosis phenomenon, the development of hybrid breeding technology and successful commercial exploitation of heterosis in maize are considered to be significant achievements and land marks in the history of biological sciences in the present century. Maize being a versatile crop, in order to harness its yield potential several genetic and agro-technique improvement strategies have been used in the past and present *viz.,* single crosses, three way crosses, double crosses, varietal hybrids, multiple hybrids, composites, synthetics and populations etc. These techniques are feasible to maize growing farmers for commercial cultivation by virtue of the crop being a highly cross pollinated species. Considering the above fact present investigation was undertaken to study heterosis in maize.

MATERIAL AND METHODS

Four females were crossed with eight males to produce 32 (4 females x 8 males) single crosses in *rabi* 2012-13. These 32 crosses along with twelve parents and one check (Rajarshi) were grown in *Kharif* 2013 in Randomized Complete Block design in two replications with the spacing of 60 cm x 20 cm, accommodating 15 plants in each row for the estimation of heterosis. Recommended package of practices were followed to raise a good crop. The data were recorded on five randomly selected plants from each genotype for the following characters i.e days to 50 per cent tasseling, days to 50per cent silking, days to maturity, plant height, length of internode, cob length, number of grains cob^{-1}, 100 grain weight, grain yield plot^{-1} and fodder yield plot^{-1} . The analysis of variance for experimental design was analysed by the method given by Panse and Sukhatme (1954). The magnitude of heterosis was calculated by mean performance of F_1 over the parent and useful heterosis was calculated as the deviation of F_1 over check variety (Shull, 1908).

RESULTS AND DISCUSSION

Data regarding mean squares due to parents, crosses and parents vs. crosses are presented in table 2. Mean squares due to parents were found to be highly significant for days to 50 per cent tasseling, days to

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Table 1. Analysis of variance for various characters in maize

Sources of variation	Degrees of freedom	Mean squares: Days to 50 % tasseling	Days to 50 % silking	Days to maturity	Plant height (cm)	Length of internode (cm)	Cob length (cm)	Cob girth (cm)	Number of grains cob^{-1}	100 grain weight(g)	Grain yield plant^{-1}(g)	Grain yield plot^{-1}(kg)	Fodder yield plot^{-1} (Kg)
Replications	1	0.54	0.18	0.18	16.10	1.6	1.38	1.45	548.59	0.80	45.53	0.090	0.029
Genotypes	44 #	12.88**	13.56**	10.07**	261.99	1.18**	2.20**	0.74	2132.59**	3.90**	147.50**	0.032**	0.017
Error	44 #	0.52	0.86	1.13	176.52	0.37	0.80	0.46	618.04	0.25	19.90	0.005	0.026

*, ** = significant at 5% and 1% level respectively. # = Degree of freedom is 44 as check (Rajarshi) is also included in the analysis.

Table 2. Analysis of variance for heterosis

Sources of variation	Degrees of freedom	Mean squares: Days to 50 % tasseling	Days to 50 % silking	Days to maturity	Plant height (cm)	Length of internode (cm)	Cob length (cm)	Cob girth (cm)	Number of grains cob^{-1}	100 grain weight(g)	Grain yield plant^{-1}(g)	Grain yield plot^{-1}(kg)	Fodder yield plot^{-1} (Kg)
Replications	1	0.55	0.28	0.102	19.34	1.61	1.32	1.31	719.76	0.87	50.09	0.095	0.001
Genotypes	43#	13.16**	13.825**	10.30**	260.37	1.17**	2.23**	0.75	2180.9**	3.99**	149.30**	0.033**	0.017
Parents (Inbreds)	11	9.55**	9.22**	10.59**	132.89	0.49	2.19**	0.38	1674.5**	4.31**	102.55**	0.022**	0.015
Crosses	31	9.69**	10.45**	8.51**	283.42	1.40**	2.31**	0.78	2429.0**	3.91**	165.74**	0.036**	0.018
Parents vs. Crosses	1	160.38**	168.75**	62.73**	948.14*	1.73**	0.28	3.97**	61.05	2.86**	153.64**	0.046**	0.044
Error	43#	0.53	0.86	1.14	180.48	0.38	0.82	0.46	618.38	0.25	20.19	0.005	0.026

*, ** = significant at 5% and 1% level respectively # = The degrees of freedom is only 43 as check (Rajarshi) is not included in the analysis

50 per cent silking, days to maturity, cob length, number of grains cob^{-1}, 100 grain weight, grain yield plant^{-1} and grain yield plot$^{-1.}$ This expressed the presence of significant variability among the parents. Significant mean squares for crosses were recorded for days to 50 per cent tasseling, days to 50 per centsilking, days to maturity, length of internode, cob length, number of grains cob^{-1}, 100 grain weight, grain yield plant^{-1} and grain yield plot$^{-1.}$. All the characters studied except fodder plot^{-1} revealed significant difference among the crosses. The presence of significant difference among parents and crosses revealed the choice of exploiting of heterosis for the above characters. The mean squares due to interaction effects of parents vs. crosses were found to be significant for days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height, length of internode, cob girth, 100 grain weight, grain yield plant^{-1} and grain yield plot^{-1} except cob length, number of grain cob^{-1} and fodder yield plot^{-1}. This indicated that the parents chosen were diverse and were with a different genetic background, and revealed the presence of average heterosis due to the significant differences in the mean performance of hybrids and parents. This result also revealed the suitability of data for estimation of heterosis. In accordance with these results, Wali *et al.* (2010), Premlatha and Kalamani (2010) and Patil (2011) has reported significant mean squares for parent vs. crosses for all the characters studied in maize.

The results on *per se* performance revealed that the cross NM-32-1-1 x NM-62-4-1 was found to be significantly superior over check Rajarshi for grain yield plant^{-1}, grain yield plot^{-1}, numbers of grains cob^{-1}, days to maturity. Similarly the cross NM-32-1-1 x NM-60-4 performed significantly superior over check Rajarshi for grain yield plant^{-1}, grain yield plot^{-1} and 100 grain weight. Another cross NM-32-1-1 x NM-78-1 showed significant superiority over check Rajarshi for number of grains cob^{-1}, grain yield plot^{-1} and days to maturity. The mean performance of thirty two crosses when compared with the check hybrid Rajarshi, the crosses NM-32-1-1 x NM-62-4-1, NM-32-1-1 x NM-60-4 and NM-32-1-1 x NM-78-1 were identified as superior crosses. Therefore these three crosses were identified as potential crosses for exploiting heterosis on the basis of *per se* performance.

The estimation of heterosis, useful heterosis over check Rajarshi revealed the response of heterosis for all the twelve characters studied. Useful heterosis over check hybrid Rajarshi were found among the crosses for all the characters except cob girth and fodder yield plot^{-1} in the desirable direction. Highest magnitude of heterosis was observed for grain yield plot^{-1} in the cross NM-32-1-1 x NM-62-4-1 (81.97%) followed by grain yield plant^{-1} (81.86 per cent) in the same cross. The extent of heterosis obtained for cob girth, cob length, 100 grain weight and plant height were low as compared to grain yield plot^{-1} and grain yield plant^{-1}. The results of similar nature on heterosis were also reported for maturity, plant height, ear length, ear height, ear diameter, 100 kernel weight and grain yield in maize by Ali *et al.* (2007), Bajaj *et al.* (2007) and Patil (2011). The highest estimate for useful heterosis over check Rajarshi were observed for grain yield plot^{-1} and grain yield plant^{-1} in the cross NM-32-1-1 x NM-62-4-1, 32.21 per cent and 32.15 per cent respectively. The extent of heterosis gives us an idea of the genetic control of the trait. Heterosis by itself whether over mid-parent or better parent can not predict us much about the superiority of hybrid over the check which is important and practical value for the plant breeding, therefore, more emphasisis should be given on useful heterosis. The cross NM-32-1-1 x NM-62-4-1 was identified to exhibit high significant useful heterosis for grain yield plot^{-1}, grain yield plant^{-1}, number of grains cob^{-1},days to 50per cent silking and days to maturity over check Rajarshi. Similarly the cross NM-32-1-1 x NM-60-4 was also identified to exhibit significant useful heterosis for grain yield plot^{-1}, grain yield plant^{-1} and 100 grain weight, days to 50per cent silking over check Rajarshi. These two crosses were also found to have significant *per se* performance for respective characters.

The level of heterosis observed in these two crosses justified the development of commercial hybrids in maize. Such potential of maize crosses for commercial exploitation of heterosis were also reported by earlier worker *viz.* Wani *et al.* (2007), Singh and Gupta (2009), Dubey *et al.* (2009), Iqbal *et al.* (2010) , Wali *et al.,* (2010) and Patil (2011). This study on heterosis has clearly indicated that heterotic response for yield and its components resulted only in selected cross combinations, indicating the pre-dominant role of non-fixable inter-allelic interactions. The above two crosses NM-32-1-1 x NM-62-4-1 and NM-32-1-1 x NM-60-4, hold promise for further evaluation and commercial exploitation of heterosis, these hybrids by chain crossing may be

Table 3. Mean performance of parents and their crosses for different characters

S. N.	Genotypes	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Lenght of internode (cm)	Cob length (cm)
1	NM-32-1-1	54.50	63.50	93.00	139.51	14.64	13.40
2	NM-44-3-1	55.00	63.00	98.00	129.28	14.32	14.90
3	NM-72-2	54.50	64.50	98.00	128.67	14.04	14.49
4	NM-2-1	58.00	67.00	95.00	140.86	14.47	13.96
5	NM-62-4-1	60.50	69.50	96.50	127.28	13.58	12.15
6	NM-60-4	60.50	69.00	97.50	127.95	14.48	12.25
7	NM-46-3-1	57.00	66.00	94.00	129.12	13.90	13.73
8	NM-26-1	58.00	66.50	98.00	132.75	13.97	11.87
9	NM-44-1	59.50	68.50	101.50	145.99	14.60	14.69
10	NM-36-5	59.50	68.50	99.00	145.31	14.50	12.91
11	NM-4-2	59.00	68.00	98.00	150.50	15.09	14.44
12	NM-78-1	58.50	67.00	98.00	137.03	15.35	13.99
13	NM-32-1-1xNM-62-4-1	55.50	63.50	92.50	143.76	13.53	14.17
14	NM-32-1-1xNM-60-4	55.00	63.00	96.00	141.19	15.21	13.49
15	NM-32-1-1xNM-46-3-1	56.50	64.00	98.00	127.51	13.89	12.26
16	NM-32-1-1xNM-26-1	52.00	61.50	94.50	151.51	15.12	14.06
17	NM-32-1-1xNM-44-1	51.50	60.00	98.50	148.02	15.87	14.40
18	NM-32-1-1xNM-36-5	53.00	61.50	98.00	177.16	16.90	15.00
19	NM-32-1-1xNM-4-2	54.00	62.50	92.50	167.03	16.11	13.23
20	NM-32-1-1xNM-78-1	56.00	64.00	95.00	166.53	15.59	14.07
21	NM-44-3-1xNM-62-4-1	57.00	66.50	94.00	146.33	14.56	14.45
22	NM-44-3-1xNM-60-4	52.50	61.50	95.50	152.45	15.80	14.24
23	NM-44-3-1xNM-46-3-1	56.00	65.00	98.50	149.81	14.68	10.68
24	NM-44-3-1xNM-26-1	58.50	67.50	97.00	139.40	14.55	11.65
25	NM-44-3-1xNM-44-1	53.50	62.50	93.50	131.47	14.63	12.30
26	NM-44-3-1xNM-36-5	56.00	65.00	92.50	145.74	15.24	14.40
27	NM-44-3-1xNM-4-2	55.50	63.50	97.00	131.85	14.05	13.16
28	NM-44-3-1xNM-78-1	58.00	66.50	95.00	130.52	15.09	13.75
29	NM-72-2xNM-62-4-1	54.50	63.50	96.00	127.32	14.69	14.81
30	NM-72-2xNM-60-4	56.00	65.00	93.00	123.32	15.15	15.13
31	NM-72-2xNM-46-3-1	52.00	60.50	95.00	132.22	13.75	12.20
32	NM-72-2xNM-26-1	57.00	65.00	93.50	146.29	14.26	13.27
33	NM-72-2xNM-44-1	53.00	60.50	97.00	141.04	14.04	14.03
34	NM-72-2xNM-36-5	52.50	62.00	92.50	145.80	15.54	12.76
35	NM-72-2xNM-4-2	56.00	65.50	96.00	132.72	13.61	13.59
36	NM-72-2xNM-78-1	57.00	66.00	93.00	143.93	12.91	15.21
37	NM-2-1xNM62-4-1	57.50	67.50	92.00	138.07	14.89	14.83
38	NM-2-1xNM60-4	54.00	63.00	99.00	145.64	14.33	12.54
39	NM-2-1xNM46-3-1	57.50	66.50	97.50	138.63	14.31	13.55
40	NM-2-1xNM-26-1	58.00	67.50	97.00	138.46	14.73	14.20
41	NM-2-1xNM-44-1	54.00	63.00	94.50	140.53	15.26	14.21
42	NM-2-1XNM-36-5	51.00	60.00	94.00	156.90	13.91	14.86
43	NM-2-1xNM-4-2	53.00	62.00	96.00	143.80	14.48	14.26
44	NM-2-1xNM-78-1	51.50	61.00	96.00	148.80	14.57	13.37
45	Rajarshi (Check)	55.00	65.50	95.50	128.51	15.46	14.28
	SE(m) ±	**0.51**	**0.66**	**0.75**	**9.39**	**0.44**	**0.64**

Table 3a. Mean performance of parents and their crosses for different characters

S. N.	Genotypes	Cob girth (cm)	Number of grainscob^{-1}	100 grain wt.(g)	Grain yiel dplant^{-1}(g)	Grain yield plot^{-1}(kg)	Fodder yield plot^{-1} (kg)
1	NM-32-1-1	11.45	200.20	23.40	47.40	0.71	1.35
2	NM-44-3-1	11.91	205.10	23.68	48.60	0.73	1.50
3	NM-72-2	12.04	228.90	24.47	54.10	0.77	1.25
4	NM-2-1	11.52	220.50	24.12	53.88	0.81	1.25
5	NM-62-4-1	11.40	161.30	22.72	32.82	0.49	1.28
6	NM-60-4	11.44	235.70	20.37	49.35	0.74	1.40
7	NM-46-3-1	11.67	231.90	23.15	50.15	0.75	1.30
8	NM-26-1	12.02	198.10	23.46	40.52	0.61	1.40
9	NM-44-1	11.20	236.50	22.65	44.51	0.67	1.25
10	NM-36-5	11.10	225.90	21.04	42.90	0.64	1.20
11	NM-4-2	11.29	279.50	23.87	59.14	0.89	1.38
12	NM-78-1	10.48	200.60	20.10	41.11	0.62	1.30
13	NM-32-1-1xNM-62-4-1	12.20	300.60	23.50	72.95	1.09	1.43
14	NM-32-1-1xNM-60-4	12.70	251.30	24.50	66.30	0.99	1.31
15	NM-32-1-1xNM-46-3-1	12.18	233.00	23.98	53.54	0.80	1.35
16	NM-32-1-1xNM-26-1	12.47	206.50	22.90	44.01	0.66	1.34
17	NM-32-1-1xNM-44-1	11.80	208.40	21.08	43.25	0.60	1.43
18	NM-32-1-1xNM-36-5	12.91	271.20	24.39	61.80	0.93	1.40
19	NM-32-1-1xNM-4-2	11.94	247.40	23.40	49.34	0.74	1.45
20	NM-32-1-1xNM-78-1	12.38	289.50	21.23	61.21	0.92	1.27
21	NM-44-3-1xNM-62-4-1	13.08	258.30	22.24	56.74	0.85	1.40
22	NM-44-3-1xNM-60-4	12.31	225.70	23.94	53.53	0.80	1.55
23	NM-44-3-1xNM-46-3-1	11.37	195.60	25.30	51.14	0.74	1.25
24	NM-44-3-1xNM-26-1	10.87	192.10	20.28	37.72	0.57	1.34
25	NM-44-3-1xNM-44-1	12.19	232.90	24.49	51.44	0.79	1.35
26	NM-44-3-1xNM-36-5	12.44	206.30	24.61	42.95	0.64	1.43
27	NM-44-3-1xNM-4-2	11.61	163.50	22.81	35.93	0.54	1.35
28	NM-44-3-1xNM-78-1	11.01	210.30	24.79	50.36	0.75	1.40
29	NM-72-2xNM-62-4-1	12.60	187.20	24.26	50.61	0.76	1.35
30	NM-72-2xNM-60-4	11.81	172.70	25.36	41.29	0.69	1.33
31	NM-72-2xNM-46-3-1	11.29	156.70	22.60	32.64	0.50	1.38
32	NM-72-2xNM-26-1	11.35	193.50	21.55	42.63	0.69	1.33
33	NM-72-2xNM-44-1	11.20	200.30	20.11	42.24	0.63	1.45
34	NM-72-2xNM-36-5	11.50	250.70	21.85	53.96	0.81	1.35
35	NM-72-2xNM-4-2	11.47	178.60	22.35	37.43	0.56	1.36
36	NM-72-2xNM-78-1	11.58	242.10	21.75	52.82	0.79	1.43
37	NM-2-1xNM62-4-1	12.82	215.00	22.49	48.11	0.72	1.32
38	NM-2-1xNM60-4	11.72	253.40	23.93	57.55	0.86	1.50
39	NM-2-1xNM46-3-1	11.69	236.60	24.14	59.12	0.89	1.58
40	NM-2-1xNM-26-1	12.78	224.20	23.45	52.68	0.79	1.40
41	NM-2-1xNM-44-1	11.73	243.80	24.66	58.69	0.88	1.40
42	NM-2-1XNM-36-5	10.85	191.60	22.69	43.81	0.69	1.33
43	NM-2-1xNM-4-2	11.51	195.30	23.57	45.86	0.69	1.35
44	NM-2-1xNM-78-1	12.64	223.10	22.85	48.57	0.73	1.03
45	Rajarshi (Check)	11.88	225.30	23.01	55.20	0.83	1.35
	SE (m) ±	**0.48**	**17.58**	**0.35**	**3.15**	**0.05**	**0.9**

Table 4. Heterosis (H1), Useful Heterosis over Rajarshi (H2)

S.N.	Crosses	Days to 50 % tasseling		Days to 50% silking		Days to maturity		Plant height	
		H1	H2	H1	H2	H1	H2	H1	H2
1	NM-32-1-1xNM-62-4-1	-3.48**	0.91	-4.51**	-3.05*	-2.37**	-3.14**	7.77	11.87
2	NM-32-1-1xNM-60-4	-4.35**	0.00	-4.91**	-3.82**	0.79	0.52	5.58	9.87
3	NM-32-1-1xNM-46-3-1	1.35	2.73**	-1.16	-2.29	4.81**	2.62*	-5.07	-0.78
4	NM-32-1-1xNM-26-1	-7.56**	-5.45**	-5.38**	-6.11**	-1.05	-1.05	11.30	17.90
5	NM-32-1-1xNM-44-1	-9.65**	-6.36**	-9.09**	-8.40**	1.29	3.14**	3.69	15.18
6	NM-32-1-1xNM-36-5	-7.02**	-3.64**	-6.82**	-6.11**	2.08*	2.62**	24.40**	37.86**
7	NM-32-1-1xNM-4-2	-4.85**	-1.82	-4.94**	-4.58**	-3.14**	-3.14**	15.19	29.97**
8	NM-32-1-1xNM-78-1	-0.88	1.82	-1.92	-2.29	-0.52	-0.52	20.44*	29.59**
9	NM-44-3-1xNM-62-4-1	-1.30	3.64**	0.38	1.53	-3.34**	-1.57	14.07	13.87
10	NM-44-3-1xNM-60-4	-9.09**	-4.55**	-6.82**	-6.11**	-2.30*	0.00	18.53*	18.63
11	NM-44-3-1xNM-46-3-1	0.00	1.82	0.78	-0.76	2.60**	3.14**	15.95	16.57
12	NM-44-3-1xNM-26-1	3.54**	6.36**	4.25**	3.05*	-1.02	1.57	6.40	8.47
13	NM-44-3-1xNM-44-1	-6.55**	-2.73*	-4.94**	-4.58**	-6.27**	-2.09*	-4.48	2.30
14	NM-44-3-1xNM-36-5	-2.18	1.82	-1.14	-0.76	-6.09**	-3.14**	6.15	13.41
15	NM-44-3-1xNM-4-2	-2.63*	0.91	-3.05*	-3.05*	-1.02	1.57	-5.75	2.60
16	NM-44-3-1xNM-78-1	2.20	5.45**	2.31	1.53	-3.06**	-0.52	-1.98	1.56
17	NM-72-2xNM-62-4-1	-5.22**	-0.91	-5.22**	-3.05*	-1.29	0.52	-0.51	-0.93
18	NM-72-2xNM-60-4	-2.61*	1.82	-2.62*	-0.76	-4.86**	-2.62*	-3.89	-4.04
19	NM-72-2xNM-46-3-1	-6.73**	-5.45**	-7.28**	-7.63**	-1.04	-0.52	2.58	2.89
20	NM-72-2xNM-26-1	1.33	3.64**	-0.76	-0.76	-4.59**	-2.09*	11.92	13.84
21	NM-72-2xNM-44-1	-7.02**	-3.64**	-9.02**	-7.63**	-2.76**	1.57	2.70	9.75
22	NM-72-2xNM-36-5	-7.89**	-4.55**	-6.77**	-5.34**	-6.09**	-3.14**	6.43	13.45
23	NM-72-2xNM-4-2	-1.32	1.82	-1.13	0.00	-2.04*	0.52	-4.92	3.28
24	NM-72-2xNM-78-1	0.88	3.64**	0.38	0.76	-5.10**	-2.62*	8.34	12.00
25	NM-2-1xNM62-4-1	-2.95**	4.55**	-1.10	3.05*	-3.92**	-3.66**	2.98	7.44
26	NM-2-1xNM60-4	-8.86**	-1.82	-7.35**	-3.82**	2.86**	3.66**	8.36	13.33
27	NM-2-1xNM46-3-1	0.00	4.55**	0.00	1.53	3.17**	2.09*	2.70	7.87
28	NM-2-1xNM-26-1	0.00	5.45**	1.12	3.05*	0.52	1.57	1.21	7.74
29	NM-2-1xNM-44-1	-8.09**	-1.82	-7.01**	-3.82**	-3.82**	-1.05	-2.02	9.35
30	NM-2-1XNM-36-5	-13.19**	-7.27**	-11.44**	-8.40**	-3.09**	-1.57	9.66	22.09*
31	NM-2-1xNM-4-2	-9.40**	-3.64**	-8.15**	-5.34**	-0.52	0.52	-1.29	11.90
32	NM-2-1xNM-78-1	-11.59**	-6.36**	-8.96**	-6.87**	-0.52	0.52	7.09	15.79
	SE m (±)	**0.63**	**0.51**	**0.80**	**0.92**	**0.92**	**1.06**	**11.63**	**13.43**

*, **= Significant at 5% and 1% level, respectively

Continued...

Table 4a. Heterosis (H1), Useful Heterosis over Rajarshi (H2)

S.N.	Crosses	Length of internode		Cob length		Cob girth		Number of grains cob^{-1}	
		H1	H2	H1	H2	H1	H2	H1	H2
1	NM-32-1-1xNM-62-4-1	-4.11	-12.46**	10.92	-0.77	6.78	2.69	66.31**	33.42**
2	NM-32-1-1xNM-60-4	4.46	-1.59	5.19	-5.53	10.97*	6.90	15.30	11.54
3	NM-32-1-1xNM-46-3-1	-2.70	-10.16*	-9.62	-14.15*	5.36	2.53	7.85	3.42
4	NM-32-1-1xNM-26-1	5.70	-2.17	11.28	-1.54	6.26	4.97	3.69	-8.34
5	NM-32-1-1xNM-44-1	8.55*	2.69	2.53	0.84	4.19	-0.67	-4.56	-7.50
6	NM-32-1-1xNM-36-5	15.99**	9.35*	14.03*	5.04	14.50**	8.67	27.29**	20.37
7	NM-32-1-1xNM-4-2	8.38*	4.24	-4.96	-7.35	5.01	0.51	3.15	9.81
8	NM-32-1-1xNM-78-1	3.97	0.87	2.74	-1.47	12.90*	4.21	44.46**	28.50*
9	NM-44-3-1xNM-62-4-1	4.37	-5.79	6.84	1.19	12.23*	10.10	40.99**	14.65
10	NM-44-3-1xNM-60-4	9.72*	2.23	4.90	-0.28	5.44	3.62	2.40	0.18
11	NM-44-3-1xNM-46-3-1	4.04	-5.01	-25.39**	-25.21**	-3.56	-4.29	-10.48	-13.18
12	NM-44-3-1xNM-26-1	2.86	-5.86	-12.96*	-18.42**	-9.15	-8.50	-4.71	-14.74
13	NM-44-3-1xNM-44-1	1.18	-5.34	-16.86**	-13.87	5.50	2.61	5.48	3.37
14	NM-44-3-1xNM-36-5	5.76	-1.39	3.56	0.84	8.13	4.71	-4.27	-8.43
15	NM-44-3-1xNM-4-2	-4.45	-9.09*	-10.29	-7.84	0.09	-2.27	-32.52**	-27.43*
16	NM-44-3-1xNM-78-1	1.72	-2.36	-4.81	-3.71	-1.65	-7.32	3.67	-6.66
17	NM-72-2xNM-62-4-1	6.37	-4.95	11.19	3.71	7.51	6.06	-4.05	-16.91
18	NM-72-2xNM-60-4	6.24	-1.97	13.16*	5.95	0.60	-0.59	-25.66**	-23.35*
19	NM-72-2xNM-46-3-1	-1.57	-11.03**	-13.54*	-14.57*	-4.77	-4.97	-31.99**	-30.45**
20	NM-72-2xNM-26-1	1.82	-7.73	0.68	-7.07	-5.65	-4.46	-9.37	-14.11
21	NM-72-2xNM-44-1	-1.96	-9.16*	-3.84	-1.75	-3.61	-5.72	-13.92	-11.10
22	NM-72-2xNM-36-5	8.90*	0.55	-6.86	-10.64	-0.61	-3.20	10.25	11.27
23	NM-72-2xNM-4-2	-6.56	-11.94**	-6.05	-4.83	-1.67	-3.45	-29.74**	-20.73*
24	NM-72-2xNM-78-1	-12.15**	-16.47**	6.81	6.51	2.84	-2.53	12.74	7.46
25	NM-2-1xNM62-4-1	6.17	-3.66	13.60*	3.85	11.87*	7.91	12.62	-4.57
26	NM-2-1xNM60-4	-1.00	-7.28	-4.31	-12.18	2.09	-1.35	11.09	12.47
27	NM-2-1xNM46-3-1	0.88	-7.41	-2.13	-5.11	0.82	-1.60	4.60	5.02
28	NM-2-1xNM-26-1	3.59	-4.69	9.95	-0.56	8.58	7.58	7.12	-0.49
29	NM-2-1xNM-44-1	4.99	-1.26	-0.80	-0.49	3.26	-1.26	6.70	8.21
30	NM-2-1XNM-36-5	-3.97	-10.00*	10.61	4.06	-4.07	-8.67	-14.16	-14.96
31	NM-2-1xNM-4-2	-2.03	-6.31	0.42	-0.14	0.92	-3.11	-21.88*	-13.32
32	NM-2-1xNM-78-1	-2.28	-5.73	-4.33	-6.37	14.91**	6.40	5.96	-0.98
	SE m(±)	**0.53**	**0.61**	**0.78**	**0.90**	**0.58**	**0.67**	**21.53**	**24.86**

*, **= Significant at 5% and 1% level, respectively

Table 4b. Heterosis (H1), Useful Heterosis over Rajarshi (H2)

S.N.	Crosses	100 grain weight		Grain yield plant^{-1}		Grain yield plot^{-1}		Fodder yield plot^{-1}	
		H1	H2	H1	H2	H1	H2	H1	H2
1	NM-32-1-1xNM-62-4-1	1.92	2.13	81.86**	32.15**	81.97**	32.21**	8.57	5.56
2	NM-32-1-1xNM-60-4	11.95**	6.45*	37.05**	20.11*	37.13**	20.18*	-4.73	-2.96
3	NM-32-1-1xNM-46-3-1	3.03	4.19	9.77	-3.01	9.77	-3.02	1.89	0.00
4	NM-32-1-1xNM-26-1	-2.25	-0.48	0.12	-20.27*	0.15	-20.24*	-2.91	-1.11
5	NM-32-1-1xNM-44-1	-8.46**	-8.41**	-5.89	-21.65*	-13.10	-27.67**	9.62	5.56
6	NM-32-1-1xNM-36-5	9.79**	6.00*	36.88**	11.96	36.90**	11.96	9.80	3.70
7	NM-32-1-1xNM-4-2	-0.97	1.69	-7.38	-10.62	-7.45	-10.63	6.42	7.41
8	NM-32-1-1xNM-78-1	-2.37	-7.74**	38.31**	10.89	38.41**	10.94	-4.15	-5.93
9	NM-44-3-1xNM-62-4-1	-4.16	-3.37	39.38**	2.79	38.91**	2.48	0.90	3.70
10	NM-44-3-1xNM-60-4	8.71**	4.04	9.29	-3.03	9.26	-3.02	6.90	14.81
11	NM-44-3-1xNM-46-3-1	8.04**	9.93**	3.57	-7.36	-0.29	-10.79	-10.71	-7.41
12	NM-44-3-1xNM-26-1	-13.98**	-11.89**	-15.35	-31.67**	-15.45	-31.72**	-7.93	-1.11
13	NM-44-3-1xNM-44-1	5.70**	6.41*	10.49	-6.81	13.68	-4.11	-1.82	0.00
14	NM-44-3-1xNM-36-5	10.05**	6.93*	-6.12	-22.19**	-6.20	-22.24*	5.56	5.56
15	NM-44-3-1xNM-4-2	-4.07	-0.89	-33.30**	-34.91**	-33.37**	-34.92**	-6.09	0.00
16	NM-44-3-1xNM-78-1	13.24**	7.71**	12.27	-8.77	12.19	-8.82	0.00	3.70
17	NM-72-2xNM-62-4-1	2.80	5.41	16.45	-8.32	20.60*	-8.34	6.93	0.00
18	NM-72-2xNM-60-4	13.13**	10.21**	-20.17**	-25.20**	-7.83	-16.13	0.00	-1.85
19	NM-72-2xNM-46-3-1	-5.09**	-1.80	-37.38**	-40.87**	-34.57**	-40.00**	7.84	1.85
20	NM-72-2xNM-26-1	-10.08**	-6.35*	-9.89	-22.77**	0.32	-16.74	0.00	-1.85
21	NM-72-2xNM-44-1	-14.64**	-12.60**	-14.33	-23.48**	-11.65	-23.50*	16.00	7.41
22	NM-72-2xNM-36-5	-3.99	-5.06	11.26	-2.25	14.83	-2.24	10.20	0.00
23	NM-72-2xNM-4-2	-7.52**	-2.87	-33.89**	-32.19**	-32.14**	-32.21**	3.24	0.37
24	NM-72-2xNM-78-1	-2.39	-5.48	10.95	-4.31	14.62	-4.29	11.76	5.56
25	NM-2-1xNM62-4-1	-3.99	-2.28	10.98	-12.84	10.92	-12.81	4.55	-2.22
26	NM-2-1xNM60-4	7.59**	4.00	11.50	4.26	11.37	4.23	13.21	11.11
27	NM-2-1xNM46-3-1	2.13	4.89	13.66	7.10	13.60	7.13	23.53	16.67
28	NM-2-1xNM-26-1	-1.43	1.91	11.62	-4.57	11.54	-4.53	5.66	3.70
29	NM-2-1xNM-44-1	5.45**	7.17*	19.30*	6.32	19.24*	6.34	12.00	3.70
30	NM-2-1XNM-36-5	0.50	-1.39	-9.46	-20.63*	-5.17	-16.80	8.16	-1.85
31	NM-2-1xNM-4-2	-1.78	2.41	-18.86**	-16.93*	-18.95*	-16.92	2.86	0.00
32	NM-2-1xNM-78-1	3.36	-0.70	2.26	-12.01	2.18	-12.02	-19.61*	-24.07*
	SE m(±)	**0.43**	**0.65**	**3.89**	**4.49**	**0.061**	**0.07**	**0.11**	**0.13**

*, **= Significant at 5% and 1% level, respectively

composited to make a gene pool. This pool may be advanced for further generations to devise and isolate lines with gene combinations for high grain yield (Saidaiah *et al.,* 2008)

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Heterotic Dual Purpose Cross Combinations in *Rabi* Sorghum

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ABSTRACT

Three lines and twenty two testers were crossed in line x tester design to produce 66 cross combinations In order to indentify the dual purpose rabi sorghum hybrids, promising hybrids were sorted out based on positive significant standard heterosis for grain yield along with fodder yield. Two crosses viz., AKRMS-80A X Rb-307-11 and AKRMS-47 A x AKSV 70 R exhibited positive significant standard heterosis for grain yield as well as fodder yield. The best dual purpose cross combination was AKRMS-80A X Rb-307-11 with standard heterosis of 28.99 per cent for grain yield per plant along with the standard heterosis of 21.90 per cent for fodder yield plant^{-1}.

In *Rabi* sorghum the grain and the fodder are of equal importance. Dual purpose sorghum hybrid is the one with high grain yield along with high fodder yield. The fodder quality of post rainy genotypes is better than *Kharif* genotypes and such good quality *Rabi* fodder has good demand and fetches good price. In this study, an effort was made to identify the high grain and fodder yielding i.e. dual purpose hybrid cross combinations produced by crossing newly developed parental lines of *Rabi* sorghum.

MATERIAL AND METHODS

The experimental material comprised of three lines *viz.,* AKRMS 80A, AKRMS 80-1-1-1A, AKRMS 47A and twenty-two testers *viz.,* Rb-307-11, Rb-400, PKV kranti as R, Rb-local 1-2, Rb-309, Rb-397-2, AKSV-47R, Rb-324, (AKR-73 x 504-1), AKSV-70R, RS-585, AKSV-219R, G-45-3-1-1, AKSV-205R, RL-5-1, RL-5-5, Rb-316-3, AKRb-356-6-2, RL-5-3, AKSV-72R, (104B x Akent 8-1-3), (275 x 104B x 1201 x Ringini x 18551 x 89022 17-1-1). Twenty-five parents and their resulting 66 hybrids along with one standard check CSH-19R were sown at Sorghum Research Unit, Dr. PDKV, Akola, during *Rabi* 2013-14 in randomized block design with three replications. The observations were recorded on five randomly selected plants plot^{-1} replication^{-1} for grain yield plant^{-1} (g) and fodder yield plant^{-1} (g). The average heterosis and heterobeltiosis were estimated as per cent increase or decrease of the mean of F_1 over its mid parent and better parent values, respectively and for over standard check for computation of standard heterosis checks CSH 19 R was used.

RESULTS AND DISCUSSION

Analysis of variance revealed the significant variation for both grain yield per plant and fodder yield plant^{-1}. To determine the heterotic potential of the hybrids, average heterosis (over mid parent), heterobeltiosis (over better parent) and standard heterosis (over standard check) were calculated for grain yield plant^{-1} and fodder yield plant^{-1}. Top ranking crosses with positive standard heterosis for grain yield are presented in Table 1. Out of sixty six crosses under study, fifteen crosses exhibited positive standard heterosis over the check CSH 19 R for grain yield plant^{-1} and appeared best for development of high yielding hybrids. But in sorghum high grain yield alone is not sufficient. Along with high grain yield, the fodder yield is also equally important character. Present need is of development of dual purpose *Rabi* sorghum hybrid with high grain yield along with high fodder yield also. The best dual purpose cross combination was AKRMS-80A X Rb-307-11 with the mean grain yield of 79.59 g. and fodder yield of 99.34 g. This cross combination recorded the highest significant standard heterosis of 28.99 per cent for grain yield per plant along with the significant standard heterosis of 21.90 per cent for fodder yield plant^{-1} (Table-2).

The second promising dual purpose cross combination was AKRMS-47 A x AKSV 70 R with the mean grain yield of 71.42 g. and fodder yield of 104.57 g. This cross combination recorded the positive significant standard heterosis of 15.76 per cent for grain yield plant^{-1} along with the positive significant standard heterosis of 28.32 per cent for fodder yield plant^{-1}. Taking in to consideration positive significant standard heterosis for grain yield plant^{-1} along with positive significant standard heterosis for fodder yield plant^{-1} these two crosses need to be evaluated in the multilocation

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Table 1. Heterotic cross combinations for grain and fodder yield per plant.

SN	Crosses	*Per se (g)*		Heterosis for grain yield plant^{-1} over			Heterosis for fodder yield plant^{-1} over		
		Grain yield plant^{-1}	Fodder yield plant^{-1}	MP	BP	SC	MP	BP	SC
1	AKRMS-80A X Rb-307-11	79.59	99.34	120.01 **	119.17 **	28.99 **	72.90**	62.25**	21.90**
2	AKRMS-47A X AKSV-70R	71.42	104.57	62.74 **	48.14 **	15.76 *	72.34**	63.18**	28.32**
3	AKRMS-80A X RS-585	70.83	85.86	66.18 **	44.75 **	14.80 *	56.92**	54.38**	5.11
4	AKRMS-47A X Rb local 1-2	67.70	82.68	83.54 **	71.13 **	9.72	47.41**	44.38	1.46
5	AKRMS-47A X Rb-309	66.69	88.39	62.40 **	56.66 **	8.08	53.15**	51.98**	8.46
6	AKRMS-80-1-1-1A X Rb-307-11	66.52	92.61	75.38 **	48.61 **	7.82	72.62**	68.66**	13.64
7	AKRMS-80A X Rb-397-2	66.43	80.62	76.92 **	71.29 **	7.66	51.67*	50.17**	-1.07
8	AKRMS-80-1-1-1A X (275 x 104B x 1201 x Ringini x 18551 x 89022 17-1-1)	66.25	101.28	75.07 **	48.60 **	7.37	90.90**	84.45**	24.28**
9	AKRMS-47A X (104B x Akent 8-1-3)	65.59	101.19	55.90 **	47.12 **	6.30	86.59**	76.71**	24.18**
10	AKRMS-47A X AKSV-219R	65.29	69.71	67.39 **	65.03 **	5.81	17.99*	14.47	-14.46*
11	AKRMS-80-1-1-1A X Rb-324	64.77	86.64	75.86 **	52.17 **	4.98	53.26**	48.98**	6.32
12	AKRMS-47A X (AKR-73 x 504-1)	63.47	79.71	49.26 **	39.55 **	2.86	40.15**	39.19**	-2.19
13	AKRMS-47A X RS-585	63.44	65.73	64.89 **	60.37 **	2.83	16.14	14.78	-19.34**
14	AKRMS-80A X (104B x Akent 8-1-3)	63.27	86.70	54.97 **	39.53 **	2.55	54.61**	48.30**	6.39
15	AKRMS-47A X Rb-316-3	61.71	74.64	46.98 **	38.94 **	0.02	34.79*	30.33**	-8.41

MP- Mid Parent**, BP-**Better Parent**, SC-** Standard Check

* - significant at 5% level of significance ** - significant at 1% level of significance

multiseason trails to find out the most stable dual purpose rabi sorghum hybrid.

Besides these two crosses, the cross AKRMS-80-1-1-1A X (275 x 104B x 1201 x Ringini x 18551 x 89022- 17-1-1) showed positive standard heterosis for grain yield per plant (7.37 %) along with positive significant standard heterosis for fodder yield per plant (24.28 %). Similarly another cross AKRMS-47A X (104B x Akent 8-1-3) also recorded positive standard heterosis for grain yield plant^{-1} (6.30per cent) along with positive significant standard heterosis for fodder yield plant^{-1} (24.18 %). Taking in to consideration positive standard heterosis for grain yield plant^{-1} along with positive significant standard heterosis for fodder yield plant^{-1}, these two crosses can

Table 2. Promising dual purpose cross combinations

S.N.	Crosses	*Per se (g)*		Standard heterosis (%)	
		Grain yield	Fodder yield	Grain yield	Fodder yield
1	AKRMS-80A X Rb-307-11	79.59	99.34	28.99**	21.90**
2	AKRMS-47A X AKSV-70R	71.42	104.57	15.76**	28.32**
3	AKRMS-80-1-1-1A X (275 x 104B x 1201 x Ringini x 18551 x 89022 17-1-1)	66.25	101.28	7.37	24.28**
4	AKRMS-47A X (104BxAkent 8-1-3)	65.59	101.19	6.30	24.18**

* - significant at 5% level of significance ** - significant at 1% level of significance

also be tested in the trials to find out the good dual purpose *Rabi* sorghum hybrid.

Thus it was concluded from the present study that the two crosses viz., AKRMS-80A X Rb-307-11 and AKRMS-47 A x AKSV 70 R appeared best crosses for development of dual purpose rabi sorghum hybrids and need to be evaluated further by their testing on large scale multilocation and multiseason trials to find out the most stable dual purpose rabi sorghum genotype for further exploitation.. Besides these two crosses, another two crosses viz., AKRMS-80-1-1-1A X (275 x 104B x 1201 x Ringini x 18551 x 89022- 17-1-1) and AKRMS-47A X (104B x Akent 8-1-3) need to be tested further. Rajguru *et al.* 2005, Umakant *et al.* 2006, Jhansi Rani *et al.* 2008 and Ghorade et al. 2014 also reported high heterosis in the top ranking crosses for both grain yield and fodder yield.

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Genetic Variability for Seed Yield and Yield Components in Land Races of Mustard

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ABSTRACT

Genetic variability and correlation studies were carried out using 200 Individual plant selection (IPS) identified from 20 land races of mustard along with 10 varieties of mustard during *Rabi* 2012 at the farm of Agril. Botany Section, College of Agriculture, Nagpur. The experiment was conducted in RBD replicated twice. Analysis of variance revealed the existence of variation among 200 IPS progenies for all the seven traits studied and hence, are suitable for selections. The range of variations was maximum for number of siliquae plant^{-1} followed by plant height, while it was lowest for 1000 seed weight and number of branches plant^{-1}. The magnitude of variation in terms of GCV and PCV was maximum for number of siliquae plant^{-1} followed by seed yield plant^{-1} and 1000 seed weight. Narrow difference between PCV and GCV was observed for the above three traits which implied that they were less influenced by environment. High heritability estimates where obtained for all the traits studied except for days to maturity for which heritability was moderate. Among the characters studied seed yield plant^{-1}, number of siliquae plant^{-1} and 1000 seed weight recorded high heritability coupled with high genetic advance as per cent of mean. Genotypic correlation worked out revealed that seed yield plant^{-1} was significant and positively correlated with number of siliquae plant^{-1}, number of branches plant^{-1}, plant height and days to maturity. Simultaneous selection for these traits might bring improvement in seed yield. Considering GCV, PCV, heritability, genetic advance as per cent of mean, seed yield plant^{-1} and number of siliquae plant^{-1} should alone be given emphasis for selecting superior IPS progenies. Based on this criteria 38 lines for number of siliquae plant^{-1}, 30 for seed yield plant^{-1} where identified as promising lines out of which 11 lines where common for both the traits.

Brassicas collectively known as rapeseed mustard are important oilseed crops of India and stands second after soybean production among eight annual edible oil seeds cultivated in our country. The current productivity level of 1190 kg ha^{-1} in India is far below than that of developed countries (2500 -3000 kg ha^{-1}) as well as the world average of about 1900 kg ha^{-1} (Yadava *et al,* 2011). Though they have the varieties with high yield potential (2000-2500 kg ha^{-1}) yet there is wide fluctuation in area, production and productivity of this crop. This fluctuation is mainly due to its cultivation on marginal lands either rainfed or with limited irrigation facilities and non availability of biotic and abiotic stress resistance / tolerant varieties for different mustard growing regions of the country.

Rapeseed - mustard crops in India are grown in diverse agro climatic conditions ranging from North Eastern / North Western hills to South under irrigated / rainfed, timely /late sown, saline soils and mixed cropping. Indian mustard accounts for about 75 - 80 per cent of the 5.8 million hectare under these crops in the country during 2009-10 crop season. Globally India account for 21.7per cent and 10.7per cent of the total acreage and production (Anonymous, 2010). Soybean, groundnut and rapeseed — mustard are the major oilseed crops in India contributing nearly 79 per cent and 88 per cent to its total acreage and production, respectively. The contribution of rapeseed - mustard to the total oilseed acreage and production is 23.7per cent and 26.0per cent, respectively. During 2009-10, rapeseed -mustard contributed 25.9 per cent and 22.0 per cent to the total oilseeds production and acreage (Anonymous, 2010). In India, the area, production and productivity was 6.69 million hectare, 6.60 million tonnes and 1145 kg ha"^{1}, respectively (Anonymous, 2011a). In Maharashtra area, production and productivity were 1200 hectares, 4000 tonnes and 308 kg ha^{-1}, respectively (Anonymous, 201la). In Vidarbha area under mustard cultivation was 865 hectares with the production of 330 tonnes and with an average productivity of 380 kg ha^{-1}. The districts in which mustard is grown were Chandrapur, Gondia, Bhandara, Gadchiroli, Nagpur and Wardha (Anonymous, 2011 b).

Main thrust in any crop improvement programme is to enhance yield. As an established fact yield is a complex trait and is dependent on many other ancillary characters which are mostly inherited quantitatively. The different traits vary in their relationship with yield in terms of their nature as well as magnitude, though they show continuous variation and are influenced by environment. The knowledge of genetic parameters of variation provides an idea about the extent of genetic improvement possible for different desirable and yield contribution characters. Hence, in this study attempt was

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made to estimate the variability parameters among the Individual plant progenies developed from the 20 land races collected from different places of Vidarbha.

MATERIAL AND METHODS

The present study was carried out during *rabi* 2012-13 with 200 individual plant selections identified from 20 land races collected from different locations of Vidarbha region of the Maharashtra along with 10 cultivated varieties of mustard. The experimental material were planted in Randomized block design replicated twice with row length of 3m and spacing between 2 rows 45 cm. Five plants were randomly selected from each genotype for recording agronomical observations. Data on Seven characters viz., days to first flower, days to maturity, plant height, number of branches plant^{-1}, number of siliquae plant^{-1}, 1000 seed weight (g) and seed yield plant^{-1} (g) were recorded. The analysis of variance for experimental design was performed to test the significance of differences between the lines for all the characters as per the methodology suggested by Panse and Sukhatme (1954), the genotypic and phenotypic coefficients of variations as per the method suggested by Burton and DeVane (1953). Heritability and genetic advance were calculated according to the method given by Burton (1952) and Johnson *et al.* (1955) respectively. The different genetic parameters ie. mean, GCV, PCV, heritability and genetic advance were estimated by the method given by Allard (1960) and Johanson *et. al.* (1955). The genotypic correlation were estimated following the method given by Singh and Choudhari (1977).

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed that the mean squares due to progenies studied were highly significant for all the 7 characters studied. ANOVA indicates that 200 IPS progenies have lot of variations among them selves and hence, are suitable for selections. The estimates of parameter of variability, heritability and genetic advance are presented in table 2. The range of variations was maximum for number of siliquae plant^{-1} followed by plant height, while it was lowest for 1000 seed weight and number of branches plant^{-1}. It indicated that there is better scope for selection and improvement for former characters and was confirmed through phenotypic and genotypic coefficients of variations. The magnitude of variation in terms of GCV and PCV was maximum for number of siliquae plant^{-1} followed by seed yield plant^{-1} and 1000 seed weight (Table 2). Higher estimates of these coefficients indicated wider diversity for these characters. Further narrow difference between PCV and GCV was observed for the above three traits which implied that they were less influenced by environment. High GCV & PCV values for number of siliquae plant^{-1}, 1000 seed weight and seed yield plant^{-1} were also reported in mustard by Kumar and Mishra (2007), Yadava *et al.*(2011) and Lende *et. al.* (2014). The reason for high magnitude of variability may be due to the fact that IPS were selected from land races belonging to different regions with different soils and climatic conditions of vidarbha.

The heritability estimates indicated the effectiveness of the character in phenotypic selection. In the present study high heritability estimates where obtained for all the traits studied except for days to maturity for which heritability was moderate. Johnson *et al.* (1955) reported that heritability and genetic advance as per cent of mean together where more useful for predicting the resultant effect of selected genotypes rather than their heritability and genetic advance as per cent of mean alone.

Among the characters studied seed yield plant^{-1}, number of siliquae plant^{-1} and 1000 seed weight recorded high heritability coupled with high genetic advance as per cent of mean. Similar to this results high heritability coupled with high genetic advance as per cent of mean where also reported by Gautami *et. al.* 2013. Therefore, selection for the traits which possessed high PCV and GCV, high heritability and genetic advance as per cent of mean is expected to result in considerable genetic gain.

The genotypic correlation coefficient was worked out among seed yield plant^{-1} and yield components and presented in Table 3. Seed yield plant^{-1} was found to be significant and positively correlated with number of siliuae plant^{-1}, number of branches plant^{-1}, plant height and days to maturity. This indicated that simultaneous selection for these traits might bring improvement in seed yield. These results are in conformation with Gautami *et al.* (2013), for number of siliquae plant^{-1}, number of branches plant^{-1} and plant height. Further number of siliquae plant^{-1}, recorded positive and significant correlation with number of branches plant^{-1}, plant height, days to first flower and days to maturity in addition to its association with seed yield plant^{-1}. 1000 seed weight which recorded high GCV, PCV, heritability and genetic advance as per cent of mean was found record negative significant association with number of siliquae plant^{-1}, number of branches plant^{-1} and days to first flower and non-significant positive association with seed yield plant^{-1}.

It is therefore suggested from the study that seed yield plant^{-1} and number of siliquae plant^{-1} should alone be given emphasis for selecting superior IPS progenies. Considering these two traits, significantly superior lines over mean where selected and presented in Table 4. Thirty eight (38) lines for number of siliquae plant^{-1}, 30 for seed yield plant^{-1} where identified as promising lines out of which 11 lines where common for both the traits. It is therefore,

Table 1. Analysis of variance for seven characters in Indian mustard

Sources of variation	df	Mean sum of squares						
		Days to first flower	Days to maturity	Plant height	No of branches plant^{-1}	No. of siliquae plant^{-1}	1000 seed weight	Seed yield plant^{-1}
Replications	1	46.46	1480.31	1.43	0.31	14417.94	0.030	47.46
Genotypes	209	16.78**	49.94*	785.32**	2.01**	12577.29*	0.664**	12.31**
Error	209	5.69	29.95	125.63	0.55	1139.74	0.006	1.29

* Significant at 5% level ** Significant at 1 % level

Note : material used in this study consisted of local material immediately after collection, hence were not stable and homozygous. Therefore the performance of same line in different replication showed high variation resulting in high Replication Mean Squares.

Table 2. Mean and variability parameters for seven characters in mustard IPS progenies

Characters	Mean	Range (Max.-Min)	GCV(%)	PCV(%)	h^2(BS)	Genetic advance	GA as % mean at 10% selection intensity
Days to first flower	46.19	14.50	5.10	7.26	49.35	2.92	6.33
Days to maturity	109.15	23.30	2.90	5.97	25.02	2.80	2.56
Plant height	169.28	113.69	10.73	12.61	72.42	27.32	16.14
No of branches plant^{-1}	4.92	6.00	17.38	23.01	57.03	1.14	23.20
No. of siliquae plant^{-1}	207.65	401.80	36.42	39.88	83.38	122.09	58.80
1000 seed weight	2.17	2.90	26.44	26.68	98.21	1.00	46.32
Seed yield plant^{-1}	6.67	17.71	35.21	39.11	81.03	3.74	56.03

Table 3. GenotypicCorrelation coefficients among seed yield and yield components in mustard

Characters	Days to maturity	Plant height	No. of branches plant^{-1}	No. of siliquae plant^{-1}	1000 seed weight	Seed yield plant^{-1}
Days to first flower	0.0639	0.2615**	0.5123**	0.4028**	-0.4636**	0.0754
Days to maturity		0.3998**	0.1073	0.1533**	0.1573**	0.2577**
Plant height			0.3930**	0.5217**	-0.0295	0.4735**
No of branches plant^{-1}				0.7208**	-0.3540**	0.4289**
No. of siliquae plant^{-1}					-0.2173**	0.5567**
1000 seed weight						0.1087

concluded from the study that these promising 27 lines should be raised and evaluated for their homozygosity and stable performance for one more year before including them in the yield trials.

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Table 4. Mean performance of no. of siliquae and seed yield plant^{-1} of the promising lines identified

S.N.	No. of siliquae plant^{-1}		Seed yield plant^{-1} (g)	
	Lines selected	Mean performance	Lines selected	Mean performance
1	L65	425.7	L65	18.51
2	L66	409.4	L101	11.91
3	L19	406	L66	11.82
4	L96	399	L119	11.42
5	L32	387.2	L124	11.07
6	L72	383.7	L11	11.03
7	L20	363.8	L161	10.91
8	L61	363.3	L165	10.74
9	L98	358.7	L61	10.62
10	L139	352.2	L55	10.6
11	L14	350.2	L110	10.45
12	L67	350	L194	10.41
13	L117	344.9	L67	10.25
14	L127	337.7	L62	10.2
15	L95	329.4	L87	10.08
16	L37	323.4	L12	10.07
17	L62	322.4	L128	10.05
18	L63	319.7	L2	9.97
19	L143	319.6	L20	9.97
20	L38	317.7	L39	9.76
21	L9	316.7	L162	9.68
22	L69	314.1	L68	9.66
23	L116	312.2	L96	9.63
24	L129	311.2	L32	9.27
25	L70	310.1	L75	9.19
26	L64	303.5	L3	9.1
27	L54	302.3	L72	9.08
28	L71	300.4	L197	9.01
29	L13	296.5	L103	8.96
30	L97	291.2	L176	8.93
31	L36	288.2	**Mean**	**6.67**
32	L147	286.9	**SE(m)±**	**0.8**
33	L128	286.7	**CD (5%)**	**2.23**
34	L90	283		
35	L112	281.7		
36	L18	279.6		
37	L34	278		
38	L142	277.1		
	Mean	**207.65**		
	SE(m)±	**23.87**		
	CD (5%)	**66.17**		

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Correlation Studies in Forage Sorghum

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ABSTRACT

The experiment was conducted during *Kharif* season of year 2011 using randomized block design with three replications. The experimental material comprised of 32 genotypes collected from at the Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The study revealed that the magnitudes of genotypic correlation coefficients are greater than phenotypic correlation coefficients for most of characters under studied. All the characters under investigation exhibited positive association at genotypic and phenotypic level with green fodder yield except leaf stem ratio. In the present studies the green fodder yield was found to be positive and significantly correlated at genotypic level with dry fodder yield, days to 50 per cent flowering, number of leaves plant^{-1}, stem girth, TSS, leaf breadth and protein. Thus it can be inferred that selection of the genotypes based on these trait either alone or in combination, will result in increasing high forage yield.

Sorghum (*Sorghum bicolour* (L.) Moench) is an important food and fodder crop of dry land agriculture. It has wider adaptability to various agro-ecological conditions especially in sub-tropical region. It is grown mainly for food and fodder purpose in Africa and India. It is grown extensively for fodder in the countries like USA, Australia and China etc. In Northern parts of India, the sorghum is grown mainly for fodder production. In the Central and Southern parts of India, it is grown as a source of food and fodder. Forage Sorghum as cereal crop has significance amongst the fodder. Sorghum is one of the most widely adapted fodder crops in drought prone areas because of its higher productivity per day coupled with better palatability and digestibility. The fodder is used as animal feed in the form of chop, hay, silage, pasture etc. It has several industrial uses. The grains are used for making bread, pop and beer.

In forage sorghum breeding programme increase in the productivity of green fodder yield is an important objective. However, yield being a complex characters govern by polygene. It will gives very little response to the direct selection under such circumstances the breeder has to modify the direction of selection after taking into consideration the relative influence of different yield contributing components of the yield.

Therefore, it becomes necessary to undertake correlation studies between fodder yield and its contributing characters. The importance of genotypic (genetic) correlation coefficients can be judge from the fact that they provide the first hand information regarding the heritable association between different yield components. And secondly give the idea regarding the importance of the character in a selection programme for yield improvement.

MATERIAL AND METHODS

The present investigation was conducted at the farm of Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. The 32 genotypes were grown in randomized block design with three replications. The genotypes were grown in the plots consisted of 4 rows with the row length of 4 meter and row to row distance 30 cm. The recommended cultural practices were followed to raise a good and healthy crop. Observations were recorded on plot basis for the three characters *viz.* days to 50per cent percent flowering, green fodder yield (t ha^{-1}) and dry fodder yield (t ha^{-1}) and on five randomly selected plants from each plot of each replication of the genotypes for the seven characters *viz.* plant height (cm), number of tillers per plant, leaf stem ratio (%), number of leaves per plant, leaf length (cm), leaf breadth (cm), stem girth (cm) and for two characters of fodder quality *viz*. TSS (per cent) and protein content (%).The analysis of variance was worked out as par the standard method (Panse and Sukhatme, 1954).The correlation were estimated from respective variances and co-variances as per the formulae suggested by Burton (1951).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences for all the characters (Table 1) indicating the

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Table 4.1. Analysis of variance for various characters in forage sorghum

Sources	df	Mean sum of squares											
		Days to 50% flowering	Plant height (cm)	Number of leaves plant^{-1}	Leaf length (cm)	Leaf breadth (cm)	Leaf stem ratio	Stem girth (cm)	TSS (%)	Number of tillers plant^{-1}	Proteins (%)	Dry fodder yield(t ha^{-1})	Green fodder yield(t/ha)
Replications	2	6.78	1100.59	1.46*	7.46	0.01	0.00	0.15	0.01	0.07	0.02	0.25	0.74
Treatments	31	101.87**	1778.90**	6.34**	78.29**	2.04**	0.01**	0.93**	0.68**	0.18	2.22**	35.35**	2.83**
Error	62	4.49	464.80	0.36	15.93	0.37	0.00	0.20	0.01	0.19	0.07	2.69	0.34

****Significant at 1% level, *Significant at 5% level**

Table 2: Genotypic (rg) and Phenotypic (rp) correlation coefficients between yield and yield contributing characters

Characters	R	Days to 50% flowering	Plant height (cm)	Number of leaves plant^{-1}	Leaf length (cm)	Leaf breadth (cm)	Leaf stem ratio	Stem girth (cm)	TSS (%)	Protein (%)	Dry fodder yield (t/ha^{-1})	Green fodder Yield (t ha^{-1})
Days to 50% flowering	**G**		-0.217*	0.880**	0.702**	0.925**	-0.404**	0.968**	0.052	0.184	0.509**	0.518**
	P		-0.121	0.764**	0.473**	0.629**	0.272**	0.631**	0.050	0.169	0.454**	0.435**
Plant height (cm)	**G**			0.043	0.251*	-0.286**	0.127	-0.026	-0.282**	-0.051	-0.068	0.150
	P			0.041	0.037	-0.153	0.039	0.032	-0.210*	-0.040	-0.049	0.059
Number of leaves per plant	**G**				0.635**	0.741**	-0.197	0.730**	0.008	0.054	0.480**	0.509**
	P				0.425**	0.571**	-0.207*	0.557**	0.014	0.071	0.393**	0.426**
Leaf length (cm)	**G**					0.705**	0.038	0.867**	-0.256*	-0.003	0.147	0.190
	P					0.455**	0.047	0.528**	-0.186	-0.015	0.081	0.116
Leaf breadth (cm)	**G**						-0.316**	0.951**	0.071	0.232*	0.287**	0.330**
	P						-0.222*	0.778**	0.033	0.198	0.107	0.213*
Leaf stem ratio	**G**							-0.236*	-0.517**	-0.374**	-0.528**	-0.601**
	P							-0.227*	-0.407**	-0.279**	-0.309**	-0.477**
Stem girth (cm)	**G**								-0.010	0.190	0.287**	0.494**
	P								-0.019	0.116	0.101	0.245*
TSS (%)	**G**									0.289**	0.410**	0.378**
	P									0.278**	0.330**	0.343**
Protein (%)	**G**										0.121	0.257*
	P										0.150	0.225*
Dry fodder yield (t/ha)	**G**											0.758**
	P											0.645**

Genotypic correlation coefficient, P-Phenotypic correlation coefficient **Significant at 1% level, *Significant at 5% level.

presence of substantial variability for all the characters except number of tillers plant^{-1} under study. The correlation coefficients were estimated among various characters at phenotypic and genotypic levels. In general, The genotypic correlation coefficient was observed to be higher than that of phenotypic correlation coefficient, indicating the existence of strong inherent association for the various characters studied. (Table 2) Green fodder yield showed positive and significant association with dry fodder yield, followed by days to 50 per cent flowering, number of leaves plant^{-1}, stem girth, TSS, leaf breadth and protein content. Thus it can be inferred that selection based on any one of these trait either alone or in combination, will result in identifying high forage yielding strains. In above case, yield components will result in corresponding increase in the green fodder yield. Therefore, the direct selection for these characters is expected to better yield results and should be given top priority in all improvement programmes as revealed by their positive and highly significant correlation coefficients. Some of the results Similar findings were reported by Singh *et al*. (2009), Prakash *et al*. (2010), and Shinde *et al*. (2010).

The characters leaf length showed positive and significant association with fodder yield. The similar findings were reported by Singh *et al*. (2009) and Prakash *et al*. (2010). While, leaf stem ratio had negative but highly significant association with green fodder yield. It suggested that the contribution of those characters towards the high green fodder yield is negligible and hence it has comparatively very less importance in breeding programme. The genotypic correlation coefficient is greater than phenotypic correlation coefficient for most of the characters under investigation. These results were in agreement with findings of Sukhchain and Singh (2009), Mahajan *et al*. (2011). All the characters under investigation exhibited positive association with green fodder yield at both genotypic and phenotypic level. Patel *et al*. (2005).

In the present studies the green fodder yield was found to be positive and significantly correlated at genotypic level with dry fodder yield, days to 50 per cent flowering, number of leaves plant^{-1}, stem girth, TSS, leaf breadth and protein. Therefore, it is suggested that selection of the genotypes based on these trait either alone or in combination will result in increasing high forage yield.

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Genetic Variability, Heritability and Genetic Advance for Yield Contributing Characters in Okra

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ABSTRACT

The experiment with fifty genotypes along with local varieties of okra was conducted on the Farm of Chilli and Vegetable Research Unit (CVRU), Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola in Randomized Block Design with three replications during *Kharif*, 2011 for genetic analysis viz. range, mean, coefficients of variability (GCV, PCV), heritability and genetic advance etc. The observations were recorded on days to 50 per cent flowering, plant height, number of primary branches plant^{-1}, number of fruiting nodes plant^{-1}, leaf area, days to first harvest, number of fruits plant^{-1}, average fruit weight, length of fruit, diameter of fruit, moisture content, protein content, yield plant^{-1} and yield ha^{-1}. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). The high values of GCV and PCV observed for number of primary branches plant^{-1}, yield plant^{-1}, yield ha^{-1}, protein content and number of fruits plant^{-1}. High heritability coupled with high genetic advance was observed for yield plant^{-1}, Yield ha^{-1} and leaf area.

Okra (*Abelmoschus esculentus* L. Moench) is one of the most important vegetable crops grown for its immature fruits in spring and rainy season from tropical to subtropical regions of the country. Breeding for crop improvement involves measures to boost yield potential, maturity and quality. The possibility of improvement in any crop is depended on variability available in the crop, wider the genetic variability in trait, better the chances of improvement of it through selection. An evaluation to detect extent of variability available for the yield attributes and their heritability values is of immense help to the breeders to select the breeding methods for improvement of that trait. Hence, an attempt was made to assess the available genetic variability in okra by partitioning of overall variability into its heritable and non-heritable components based on genetic parameters likes genotypic coefficient of variation, heritability and expected genetic advance. Therefore, the present study was undertaken with the objective of assessing the phenotypic and genotypic variability, heritability and genetic advance for yield and yield components.

MATERIAL AND METHODS

The present investigation was conducted on the field of Chilli and Vegetable Research Unit (CVRU), Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra state during the *Kharif*, 2011. The soil was medium black, with clay, fairly leveled and uniform in topography with appropriate drainage. The material under study was constituted of 50 genotypes of okra obtained from National Bureau of Plant Genetic Resources (NBPGR), New Delhi, Chilli and Vegetable Research Unit (CVRU); Dr. PDKV.; Akola, Marathwada Agriculture University; Parbhani and local genotypes of Maharashtra, Gadchiroli. The observations on various characters were recorded on five competitive randomly selected plants in each plot and were averaged.

Analysis of genotypic and phenotypic coefficients of variations were estimated as per the formula suggested by Burton and Devane (1953). Heritability in broad sense and genetic advance calculated by formula given by Lush (1949) and Johnson *et al*. (1955a).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the traits under study (Table 1) which indicated that the genotypes differ significantly for all the traits.

The mean and range values for all the traits evaluated are presented in Table 2. A wide range of variation observed for plant height at the time of last harvesting ranged from 111 .93 cm (IC-117011) to 179.00 cm (GO-2), number of primary branches ranged from 0.87 (IC-117034) to 6 (AKOV-103), number of fruiting nodes plant^{-1} 22.33 (IC-117034) to 59.53 (AKOV-103), leaf area 143.58 cm^2 (HRB-107-4) to 404.42 cm^2 (IC-90298), number of fruits plant^{-1} 1.35 (IC-117034) to 25.97 (AKOV-106), average weight of fruit 8.87 g (IC-117034) to 23.98 g (AKOV-103), length of fruit ranged from 7.80

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Table 1. Analysis of variance for various characters in okra.

S. N.	Characters	Replication	Treatment	Error
1	Degree of freedom	2	49	98
2	Days to 50% flowering	3.49	13.43**	2.26
3	Plant height(cm)	429.27	734.25**	143.09
4	No. of Primary Branches plant^{-1}	1.02	3.00**	0.48
5	No. of Fruiting nodes plant^{-1}	40.94	173.44**	22.28
6	Leaf area (cm^2)	6860.38	9694.82**	1677.08
7	Days to first harvest	6.81	26.86**	6.74
8	No. of fruits plant^{-1}	18.40	83.54**	10.22
9	Average Fruit weight (g)	5.84	22.74**	3.41
10	Length of Fruit(cm)	6.98	4.32**	2.78
11	Diameter Of Fruit	0.026	0.171**	0.027
12	Moisture content, %	25.84	35.44**	9.91
13	Protein content, %	0.04	103.21**	0.02
14	Yield plant^{-1} (gm)	2741.42	20677.90**	2103.98
15	Yield ha^{-1} (q)	1139	6260.95**	703.76

Table 2. Range, mean and estimates of genetic parameters in okra.

S. N.	Character	Range	Mean	GCV%	PCV%	h^2%	GA
1	Days to 50% to flowering	39.00-49.00	44.35	4.35	5.51	62.3	3.13
2	Plant height (cm)	111.93-179.00	145.75	9.63	12.65	57.9	22.01
3	Number of Primary Branches plant^{-1}	0.86-6.00	2.61	35.11	44.01	63.6	1.51
4	Number of Fruiting nodes plant^{-1}	22.33-61.53	39.42	18.00	21.63	69.3	12.18
5	Leaf area (cm^2)	143.58-404.42	267.56	19.32	24.65	61.4	83.48
6	Days to first harvest	44.00-54.00	46.89	5.52	7.82	49.9	3.77
7	Number of fruits plant^{-1}	1.35-25.97	15.99	30.92	36.83	70.5	8.55
8	Average fruit weight(g)	8.87-23.98	14.95	16.98	21.00	65.4	4.22
9	Length of fruit (cm)	7.80-13.93	10.95	6.55	16.58	15.6	0.58
10	Diameter Of fruit(cm)	1.14-2.39	1.42	15.50	19.33	64.3	0.36
11	Moisture content, %	76.85-105.86	88.29	3.30	4.86	46.2	4.08
12	Protein content, %	11.06-30.01	18.82	31.16	31.17	99.9	12.08
13	Yield plant^{-1} (g)	26.48-405.58	232.47	33.85	39.18	74.6	140.03
14	Yield ha^{-1} (q)	14.51-225.32	129.09	33.34	39.17	72.5	75.48

cm (IC-117020) to 13.93 cm (IC-33332), diameter of fruit ranged from 1.14 cm (Akola Bahar) to 2.39 cm (IC-117020), yield per plant ranged from 26.48 g (IC-117034) to 405.58 g (AKOV-103). The range of mean values could present a rough estimate about the variation of magnitude of variability present among different genotypes. But the estimates of genotypic and phenotypic coefficients are of greater use in determining the content of variability present within the material.

Estimates of variability and genetic parameters are given in Table 2. The number of primary branches per plant had the highest GCV of (35.11%) followed by yield per plant (33.85%), yield ha^{-1} (33.34%), protein content (31.16%) and number of fruits plant^{-1} (30.92 %).

The moderate GCV of 19.32 per cent, 18.00 per cent, 16.98 per cent, 15.50 per cent, 9.63 per cent were exhibited for leaf area, number of fruiting nodes per plant, average fruit weight, diameter of fruit and plant height respectively. The estimate of

GCV was found to be lowest for moisture content (3.30 %). Similarly the number of branches plant^{-1} had highest PCV (44.01%) followed by yield plant^{-1} (39.18 %), Yield ha^{-1} (39.17%), protein content (31.17%) and number of fruits per plant (36.83%). Moderate PCV of 24.65 per cent, 21.63 per cent, 21.00 per cent, 19.33 per cent, 12.65 per cent were exhibited for leaf area, number of fruiting nodes per plant, average fruit weight, diameter of fruit and plant height, respectively. PCV recorded lowest for moisture content (4.86%).

The high magnitude of GCV, PCV value was observed for number of primary branches plant^{-1}, yield plant^{-1}, yield ha^{-1}, protein content and number of fruits plant^{-1} indicating maximum variability among the genotypes selected for evaluation and thus these trait provides better chance of selection of desirable genotypes. The similar results were reported earlier by Dakahe *et al*. (2007).

Highest magnitude of heritability was observed for protein content (99.9 %) followed by yield per plant (74.6 %), yield per hectare (72.5 %), number of fruits per plant (70.5 %), number of fruiting nodes per plant (69.3%) indicating major role of genotype and ultimately less environmental influence and high heritability suggests that selection would be successful for these traits. These results confirm the earlier findings of Dudi and Dhankar (1994). Yield plant^{-1}, yield ha^{-1} and leaf area showed high heritability with high genetic advance indicating the presence of additive gene action and direct selection for such traits is rewarding in crop improvement. These results as in accordance with result reported by Singh *et al*. (2007). High heritability coupled with low genetic advance for diameter of fruit attributed to the action of non additive gene effects including dominance and epistasis. Hence, straight selection has limited scope for improving these traits.

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Path Coefficient and Correlation Response for Yield and Yield Contributing Traits in Vegetable Type Genotypes in Pigeon Pea

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ABSTRACT

Genetic analysis of 24 vegetable type genotypes in Pigeon pea was studied by using variability,correlation and path coefficient analysis to find out the variation, association among characters and to measure the direct and indirect contribution of eleven characters on green pod yield per plant. The genotypic correlation studies pod length (0.2266), pod width (0.1127), seed per pod (0.0026),100 green pod weight (0.0383), 100green seed weight (0.3583), shelling percentage (0.4283), number of flower cluster (0.2260) indicated that green pod yield plant^{-1} exhibited stable positive association with traits expect days to 50 per cent flowering (-0.1917), number of primary branches (-0.0479) and TSS (-0.0342). While the phenotypic correlation revealed that, days to 50 per cent flowering (-0.1731), number of primary branches (-0.0358) and TSS (-0.0387) were negatively correlated and the rest of all characters were positively correlatedwith green pod yield plant^{-1}. The direct effects of path coefficient analysis revealed that the greenpod yield plant^{-1} had positive and significant with days to 50 per cent flowering (0.0588), pod width (0.9276), pod length (0.4526), seed pod^{-1} (0.0062), 100 greenpod weight (0.0652), 100green seed weight (0.2128), shelling percentage (0.3972), number of flower cluster (0.3709) and the rest of the effects of few characters were negative for number of primary branches(-0.0246) and TSS (-0.0068). Moreover, it was noticed that, high indirect contribution was contributed through green pod yield per pod with most of the yield contributing traits. Hence, the traits*viz.*, 100 green pod weight, days to 50 per cent flowering, seeds pod^{-1} and 100green seed weight should be given more consideration while deciding about selection criteria for vegetable type genotypes in pigeonpea.

Pigeonpea (*Cajanus cajan* (L.) is one of the most important food legumes grown in over 82 countries across the globe, it ranks as the world's fifth most important pulse crop. The crop is cultivated in an estimated area of 2.9 million hectares in the world with an average of 684 kg ha^{-1}. Among legumes, pigeonpea or red gram occupies an important place in rainfed agriculture. Globally, it is cultivated on 4.67 million hectares, out of which, 3.30 million hectares is confined to India alone. Although the crop is known to be grown in 22 countries, the major producers are only a few. The major pigeon pea producing areas in the world are India, Eastern Africa, Central and South America, the Caribbean and West Indies, India with a total area of 2.6 million hectares and an average yield of 719 kg ha^{-1} produces nearly 92 per cent of the world's entire pigeonpea crop, though the average seed yields are relatively low, the crop can yield 16-29 qt ha^{-1} under favorable management; while an exceptional yield of 7-8 qt ha^{-1} under dry land condition has been reported(Gowda *et al.,* 2011). The average yields of green pod are relatively vary, as per the crop management under favorable conditions and yield with range of 36-49 q ha^{-1} (Saxena *et al*., 2010b). About 90per cent of pigeon pea constituting medium and late maturing genotypes is either inter cropped. It is mainly cultivated for its dry seeds and green vegetables in dry areas of the tropics and subtropics.Pigeon pea is highly proteimous crop and the seed can be prepared into various meals and served as substitute for cow pea and green pea.

Pigeonpea is cultivated in a wide range of cropping systems and so is its usage. It is energy rich but is cultivated largely under energy starvation condition. In some parts of India including Gujarat, Karnataka, Maharashtra, Tamilnadu, Madhya Pradesh and Andra Pradesh the use of immature shelled seeds is very common as fresh vegetable. It can become one of the most nutritionally rich vegetables of the daily cuisine, especially for the poor in India, Nepal and Myanmar.

India is world's biggest home of vegetarian in habitants and legumes are main source of protein in their diet, pods are consumed fresh, or processed as vegetable either dried seed are used as *dal* or variety of preparation. A vegetable type pigeon pea of perennial nature has been identified and explored from Vaishali district of Bihar (Singh, 2012).

The pigeonpea is well balanced nutritionally and an excellent source of protein whether eaten as a green

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pea or as dried grain. In addition to protein, pigeonpea provides carbohydrates and 5-fold higher levels of Vitamin A and C. Pigeonpea seeds are known to be rich in proteins (generally varying from 18 to 25 per cent and as high as 32 per cent), carbohydrates and minerals. Likewise, the seeds are rich in sulphur-containing amino acids, methionine and cysteine. Its abundance in protein makes it an ideal supplement to traditional cereal, banana or tuber-based diets of poor farmers that are generally protein deficient.Vegetable pigeonpea a highly nutritive potential crop for all ages.

Vegetable pigeonpea is a good source of protein, vitamins (A,C, B complex), minerals (Ca, Fe, Zn, Cu), carbohydrates and dietary fiber. In comparison to green peas (*Pisumsativum*), the vegetable pigeonpea has five times more beta carotene content, three times more thiamine, riboflvin and niacin content. Besides it has higher shelling percent (72 %) than that of green peas (53per cent). These all factors indicate that pigeonpea is nutritionally rich vegetable and it can be used in daily cuisine(Saxena *et al.* 2010a).

The other food items that can be prepared from pigeonpea are fresh sprouts, Tempe, ketchup, noodles, snacks and various extruded food products by Sexena *et al*. (2010c). Pigeonpea floor is an excellent component in the snacks industry and been recommended as an ingredient to increase the nutritional value of pasta without affecting its sensory properties.In India, de-hulled split cotyledons of dry pigeonpea seed are cooked to make *dal* or *sambar* for eating with *chapati* or rice; while in southern and eastern Africa and South America, whole dry seeds are used for porridge, and its green seeds are used as fresh, frozen, or canned vegetable.(Gowda*et al.*2011).

Crop yield is one of the complex characters controlled by several interacting genotypic and environmental factors. There are quite few yield components which are less complex, highly inherited and less influenced by the environmental changes. In the present study, the genetic variation among pigeon pea genotypes was studied, for improvement of the crop yield based on the available breeding strategies for selection of parental lines.

The objectives of this study were to evaluate the variability, degree of association between green pod yield components and morphological traits and to determine the direct and indirect effects of yield and its component traits on green pod yield in pigeonpea grown for vegetable purpose.

MATERIAL AND METHODS

The field experiment was conducted during the *Kharif* season of 2013-14 the field of Agril. Botany, Department, Dr. Pajabrao Deshmukh Krishi Vidyapeeth, Akola. The experimental material consisted 24 germplasm lines of pigeon pea along with a two checks GT-100 and ICP-7035 for yield and other agronomic characters, the experiment was laid out in a Randomized Complete Block Design with three replications. On the basis of yield contributing traits, vegetable type pigeon pea germplasm were selected from the 91 different lines, which were collected from different research stations working on vegetable type pigeon pea in India. The twenty four genotypes *viz.*, PT-04-253, BDN-2004-3, AKTM-10-4, AKTM-10-6, AKTM-11-18, BDN-2, RPS 2007-10, AKTM-11-11, BDN-2004, AKTM-11-17, BDN-2005, PT-04-254, AKTM-10-10, BDN-2001-09, AKTM-11-24, AKTM-11-07, AKTM-11-10, BDN-2010-3, AKTM-11-12, BDN-2001-07, PKV-TARA,ICPL-87, ICP-7035(C) and GT-100 (C).The following data was collected on days to 50 percent (per cent) flowering, pod length (cm), pod width (cm), plant height (cm), seedper pod,100 green pod weight (g), 100 green seed weight (g), shelling percentage (%), number of flower cluster,number of primary branches, TSS percentage (%) and green pod yield (g plant^{-1}).Genetic and phenotypic coefficients of variance was estimated as suggested by Burton (1951) and heritability as suggested by Johnson *et al*. 1955. Genotypic and phenotypic correlation was estimated as suggested by Singh and Chaoudhari (1977) and Path coefficient analysis was estimated as suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Variability studies

Variability studies reveled that genotypic and phenotypic coefficient of variation were of high magnitude for plant height,100 green pod weight,100 green seed weight, Shelling percentage (%t), TSS (%), days to50per cent flowering, pod length, pod width as well as for number of primary branches. The analysis revealed significant differences among all genotypes for all the characters presence of considerable amount genetic variability in the materials under study. While, looking to the estimates of GCV and PCV (Table 1), it was observed that the GCV and PCV were high magnitude for TSS (per cent) followed by

100 green seed weight, pod length, 100 green pod weight, number of primary branches and number of flower cluster. The estimate of high heritability (bs) accompanied with high-expected genetic advance for 100 green pod weight and days to 50 per cent flowering indicating the presence of additive gene action in the expression of these characters. This suggesting that such traits can be improved by direct selection.

The magnitutudal difference between PCV and GCV estimate was maximum for plant height, number of primary branches, number of flower cluster and 100 green seed weight, suggesting influence of environment on these traits. However, the difference between PCV and GCV estimate was minimum for 100 green pod weight, pod length, pod width, TSS (%), Day to 50per cent flowering, seeds pod^{-1} and shelling percentage (%) suggesting little influence of environment on these traits and one of may rely on phenotypic value for direct selection.

Ponnuswamy *et al*. (1983) reported that significant differences were observed among the eight vegetable soybean varieties for all the characters studied. The highest values of heritability and genetic advance were observed for number of green pods per plant and green pod yield plant^{-1}. The magnitude of GCV for all the traits, suggesting the role of environmental variance. The characters *viz.*, pod width, plant height and shelling percentage (%) exhibited very low GCV and PCV estimate suggesting the narrow range of variation for traits. These results are in agreement with the earlier findings of Chetukuri *et al*. (2013) in pigeonpea.

The estimation of heritability (bs) were of high magnitude for 100 green pod weight and days to 50 per cent flowering indicating the major role of genotypic and ultimately less environmental influence.

Sureja *et al*. (2000) reported genetic variability for pod yield in pea and its component characters. High heritability in association with high genetic advance observed for plant height, pod yield plant^{-1}, number of pods plant^{-1}, seed yield per plant, number of primary branches and 100 seed weight.Green pod yield, the character of prime importance had the moderate estimate of heritability but high genetic advance when compared with other characters. The present results are in accordance with the results obtained by Nausherwan *et al*. (2008) with respect to genetic advance.

Genotypic and phenotypic correlation analysis

The genotypic and phenotypic correlation for the association among the characters studied for the 24 genotypes were shown in Table 2. The genotypic correlation of green pod yield plant^{-1} was found to be positively correlated with pod length (0.2266), pod width (0.1127), seed pod^{-1} (0.0026), 100 green pod weight (0.0383), 100 green seed weight (0.3583), shelling percentage (0.4283), number of flower cluster (0.2260) and the days to 50 per cent flowering (-0.1917), number of primary branches (-0.0479) and TSS (-0.0342) were negatively correlated with green pod yield. The phenotypic

Table 1. Characters evaluated in vegetable type pigeonpea

S.N.	Characters	Mean	Range	GCV	PCV	C.V.(%)	Heritability (h^2) (BS)	Genetic Advance (GA)
1	Days to 50% flowering	125.34	110-140	5.35	5.85	2.37	0.83	12.63
2	Pod length (cm)	5.53	4.6-7.0	10.98	11.45	3.26	0.91	1.20
3	Pod width (mm)	12.85	11.4-14.3	5.33	5.47	1.22	0.95	1.37
4	Plant height (cm)	187.82	120-220	5.63	8.55	6.43	0.43	14.36
5	Seed per pod	3.66	3.2-4.2	7.09	7.51	2.49	0.88	0.50
6	100 green pod weight (g)	131.23	105.3-161.2	9.85	9.93	1.31	0.98	26.11
7	100 green seed weight (g)	19.39	8.3-25.3	11.36	13.26	6.83	0.73	3.89
8	Shelling percentage (%)	65.82	53.8-76.4	6.59	7.07	2.55	0.86	8.34
9	No. of flower cluster	4.57	3.5-5.6	8.51	11.54	7.87	0.54	0.59
10	No. of primary branches	3.46	2.5-4.5	8.82	11.92	8.01	0.54	0.46
11	TSS%	12.95	8.5-18.5	18.05	18.20	2.33	0.98	4.77

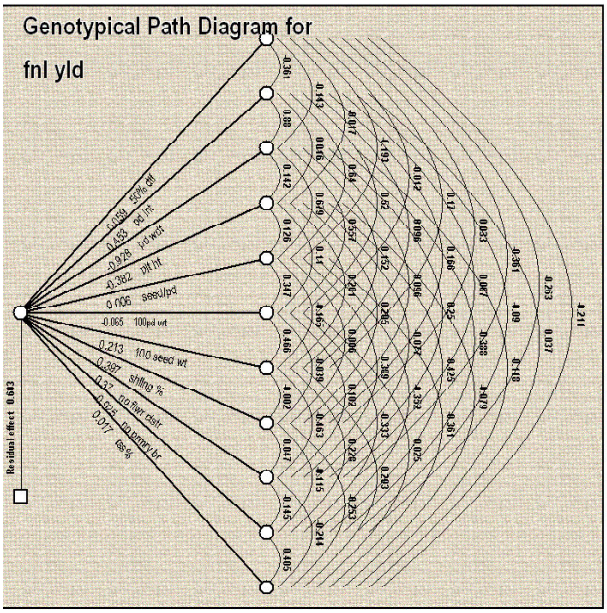

Fig. 1. The Path Diagram of yield and yield contributing characteristics in vegetable type Pigeonpea.

correlation of green pod yield plant^{-1} was found to be positively correlated with pod length (0.2184), pod width (0.1098), seed pod^{-1} (0.0034), 100 green pod weight (0.0375), 100 green seed weight (0.3105), shelling percentage (0.4006), number of flower cluster (0.1621) and days to 50 per cent flowering (-0.1731), number of primary branches (-0.0358) and TSS (-0.0387) were negatively correlated.

The genotypic correlation of days to 50per cent flowering was positively correlated with 100 green seed weight and shelling percentage (%), but negatively correlated with pod length, pod width, plant height, seed pod^{-1}, 100 green pod weight, number of flower cluster, number of primary branches. The genetic correlation of pod length was positively correlated with pod width, plant height, seed pod^{-1}, 100green pod weight, 100 green seed weight, shelling percentage (%), number of flower cluster and TSS, while number of primary branches was negatively correlated.The genotypic correlation of pod width was positively correlated with all traits except number primary branches and TSS.The genotypic and phenotypic correlation of pod width was negatively correlated with number of primary branches and TSS, while plant height, seed pod^{-1}, 100 green pod weight, 100 green seed weight, shelling percentage (%), and number of flower clusterwere positively correlated.The genetic and phenotypic correlation of seed per pod were positively correlated with 100 green pod weight, shelling percentage (%) and number of flower cluster, while negatively correlated with 100 green seed weight, number of primary branches and TSS.The genotypic and phenotypic correlation of 100 green pod weightwas positively correlated with 100 green seed weight, number of flower cluster and TSS (%), while negatively correlated with shelling percentage (per cent) and number of primary branches.

Number of pods plant^{-1} had significant positive correlations with pod length,number of branches plant^{-1} at phenotypic level. Whereas, at genotypic level this traitshowed significant positive correlation with number of branches plant^{-1}, pod length andTSS(%).Also significantly negative correlated with days to maturity at both phenotypicand genotypic level. In vegetable type Soybean; Rajput *et al*. (1986), Mishra *et al.* (1988), Amaranath (1986), Kalaimagal (1991) and Nirmala Kumari (1986) have reported positive correlation of number of pods plant^{-1} with maximum number of yield contributing characters**.**

In vegetable soybean, pod width exhibited positive significant correlation with 100 seed weight, TSS (%) at both phenotypic and genotypic level including number ofbranches per plant at genotypic levels. These results are in accordance with the report of Ziqiang Wang *et al*. (2001), where 100 green seed weight exhibited positive significant correlationwith pod width.These results are in conformity with the reports of Ziqiang Wang *et al.* (2001) where100 green seed weight exhibited significantly positive correlation with pod lengthand pod width. Also, reported that the increase or decreases in the pod length results in the increase or decreases in the 100 green seed weight which in turn influenced the green pod yield of the plant.

Path coefficient of Analysis

The results of path coefficients were partitioned into direct and indirect effects through various yield contributing characters as given in Table 3. The direct effects of days to 50 per cent flowering (0.0588), pod width (0.9276), pod length (0.4526), seed pod^{-1} (0.0062), 100 green pod weight (0.0652), 100 green seed weight (0.2128), shelling percentage (0.3972), number of flower cluster (0.3709)were positive and the effect of few

characters *viz.*, number of primary branches(-0.0246) and TSS (-0.0068)were negative on green pod yield plant^{-1}. The highest direct effect was exhibited by 100 green seed weight (0.2128)and it was followed by 100 green pod weight(0.0652). The highest direct effect was exhibited by seed pod^{-1} and followed by 100 green seed weight.Figure 1 showed the Path Diagram of yield and yield contributing characteristics in vegetable type pigeonpea.

Days to 50 per cent flowering, pod width, plant height, number of flower cluster and number of primary branches showed negative indirect effect on green pod yield plant^{-1} which indicating the effect of these characters. The character *viz*., seed pod^{-1}, pod length, 100 green seed weight, 100 green pod weight and green pod shelling percentage (%) had positive direct effect on green pod yield plant^{-1} while, some other traits such as days to 50 per cent flowering, seed pod^{-1} and 100 green pod weight. Similar results were obtained by Rajput *et al*. (1986), Mishra *et al.* (1988) and Nausherwan *et al*. (2008).

On the basis of path coefficient studies, Teerawat (2012) suggested that the number of pods plant^{-1}, green pod weight and plant height were important characters that should be taken into account as selection criteria in improving marketable pod yield of the vegetable soybean. As per Vijayalakshmi *et al*. (2013), it was noticed that most of the yield components showed the indirect contribution towards green pod yield. Also, number of seed pod^{-1} and number seed plant^{-1} should be given more consideration while deciding about selection criteria of vegetable type genotypes in soybean.

Thus it is concluded that, estimate of high heritability (bs) accompanied with high-expected genetic advance for 100 green pod weight and days to 50 per cent flowering indicating the presence of additive gene action in the expression of these characters. This suggesting that such traits can be improved by direct selection.The genotypic correlation of green pod yield plant^{-1} was found to be positively correlated with pod length, pod width, seed per pod,100 green pod weight, 100 green seed weight, shelling percentage, number of flower cluster.The green pod yield plant^{-1} showed the direct positive effects of characters like, days to 50per cent flowering, pod width, pod length, seed per pod, 100 green pod weight, 100 green seed weight, shelling percentage, number of flower cluster. Therefor emphasis should be given to 100 green pod weight, seed pod^{-1}, 100 green seed weight, shelling percentage and number of flower cluster while selecting genotypes for high green pod yield plant^{-1} in vegetable Pigeon pea.

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Heterosis in Forage Sorghum and its Relationship with Combining Ability

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ABSTRACT

'9x9' diallel crosses of forage sorghum were evaluated with one hybrid check in RBD design for mean performance, types of heterosis. Among the parents AKFR-89 and among the crosses IS-23960 x IS-22450, IS-23980 x IS- 23963 and IS-23980 x IS-22450 recorded significantly, highest total green fodder yield and also possessed the desirable morphological as well as quality characters like low HCN content and high protein per cent. Out of six best crosses, two crosses exhibited >150 per cent average heterosis and heterobeltiosis and four crosses exhibited approx. 75 per cent average heterosis and heterobeltiosis. So far as useful heterosis is concerned hybrid IS-23980 x IS-23960 exhibited more than 100 per cent useful heterosis and others exhibited more than 50 per cent useful heterosis. Significance of gca and sca variances for most of the characters indicated the importance of both additive and non-additive gene actions for the control of fodder characters under study. Cross IS-23980 x IS-23960 exhibited maximum *per se* performance, heterosis and significant sca effects for total green fodder yield along with significant sca effects for number of leaves plant^{-1}, green and dry fodder yield productivity per day, HCN content and protein per cent.

Fodder sorghum, the improvement in the past was mainly based on selection in the locally adapted types and hybrid population. But during recent years, hybrid vigor and selection of parents on the basis of combining ability have open up a new way of approach in crop improvement. Therefore, the major objectives in forage sorghum breeding is to develop hybrids both for single cut and multi cut with high tonnage, better quality good seed yield and resistance to insects, pests and diseases and to increase the fodder yield of forage sorghum per unit area per unit time, the concept of breeding multi cut hybrids was coined. Paroda *et al.* (1974) had advocated the development of multi cut hybrids in forage sorghum for quantum jump in yield. In the present investigation efforts are being made to estimate the i) mean performances of parents and hybrids, ii) heterosis, heterobeltiosis and useful heterosis and iii) GCA and SCA effects using the diallel analysis in forage sorghum.

MATERIAL AND METHODS

Study was conducted at Sorghum Research Unit, Dr. P.D.K.V. Akola. In Rabi 2006-2007, nine forage genotypes were crossed in diallel fashion (excluding reciprocals) and sufficient F1 seed was obtained, which was evaluated in kharif 2007. The experimental material comprised of 46 genotypes (32 hybrids, 9 parents and one check AKFSH-6). The experiment was conducted in Randomized Block Design (RBD) with three replications. Experimental plot size of 2.08 m x 0.50m and spacing of 25cm x 16cm was adopted to raise the forage crop. The observations were recorded on randomly selected five plants in each plot in each replication for the 11 characters viz. plant height (cm), number of leaves per plant, length of leaves (cm), breadth of leaves (cm), leaf: stem ratio (at I and II cut), green fodder yield (Kg net^{-1} plot at I and II cut), dry fodder yield (Kg net^{-1} plot at I and II cut), Total GFY (Kg net^{-1} plot), Total DFY (Kg net^{-1} plot), Total GFY (q ha^{-1}), Total DFY (q ha^{-1}), green and dry fodder yield productivity per day (q ha^{-1}), HCN content (ppm) and protein (per cent). Data was subjected to statistical analysis using diallel analysis as suggested by Griffing (1956) Method-II (F_1's and parents), Model-I (fixed effect model).

RESULTS AND DISCUSSION

Among the parents AKFR-89 recorded significantly, highest total green fodder yield and also possessed the desirable morphological as well as quality characters like low HCN content and high protein per cent. While among the crosses IS-23960 x IS-22450, IS-23980 x IS-23963 and IS-23980 x IS-22450 exhibited significantly higher green as well as dry fodder yield along with higher plant height, number of leaves per plant, leaf : stem ratio, length of leaves, breadth of leaves, green and dry fodder yield productivity per day, protein per cent as well as low HCN content.

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Heterosis

Primary aim of the study was to identify superior cross combinations which will exhibit good amount of heterosis for fodder yield and its component traits. Data presented in Table 1, revealed that cross SSG-59-3 x IS-22450 exhibited highest significant heterosis for both total green and dry fodder yield and also for morphological traits like plant height, number of leaves per plant, length of leaves, breadth of leaves, green fodder yield productivity per day, dry fodder yield productivity per day and protein content, a quality character. Along with around 150 per cent average heterosis and heterobeltiosis this cross also exhibited more than 50 per cent useful heterosis. While the cross IS-23980 x IS-23960 exhibited significant heterosis for both green and dry fodder yield and for other characters like number of leaves per plant, length of leaves, green and dry fodder productivity per day, low HCN content and protein percentage. This cross exhibited more than 100 per cent average heterosis, heterobeltiosis and useful heterosis for green fodder yield. Other crosses IS-23960 x IS-22450, IS- 23980 x IS-22450 exhibited significant heterosis, heterbeltiosis and useful heterosis over pre released hybrid check AKFSH-6 for yield and other seven characters. The crosses viz. M-48273x IS22450, M- 48212 x IS-23960 ranked eighth and ninth respectively in mean performance and exhibited significant heterosis for total green and dry fodder yield over mid parent and also for few other yield components.

Maximum heterosis for green fodder yield over mid parental value of 159.39 per cent has been observed in cross SSG-59-3 x IS 22450. Similarly, maximum heterobeltiosis was observed to be 153.33 per cent in cross IS 23980 x IS 23960. Pathak and Sanghi (1988[a]) recorded highest degree of heterosis up to 159.70 per cent and heterobeltiosis upto 248.3per cent for green fodder yield. Similar results were also noted by Kukadia and Singhania (1982) and Patil and Bapat (1991) in their studies on sorghum. Several researchers noted significant heterosis in desirable direction for different traits in sorghum. Kirby and Atkins (1968) for plant height, stalk diameter and number of leaves, Sangwan *et al.* (1972), for protein and sugar content, Shankaragowda *et al.* (1972) for days to 50per cent flowering, Patil and Bapat (1991) for stem thickness, leaf weight and stem weight, Thawari *et al.* (2000) for plant height, number of leaves plant^{-1}, leaf length, leaf: stem ratio and stem girth.

The magnitude of heterosis and heterobeltiosis for total dry fodder yield ranged from -64.65 to 274.98 per cent and -68.10 to 232.46 per cent, respectively. The cross SSG-59-3 x IS-22450 recorded maximum heterosis (274.98 per cent) and heterobeltiosis (232.46 %) followed by cross IS-23980 x IS-22450 (226.58 and 162.22 per cent, respectively). As regards standard heterosis ranged from -78.85 to 73.17 per cent and 14 crosses exhibited significantly positive standard heterosis for total dry fodder yield. The cross M- 48273 x AKFR-89 (73.17 %) recorded maximum standard heterosis followed by IS-23980 x IS- 22450 (66.75 %) and SSG-59-3 x IS-22450 (65.66 %)

Considering the gca effects of parents, sca effects of crosses, *per se* performance of parents and crosses along with average heterosis, heterobeltiosis and useful heterosis for fodder yield and its component character it appears that six crosses viz, SSG-59-3 x IS-22450, IS-23980 x IS-23960, IS- 23960 x IS-22450, IS-23960 x IS-22450, IS-23980 x IS-22450, IS-23980 x IS-23963 and IS-23960 x SGL-87 are the best desirable crosses for carrying in further generation amongst all the crosses (Table 2). Out of which former two hybrids recorded more than 150 per cent average heterosis and heterobeltiosis and later 4 hybrids recorded approximately 75 per cent average heterosis and heterobeltiosis. As regards the useful heterosis expressed by above mentioned six crosses, hybrid IS-23980 x IS-23960 exhibited more than 100 per cent useful heterosis and others exhibited more than 50 per cent useful heterosis.

The elite hybrids listed in Table 2 involved the parents with H x H gca and H x L gca. Only cross SSG-59-3 x IS-22450 involved parents having L x L gca effects. This has been observed because of higher significance of the characters like plant height, number of leaves and stem girth. However, Paroda *et al.* (1979) reported that elite crosses in general involved either both or at least one parent as good general combiner. Similarly, Shekar *et al.* (1987) also opined that involvement of at least one good general combiner was necessary for obtaining heterotic hybrids.

Combining ability analysis

In present study, it has been observed that both gca and sca variances were highly significant for all the characters under study. This indicates the importance of

both additive and non-additive gene action for the development of all the characters under study. According to the results of Monpara and Sanghi (1982) highly significance of gca and sca variances for the characters like days to flowering, plant height, number of leaves per plant, leaf length, leaf breadth, flag leaf area, green fodder and dry matter yield and crude protein percentage, the results obtained in present study are in agreement with them and results reported by various workers viz. Gfrewal *et al.* (1994), Katiyar *et al.* (1999) and Parmar and Tikka (2005).

General combining ability

It is revealed from the data in Table 2 that, none of the parents exhibited significant and desirable gca effects for all the characters under study. However, for most important characters i.e. green and dry fodder yield two parents IS-23980 and AKFR-89 showed positive gca effects in desirable direction. Along with yield these two parents showed significant and positive gca effects in desirable direction for other yield components. Therefore, from yield point of view these parents appear to be good general combiners. Further, amongst nine parent IS-23963 and IS-23960 exhibited significant and positive gca effects in desirable direction for plant height and HCN content. Moreover along with these characters IS-23960 also exhibited significant gca effects for breadth of leaves, green fodder yield, as well as green fodder productivity per day. Similarly SGL-87 exhibited positive and significant gca effect in desirable direction for plant height, leaf: stem ratio (I cut), total green fodder yield and protein per cent. The other parents M-48212 and M-48273 exhibited significant gca effects for leaf: stem ratio (I cut) and protein (%), respectively and are identified as good general combiners for these traits.

Parent SSG-59-3 showed significant and positive gca effects for length of leaves and protein per cent and identified as good general combiner for these traits. While parent IS-22450 exhibited significant gca effects in desirable negative direction for HCN content. The parents which exhibited significant gca effects in desirable direction are categorized as good general combiner for that particular traits. Hence these parents may be useful for improvement in those particular characters. Sharma *et al.* (1984), Khambalkar (1997), Sumalini *et al.* (2005) and Mukesh Mohan *et al.* (2007) in their combining abiltiy studies pointed out good parents on the basis of gca effects which supports the interference drawn above.

Specific combining ability effects:

Specific combining ability value is an indicative of heterosis. Therefore the crosses exhibiting desirable sca effects for yield and other component characters are of importance for farther utilization in the breeding program. Data presented in Table 3 revealed that the cross IS-23980 x IS-23960 exhibited maximum *per se* performance for total green fodder yield with significant sca effects for yield along with significant sca effects for number of leaves per plant, green and dry fodder yield productivity day^{-1}, HCN content and protein per cent. In this cross parent IS- 23980 is good general combiner for plant height, number of leaves per plant, length of leaves, breadth of leaves, leaf: stem ratio, total green and dry fodder yield and yield productivity per day and HCN content, while other parent IS-23960 is good general combiner only for plant height and low HCN content. Cross IS-23980 x IS-23963 ranked third in *Per se* performance (mean) but showed significant sca effects for yield and other six yield components. Further, crosses M-48273 X AKFR- 89 and SSG-59-3 x IS-22450 ranked second and fourth respectively in *per se* performance (mean) but showed significant sca effects for five important characters including total green fodder yield and total dry fodder yield. Rao (1970) also pointed out that crosses where sca effects are high should be selected for yield. Parmar and Tikka (2005) and Mukesh Mohan *et al.* (2007) also studied the sca effects in different crosses and indicated superior crosses on the basis of sca effects.

The parent IS-23980 was categorized as good general combiner and exhibited better crosses with parents viz., IS-23960, IS-23963 and IS-22450, which exhibited medium general combining ability on the basis of their gca effects. It is seen that at least one of the parent with high gca effect is essential for getting superior cross combination. Similar findings have been reported by Govil and Murthy (1973), Paroda *et al.* (1979) and Shekar *et al.* (1987). Therefore, it is concluded that for getting good hybrid combinations, gca of the parents is very important one. It is also observed that although the parents M-48212, M-48273 and IS-22450 were poor general combiners but they recorded good yield performance.

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CSH-35 A Potential High Yielding National Release Sorghum Hybrid with Excellent Grain, Fodder and Organoleptic Quality

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ABSTRACT

The kharif sorghum hybrid CSH-35 (SPH-1705) has been developed by heterosis breeding method using a new diverse female line AKMS 30 A and the restorer AKR 456. The *Kharif* sorghum hybrid CSH 35 gave average grain yield of 41.90 q ha^{-1} in Zone-II during three years and has shown superiority of 7.90per cent and 29.54per cent over check hybrids CSH 16 (38.83q ha^{-1}) and CSH 23 (32.34q ha^{-1}), respectively. Similarly for fodder yield, *Kharif* sorghum hybrid CSH 35 had recorded average fodder yield of 126.81 q ha^{-1} in Zone-II during three years and has shown superiority of 6.63 per cent and 29.16 per cent over check hybrids CSH 16 (118.93q ha^{-1}) and CSH 23 (98.18 q ha^{-1}), respectively. Further this hybrid recorded promising performance against major pest and diseases as compared to the checks. Nutritional constituents responsible for roti making quality of CSH 35 were better as compared to the national checks. Also the organoleptic quality of the roti prepared from the sorghum hybrid CSH 35 was the best among all the testing entries with the DMRT rank of 1 as compared to the checks CSH 16 (with the DMRT rank of 6) and CSH 23 (with DMRT rank of 10). The hybrid seed production of this hybrid is easy due to synchronous flowering (nicking) of both male and female parents.

Sorghum (*Sorghum bicolor* (L) Moench) is one of the important food crops of the world. Sorghum is the fifth most important cereal crop on the global level. In India sorghum is cultivated during both rainy (*Kharif*) and post rainy (*Rabi*) season. Maharashtra is the largest sorghum grower (54 %) area and produces (49.5%) followed by Karnataka, Madhya Pradesh and Andhra Pradesh (Anonymous, 2012). This is the most assured crop of the rainfed agriculture with highest biomass production even under scarcity seasons. Being C4 plant it can utilize sunlight and water efficiently. Sorghum is one of the most nutritious cereals and is an important dry land crop grown in marginal lands, with minimum inputs. It is recognized worldwide as a smart crop capable of providing food, feed, fodder and fuel especially under moderate inputs especially in water deficit environments. It is also the base crop on which many inter and sequence cropping systems are built upon. A temporary setback in popularity of millets, especially sorghum was imminent because of abundant availability of fine cereals through government policy and programs. In the context of rising input costs, now it is realized that sorghum is of prime importance for the sustained livelihood of the rural poor farmers who cannot afford purchased inputs. Further , the urban poor consumers having limited purchasing power will benefit if nutritive millet grains are also made available as rice and wheat at low cost. Increasing industrial utilization, greater use as quality forage and as adjunct in food and feed mixes can dramatically alter the demand for sorghum. Keeping this fact in consideration, a superior dual purpose new kharif sorghum hybrid CSH-35 has been developed by Sorghum Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra). This hybrid has been identified for released for the Zone-II (Maharashtra, Karnataka, Madhya Pradesh, South Gujarat and North Andhra Pradesh) of India at National Level during the Varietal Identification Committee Meeting held on 19th August, 2014 (Anonymous, 2014).

MATERIAL AND METHODS

The *Kharif* sorghum hybrid CSH-35 (SPH-1705) has been developed by heterosis breeding method using a new diverse female line AKMS 30 A and the restorer AKR 456. There is strong need to increase genetic diversity and exploit indigenous and exotic germplasm to develop diverse sorghum parents. Therefore, Sorghum Research Unit, Dr. PDKV, Akola has been consciously involved in the development of diverse parents with good grain and fodder quality and as a result of these deliberate and

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conscious efforts, the female parent AKMS 30 A has been bred at Akola with the pedigree – [(2077 B x B 57319) x 296 B)- Selection- 10-1]. Further, the male parent AKR 504 of the hybrid has also been developed with the pedigree- [(AKR 426-2 x AKR 436)- Selection- 2-3].This hybrid has been tested in All India Co-ordinated Sorghum Improvement Project (AICSIP) multilocation trials during- 2011 (IHT- Initial Hybrid Trial), 2012 (AHT Ist year- Advance Hybrid Trial) and 2013 (AHT IInd year- Advance Hybrid Trial) along with the national released checks This hybrid has been tested for grain yield, fodder yield, reaction to major pest and diseases. Similarly the grain and stover quality parameters as well as organoleptic properties of the roti have also been assessed in the AICSIP trials. AICSIP- Parental Line Trial (PLT) was also conducted to test the synchronous maturity of the male and female parents of the hybrid. The statistical analysis was carried out according to Panse and Sukhatme (1967) for enterpreting the results.

RESULTS AND DISCUSSION

The performance of CSH 35 All India Coordinated Sorghum Improvement Project (AICSIP) multilocation and multiseason trials is presented below.

Grain and fodder yield of CSH 35 in three years of AICSIP Trials

In All India Coordinated Sorghum Improvement Project (AICSIP) multilocation and multiseason trials, kharif sorghum hybrid CSH 35 was tested at national level for three years across 29 locations for grain yield and 30 locations for fodder yield in zone-II project testing. For grain yield, the kharif sorghum hybrid CSH 35 gave average grain yield of 41.90 q ha^{-1} in Zone-II during three years and has shown superiority of 7.90 per cent and 29.54 per cent over check hybrids CSH 16 (38.83q ha^{-1}) and CSH 23 (32.34q ha^{-1}), respectively (Table 1). While for fodder yield, kharif sorghum hybrid CSH 35 had recorded average fodder yield of 126.81 q ha^{-1} in Zone-II during three years and has shown superiority of 6.63per cent and 29.16 per cent over check hybrids CSH 16 (118.93q ha^{-1}) and CSH 23 (98.18 q ha^{-1}), respectively (Table-2). Rajguru et al. 2005, Jhansi Rani *et al.* 2008 and Ghorade *et al.* 2014 also reported high grain and fodder yielding cross combinations in their study.

Reaction to major diseases and pest in AICSIP trials

The *Kharif* sorghum hybrid CSH 35 had better performance for some of the diseases and pests as compared to the checks in the project pathology and entomology trials conducted during 2011-2013. Among the diseases, Egrot per cent of CSH-35 was less (7.2) as compared to the checks CSH 16 (8.9per cent) and CSH 23 (10.0). Rust attack on CSH-35 was less (2.2) as compared to checks CSH 16 (2.3) and CSH 23 (2.7). Grain affected per cent was also less in CSH 35 (25.1) as compared to the checks CSH 16 (28.8) and CSH 23 (26.8) (Table 3).

Among the important insect pest of sorghum, the hybrid CSH 35 had better performance for most of the insect pests. CSH 35 had shown less shoot fly dead heart per cent at 28 DAE (64.07) as compared to CSH 16 (67.14) and CSH 23 (65.99). CSH 35 had recorded less HB-PDR (3.34) as compared to CSH 16 (3.40). Stem borer leaf injury rating at 35 DAE was less in CSH 35 (3.78) as compared to the checks CSH 16 (4.22) and CSH 23 (4.45). For stem borer dead hearts per cent at 45 DAE, CSH 35 showed less infestation (12.16) as compared to CSH 16 (12.60). Stem borer stem tunneling per cent was also less in CSH 35 (5.33) while it was 7.0 in CSH 16 and 7.26 in CSH 23. (Table 4).

Nutritional constituents responsible for roti quality

Nutritional constituents responsible for roti making quality of CSH 35 were better as compared to the checks. Water absorption capacity of CSH 35 was more (112 ml $100g^{-1}$) as compared to the check CSH 16 and CSH 23 (108 ml $100g^{-1}$) indicating the better roti quality as this parameter is positively correlated to the roti quality. Crude protein content (per cent) of CSH 35 was more (9.68 %) as compared to CSH 16 (9.04 %) and CSH 23 (8.66 %). Total sugar per cent of SPH 1705 was higher (1.66%) as compared to check CSH 16 (1.54%) indicating good amylolyptic activity while preparation of roti and also good taste of roti. (Table 5)

Organoleptic quality of roti

Organoleptic parameters the ranking was done using Duncan Multiple Range Test (DMRT) (Amerine *et al.* 1980). The DMRT rank of 1 indicates the best

Table 1. Summery of grain yield data in AICSIP Hybrid Trials

Traits	Years of Testing	No. of Trials	Proposed hybrid CSH 35	Check Hybrids CSH 16	Check Hybrids CSH 23	CD 5%
Grain yield (Kg)	2011	5	4469	4133	3942	632
	2012	13	4131	4004	2795	459
	2013	11	4131	3625	3454	472
	Mean	**29**	**4189.93**	**3883.10**	**3234.45**	
% increase or decrease over the checks and qualifying hybrids	2011	5		8.13	13.37	
	2012	13		3.17	47.80	
	2013	11		13.96	4.95	
	Mean	**29**		**7.90**	**29.54**	
Frequency in the top 5 group pooled for 3 years			**14/29**	**9/29**	**2/29**	

Table: 2- Summery of fodder yield data in AICSIP Hybrid Trials

Traits	Years of Testing	No. of Trials	Proposed hybrid CSH 35	Check Hybrids CSH 16	Check Hybrids CSH 23	CD 5%
Fodder yield (kg)	2011	5	16534	14541	11292	2168
	2012	13	12185	10871	8952	1553
	2013	12	11600	11224	9942	1287
	Mean	**30**	**12681.4**	**11893.27**	**9818.27**	
% increase or decrease over the checks and qualifying hybrids	2011			13.71	46.42	
	2012			12.09	36.11	
	2013			3.35	16.68	
	Mean			**6.63**	**29.16**	
Frequency in the top 5 group pooled for 3 years			**14/30**	**8/30**	**2/30**	

performance for the organoleptic parameters. Organoleptic quality of the roti prepared from the sorghum hybrid CSH 35 was the best among all the testing entries with the DMRT rank of 1 as compared to the checks CSH 16 with the DMRT rank of 6 and CSH 23 with DMRT rank of 10 (Table 6). Roti prepared from CSH 35 was superior to that of CSH 16 and CSH 23 in all organoleptic quality parameters like color and appearance, flavour, texture, taste and overall acceptability. All these parameters were in the category of "Like very much (Very good)" while the checks CSH 16 and CSH 23 were in the category of "Like moderately" (Table-6). Chavan *et al.* 2013 also reported

Table: 3. Reaction to major diseases (Overall mean of 2011 to 2013)

Name of disease	No. of Trials	Proposed hybrid CSH 35	Check Hybrids CSH 16	Check Hybrids CSH 23
Grain mold field grade (1-9)	11	4.1	3.5	4.1
Grain mold threshed grade (1-9)	8	4.7	3.9	4.7
Fusarium (%)	5	22.4	20.6	21.7
Curvularia (%)	5	21.2	17.9	21.0
Other fungi (%)	4	13.0	13.9	15.9
Ergot (%)	3	7.2	8.9	10.0
Sooty stripe (1-9)	2	2.5	1.7	1.3
Anthrocnose (1-9)	4	3.1	3.	2.7
Zonate leaf spot (1-9)	4	2.7	2.2	2.4
Rust (1-9)	4	2.2	2.3	2.7
Leaf blight (1-9)	5	2.8	2.6	2.7
Grain affected (%)	3	25.1	28.8	26.8
Germination (%)	6	63.5	63.8	64.6

* Grade-1 = Immune, Grade- 9 = Highly susceptible

Table: 4. Reaction to major Insect Pests (Overall mean of 2011 to 2013)

Name of Pest	No. of Trials	Proposed hybrid CSH 35	Check Hybrids CSH 16	Check Hybrids CSH 23
Shoot fly pest (dead heart % at 28 DAE)	11	64.0	67.1	65.9
Shoot fly pest (dead heart % at peak time)	6	73.0	78.0	71.0
HB-PDR (1-9)	5	3.3	3.4	2.9
Stem borer leaf injury rating at 35 DAE (1-9)	6	3.7	4.2	4.4
Stem borer dead hearts (%) 45 DAE	9	12.1	12.6	12.1
Stem borer stem tunneling (%)	2	5.3	7	7.2
Stem borer peduncle tunneling (%)	1	6.3	5.2	4.7
Overall resistance rating (1-9)	5	5.9	5.7	6.4
MTDR(1-9)	5	2	1.8	1.6

* Grade-1 = Low, Grade- 9 = High

Table: 5. Data on Nutritional constituents responsible for roti quality. (Location –Dharwad- 2012 & 2013**)**

Name of Parameter	Proposed hybrid CSH 35	Check Hybrids CSH 16	Check Hybrids CSH 23	Check Hybrids CSH 25
Hectoliter weight (kg hl^{-1})	76.76	77.65	75.33	75.70
Water absorption (ml $100g^{-1}$)	112.00	108.00	108.00	102.00
Crude protein (%)	9.68	9.04	8.66	8.89
Soluble proteins (%)	1.21	1.67	1.58	1.56
Total sugars (%)	1.66	1.54	1.72	1.51
Starch (%)	43.12	47.75	50.60	47.78
Free amino acids (mg $100g^{-1}$)	84.26	76.24	76.41	77.38
Phenolics (%)	2.36	2.13	2.46	1.99

Table 6. Data on Organoleptic quality of roti. (Location –Dharwad -2012)

Quality characteristic	Proposed hybrid	Check Hybrids		
	CSH 35	CSH 16	CSH 23	CSH 25
Water required for dough (ml $100g^{-1}$)	110	110	100	90
Kneading quality	1	1	1	1
Spreading quality	1	1	1	1
Organoleptic quality parameters				
Colour and appearance	8.6	7.0	6.6	8.2
Flavour	8.0	7.6	6.8	8.2
Texture	8.2	7.6	7.2	7.8
Taste	8.4	7.4	7.2	7.6
Overall acceptability	8.30	7.40	6.95	7.95
Rank by DMRT	1	6	10	4
Loss in weight during storage (%)				
4 hrs	2.11	1.73	2.39	2.01
8 hrs	2.95	2.58	3.14	3.55
24 hrs	4.64	4.17	5.67	5.41

Kneading quality of dough, **score**:- Good=1 , Fair= 2, Poor= 3. **Spreading quality of roti, score**:- Easy spreading without cracks=1, Slightly difficult to spread with minute cracks=2, Difficult to spread with cracks=3. **Sensory score** :- Like extremely (Excellent)-9, Like very much (Very good)-8, Like moderately -7, Like slightly-6, Neither like nor dislike-5, Dislike slightly-4, Dislike moderately-3, Dislike very much-2, Dislike extremely-1.

DMRT- Duncan's Multiple Range Test

Table: 7. Data on Stover quality. (2012 & 2013)

Name of Parameter	No. of Trials	Proposed hybrid	Check Hybrids		
		CSH 35	CSH 16	CSH 23	CSH 25
Crude Protein (%)	6	7.43	7.40	7.71	7.73
IVOMD (%)	6	45.14	44.86	45.90	45.16
NDF%	5	59.61	60.24	59.13	59.40
ADF%	5	45.32	45.31	44.23	45.46
Dry matter (%)	2	91.14	91.86	91.71	92.02
Ash content (%)	5	9.06	9.48	9.14	9.57
Metabolizable energy (ml/kg)	5	6.42	6.33	6.56	6.41
Lignin (%)	5	5.24	5.21	5.12	5.24

IVOMD-Invitro Organic Matter Digestibility, **NDF**- Neuter Detergent Fiber, **ADF**- Acid Detergent Fiber

Table: 8. Parental line trial (PLT) of parents of CSH 35 (AKMS 30 A x AKR 504)

(Year – Rabi 2012-2013, **Locations**- Nandyal, Parbhani and Hagari)

SN	Parent	Days to 50% flowering
1	AKMS 30 A(Female parent of CSH 35)	67
2	AKR 504 (Male parent of CSH 35)	66

the organoleptic properties of rabi sorghum genotypes.

Data on stover quality

Stover quality parameters of CSH 35 were better as compared to the checks. Crude protein (%) of CSH 35 was more (7.43%) as compared to the check CSH 16 (7.40 %). IVOMD (per cent) of CSH 35 was more (45.15 %) as compared to the checks CSH 16 (44.86 %). Metabolizable energy of CSH 35 was better (6.42 ml kg^{-1}) as compared to check CSH 16 (6.33 ml kg^{-1}) (Table 7). Umakanth *et.al.* 2014 also reported stover quality parameters of brown mid rib mutations.

Synchronous flowering of the parents of the hybrid

Based on the data of PLT (Parental Line Trial) at AICSIP level, it was found that flowering of male and female parents of this hybrid was synchronous. Thus, there is no need of staggered sowing of male and female parents for hybrid seed production programme and the seed production is also expected to be economical. (Table-8)

CONCLUSION

The major challenge facing sorghum research and development workers is to provide technologies that will enable the agricultural sector to affect transformation of "subsistence farming" to a sustainable "market oriented" enterprise successfully competing with rest of the world. Therefore, development of strategies/ products for resolving the constraints which inhibit the increased use of improved technologies/ products in cost effective manner. Taking in to consideration the superior performance of the *Kharif* sorghum hybrid CSH 35 for grain as well as fodder yield along with the excellent quality characters, this hybrid has been identified for release by the identified for released for the Zone-II (Maharashtra, Karnataka, Madhya Pradesh, South Gujarat and North Andhra Pradesh) of India at National Level during the recently held Varietal Identification Committee Meeting on 19th August, 2014 held at Directorate of Sorghum Research (DSR), Hyderabad. Thus, in line of strategy of sorghum with the goal of attaining food security and maintaining diversity in sorghum cultivation, the hybrid CSH-35 may prove its significance and may prove as a 'milestone' in sorghum breeding programme.

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Mutagenic Effectiveness and Efficiency of Gamma Radiation in Mungbean

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ABSTRACT

The study on mutagenic effectiveness and efficiency of gamma rays in mungbean was carried out at Department of Agricultural Botany, Dr. P.D.K.V Akola. Seeds of PKV Green gold, AKM-8802 and AKM-4 of mungbean were exposed to gamma ray doses (at 15, 25 and 35kR) to obtain the spectrum and frequency of chlorophyll mutations in M_1 generation. The results revealed that treatment 15kR gamma ray was found more efficient and effective in PKV Green gold and 35kR treatment in AKM-8802 and AKM-4. The maximum (19) loci mutated found in 35kR dose of AKM-8802 while minimum (11) loci mutated shown in 35kR dose of PKV Green gold. There are total 135 loci were mutated in three varieties by 15, 25 and 35kR doses of gamma rays. It can be expected that modern mutation breeding technologies in combination with refined selection methods applicable to large populations will continue to be of great potential for the improvement of both sexually and vegetative propagated crop plants.

Mungbean is one of the most important pulse crop grown in India. Significant genetic improvement in this crop could not be made in the recent past, which could be attributed to relatively low genetic variability for yield potential in available genotypes. Pulses constitute an important ingredient in predominantly vegetarian diet and are important as source of protein that nutritionally balances the proteins from cereal grains. India is the largest producer of mungbean in the world. Greengram belongs to family Leguminoceae and sub-family Papilionaceae. It has 12 pairs of chromosomes (2n=24). Green gram is originated in India and Central Asia.

The traditional breeding methods for self pollinated crops largely depend on natural variability already present in the crop. Green gram being self pollinated, the naturally existing genetic variability may not be sufficient to achieve desire improvement. Each kind of breeding method involves creation and utilization of genetic variability by means of hybridization, recombination and selection. Alternatively, mutation breeding is the best method to create the new genetic variability of a species considerably within a short time.

Induced mutations was used to generate genetic variability and have been successfully utilized to improve yield and yield components of various pulse crops. The breeding objectives in green gram are to develop varieties with high yield, early maturity, high protein and resistant to diseases and insects-pests. To achieve these objectives and bring about desired improvement in crop the most sophisticated techniques of mutation breeding can be exploited by the plant breeders. The present study was undertaken to study and compare the effectiveness and efficiency of different doses of induced mutation.

MATERIAL AND METHODS

The present investigation was conducted at the field of Department of Agricultural Botany, Dr. PDKV, Akola, Maharashtra during *Kharif* 2010. For the present study three varieties of mungbean viz., AKM-4, AKM-8802, and PKV Green gold were used. The seed of varieties were collected from Pulses Research Unit, Dr. PDKV Akola. Eighty gram seeds of each variety was irradiated with 15, 25 and 35kR Gamma rays at Bhabha Atomic Research Centre, Trombay, Mumbai.

Total twelve treatment comprised of treated seeds three varieties with three different doses gamma rays along with one control for each genotype were sown to raise M_1 generation in randomized block design at the research field of Department of Agricultural Botany, Dr. PDKV, Akola during summer 2010. The M_1 generation was observed for different parameters besides population screened for chlorophyll mutants. Seeds from each plant of M_1 generation was harvested separately.

The M_2 generation was raised in *Kharif* 2010. Plants to row progenies were raised from all the harvested seeds from each treatment. The treated populations were carefully screened for chlorophyll mutations where as viable chlorophyll mutations were scored throughout the

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life period of the plants. The spectrum of chlorophyll and morphological mutations were scored treatment wise to study mutagenic effectiveness and efficiency of each treatment as suggested by Gaul (1958) and Konzak *et al.* (1965) respectively.

RESULTS AND DISCUSSION

Different types of mutants isolated from various treatments of gamma rays on the basis of morphological changes have been discussed in present investigation. They are explained as under.

Six types of chlorophyll mutants were recorded in the present investigation Albina, Xantha, Variegated leaf, White streak leaf, persistent yellow leaf and Chlorina. The frequency of chlorophyll mutations was higher in variety AKM-8802(0.23 %) followed by AKM-4 (0.10%) and PKV Green gold (0.06 %). Among different chlorophyll mutations, Xantha exhibited the highest frequency followed by persistant yellow leaf, Chlorina, Albina, White streak leaf and Variegated leaf. The earlier findings of Chontira *et al.* (2005) were similar to the present findings.

Tall type of mutant showed increased in height with more or equal number of branching. These types of mutants were found in almost all the treatments except T_6 i.e. AKM-8802 treated with 15kR gamma rays. The maximum frequency was recorded in 25kR dose applied to AKM-8802 i.e. T_7 (0.12 %). Similar induced mutations were recorded by Barshile *et al.* (2009) in chickpea. Tall mutants of mungbean are likely to be useful for intercropping with the tall growing cereals like sorghum or maize.

Height of plant was reduced in dwarf mutant. In some dwarf mutants pod formation was badly affected. This type of mutant was recovered in almost all the treatments. The maximum frequency was recorded in 25kR dose affected to AKM-8802 i.e. T_7 (0.20 %). The similar mutants were found by Grover and Virk (1984) in green gram.

One plant with single leaflet without pedicel was observed in 35kR dose applied to AKM-8802 i.e. T_8 (0.02 %). The variant was also reported by Gautam and Mittal (1998) and Chontira *et al.* (2005).

The plant bearing different number of leaflets per leaf varied from 2 to 8. They were called as bifoliate, quadrafoliate, pentafoliate, hexafoliate and octafoliate leaf mutants. This variation is limited to few leaves in seedling while subsequent leaves are normal. The frequency of quadrafoliate was maximum followed by pentafoliate, hexafoliate and octafoliate. Similar mutants were recorded by Grover and Virk (1984) in Green gram and Chontira *et al.* (2005). The leaflet variation may be useful as seedling markers although subsequent younger leaves on the plant may be normal trifoliate.

The viny mutant plant with weak, slender, delicate, hallow stem and showing creeping habit was observed. Grover and Virk (1984) did came across such viny mutations in mungbean. The leaves of broad leaflet mutants were quite wider than the normal leaf. The maximum frequency was recorded in AKM-4 followed by AKM-8802 and PKV Green gold. In earlier studies, broad leaf mutant were also recorded by Singh and Yadav (1991) in green gram.

In narrow leaflet mutants leaves were narrow as compared to controls. This type of mutant was recorded in AKM-8802 only. Similar mutant observed by Chontira *et al.* (2005) and Sharma *et al.* (2008). The plant shown dark green thick crumpled leaves. The frequency of dark green thick crumpled leaves mutant was higher in AKM-4 followed by AKM-8802 and PKV Green gold. Tickoo (1987) recorded the frequency of this mutant in Green gram with gamma rays.

Serrated leaflet mutants were found mostly in AKM-8802 genotype followed by AKM-4 and highest frequency was in 35kR dose in AKM-8802 i.e. T8 (0.05%). Grover and Virk (1984) reported same type of leaf in Green gram. The frequency of rounded leaf mutants were in AKM-4 followed by AKM-8802 and PKV Green gold. Earlier findings were same recorded by Chontira et al. (2005) and Bundhopadhyay and Bose (1983).

The small leaflet leaflet size found decreased as to that of control. The mutants were observed in T_6 and T_4. Such small leaves were also recorded by Patil and Mouli (1978) with gamma rays. One of leaf shape mutant had wrinkle on it. They were observed only in AKM-8802 genotype. Chontira *et al.* (2005) reported the same results.

Mutation frequency of each visible mutant in M_2 generation was calculated as suggested by Gaul (1958). It is represented in Table 1. The table revealed that treatments with higher doses of 25 and 35 kR gamma rays

Table1: Spectrum of induced mutations in different treatments of gamma rays in M_1 generation (%)

S.N.	Type of Mutation	PKV Green gold			AKM-8802			AKM-4		
		15kR	25 kR	35 kR	15 kR	25 kR	35 kR	15 kR	25 kR	35 kR
1	Chlorophyll mutants									
a	Albina	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
b	Xantha	0.00	0.02	0.02	0.00	0.02	0.02	0.02	0.02	0.02
c	Variegated leaf	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d	White streak leaf	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
e	Persistant Yellow leaf	0.00	0.00	0.00	0.02	0.07	0.02	0.00	0.00	0.02
f	Chlorina	0.00	0.00	0.00	0.02	0.02	0.00	0.00	0.02	0
	Total chlorophyll mutant	0.02	0.02	0.02	0.08	0.11	0.04	0.02	0.04	0.04
2	Dwarf	0.07	0.14	0.05	0.04	0.20	0.19	0.09	0.11	0.15
3	Tall	0.09	0.09	0.07	0.00	0.12	0.11	0.14	0.14	0.07
4	Early Maturing	0.04	0.00	0.02	0.02	0.02	0.00	0.00	0.02	0.05
5	Late maturing	0.04	0.02	0.02	0.09	0.00	0.05	0.00	0.04	0.00
6	High podding	0.07	0.07	0.02	0.09	0.12	0.08	0.09	0.16	0.15
7	Crumpled leaf	0.04	0.00	0.00	0.00	0.12	0.05	0.02	0.04	0.05
8	High branching	0.04	0.04	0.02	0.02	0.05	0.11	0.09	0.09	0.15
9	Small leaf	0.00	0.00	0.05	0.02	0.00	0.00	0.00	0.00	0.00
10	Narrow leaf	0.00	0.00	0.00	0.02	0.05	0.05	0.00	0.00	0.00
11	Leaf shape									
a	Long	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.02
b	Ovate	0.00	0.00	0.00	0.04	0.00	0.05	0.00	0.11	0.00
	Total leaf shape mutant	0.00	0.04	0.00	0.04	0.00	0.05	0.00	0.11	0.02
12	Short pod	0.00	0.04	0.00	0.00	0.00	0.11	0.00	0.04	0.00
13	Wrinkled leaf	0.00	0.00	0	0.02	0.05	0.02	0.00	0.00	0.00
14	Sturdy strong stem	0.04	0.07	0	0.07	0.07	0.08	0.00	0.04	0.00
15	Broad leaflet	0.00	0.04	0.02	0.049	0.02	0.00	0.04	0.09	0.05
16	Leaflet number variations									
a	Unifoliate with no branching	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
b	Bifoliate	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
c	Quadrafoliate	0.11	0.04	0.02	0.07	0.12	0.11	0.11	0.16	0.07
d	Pentafoliate	0.02	0.12	0	0.07	0.05	0.05	0.19	0.09	0.12
e	Hexafoliate	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
f	Octafoliate	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
	Total Leaflet number variations	0.13	0.16	0.02	0.14	0.17	0.20	0.32	0.25	0.19
17	Reddish stem	0.02	0.02	0.00	0.00	0.00	0.00	0.16	0.07	0.02
18	Serrated leaf margin	0.00	0.00	0.00	0.04	0.00	0.05	0.04	0.00	0.00
19	Viny mutant	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
20	Bold seeded	0.04	0.07	0.05	0.00	0.00	0.00	0.04	0.07	0.07
	Total	1.82	3.14	3.37						
	Dose-wise total over varieties:									
	Doses	15kR			25kR			35kR		
	Total	2.44			3.28			2.65		

Table 2: Mutagenic efficiency and effectiveness of different treatment of gamma rays in M_2 generation.

Genotype	Treatment doses	Percent lethality	Mutant100^{-1} M_2 plant	Mutagenic efficiency	Mutagenic effectiveness
		(L)	(MP)	(MP/L)	(MP/kR)
PKV Green gold	15kR	2.43	0.75	0.309	0.0500
	25kR	3.93	0.93	0.237	0.0372
	35kR	3.53	0.44	0.125	0.0126
AKM-8802	15kR	3.61	0.89	0.247	0.0593
	25kR	2.56	1.25	0.488	0.0500
	35kR	2.85	1.43	0.502	0.0409
AKM-4	15kR	4.60	1.17	0.254	0.0780
	25kR	4.46	1.47	0.330	0.0588
	35kR	2.70	1.11	0.411	0.0317

kR= Dose of gamma radiation in kilo Roentgen

induced higher mutation frequency in all three genotypes.

In overall sums over the varieties the mutation frequency was maximum in AKM-4 with frequency 3.37 per cent followed by AKM- 8802 (3.14%) and PKV Green gold (1.82%). When the frequency of three varieties mutations summed over the doses the highest frequency was with 25 kR dose (3.28%) followed by 35kR (2.65%) and least with 15kR (2.44%).

The efficiency and effectiveness of gamma rays were estimated as suggested by Konzak *et al.* (1965) and are presented in Table 2.

From Table 2 it is observed that in PKV Green gold mutagenic efficiency was minimum 35kR dose i.e. in T_4 (0.125) and maximum 15 kR i.e. in T_1 (0.309). In AKM-8802, it was minimum in 15kR T6 (0.247) and maximum 35kR i.e. in T_8 (0.502). In AKM-4, it was minimum 15kR i.e. in T_{10} (0.254) and maximum 35kR i.e. in T_{12} (0.411). In all treatments mutagenic efficiency was more in AKM-8802.

The mutagenic effectiveness was found maximum in 15kR doses in all the three varieties i.e. T_2 (0.050), T_6 (0.059) and T_{10} (0.078). While minimum in 35kR dose i.e. T_4 (0.012), T8 (0.040) and T_{12} (0.031) in genotypes PKV Green gold, AKM-8802 and AKM-4 respectively.

The increased dose of gamma rays increased the mutation frequency. Yadav (1987) in *V. radiata* reported increased in frequency with increased doses of mutagenic treatments. Tickoo *et. al.* (1987) studied frequency of induced macromutation in *V. radiata* with gamma rays. Similarly, Tonacimuthu and Babu (1988) observed frequency of chlorophyll mutations increased with dosage. It indicated that the doses of gamma rays had been within the useful limit to induce broad mutation spectrum.

Mutagenic effectiveness is a measure of the frequency of mutations induced by a unit dose of mutagen (kR), while mutagenic efficiency gives an idea of the proportion of mutations in relation to undesirable changes like lethality or sterility. The concept of mutagenic efficiency and effectiveness was enunciated by Ehrenberg (1960) and was further utilized by Konzak (1965).

In the present investigations treatment 15kR gamma rays was found to be more efficient and effective in PKV Green gold while 35kR treatment was better in AKM-8802 and AKM-4. It showed differential genotypic response to different doses of mutagens. The selected treatments were found effective in inducing wider range of mutation in mungbean. Birhman *et al.* (1980) and Sharma and Haque (1997) recorded the similar results in mungbean

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PKV PINK : A New Safflower Variety Released for Vidarbha Region of Maharashtra

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ABSTRACT

High yielding safflower variety PKV Pink (AKS 311) which produced 19.7 per cent higher yield over check Bhima and 23.6 per cent higher over AKS 207, was released during the year 2011 for Vidarbha region of Maharashtra State. It has got high oil content (33 per cent) and low test weight (HSW 3.7 g). It is tolerant to wilt and have distinctness in petal colour (Pale yellow turns to pink and remain pink after fading)

Safflower is an important *Rabi* oilseed crop of Vidarbha which is grown under rainfed and irrigated conditions. This crop is basically drought tolerant and therefore comes up well in minimal irrigations. If this crop is provided with 2- 3 irrigations, the crop can surpass yield of many *Rabi* crops. However, the area under this crop is declining all over the country. At present the area, production and productivity of Vidarbha was 16 thousand hectares, 12 thousand tones and 779 kg ha^{-1}, respectively, and of Maharashtra 231 thousand hectares, 154 thousand tones and 665 kg ha^{-1}, respectively and of India 377 thousand hectares, 240 thousand tones and 637 kg ha^{-1}, respectively.

In this region of Maharashtra mostly Bhima variety of safflower is under cultivation. Recently one variety developed by Dr, Panjabrao Deshmukh Krishi Vidyapeeth, Akola i.e. AKS 207 was added in the list and choice was left to the farmers. However, now again we have released one more variety of safflower, i.e PKV Pink which will definitely replace the ruling varieties in the region (PDKV, 2011).

MATERIAL AND METHODS

The genotype PKV Pink (AKS- 311) was tested first time in preliminary yield trial (PYT) during 2007-08 at Akola location. Looking to its performance , it was promoted to multilocaton vatrital trial (MVT) and tested at seven locations, viz, Akola, Achalpur,Amravati, Buldana, Nagpur, Yavatmal, Washim for three years 2008-09,2009-10 and 2010-11with different sets of 10-12 entries. The net plot size was 4.6 m x 1.35 m (3 Rows) with spacing of 45cm x 20 cm. The experimental design was Randomized Block Design (RBD) with three replications. Every year at all locations the crop was sown in the last week of September under rainfed conditions. A common dose of fertilizer 25 : 25 : 0 NPK kg ha^{-1} was applied at the time of sowing. A recommended agronomic package of practices were followed during the course of evaluation.

PKV pink is a cross derivative developed by pedigree method of breeding from the cross NARI 6 x JLSF 344. The objective of the project was to develop high yielding variety coupled with disease resistant (PDKV, 2011).

RESULTS AND DISCUSSION

Yield potential of PKV Pink was confirmed at research field of Oilseeds Research Unit, Dr. PDKV , Akola in PYT during 2007-08 (Table 1). It produced 12.5 per cent higher (2162 kg ha^{-1}) seed yield over check AKS 207 (1921 kg ha^{-1}) and oil yield was 26.7 per cent higher (696 kg ha^{-1}) over AKS 207 (550 kg ha^{-1}). Looking to this performance it was promoted to MVT and tested for three years (2008-09 to 2010-11) at seven locations in Vidarbha region of Maharashtra. PKV Pink produces average seed yield of 1576 kg ha^{-1} which was 23.6 per cent and 19.7 per cent more than the yield of AKS 207 and Bhima respectively with significant superiority (Table 2). Oil yielding ability of PKV Pink was more pronounced with mean oil yield of 521 kg ha^{-1} and the increase over the checks 27.1 per cent (Bhima) and 30.9 per cent (AKS 207) (Table 3). Oil recovery of PKV Pink was confirmed on mini oil expeller (Table 4) and oil content was confirmed on Soxhlet's method (Table 5). It showed similar trend.

PKV Pink was also tested at State level (Table 6) and in AICRP breeding trials (Table 7). In IVT (Irrigated) it produced 5.54 per cent higher oil yield (400 kg ha^{-1}) over national check A 1 (379 kg ha^{-1}).

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Table 1. Seed and Oil Yield performance of PKV Pink in Preliminary Yield Trial (2007-08).

Location	Particular	Proposed variety PKV Pink	AKS 207 (c)	SE m ±	C.D. (5%)	CV (%)
Akola	Seed Yield (Kg/ha)	2162	1921 (12.5)	100.8	285.3	10.1
	Oil yield (kg/ha)	696	550 (26.7)	-	-	-
	Oil content (%)	32.2	28.6	-	-	-

Figures in parenthesis indicated per cent increase.
Source: RRC report of safflower breeding of Dr. PDKV, Akola 2007-08

Table 2. Seed Yield performance of PKV Pink in Multilocation Varietal Trial (2008-09, 2009-10 and 2010-11) Seed yield (kg ha^{-1})

Year	Locations	Proposed variety PKV Pink	AKS 207 (c)	Bhima (c)	SE m ±	C.D. (5%)	CV (%)
2008-09	Akola@	1906	1696	1820	149.4	NS	14.3
	Achalpur	2469	2228	1879	141.9	425.4	11.4
	Amravati	1027	932	791	82.7	247.9	14.2
	Buldana	1224	1401	1248	55.0	164.9	7.5
	Yavatmal	1392	1272	1200	166.6	478.7	19.6
	Washim	1675*	1213	1047	81.2	243.4	9.5
Mean of 5 locations		**1557**	**1409**	**1233**	**62.9**	**187.6**	**10.5**
% increase		**10.5**	**26.3**	**-**	**-**	**-**	
2009-10	Akola	1336*	518	590	60.5	175.9	15.0
	Nagpur	977	1115	1126	98.6	286.6	17.7
	Yavatmal	1167	1288	1264	80.4	233.6	10.7
	Washim	1718	1422	1771	247.1	718.3	16.8
Mean of 4 locations		**1300**	**1086**	**1188**	**127.5**	**396.9**	**21.3**
% increase	-	**19.7**	**9.4**	-	-	-	
2010-11	Akola	1755*	1261	1527	65.7	193.2	8.0
	Yavatmal	1852	1006	1557	163.2	478.7	19.6
	Washim	2497	1841	2389	88.6	272.2	13.5
	Bhuldana	1276	966	855	186.7	533.0	7.4
	Amravati	1610	1449	1127	187.9	526.3	18.7
	Nagpur	1670*	1213	1382	71.1	208.3	12.0
Mean of 6 locations		**1777***	**1289**	**1473**	**73.9**	**220.6**	**11.9**
% increase	-	**37.5**	**20.3**	**-**	**-**	**-**	
Overall mean 15 Loc.		**1576***	**1275**	**1317**	**50.1**	**142.4**	**14.1**
% Increase	-	**23.6**	**19.7**	**-**	**-**	**-**	

* Indicated significant superiority over best check @ Not considered for averaging.

Source: RRC report of safflower breeding of PDKV, Akola 2008-09. 2009-10 and 2010-11.

Table 3. Oil yield of PKV Pink in Multilocation Varietal Trial (2008-09, 2009-10 and 2010-11)

Trial	Year	No. of test	Oil yield (kg ha^{-1})		
			Proposed variety PKV Pink	AKS 207 (c)	Bhima (c)
MVT	2008-09	5	518 (33.3)	441 (31.3)	386 (31.3)
MVT	2009-10	4	426 (32.8)	337 (31.0)	371 (31.2)
MVT	2010-11	6	586 (33.0)	402 (31.2)	457 (31.0)
Overall mean of MVT		15	521 (33.0)	398 (31.2)	410 (31.2)
% increase		-	30.9	27.1	

Figures in parenthesis indicated per cent oil content

Table 4. Oil recovery of PKV Pink on mini oil expeller

Variety	Quantity of seed crushed (Kg)	Oil recovery (kg)	% Oil recovery
Proposed variety PKV Pink	5	1.516	30.32
AKS 207 (c)	5	1.354	27.08
Bhima (c)	5	1.406	28.12

N.B. Oil was extracted at M/s. Shri. Gajanan Oil Mill, Akola Road, Malegaon.

Table 5. Confirmation of oil content in PKV Pink by Soxhlet's method.

Variety	Oil content %
Proposed variety PKV Pink	32.15
AKS 207 (c)	29.20
Bhima (c)	28.07

N.B. Oil estimation was done at Nagarjun Medicinal Plant Garden, Dr. PDKV Akola

Table 6. Seed yield of PKV Pink in State Multilocation Varietal Trial (2009-10)

Year	Locations	Proposed variety PKV Pink	AKS 207 (C)	Bhima (C)	PBNS 12 (C)	Nari 38 (C)	Phule Kusuma (C)	SE (m) ±	CD at 5%	CV %
2009-10	Solapur	1235	1047	1084	1082	923	1141	90.8	260.8	13.9
	Mohol	843	548	655	623	456	730	41.0	118.0	11.8
	Akola	1127	660	1074	837	996	998	89.7	257.8	17.7
	Parbhani	1436	880	1616	1430	891	1524	70.6	203.0	13.2
	Phaltan@	1001	1027	1076	1032	1182	875	129.3	NS	21.6
	Overall Mean	**1128**	**832**	**1101**	**1001**	**890**	**1054**	-	-	-
	%increase		**35.6**	**2.5**	**12.7**	**26.7**	**7.0**			

@Not considered for averaging.

Source: RRC report safflower breeding of Dr. PDKV Akola 2009-10

Table 7. Yield performance of PKV Pink in Project Trials (AICRP) (2008-09)

Trial	Particular	Proposed variety PKV Pink	A 1 (NC)	SE m ±	CD (5%)	CV (%)
IVT - Rainfed (10 locations)	Seed yield (Kg/ha)	1292	1402 (-7.84)	37	103	15.2
	Oil yield (kg/ha)	296	304 (-2.63)	-	-	-
IVT - Irrigated (10 locations)	Seed yield (Kg/ha)	1539	1658 (-7.17)	33	93	12.1
	Oil yield (kg/ha)	400	379 (5.54)	-	-	-
IVT - Rainfed and Irrigated	Seed yield (Kg/ha)	1416	1530(-7.5)	25	69	13.6
(20 Loc.)	Oil yield (kg/ha)	345	339(1.7)	-	-	-
Oil content (%) Rainfed		25	23			
Oil content (%) Irrigated		25	23			

Figures in parenthesis indicated per cent increase/decrease of yield over National check A 1.

Rainfed centers (10): Akola, Annigeri, Arnej, Bijapur, Dhandhuka, Dharwad, Latur, Raichur, Solapur and Tandur.

Irrigated centers (10): Berhampore, Hiriyur, Indore, Jalna (Krishidhan), Jalna (Mahyco), Mauranipur, Parbhani, Phaltan, Raipur and Udaipur.

Source: Annual Report of AICRP (Safflower) 2008-09

Table 8. Duration in days

Variety	PYT (07-08)	MVT (08-09)	MVT (09-10)	MVT (10-11)	IVT (Rainfed) (08-09)	Mean of rainfed trials	IVT (Irrigated) (08-09)
PKV Pink	134	135	135	143	128	135	136
AKS 207 (c)	122	129	130	139	-	130	-
Bhima (c)	-	133	136	141	-	137	-
A 1 (NC)	-	-	-		127	-	136

Source : RRC report of safflower breeding of PDKV, Akola2007-08, 2008-09. 2009-10, 2010-11 and Annual Report of AICRP (Safflower) 2008-09.

Table 9. Average Ancillary Observations over the years (2008-09, 2009-10 and 2010-11) in MVTs conducted at University level

S. N.	Observations	Mean of all MVTs		
		Proposedvariety PKV Pink	AKS 207 (C)	Bhima (C)
1	Days to 50% flowering	84	78	85
2	Days to maturity	138	133	137
3	Plant height (cm)	77.1	74.1	74.6
4	No. of branches/plant	7.1	8.9	8.5
5	No. of effective capitula/plant	17.7	20.4	20.1
6	No. of seeds/ capitulum	32.4	23.0	24.6
7	100 seed weight (g)	3.8	6.0	5.7
8	Volume weight (g)	572	535	541
9	Oil content (%)	33.0	31.2	31.2

Table 10. Ancillary observations recorded in Initial Varietal Trial (AICRP) 2008-09

S. N.	Observations	IVT (Rainfed)		IVT (Irrigated)	
		Proposed variety PKV Pink	A 1 (C)	Proposed varietyPKV Pink	A 1 (C)
1	Oil content (%)	25.0	23.0	25.0	23.0
2	Hull content (%)	48.6	46.8	46.7	54.2
3	Days to 50% flowering	81	80	98	98
4	Days to maturity	128	127	136	136
5	No. of effective capitula/plant	17.7	19.8	22.5	25.3
6	No. of seeds/ capitulum	32.0	22.0	34	26
7	100 seed weight (g)	4.1	5.9	4.1	5.7
8	Volume weight (g)	660	645	554	542
9	Harvest index (%)	29	31	30	30
10	Biological yield (kg/ha)	5440	5371	7846	7547
11	Plant height (cm)	75	72	105	101

Source: Annual Report of AICRP (Safflower) 2008-09.

Table 11. Reaction of PKV Pink to wilt (%) (2008-09) (AICRP)

Genotype	Particulars	Locations				
		Solapur	Tandur	Phaltan	DOR, Hyderabad	Annigeri
Wilt (%)						
Proposed varietyPKV Pink		2.9	28.6	1.4	8.3	-
A 1 (C)		53.3	50.0	53.5	29.2	-

Source: Annual Report of AICRP (Safflower) 2008-09.

Table 12. Comparative assessment of yield gain from safflower varieties in relation to fertilizer input under rainfed conditions (Akola, 2010-11)

Treatment	Seed yield (kg/ha)	Gross return	Cost of cultivation	Net return	B:C ratio
F_0 – No RDF	770	16940	7400	9540	2.29
F_1 – 50% RDF	1031	22682	7800	14882	2.91
F_2 – 100% RDF	1313	28886	8200	20686	3.52
F_3 – 150 % RDF	1465	32230	8600	23630	3.74
SE (m) $\pm$	21.4				
CD at 5%	63.3				
CV%	5.6				
Variety					
V_1-AKS 311	1288	28336	8000	20336	3.54
V_2 – AKS 207	954	20988	8000	12988	2.62
V_3 – Bhima	1191	26202	8000	18202	3.28
SE (m) $\pm$	28.9				
CD at 5%	114.3				
CV%	8.8				
Interaction	NS				

Table 13. Results of adaptive trials of safflower variety PKV Pink (2010-11)

S. N.	Name and address of cultivators	Date of sowing	Seed yield (kg/ha)		% increase over
			Proposed variety PKV Pink	Check AKS 207	
1	Shri. Ramdas Shankar Marge, Panchagavan, Tq. Telhara, Dist. Akola	4-10-10	1300	1050	23.8
2	Shri. Duttraya Anand Daud, Ner, Tq. Telhara, Dist. Akola	8-10-10	1100	800	37.5
3	Shri Amol Punjaji Dhame, Mahagaon, Tq. Karanja Dist. Washim	2-10-10	1250	900	38.9
4	Shri Gajanan Janakrao Deshmukh, Kavatha, Tq. Balapur , Dist. Akola	11-10-10	1150	850	35.3
5	Shri. Vitthal Sadashiv Ambuskar, Kavatha, Tq. Balapur , Dist. Akola	14-10-10	1200	900	33.3
6	Shri. Prashant Vijayrao Wankhade, At Post Shendurjana, Tq. Arni, Dist. Yavatmal	28-9-10	1300	1100	18.2
7	Shri. Vinod Shriram Dhore, Digras, Tq. Digras Dist. Yavatmal	18-10-10	1250	1000	25.0
8	Shri. Rubin Giris Aggrawal, Pusad Tq. Pusad Dist. Yavatmal	29-9-10	1000	800	25.0
9	Shri. Nilesh Sadashivrao Pote, Songaon, Tq. Anjangao Surji, Dist. Amravati	1-10-10	1500	1200	25.0
10	Shri Skharam Khadse Agar Tq. Dist. Akola	1-10-10	1420	1170	21.4
11	Shri Nandkishor Duttraya KalneAgar Tq.Dist. Akola	2-10-10	1250	1280	-2.3
12	Shri Arun Mehkare Agar Tq. Dist. Akola	28-9-10	1400	1100	27.3
13	Shri. Kishor Khole Agar Tq. Dist Akola	29-9-10	1520	1220	24.6
14	Shri. Ganesh Kukade Agar Tq. Dist. Akola	30-9-10	1640	1480	10.8
15	Shri. Shrikant Gajanan Alshi ,Amdapur, Tq. Chikhali, Dist. Bhuldhana	4-10-10	1580	1300	21.5
	Mean	**-**	**1324**	**1077**	
	% Increase over Check	**-**	**-**	**22.9**	

The number of days to maturity of PKV Pink is similar to Bhima (Table 8). Table 9 and 10 revealed that hundred seed weight of PKV Pink was less, number of seeds/capitulum was more and volume weight (g/1000 ml) was more. Differences in pest infestations among the varieties were not noticed. However, PKV Pink showed tolerance to wilt at Solapur, Tandur, Phaltan and DOR, Hyderabad (Table 11).

In agronomic trial yield of safflower was significantly influenced by various fertilizer levels. The highest seed yield (1465 kg ha^{-1}) was obtained by 150 per cent RDF which were statistically significant over 100 per cent RDF. The yield of PKV Pink was found to be highest (1288 kg ha^{-1}).Gross returns (28336), net return (20336) and B:C ratio (3.54) followed the same trend (Table 12).

In adaptive trials conducted in Vidarbha region during *Rabi* 2010-2011, PKV Pink produced 22.9 per cent higher yields compared to check AKS 207 (Table 13).

Looking to the performance of PKV Pink and desirable traits in it like higher yield, higher oil, low seed

rates per hectare due to low HSW, higher volume weight and tolerance to wilt, it was released for general cultivation in Vidarbha region of Maharashtra (Annonymous, 2011).

Description of safflower variety PKV Pink and its agronomic requirement

1.	Days to 50% flowering (DAS)	:	80-83
2.	Days to maturity (seed to seed)	:	135-140
3.	Maturity group	:	Medium
4	Plant height (cm)	:	70-80
5	Distinguishing morphological characters	:	Distinct petal colour, pale yellow turn to pink and remain pink after fading.
6.	Reaction to major pests and disease	:	Tolerant to wilt in field condition
7.	Seed colour	:	White
8.	Hundred seed weight(g)	:	3.5 – 4.0 (small)
9.	Oil content (per cent)	:	33
10.	Spacing	:	45 cm x 20 cm
11.	Plant population ha^{-1}	:	1,11,000
12.	Seed rate ha^{-1}	:	10 kg
13.	Fertilizer dose	:	25 : 25 : 0 NPK kg ha^{-1} (Rainfed)40 : 40 : 0 NPK kg ha^{-1} (Irrigated)
14.	Productivity potential	:	25 q ha^{-1}

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Manifestation of Standard Heterosis for Yield and its Components in Castor

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ABSTRACT

Standard heterosis was estimated in castor (*Ricinus communis* L.) in a set of 15 parents involving five female and ten male parents during *Kharif* 2010-11. The crosses involving AKC-1 as female parent recorded the highest standard heterosis over all the three checks GCH-4, AKC-1 and 48-1, for seed yield indicating the potential of this parent in heterosis breeding.The standard heterosis based on these standard checks viz,; GCH-4, AKC-1 and 48-1 revealed that the cross AKC-1 X OTC 30-11 exhibited highest standard heterosis over the check GCH4 (72.54%), AKC-1 (96.30%) and 48-1(71.04%) for seed yield plant^{-1}.

Castor is a non-edible oilseed crop cultivated around the world because of commercial importance of its oil. There are varied industrial applications of castor oil and its derivatives. Papova (1926) reported 42 to 58 per cent oil in castor seed whereas Li Wang (2007) reported 35 to 55 per cent oil in castor seed. The oil is mainly used as lubricant because of its property to remain liquid at very low temperatures (–32°C), high density and viscosity (18 times higher than that of any other vegetable oil). Castor oil and its derivatives have wide range of uses in the manufacture of lubricants, plastics, adhesives, waxes, polishes, coating applications, inks, paints.

Besides India, Brazil and China are the most important castor growing countries in the world. India contributes more than one third of the world production of castor oil and meets about 80 per cent world castor oil demands. Hence, castor plays an important role in Indian economy by earning valuable foreign exchange (Rs. 800 crores per annum).

The phenomenon of heterosis has proved to be the most important genetic tool in enhancing the yield of cross pollinated species in general and particularly in castor. With the availability of cent per cent pistillate lines in castor, exploitation of hybrid vigour on commercial scale has become feasible and economical (Gopani *et al*., 1968). The spectacular advancement in production and productivity of castor has been witnessed in India especially in Gujarat state which was mainly due to release of new hybrids and their adaptation by farmers.

MATERIAL AND METHODS

Five females viz., AKC-1, 48-1, DCS-9, Aruna, AKD-1crossed with ten males viz., OTC 30-11,Jorhat Local, RG 5954, RG 6301, RG 7301, KA-51, KA-57, SKP-9SKP-67, TRC-115) to produce 50 F_1's. These 50 F_1's along with three checks i.e. GCH-4, AKC-1 and 48-1 were evaluated in randomized complete block design with 3 replications at the field of AICRP for Dryland Agriculture Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during *Kharif* 2010-11.

The data were recorded for days to 50 per cent flowering, days to maturity of primary spikes, plant height, effective length of primary spikes, effective length of secondary spikes, effective length of tertiary spikes, total number of capsules, 100 seed weight, seed yield and oil content. Analysis of variance was carried out as standard^{-1} method (Panse and Sukhatme, 1954).The standard heterosis magnitudes were calculated to know the extent of heterosis.

RESULTS AND DISCUSSION

The analysis of variance for various characters under study has been presented in Table 1.The variation among the crosses was highly significant for all characters except for effective length of tertiary spikes indicating the presence of substantial amount of genetic variability for these characters.

The cross AKD-1 x SKP-9 recorded lowest number of days to 50 per cent flowering (68.33 days) followed by AKD-1 x KA-57 (70days) and AKD-1 x RG 5954 (72.67days). The cross AKD-1 x KA- 57 (119.33 days) was observed to be earliest in maturity followed by AKD-1 x RG 7301 (120.33 days) and AKD-1 x Jorhot Local (120.67days). Lowest plant height was found in the cross AKD-1 x SKP-67 (41.33cm) followed by AKD-1 x TRC-115 (52.44cm), AKD-1 x RG 7301and AKD-1 x KA 57 (60.78cm). This indicated the potential of the female parent AKD-1 in imparting earliness and dwarfness in

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Table 1. Analysis of variances for various characters

Source of variation	DF	Mean sum of squares									
		Days to 50% flowering of primary spikes	Days to maturity of primary spikes	Plant height (cm)	Effective length of primary spikes	Effective length of secondary spikes	Effective ength of tertiary spikes	Total number of capsule plant^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)	Oil content (%)
	1	2	3	4	5	6	7	8	9	10	
Replication	2	50.04**	10.59	1617.55**	50.34	1.13	40.01	4274.22**	3.80	2481.99**	4.51**
Treatments	52	85.85**	100.16**	759.35**	95.23**	15.44**	10.09	211.83**	8.79**	139.40**	18.01**
Error	104	14.77	15.53	127.64	18.23	5.69	8.84	98.37	5.85	81.57	0.03

Note:* Significant at 5% level of significance. ** Significant at 1% level of significance

castor. The cross Aruna x KA-57 recorded maximum effective length of primary spike (44.22cm) and secondary spike (22.89cm). Highest number of capsules was found in the cross AKC-1 x KA-51 (64.78). For the characters, 100 seed weight and oil content, the crosses DCS-9 x RG 6301 (29.48g) and AKD-1 x RG 6301 (53.6%) respectively were found to be promising and may be indicating the role of male parent RG 6301 in these characters. The cross AKC-1 x OTC 30-11 exhibited highest seed yield per plant (51.04g) followed by AKC-1 x KA-51 (57.16g) and AKC-1 x TRC 115 (52.19g).

Commercial exploitation of heterosis in castor is regarded as one of the major breakthrough in the field of castor improvement. Castor is highly cross pollinated crop and with the availability of 100 per cent pistillate lines, heterosis has been successfully exploited in castor and in India first castor hybrid GCH 3 (TSP-10 R x J 1) was released for general cultivation in Gujarat as early as 1968 (Gopani *et al*., 1968). The measure of heterosis over mid parent/better parent value has relatively limited importance and is of more academic interest. On other hand, the heterosis measured over the standard checks is of much practical importance.

In the present study, the existence of standard heterosis was evident and good number of crosses showed significant standard heterosis over the standard checks

Table 2. The crosses showing highest mean and standard heterosis over the checks GCH 4, AKC 1and 48-1

S.N.	Characters	Name of the cross	Mean	Standard heterosis over GCH 4	Standard heterosis over AKC-1	Standard heterosis over 48-1
1	**Days to 50% flowering of primary spikes**	AKD-1× SKP 9	68.33	-18.33	-15.64	-16.33
		AKD-1× KA 57	70.00	-16.34	-13.58	-14.29
		AKD-1× RG 5954	72.67	-13.15	-10.29	-11.02
2	**Days to maturity of primary spikes**	AKD 1 x KA57	119.33	-11.60	-7.01	-9.13
		AKD 1 x RG 7301	120.33	-10.86	-6.23	-8.37
		AKD 1 x Jorhat Local	120.67	-10.62	-5.97	-8.12
3	**Plant height (cm)**	AKD-1× SKP 67	41.33	-33.45	-50.00	-54.74
		AKD-1× TRC 115	52.44	-15.56	-36.56	-42.58
		AKD-1× RG 7301	60.78	-2.14	-26.48	-33.45
4	**Effective length of primary spikes**	Aruna× KA 57	44.22	44.19	49.05	67.95
		Aruna× RG 6301	43.44	41.65	46.43	65.00
		DCS-9× RG 7301	41.44	35.13	39.68	57.40
5	**Effective length of secondary spikes**	Aruna× KA 57	22.89	46.07	53.72	24.87
		AKC-1 × KA 57	22.33	42.52	49.99	21.84
		Aruna× KA 51	21.44	36.85	44.02	16.99
6	**Total number of capsule plant^{-1}**	AKC-1 × KA 51	64.78	52.20	74.56	51.42
		Aruna× KA 57	61.33	44.11	65.27	43.37
		Aruna× KA 51	60.00	40.98	61.68	40.25
7	**100 seed weight (g)**	DCS-9× RG 6301	29.48	27.03	28.19	27.80
		AKC-1 × OTC 30 -11	29.27	26.10	27.25	26.86
		48-1× RG 5954	29.16	25.64	26.78	26.40
8	**Seed yield plant^{-1} (g)**	AKC-1 × OTC 30-11	51.04	72.54	96.30	71.04
		AKC-1 × KA 51	46.90	58.54	80.37	57.16
		AKC-1 × TRC 115	45.41	53.53	74.67	52.19
9	**Oil content (%)**	AKD-1× RG 6301	53.60	13.78	12.20	13.34
		DCS-9× KA 57	51.40	9.11	7.60	8.69
		AKD-1× SKP 9	51.22	8.72	7.22	8.31

GCH-4, AKC-1 and 48-1 for various traits in desired direction.

The crosses showing maximum standard heterosis over the checks GCH-4, AKC-1 and 48-1 for different characters in desired direction are given in Table 2. The highest standard heterosis in desirable direction was recorded by the cross AKD1 x SKP 9 for days to maturity of primary spikes over the check GCH-4 (-18.33%), AKC-1 (-15.64%) and 48-1 (-16.33%) followed bythe cross AKD 1 x KA 57 (-16.34 % over GCH 4, -13.58 % over AKC 1 and -14.29% over 48-1). This cross AKD 1 X KA 57 also ranked first in respect of days to maturity of primary spikes with the tune of standard heterosis of -11.60 per cent over GCH 4, -7.01per cent over AKC 1 and -9.13 per cent over 48-1. For the character, plant height, the highest magnitude of standard heterosis over GCH 4 (-33.45%), AKC 1(-50%) and 48-1 (-54.74%) was found in the cross AKD 1 x SKP 67. Thus , it indicated that the female parent AKD 1 may be involved for expression of heterosis for earliness and dwarfness.

The cross Aruna x KA 57 recorded highest standard heterosis for two characters i.e effective length of primary and secondary spikes over GCH 4 (44.19% and 46.07%), over AKC 1 (49.05% and 53.72%) and over 48-1 (67.95% and 24.87%) suggesting that this cross can be utilized for enhancing pistilateness in castor. For the character, total number of capsules per plant, the cross AKC 1 x KA 51 showed highest standard heterosis over GCH 4 (52.20%), AKC 1 (74.56%) and 48-1 (51.42%) whereas for 100 seed weight, the cross DCS 9 x RG 6301 recorded maximum standard heterosis over GCH 4 (27.03%), AKC 1 (28.19%) and 48-1 (27.80%).

The yield superiority of the cross over best cultivated varieties is important and essential from commercial cultivation point of view. The checks GCH 4, AKC-1 and 48-1 were used in order to obtain the information on the superiority of the crosses over GCH 4, AKC-1 and 48-1.

The crosses involving AKC 1 as female parent expressed maximum standard heterosis indicating its potentiality for improvement of seed yield in castor. The crosses AKC 1 x OTC 30-11, AKC 1 x KA 51 and AKC 1 x TRC 115 showed highest standard heterosis for seed yield per plant over GCH 4 (72.54%, 58.54% and 53.53%) AKC 1 (96.30%, 80.37% and 74.67%) and 48-1 (71.04%, 57.16% and 52.19%).For oil content, maximum standard heterosis was found in the cross AKD 1 x RG 6301 over GCH 4 (13.78%), AKC 1 (12.20%) and 48-1 (13.34%).

The occurrence of heterosis as observed in present study has also been reported by several workers for different characters by Chaudhari, 2007, Thakker *et al*., 2005, Dangaria *et al.,* 1987 and Joshi *et al*., 2001.Relatively moderate to low heterosis for days to 50 per cent flowering and maturity observed in present investigation was also reported by Mehta *et al*. (1991)

Overall results heterosis analysis revealed the importance of the female parent AKD 1 in imparting earliness and dwarfness, Aruna for enhancing pistilatness and AKC 1 for improving the yield potential in castor.The crosses AKC 1 x OTC 30-11, AKC 1 x KA 51 and AKC 1 x TRC 115 showed maximum standard heterosis for seed yield plant^{-1} over the checks GCH 4 , AKC 1 and 48-1 and can be utilized to exploit heterosis in castor.

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Evaluation of Elite Safflower Genotype for Callus Growth Parameters and Proline Content Under *In Vitro* Saline Stress Condition

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ABSTRACT

Salinity is one of the major problems that affect plant growth and development in arid and semi arid regions. The reasons of the formation of salty soil are different climatic factors, weathearing of parental rocks, oceans and using salty water for irrigation. The investigation was conducted in order to evaluate callus growth, relative water content and proline content in different saline stress conditions using various concentrations (0, 50,100,200,300,400 mM) of NaCl medium and compared with control (un-stressed) callus medium for elite safflower genotype PKV pink. The results showed inversely proportional relationship between visible callus growth, relative water content (RWC) with different induced saline stress medium. While, proline content was progressively increased upto certain limited saline stress and further starts decline. In recent years, tissue culture based *In vitro* selection has emerged as a feasible and cost effective tool for developing stress tolerance plants. The above studied parameters are primarily useful for optimizing the *in-vitro* selection regime i.e 150 mM saline stress for callus growth. Also, the confirmation by biochemical assay i.e. proline content found to be useful in screening saline tolerance in PKV pink safflower genotype.

Safflower (*Carthamus tinctorius* L.) a member of the family *Asteraceae*, is an annual herbaceous plant growing in arid and semi-arid regions (Pahlvan *et al*.,2004). It is one of the oldest oil seed crop and researchers have suggested that it originates from eastern Mediterranean (Baydar *et al.,* 2003). Historically, Safflower has been mainly cultivated for medicinal purposes and extracting cartamin from its florests which is used for coloring foods and clothes (Knight, 2007). Spineless genotypes of safflower also used as cut flowers in Western Europe, Japan and America.

Various abiotic stresses like salt, drought, cold, etc. affect the growth and development of crop and reduce the ultimate yield. Among these, salinity is one of the major constraint limiting seed production. To cope up the adverse effects of saline, breeders are continuing to look for the genetic diversity which provide tolerance to salinity on one hand and reduce the yield on the other hand. But breeding for salinity tolerant is a slow process. So, recently many approaches have been used in selection of saline tolerance safflower genotype such as using salinity tolerant variety, simulating saline conditions in greenhouse experiments or using *In vitro* culture. In-vitro culture technique minimizes environmental variation due to defined nutrient media, controlled conditions and homogeneity of stress application Gupta et al.,2014. Such applications also enable us to study large plant populations and stress treatment not only in off season but also in limited space and short time of duration (Sakthivelu *et al*.,2008).Many researchers suggests that callus tissue could also be considered as a target materials for selection of tolerant genotypes. The *In vitro* selection technique for salinity tolerance has also been used in sugarcane (Patade *et al.*, 2006), Bermudagrass (Lu *et al.*, 2007) and Potato (Queiros *et al.,* 2007)

MATERIAL AND METHODS

Plant Material

Safflower seeds genotype i.e. PKV-Pink having oil content 33per cent were obtained from Oilseed Research Unit Dr. Panjabrao Deshmukh Agricultural University, Akola. Maharastra, India. Firstly, the seeds were washed with 1per cent Tween-20 detergent for 5 min, further sterilised in 0.1per cent Mercuric chloride ($HgCl_2$) for 10 min and rinsed in sterile distilled water. Surface sterilised seeds were then transferred to 0.5 X MS medium for germination. After 8-10 days of germination cotyledonary leaves from germinated seedlings were isolated to obtain the explant size of about 0.5-1cm^2 each.

Culture Conditions

The MS (Murashige and Skoog,1962) medium with 2,4-D and KIN (1mg L^{-1}) each with 3per cent sucrose and solidifying agent i.e., bacteriological agar at 0.8per cent was used for callus induction. The pH of the medium was adjusted to 5.8 with 1N NaOH or 1N HCl before autoclaving at 121ºC for 15 min. *In-vitro* cultures were incubated in growth room under dark condition at 25±2ºC for 3-4 weeks.

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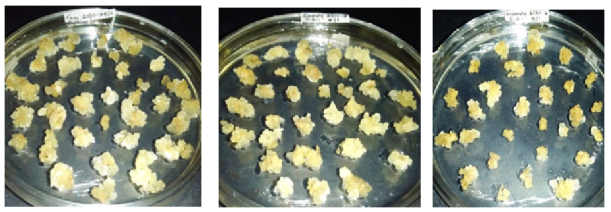
In order to investigate the response of safflower genotype to salinity stress, the four weeks old calli were subcultured on MS media containing different concentrations of NaCl (50, 100, 200, 300, 400 mM). These culture media supplemented with the same hormone combinations for callus induction. Three weeks after NaCl treatment, the visible callus growth, RWC were determined:

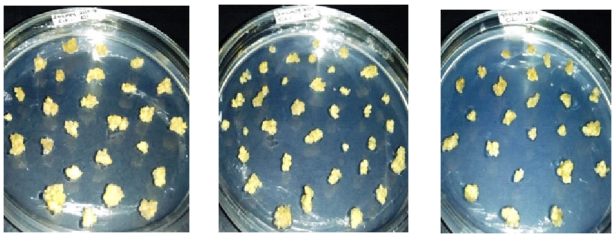
RWC= [(FW-DW)/DW]×100, whereas, FW and DW are the callus fresh and dry weights, respectively. Fresh callus samples were dried in an oven set at 50°C for 24 h and RWC was calculated by above formula (Errabi *et al.*, 2006). Proline estimation of control and stress calli was carried out by method suggested by Rahman *et al.*, 2013.

RESULTS AND DISCUSSION

The calli from unstressed media were large as compared to calli on stress medium (50, 100, 200, 300, 400 mM). The calli lost their compactness and became smaller with strong browning and necrosis with increasing NaCl concentration.(**fig** 1).



A) Control(unstress) B) 50mM C) 100mM



D) 200mM E) 300mM F) 400mM

Fig 1. The visible growth of calli on different NaCl stress medium after 3-weeks of PKV-Pink safflower genotype.

The increasing NaCl in the medium significantly brings down the weight of calli and their RWC respectively (Fig 2). The highest RWC was recorded on unstressed calli and 50mM stressed calli. Inline result of callus growth and RWC was observed by (Kakaei et al.,2013) while working on NaCl and PEG induced osmotic stress on callus growth parameters in Safflower.

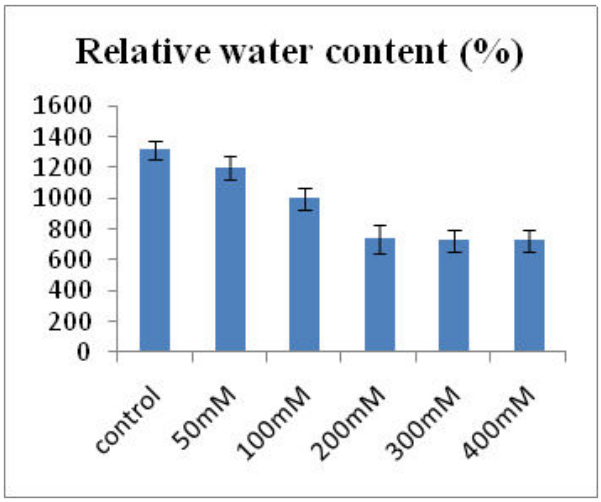


Fig 2. Graphical representation of RWC content of unstress and stress calli

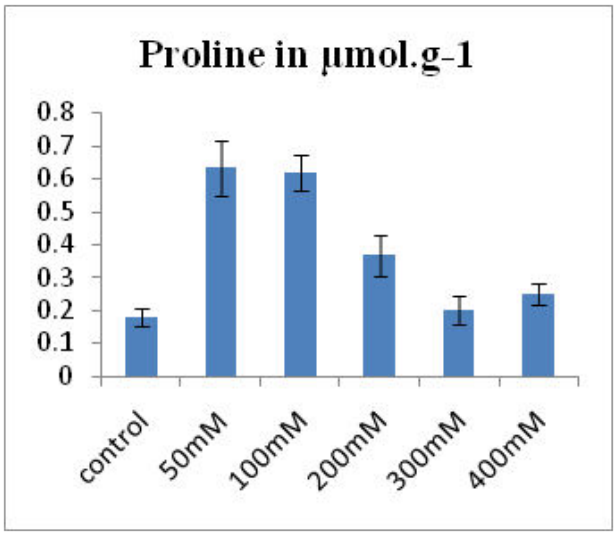


Fig 3. Graphical representation of Proline content of unstress and stress calli

Salinity reduces the ability of plants to take up water, which quickly reduces the growth rate, as well as a number of metabolic changes identical to those caused by water stress (Munns, 2002). As a consequence, salt stress often activates similar cell-signalling pathways (Shinozaki and Yamaguchi-Shinozaki, 2000). Proline is a major component for osmoregulation under stress conditions. The proline content was estimated from different salt stressed calli. Under control conditions the proline accumulation was less the accumulation was highest at 50 mM NaCl concentration followed by 100 mM further declined with increase in NaCl concentrations. Thus the results clearly indicates that salt stress has

significant effect on proline accumulation. The accumulation was higher up to 100 mM NaCl stress that might be due to stress tolerance further decreased due to break of defence mechanism. The similar finding was observed by (Rahman et al.,2013) while working on stress NaCl stress callus culture of *Datura metel* and *D. Stramoniu*.

CONCLUSION

Results of this study showed that saline stress induced by high concentrations of NaCl can significantly reduce callus growth rate, relative water content. However, calluses under high saline pressure were able to adapt to the stress, created in the culture medium up to certain levels. The long-term culture of these calli, which seem to tolerate high osmotic pressures, will allow us in further to regenerate plants with the aim of selecting lines tolerant to saline stress, and also to study the mechanism of cell tolerance to high saline pressures.

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Evaluation of Wheat Genotypes for High Temperature Tolerance Under Field Conditions

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ABSTRACT

Wheat (*Triticum aestivum* L.) is the second most important cereal crop after rice in India and the improvement in its productivity has played a key role in making the country self sufficient in food production. An experiment was carried out at the research field of Wheat Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, to evaluate the wheat genotypes for high temperature tolerance under field conditions. High temperature stress was induced by manipulation of the sowing dates. 20 promising genotypes were sown under natural field conditions on 25 th November (control-normal sown) and 25th December (high temperature stress- la te sowing).Results revealed that delayed sowing negatively affected growth attributes viz., plant height and number of productive tillers m^{-2} as compare to timely sown crop. Chlorophyll content index, relative water content were also reduced at grain filling stage under delayed sowing . Heat stress results in forced maturity of crop, by reducing the reproductive phase and development of poor sink due to shriveled grains. However, catalase enzyme activity was increased under delayed sowing. The data recorded on the above traits indicated wide range of variabity in the genotypes. Genotype AKAW-4627 was found to be heat tolerant coupled with high grain yield.

Wheat (*Triticum aestivum* L.) is the second most important cereal crop after rice in India and the improvement in its productivity has played a key role in making the country self sufficient in food production. In India alone around 13.5 million hectares of wheat is heat stressed . During past few years, more than 50per cent sowing of wheat often gets delayed till December or early January causing substantial loss in grain yield. Amongst several constraints which affects wheat productivity, delayed sowing ranks at the top as it exposes the crop to high temperature stress at anthesis / grain filling stage. All morphological, physiological, biochemical and phenological traits are affected by heat stress. Heat stress results in forced maturity of crop, by reducing the reproductive phase and development of poor sink due to shriveled and reduced number of grains.

In Maharashtra, the life cycle of the crop covers a period from October November to march April during which thermal and photo period undergo gradual changes. During vegetative phase the temperature ranges from 35.2^{0}C down to 20^{0}C maximum and 17.1 to 6.6^{0}C minimum. Under this thermal regime, the wheat plant completes its vegetative phase and switches over to reproductive phases. Important physiological changes occur during this period. Under Akola condition clear sky facilitates maximum radiation in day and rapid loss of heat in nights resulting in high diurnal fluctuations in temperature range from 35^{0}C to 17^{0}C. In wheat, mean maximum temperature during grain development between 25 to 32^{0}C is considered moderately high temperature and 35 to 40^{0}C is considered very high temperature (Stone and Nicolas, 1995). A temperature between 17 and 23^{0}C is generally recognized as the optimum range for wheat vegetative growth, whereas 0 and 37^{0}C are considered the minimum and maximum tolerable limits respectively. High night time temperature (>14^{0}C) decreases photosynthesis, spikelet fertility, grains per spike, grain size and decreased grain filling duration by 3 to 7 days and grain yield (>20^{0}C) ,decreasing yields by 3 to 5per cent per 1^{0}C increase above normal conditions (Gibson and Paulsen, 1999). The late sown wheat crop gets exposed to maximum temperature of above 35^{0}C during grain growth period, which causes yield reduction of 270 kg ha^{-1} $degree^{-1}$ rise in temperature (Nagarajan and Rane, 2002). High temperature after anthesis up to maturity adversely affects fertilization and grain development, decreases grain size due to high respiration rate and decrease in rate of starch synthesis, which reduces grain weight because of forced grain development (Stone and Nicolas, 1994). Increasing the activities of antioxidative enzymes increases tolerance of plant to stress (Sairam and Srivastava 2001, Sarkar *et al*.2001, Gratao *et al.* 2006).

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Heat tolerance is complex physiological process (Gusta and Chen, 1987) thus selecting heat tolerant genotypes based upon their physiological traits and higher yield is important. However, no single trait fully explains why some wheat varieties are able to yield satisfactorily even under stress conditions. There are several major aspects of thermo tolerance from the morphological, physiological, biochemical and phenological levels.Keeping in view above points an experiment was carried out to evaluate wheat genotypes for high temperature tolerance under field conditions.

MATERIAL AND METHODS

The experiment was carried out during *Rabi* 2010-11 and 2011-12, at Wheat Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, to evaluate the wheat genotypes for high temperature tolerance under field conditions. High temperature stress was induced by manipulation of the sowing dates. Treatment comprise of 40 combinations of two sowing dates and 20 promising genotypes of wheat. Wheat genotypes selected have different characteristics in terms of species, duration, adaptation, input requirement and morphology. Wheat genotypes were sown under natural field conditions on 25 th November (control-normal sowing) and 25 th December (high temperature stress- late sowing). Experiment was replicated thrice in split plot design assigning sowing dates in main plots and genotypes in the sub-plots, The experimental site was fairly leveled and uniform in topography. The soil of the experimental site was clayey in texture having organic carbon 0.63 per cent, available nitrogen 238.3 kg ha^{-1}, available phosphorus14.6 kg ha^{-1}, K_2O 266 kg ha^{-1}, pH 7.8, EC 0.77ds m^{-1}, field capacity 38.25per cent and permanent wilting point 17.21per cent. The experiment was carried out on the same site with same randomization during both the years and pooled data is presented in Table 1 and 2.Plant height was measured in cm from the base of the plant (ground level) to the tip of the plant excluding the awns of ear head at maturity .Tillers bearing ear heads were counted in one square meter area from the net plot of each treatment before harvesting and expressed as number of productive tillers m^{-2}. Days to anthesis were recorded by counting total number of days required from sowing to the day on which 50 per cent plants from each plot were flowered. Days to maturity were recorded at the stage when all the plants in the plot showed natural senescence and the grains become very hard. Each plots were tested by taking grains between teeth and crushed. When sound was noticed, the plot treated as matured. Total number of days from sowing to maturity were counted and expressed as days to maturity. The chlorophyll content index (CCI) of intact three flag leaves was measured by using an instrument 'CCM 200 plus Optiscience' at 60 and 75 days after sowing The observations were recorded during the day time between 11 a.m. to 14 p.m. Relative water content (RWC %) of three flag leaves was estimated by using relative turgidity technique 75 days after sowing (grain filling stage).The standard procedure given by Barrs and Weatherley (1962) was used. Enzyme catalase activity(EC 1.11.1.6) of flag leaves was estimated as per procedure given by Sinha (1972) at 60 and 90 DAS, respectively under both normal and late sown conditions. For grain weight $spike^{-1}$ (g) total numbers of grains obtained from ear heads of five selected plants were weighted on electronic balance and mean grain weight $spike^{-1}$ in gram was calculated for each treatment. Random samples of grains were drawn from each treatment net plot yield to determine1000 grain weight (g). One thousand grains were counted manually and their weights were recorded and expressed in gram. After threshing and winnowing, grain yield per net plot was recorded in kg $plot^{-1}$ and finally expressed as kg ha^{-1}. Mean maximum temperature was higher by 3.21^{0}C under late sown wheat crop (36.0^{0}C) as compared to normal sown crop (32.79) from 50per cent heading to crop maturity. Similarly mean minimum temperature was higher by 2.54^{0}C under late sown crop (17.56^{0}C) as against normal sown crop (15.02^{0}C). In respect to average temperature, 2.87^{0}C increase in temperature was found in late sown wheat crop 36/17.56^{0}C (26.78^{0}C) as against 32.79/15.02^{0}C (23.91^{0}C) temperature recorded under normal sown condition.

RESULTS AND DISCUSSION

Data presented in Table 1 indicated that plant height of wheat was reduced by 9.60 per cent due to high temperature stress induced by late sowing (86.94 cm) over normal sown (96.18 cm). Genotype AKDW-2997-16 exhibited lowest plant height (83.14 cm) and AKDW- 3931-2 the highest (111.10 cm). Lowest plant height was recorded in genotype AKDW 2997-16 in normal sown (87.22 cm) and late sown crop (79.06 cm). Decrease in plant height under late sowing may be due to inhibition cell elongation above 32^{0}C. It was reported by Allan *et al.* (1962) that temperatures above 32^{0}C reduce wheat coleoptiles length by inhibiting cell elongation. Singh and Pal (2003) reported 10per cent reduced plant height under

delayed sowing by one month under pot experiment. Mukherjee (2012), Nidhi Srivastava *et al*. (2012) also reported the similar findings. The significant variations in this character was due to their genetic potential and the environment response under normal and late sown condition at maturity. Khan *et al*.(2007) opined that decrease in plant height must have been occurred due to shortness in growth period as well as photosynthetic period because of terminal heat stress in association with late sowing. Significantly higher number of productive tillers m^{-2} (318.06) were recorded in normal sowing (25th November) as compared to late sowing (25th December) i.e., 272.68 (Table 1). High temperature stress induced by late sowing caused 14.3per cent reduction in number of productive tillers m^{-2}.Number of productive tillers m^{-2} recorded in Lok-1 (346.5), AKAW-4705 (346.42), AKAW 3997 (332), AKAW-4627 (317.76) and NIAW-34 (312.25) were significantly higher than the general mean of all genotypes (295.37). On the contrary, lowest was observed in genotype AKAW-4210-6 (270.08). The genotype AKAW 4210-6, though showed lowest number of productive tillers but showed highest grain weight spike^{-1} (g) resulted into higher grain yield ha^{-1} next to AKAW-4627. The reduced number of productive tillers m^{-2} was due to increased mortality of productive tillers occurring because of intense competition for the limited resources under high temperature stress. The tillers have to compete for the resources (assimilates and nitrogen) from elongating stem in the background of shorter crop growth duration under late sowing. Similar results were also reported by Khan *et al*. (2007), Bahar *et al*. (2008), Anonymous (2009), Kalita *et al*. (2009), Mukherjee (2012). Genotypic variations were also found in present investigation for this trait. Mukherjee(2012) stated that productive tillers considered as the most important yield determinant varied significantly under different dates and genotypes and recorded 310 productive tillers under 15th November and 208 m^{-2} under 25th December sowing respectively. Overall average days from sowing to 50per cent anthesis were 62.91(Table 1) . High temperature stress induced by late sowing exhibited 6.65 days earlier 50 per cent anthesis than normal sowing in wheat . Venkatraman and Singh (2009) reported 8 days differences and Manju Zacharias *et al*. (2010) reported 5 days difference stating that high temperature caused hastening of anthesis in wheat. Genotypes AKAW-4636, AKAW-3997 and AKDW-4021 required maximum days. Whereas, genotypes Lok-1, AKAW-4627, MACS-1967, AKAW -4210-6 and AKAW-3931-2 required minimum days for 50 per cent anthesis. The genotype AKAW-4627 recommended for late sown condition showed only 3.7per cent decrease in days to 50per cent anthesis under late sown condition during the normal sowing. This indicated the possibility of escaping nature of AKAW-4627 under high temperature regime of late sown condition, which could be a desirable phenological character of wheat for late sown condition. Significantly maximum days were required from sowing to maturity under normal sown crop (104.8 days) relative to late sown crop (92.48). High temperature stress induced by late sowing induced forced maturity by 12.32 days (11.8per cent) f as compared to normal sowing. Significantly maximum days were required in genotype AKAW- 4636 (103.33) than all the genotypes indicating long growth cycle. However, genotype AKAW-4627 (95.83) completed its life cycle in minimum days and it was followed by MACS-1967 (95.92), Lok 1 (96.33), AKDW-3931-2 (97.08), AKAW-4210-6 (97.25), AKAW-4493 (97.50) and AKAW-4739 (97.67) indicating their earliness. High temperature stress of 2.87^{0}C at post anthesis reduced the duration by 12.32 days. Parry and Swaminathan (1992) reported that an increase of 0.5^{0}C temperature resulted in decrease in the duration of wheat crop by 7 days. It would thus be seen that sowing date influence was of greater order on the post flowering period as it clearly seen by increased average temperature of 2.87^{0}C under late sown condition (36/17.56^{0}C) compared to normal sown condition (32.79/15.02 ^{0}C) during reproductive growth period from 50per cent heading to maturity. The present results are in conformity with those of Venkatramanan and Singh (2009) who stated that high day and night temperatures stress (+2.4^{0}C) affected the crop phenology by reducing days to flowering and maturity. Chlorophyll content index of flag leaves was decreased during grain growth period (at 75 DAS) under high temperature stress induced by late sowing (Table 1). At 75 DAS ,CCI was found to be significantly decreased by 3.4 per cent under late sown condition (24.29) in comparison to normal sown wheat crop (25.15). Wheat genotypes, AKDW-4021 (34.41), AKDW-4749 (34.11), NIDW-295 (31.07) had consistently registered significantly higher CCI than the general mean at 75 and 60 DAS. Significantly maximum CCI value was registered in NIDW- 295 (35.48), followed by AKDW-4749(35.61) and AKDW-4021(35.0), under late sown condition. However, minimum CCI was found in MACS-1967 (14.81) under late sown condition. Though there was reduction in CCI under late sown condition in comparison

Table 1 : Effect of sowing dates and wheat genotypes on growth, morpho-physiological and phonological traits of wheat .

S.N.	Genotypes	Plant height at maturity			Productive tillers m^{-2}			Days to maturity			Days to anthesis			Chlorophyll content index at 60 DAS			Chlorophyll content index at 75 DAS		
		N	L	M	N	L	M	N	L	M	N	L	M	N	L	M	N	L	M
1	AKDW 4021	87.95	81.13	84.54	289.17	267.83	278.50	71.83	63.50	67.67	105.50	95.50	100.50	30.96	37.59	34.27	33.81	35.00	34.41
2	AKDW 2997-16	87.22	79.06	83.14	313.33	273.50	293.42	71.50	61.83	66.67	106.33	94.00	100.17	21.43	24.58	23.01	20.24	25.68	22.96
3	AKDW 4749	88.22	80.06	84.14	289.17	253.00	271.08	71.00	62.67	66.83	104.33	91.83	98.08	31.78	35.23	33.51	32.61	35.61	34.11
4	AKDW 4750	96.80	85.67	91.23	295.33	234.50	264.92	68.67	61.33	65.00	105.17	92.00	98.58	27.08	30.89	28.98	26.97	31.00	28.99
5	AKDW 4132-3	97.86	86.39	92.13	307.83	260.0	283.92	64.00	58.00	61.00	104.67	91.33	98.00	26.95	29.73	28.34	23.36	22.10	22.73
6	AKDW 3931-2	117.03	105.17	111.10	248.00	226.50	237.25	61.83	56.67	59.25	103.17	91.00	97.08	26.54	26.45	26.50	28.10	17.73	22.92
7	HD 2189	107.61	94.94	101.28	298.00	265.00	281.50	65.50	58.50	62.00	104.50	93.33	98.92	24.25	26.60	25.42	24.31	20.59	22.45
8	NIDW 295	92.29	84.17	88.23	326.50	277.33	301.92	71.67	60.83	66.25	106.33	92.33	99.33	24.36	32.71	28.53	26.67	35.48	31.07
9	NIAW 34	98.44	86.67	92.55	338.33	286.17	312.25	61.67	57.50	59.58	102.83	91.67	97.25	26.42	26.43	26.42	23.65	20.23	21.94
10	AKAW 4627	96.83	89.83	93.33	330.34	305.17	317.76	58.50	56.33	57.42	101.00	90.67	95.83	26.10	25.04	25.57	23.15	17.30	20.23
11	LOK 1	96.00	87.89	91.95	360.00	333.00	346.50	57.33	54.00	55.67	102.17	90.50	96.33	25.38	26.25	25.82	22.04	18.54	20.29
12	MACS 1967	113.56	97.11	105.33	300.50	264.33	282.42	61.50	55.50	58.50	101.33	90.50	95.92	21.66	24.18	22.92	24.20	14.81	19.50
13	AKAW 3997	96.22	88.11	92.17	368.50	295.50	332.00	72.17	62.17	67.17	106.50	93.33	99.92	19.05	25.66	22.35	24.75	26.67	25.71
14	AKAW 4073	93.72	83.72	88.72	312.67	272.50	292.58	70.67	62.50	66.58	107.17	93.33	100.25	27.21	33.12	30.16	30.87	28.06	29.47
15	AKAW 4210-6	91.78	89.00	90.39	291.84	249.33	270.08	61.00	56.67	58.83	102.83	91.67	97.25	25.43	24.60	25.01	24.95	28.37	26.66
16	AKAW 4493	93.22	83.11	88.17	327.83	273.00	300.42	63.17	58.17	60.67	103.50	91.50	97.50	23.86	24.92	24.39	22.05	15.43	18.74
17	AKAW 4705	90.67	82.67	86.67	394.50	298.33	346.42	64.67	60.00	62.33	105.67	93.17	99.42	23.42	24.70	24.06	22.22	20.10	21.16
18	AKAW 4731	91.17	83.11	87.14	312.17	283.67	297.92	69.17	62.17	65.67	109.00	94.00	101.50	21.11	27.41	24.26	23.50	26.19	24.85
19	AKAW 4636	97.11	90.95	94.03	321.33	255.50	288.42	73.17	63.33	68.25	110.33	96.33	103.33	18.76	26.24	22.50	22.49	26.06	24.28
20	AKAW 4739	90.00	80.00	85.00	333.50	276.83	305.17	65.67	60.00	62.83	103.67	91.67	97.67	26.50	25.11	25.81	23.22	20.89	22.05
Mean (S.D.)		96.18	86.94	91.56	318.06	272.68	295.37	66.23	59.58	62.91	104.8	92.48	98.64	24.91	27.87	26.39	25.15	24.29	24.72
CD at 5%	Sowing dates		1.15			7.48			0.83			0.25			0.76			0.46	
Genotypes			2.18			14.22			0.75			0.45			1.54			2.21	
(SxG)			3.08			20.13			1.06			0.64			2.18			3.14	

to normal sowing, most of the genotypes viz., AKDW-4021, AKDW-4749, AKDW-4750, NIDW-295, AKAW-3997, AKAW-4210-6, AKAW-4731, AKAW-4636 had registered higher values under late sown condition as compared to normal sown condition during the present investigation, Table 1 indicated that chlorophyll content index of flag leaves decreased during grain growth period (at 60 and 75 DAS) under high temperature stress induced by late sowing .This may be due to loss of chlorophyll by high day temperature (35.35 to 36.87 ^{0} c) after anthesis as compared to normal sown condition(32.10 to 33.62 ^{0}c). The high temperature hastened the leaf senescence and crop maturity with squeezed reproductive phase in late sown crop. Leaf senescence is the key development state in the life of plant, and is characterized by cell death through highly regulated, genetically controlled process (Chandlee 2001), chlorophyll loss, oxidative stress (Upadhyaya *et al*., 2008). The results obtained in present investigation are in conformity with those of Rane and Chauhan (2002) , Anonymous (2009),Pandey and Srivastava (2009) and Ram *et al.*(2012). Anonymous (2009) indicated that chlorophyll content index of flag leaves was reduced under late sown condition as compared to normal sown wheat crop during grain growth period. Ram *et al.*(2012) mentioned that CCI was about 44 at anthesis and less than 10 at 20 days after anthesis. Relative water content plays a vital role in metabolic and physiological processes that are occurring in plant tissue. Table 2 indicate that RWC was found significantly higher under normal sown condition (88.90%) as compared to late sown condition (79.57%).The reduction of 10.5per cent RWC was caused due to high temperature stress induced by late sowing .Among the genotypes, variation in RWC (%) was found in the range of 78.91per cent to 88.70per cent . Significantly higher RWC was maintained in genotype AKDW-4750 (88.70 %) than the rest of the genotypes and remained at par with AKDW 4021(88.24 %). However, lowest RWC was recorded in MACS-1967 (78.9 %). Greater reduction was recorded under late sown condition by 10 per cent at 75 DAS representing grain filling stage might be due to decrease in uptake of the water from soil as well as rapid loss due to increased transpiration . Similar results were reported by Rane *et al*. (2001),Yadav and Jaiswal (2001),Almeselmani *et al.* (2009), Meena *et al.*(2011). Interaction effect was significant. Significantly highest RWC was maintained by genotype AKDW-4749 (92.52 %) and remained at par with AKDW-4021(92.29 %) and AKAW-3997 (92.01per cent) under normal sown condition .However, Lowest RWC was noticed in genotype HD-2189 (73.95 %) under late sown condition. Almeselmani *et al.* (2009) who stated that water potential was significantly reduced at anthesis, at 7 and 15 days after anthesis in wheat genotypes (susceptible to temperature and tolerant) in heat stress treatment (25/35 ^{0}c temperature stress) and greater reduction was recorded in susceptible genotype PBW-343. Saxena *et al.* (2011) reported that, relative water content was found to be high in high yielding cultivars under early and late growing condition in wheat, maintaining higher water potential . Shubhra (2005) observed lower RWC in thermo tolerant wheat genotype WH-730 as against the moderately thermo sensitive wheat variety UP-2565 under high temperature stress but the effect of high temperature stress on RWC was more severe in moderately thermo sensitive variety UP-2565 (30 %) than the thermo tolerant wheat genotype WH-730 where 6 per cent decline in RWC was noted .Further he reported that high temperature lead to 18 per cent decline in RWC of the flag leaf relative to control .

It was observed that enzyme catalase activity increased under high temperature stress induced by late sowing at heading (60 DAS) as well as near maturity (90 DAS) as compared to normal sown crop (Table 2). Genotype AKAW-4627 showed high grain yield under late sown condition maintained better values at 60 DAS(7.08) and highest value at 90 DAS(5.83) showing stable performance in average and under high temperature stress ,also indicate its tolerance capacity. At 60 DAS, catalase activity (116 %) increased significantly under late sown condition (4.24) in comparison to normal sowing (1.96). At 90 DAS,catalase activity significantly increased under late sowing (2.57) compared to normal sowing (2.38). There was increase of 8 per cent in catalase activity due to high temperature stress induced by late sowing. Similar results were also reported by Almeselmani (2006) who stated that with delay in planting in wheat there was significant increase in activity of catalase at all stages of crop growth. The tolerant wheat genotype HD-2815 showed greatest increase at all stages of plant growth. Catalase activities also associated with the scavenging of H_2O_2 and an increase in its activity is related with increase in stress tolerance (Upadhyaya *et al*., 1990, and Foyer *et al*., 1997). Present findings are in conformity with those of Renu Munjal *et al*. (2011). They recorded that wheat genotypes were subjected to high temperature stress after anthesis by late sowing and reported that high grain yield under

heat stress condition was found associated with higher catalase enzyme activity. Vanita Jain *et al*. (2011) also stated that wheat genotype Uniculum flag leaves had higher catalase activities of low N than Kalyansona (highly sensitive to low N stress), though the Kalyansona maintained higher green leaf areas. Grain weight spike^{-1} (g) was found significantly higher under normal sown condition (1.61 g) relative to late sown condition (1.44 g) in wheat (Table 2). The reduction in grain weight spike^{-1} to the extent of 10.6 per cent was caused due to high temperature stress induced by late sowing. Among the wheat genotypes tested second top ranking genotype AKAW-4210-6 in grain yield (kg ha^{-1}) has recorded significantly highest grain weight spike^{-1} of 1.82 g. However, lowest (1.2 g) grain weight spike^{-1} was recorded in Lok-1 and AKAW 4705. Genotype AKAW-4210-6 recorded highest grain weight spike^{-1} of 1.92 and 1.72 g under normal and late sowing, respectively over all the genotypes. In the present investigation, decrease in grain weight spike^{-1} under late sown condition (high temperature stress of 2.87 ^{o}C) and some genotypes was mainly due to reduction in grain number earhead^{-1} as well shriveled grain because of competition for assimilate between grains of the same ear head has been much prominent and they could not get sufficient assimilate (source limitation of grain development). However, some genotypes increased and maintained grain weight spike^{-1} under late sown conditions, the survival grains could get sufficient source potential and developed fully. These present results are in agreement with those of Spiertz (1974), Bahar *et al*. (2008), Anonymous (2009), Ercoli *et al*. (2009), Pandey and Srivastava (2009), Rane *et al*. (2009), Mukherjee (2012). Spiertz (1974) reported that with high temperatures after anthesis, increasing leaf senescence is coupled to a significant increase in the respiration rates in the grains. Such a response, depending on its extent, might trigger decreased carbohydrates availability (Thornley, 1971) justifying the decline in grain weight.1000 grain weight (g) indicated that normal sowing (41.11 g) increased 1000 grain weight as compared to late sowing (38.52 g). The high temperature stress induced by late sowing caused 6.3 per cent reduction in 1000 grain weight. Among the genotypes, significant variation in 1000 grain weight was found ranging from 33.50 to 48.13 g. 1000 grain weight of Lok-1 (48.13 g) was found significantly highest and showed parity with genotype MACS-1967 (46.76 g). Next to MACS-1967 were AKDW-4749 (45.97 g), AKDW-3931-2 (45.94 g), AKDW 4132-3 (45.78 g), AKDW-4750 (45.70 g) and NIDW-295 (42.13 g) recorded significantly higher grain weight than the mean (39.82 g). Lowest test weight was recorded in AKAW-4493 (33.50 g).Interaction effect between sowing dates and genotypes was found statistically significant for test weight of 1000 grains. Early duration genotype Lok 1 when sown under normal condition exhibited significantly highest 1000 grain weight (50.27 g) over all combinations. AKDW 3931-2 (47.83 g) and AKDW-4750 (47.34 g) were next two significantly superior genotypes after Lok-1 under normal sown condition. Whereas, under late sowing, AKDW-4132-3, one of the high yielding genotypes recorded significantly highest (46.40 g) grain weight followed by MACS- 1967 (46.38 g), AKDW-4749 (46.23 g), Lok-1 (45.98 g), AKDW-4750 (44.06 g) and AKDW-3931-2 (44.05 g). On the contrary, genotype AKAW- 3997 (34.85 g) and AKAW 4493 (30.96 g) showed lowest 1000 grain weight under normal and late sown condition respectively. All the wheat genotypes showed reduction in 1000 grain weight due to high temperature stress of 2.87 ^{0}C induced by late sowing except AKDW-4132-3 (2.8per cent) and AKDW-4749 (1.1per cent) increase in test weight under late sown condition. Genotype AKAW-4493 showed highest (14.1per cent) reduction in 1000 grain weight(table 2). . The reduction in 1000 grain weight under late sowing was mainly due to high temperature of 2.87^{0}C, reduction in grain growth period and shriveling of grains. The reduction in grain weight under late sowing and high temperature was reported by Al-Khatib and Paulsen (1984), for their he explained loss in grain weight under late sowing as a result of injury caused by high temperature during the grain development, high temperature during pre and post anthesis under field condition (Wardlaw, 2002), negative influence on the movement of photosynthetic products to the developing kernel and inhibits the starch synthesis (Bahar *et al*., 2011), reduction in growth period and shriveling of grain (Mukherjee, 2012). Dias and Lidon (2009^{a}) reported that the increasing temperature from 25/14^{0} C to 31/20^{0}C during grain growth, decreases grain size and promotes grain shrinking thus implicating a reduction of individual grain weight which was observed in present investigation under late sown condition a temperature regime of 36/17.56^{0}C.

A significant difference in the mean values for 1000 grain weight was observed between different genotypes and interaction between sowing dates and genotypes. Similar results were reported by Khan *et al*.

Table 2 : Effect of sowing dates and wheat genotypes on growth, morpho-physiological, biochemical and yield attributes of wheat

S. N.	Genotypes	Relative water content(%) at 75 DAS			Catalase activity (units g^{-1} fw min^{-1}) at 60 DAS			Catalase activity (units g^{-1} fw min^{-1}) at 90 DAS			Grain weight $spike^{-1}$ (g)			1000 grain weight (g)			Grain yield (kg ha^{-1})		
		N	L	M	N	L	M	N	L	M	N	L	M	N	L	M	N	L	M
1	AKDW 4021	92.29	84.18	88.24	0.00	12.92	6.46	1.67	4.58	3.13	1.73	1.41	1.57	37.17	34.58	35.87	4352	3729	4040
2	AKDW 2997-16	91.03	81.40	86.22	0.00	3.34	1.67	1.67	2.09	1.88	1.61	1.50	1.56	38.78	38.45	38.62	4336	3925	4130
3	AKDW 4749	92.52	80.10	86.31	2.92	3.49	3.20	1.66	2.09	1.87	1.75	1.66	1.71	45.72	46.23	45.97	4083	3914	3998
4	AKDW 4750	91.19	86.21	88.70	4.16	13.33	8.75	1.67	5.43	3.55	1.87	1.57	1.72	47.34	44.06	45.70	4504	3722	4113
5	AKDW 4132-3	91.40	79.80	85.60	0.00	2.92	1.46	3.34	2.09	2.71	1.81	1.66	1.74	45.15	46.40	45.78	4575	4020	4297
6	AKDW 3931-2	84.05	76.11	80.08	0.00	3.34	1.67	1.67	2.09	1.88	1.63	1.58	1.60	47.83	44.05	45.94	3518	3459	3488
7	HD 2189	87.28	73.95	80.62	0.00	3.33	1.67	1.67	1.67	1.67	1.64	1.31	1.47	37.57	35.74	36.65	3920	3647	3784
8	NIDW 295	90.78	82.10	86.44	2.09	3.75	2.92	3.34	2.09	2.71	1.69	1.37	1.53	42.83	41.43	42.13	4574	3823	4199
9	NIAW 34	85.84	75.45	80.64	3.34	2.09	2.71	2.50	2.09	2.29	1.39	1.39	1.39	41.32	36.20	38.76	4481	4109	4295
10	AKAW 4627	85.81	78.90	82.35	7.50	6.67	7.08	1.67	5.83	3.75	1.60	1.58	1.59	41.45	37.01	39.23	4854	4717	4785
11	LOK 1	88.22	74.60	81.41	5.42	1.67	3.54	2.50	1.67	2.09	1.34	1.06	1.20	50.27	45.98	48.13	4523	3937	4230
12	MACS 1967	81.79	76.04	78.91	1.67	2.92	2.29	3.34	1.67	2.51	1.45	1.47	1.46	47.15	46.38	46.76	3182	3140	3161
13	AKAW 3997	92.01	83.01	87.51	2.09	2.09	2.09	2.50	2.10	2.30	1.36	1.14	1.25	34.85	34.50	34.67	4655	3945	4300
14	AKAW 4073	90.55	83.21	86.88	2.50	3.34	2.92	3.34	2.50	2.92	1.73	1.35	1.54	36.42	33.39	34.90	4274	3993	4133
15	AKAW 4210-6	90.38	78.86	84.62	0.00	4.59	2.29	1.67	2.09	1.88	1.92	1.72	1.82	43.16	38.94	41.05	4570	4417	4494
16	AKAW 4493	86.01	75.06	80.53	2.92	2.92	2.92	2.50	1.67	2.09	1.37	1.11	1.24	36.05	30.96	33.50	4109	3663	3886
17	AKAW 4705	89.51	81.98	85.74	0.02	2.92	1.47	2.50	2.09	2.29	1.17	1.23	1.20	36.45	32.44	34.44	4330	3797	4063
18	AKAW 4731	90.51	81.97	86.24	0.41	4.17	2.29	3.33	1.67	2.50	1.55	1.42	1.48	36.96	34.70	35.83	3895	3759	3827
19	AKAW 4636	88.41	80.49	84.45	2.92	2.50	2.71	1.67	2.92	2.29	1.56	1.56	1.56	39.84	37.00	38.42	4088	3521	3804
20	AKAW 4739	88.53	78.04	83.29	1.25	2.50	1.88	3.34	2.92	3.13	1.64	1.44	1.54	35.93	32.08	34.01	4515	3861	4188
Mean (S.D.)		88.90	79.57	84.24	1.96	4.24	3.10	2.38	2.57	2,48	1.61	1.44	1.52	41.11	38.52	39.82	4267	3855	4061
CD at 5% Sowing dates			1.04			0.055			0.021			0.03			0.42			99.39	
Genotypes			1.49			0.114			0.043			0.11			1.65			105.32	
(SxG)			2.10			0.16			0.061			0.12			2.34			148.96	

(2007), Ahmed *et al*. (2010), Singh *et al.* (2012), Nidhi Srivastava (2012). Nidhi Srivastava (2012) stated that the temperature tolerant genotype UP-2338 showed minimum reduction (5.5per cent) in 1000 grain under late sown condition than the susceptible genotype i.e. VL 421.In respect to grain yield,it was evident that, crop sown on 25th November (normal sowing) recorded the significantly higher grain yield of 4267 Kg ha^{-1}) as compared to the crop sown on 25th December (late sowing) i.e., 3855 Kg ha^{-1} (Table 2). Grain yield ranged from 3182 to 4854 Kg ha^{-1} under normal sowing and 3140 to 4717 Kg ha^{-1} under late sowing in present investigation. The 9.7 per centreduction in grain yield under late sown condition caused due to high temperature stress of 2.87^{0}C occurred at post anthesis stage. The increase in yield under normal sowing on 25th November might be due to higher yield attributes viz., higher productive tillers m^{-2} , more grain weight $spike^{-1}$, more 1000 grain weight, more days to maturity, higher relative water content per cent., high chlorophyll content index. The early duration genotype AKAW-4627 recorded the significantly highest mean grain yield of 4785 kg ha^{-1} (normal sowing-4854 and late sowing-4717 kg ha^{-1}) among all the wheat genotypes followed by AKDW-4210-6(4493 kg ha^{-1}),AKAW-3997 (4300 kg ha^{-1}), AKAW-4132-3 (4297 kg ha^{-1}), NIAW-34 (4295 kg ha^{-1}), and Lok-1 (4230 kg ha^{-1}). Ilyas *et al.,(*2013) reported 13.6per cent decline in grain yield ha^{-1} due to late planting (2 December) compared to normal planting (15 th November). Genotypic differences in grain yield might be due to genetic potential of different varieties to express in terms yield attributing traits in differential environmental condition. Significant differences in grain yield among the wheat genotypes were also reported by Ram *et al*.(2012)

CONCLUSION

It can be concluded that ,high temperature stress negatively affected different traits resulted into 9.6 per cent yield reduction. Whereas, on the basis of enzyme catalase activity, earliness, productive tillers m^2, grain weight $spike^{-1}$ coupled with high grain yield under late sowing (high temperature stress) genotypes viz., AKAW-4627 and AKAW-4210-6 are identified as highly thermo tolerant.

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Evaluation of Fatty Acid Composition in Cotton Genotypes

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ABSTRACT

Cotton is an important fibre crop which plays significant role in Indian economy and as a by-product, cotton seed is used for extraction of edible oil. Seeds of adapted cultivars, parental lines, advance breeding lines and selected germplasm accessions of cotton were characterized for the different fatty acids. Considerable variability for fatty acid contents was observed. GCV as compared to ECV was found to be higher indicating the importance of genetic contribution towards these characters. High heritability coupled with high genetic advance was observed for Stearic acid, Arachidic acid, Myristic acid, Palmetoeic acid and Linolenic acid, indicating the possibility of improvement of these traits through selection. High heritability accompanied with high genetic gain indicates that these traits are under the control of additive gene action. Correlations were found between the several major and minor fatty acids. The results obtained indicated that breeding for a genotype with modified oil composition should be feasible but the range of variation observed within the genotypes studied was insufficient to provide useful traits for breeding. A more extensive survey of cottonseed genotypes will be needed for this purpose.

Cotton (*Gossypium* spp.) is an important fibre crop and plays a vital role as a cash crop in commerce of many countries. Cotton, also known as "King of fibres" plays a remarkable role in Indian economy.

The cotton seed, which is by product, is an important source of edible oil. Cottonseed oil is cooking oil extracted from the seeds of cotton plant of various species, mainly *Gossypium hirsutum* L. and *Gossypium herbaceum* L. Its oil is typically composed of palmitic acid (C16:0), oleic acid (C18:1), and linoleic acid (C18:2) Liu *et al.* (2002). The relatively high level of palmitic acid provides a degree of stability to the oil that makes it suitable for high-temperature applications, but is nutritionally undesirable because of the low-density lipoprotein cholesterol-raising properties of this saturated fatty acid (Cox *et al.,*1995). It also has disadvantages that have resulted in some food companies limiting their use of the oil. Specifically, the oxidative stability of cottonseed oil can be lower than for other vegetable oils because of its high concentration of linoleic acid (18:2). When used for frying, this instability accelerates the formation of off-flavors (rancidity) and shortens oil life. To compensate it, cottonseed oil can be partially hydrogenated, which reduces the level of linoleic acid (18:2) and improves the oil's stability, but the process also forms undesirable trans-fatty acids that raise serum low-density lipoprotein cholesterol levels (Sacks and Katan, 2002). Although cottonseed oil has recently been shown to lower total serum cholesterol compared with corn (*Zea mays*) oil (Radcliffe *et al.,*2001), it ensured thus by lowering the level of the desirable high-density lipoprotein cholesterol without reducing the level of the undesirable low density lipoprotein cholesterol, presumably because of its significant content of palmitic acid.

The processed cotton seed oil is the fifth leading vegetable oil in the world. Refined cotton seed oils free from phenolic compound; gossypol and it can be directly used as cooking medium. Chemical analysis showed that by and large cotton seed oil and groundnut oil have similar physiochemical properties except free fatty acids which indicate the better keeping quality of cotton seed oil. Cotton seed oilis generally considered as healthy vegetable oil. It is cholesterol free and hence termed as "Heart oil". In India nearly entire cotton seed oil being utilized for edible purposes and mostly for Vanaspati, only small quantity (5-10 %) is used for manufacturing soaps (Ashokkumar, 2006). It has high level of antioxidants (Vitamin E) that contribute to its long life in the cooking or on the shelf. Breeding for the improvement of cotton seed oil has not made much progress. Marked differences were observed in oil composition between varieties within the species. Consequently, a series of studies is underway to determine the variation that exists in fatty acid composition of cotton germplasm as we know variability must be present in character under improvement

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and to start a new breeding programme for developing cotton plants with modified oil properties. As a first step in this process, our objective was to evaluate the fatty acid variation existing in seeds of commercially acceptable cotton genotypes. The present study included 35 genotypes from germplasm, varieties and advanced breeding lines.

MATERIAL AND METHODS

Plant material

A total of 35 cotton genotypes were used for the study. Cotton seed samples from popular cultivars and parental lines (11), high yielding advance breeding lines (19) and selected germplasm accessions (5) collected from Central Institute for Cotton Research, Nagpur and Cotton Research Unit, Dr. PDKV, Akola , which were characterized for contents of fatty acid. Replicated seed samples from each of the genotype were harvested and used for estimation of fatty acid profile.

Fatty acid estimation

Randomly chosen sound mature seeds of cotton were obtained from each parent, commercially released varieties/hybrids and germplasm lines. A small portion of the distal end removed and middle portion of the seed was used for the analysis. According to Kartha (1963) and Zeile *et al.*, (1993), tissue samples from the middle sections of cotton seed gave optimal representation for fatty acid composition and iodine value (IV). Preliminary evaluation of thirty five genotypes were subjected to fatty acid analysis using a modified method of Young and Waller (1972). A brief summary of this method is as follows.

Esterification procedure (Young and Waller, 1972)

Ten seeds from each replication were taken from the genotypes and used for sample preparation. Esterification procedure involved solvent extraction and esterification of the fatty acids to form fatty acid methyl esters (FAME).

1. Seeds were ground to fine paste in mortar and pestle and about 0.25 g paste used for analysis. These cotton samples were placed in test tube to which 2 ml of petroleum ether (HPLC grade, boiling range 35-60^0 C) was added, the tubes were sealed with Teflon-lined caps, vortexed and allowed to stand overnight at room temperature for extraction.
2. The next day,2 ml of 0.5 NNaOH was added; tubes were vortexed and heated at 90^{0}C in water bath for 5 minutes.
3. After saponification tubes were cooled and 2 ml of boron triflouride in methanol (12%) (Sigma, Aldrich) was added; tubes were vortexed and heated at 90^{0}C in water bath for 5 minutes.
4. After cooling 2 ml of deionized water and 2 ml petroleum ether was added to stop the reaction. Then samples were vortexed and kept for 30 minutes, which leads to formation of two phases.
5. After phase separation, 1.5 ml of the upper phase (FAME) was removed by pipette into 2 ml screw cap glass auto sampler vials fitted with a septum and used for gas chromatography analysis.

b. Gas chromatography analysis

A gas chromatograph, model GC-2010 equipped with automatic sample injector AOC-20i, flame ionization detector (Shimadzu, Kyoto, Japan) and fitted with a narrow bore capillary column: Rtx- (film thickness-0.25µm; I.D-0.25 mm; length-30m) was used to separate methyl esters. The initial column temperature was set at 170 ^{0}C and held for 3 minutes, then programmed at an increase of 10 ^{0}C per minute to a final temperature of 230^{0}C, at which it was held for 1 minute. Injector and detector temperature were both set at 250^{0}C. The flow rates for nitrogen (carrier gas), hydrogen and air were 45, 40 and 400 ml per minute, respectively. A split ratio of 10:1 was employed and 1µl of sample was injected using an auto sampler. The fatty acid methyl ester was identified by a comparison of retention time to standard methyl ester fatty acid mixtures (Sigma, Aldrich). Concentration of each fatty acid was recorded by normalization of peak areas as per cent of particular fatty acid.

Ten fatty acids *viz*., Myristic acid (14:0), Palmitic acid (16:0),Palmetoeic acid (16:1), Stearic acid (18:0), Oleic acid (18:1), Linoleic acid (18:2), Linolenic acid (18:3), Arachidic acid (20:0), Behenic acid (22:0) andlignoceric acid (24:0). Among these, Palmitic, Stearic, Arachidic,Behenicand Lignoceric acid are unsaturated fatty acids with no double bonds in their fatty acid chain, oleic acid monounsaturated fatty acid with single double bond and linoleic acid is polyunsaturated fatty acid with two double bonds in fatty acid chain. The values in the brackets indicate the number of carbon atoms and the number of double bonds in the fatty acid chain.

Table 1. ANOVA and variability for different fatty acid in *G. hirsutum* genotype.

S.N.	Items	Myristic Acid (14:0)	Palmitic Acid (16:0)	Palmetoeic Acid (16:1)	Stearic Acid (18:0)	Oleic Acid (18:1)	Linoleic Acid (18:2)	Linolenic Acid (18:3)	Arachidic Acid (20:0)	Behenic Acid (22:0)	Lignoceric Acid (24:0)
1	Mean squares	0.016**	2.61**	0.006**	0.22**	3.34**	5.11**	0.0036**	0.003**	0.002**	0.001
2	Mean ± SE (m)	0.757± 0.023	23.784± 0.242	0.520± 0.016	2.396± 0.047	17.894± 0.118	53.894± 0.213	0.347± 0.018	0.236± 0.014	0.104± 0.019	0.067± 0.019
3	Range	0.537-0.918	21.16-26.12	0.432-0.638	1.925-3.405	15.09-20.83	51.30-57.93	0.27 - 0.47	0.17-0.32	0.03 - 0.19	0.029 - 0.113
4	CD(5%)	0.047	0.491	0.033	0.096	0.239	0.433	0.037	0.028	0.040	0.040
5	ECV (%)	4.4	1.46	4.521	2.829	0.946	0.569	7.607	8.556	26.921	42.161
6	GCV(%)	11.51	4.695	10.201	13.735	7.195	2.939	11.088	15.366	29.129	15.825
7	PCV(%)	12.32	4.91	11.15	14.02	7.25	2.99	13.44	17.58	39.66	45.03
8	h^2 (bs)	0.873	0.912	0.836	0.959	0.983	0.964	0.68	0.763	0.539	0.123
9	GA as % of mean	22.14	9.23	19.21	27.71	14.69	5.94	18.83	27.65	44.06	11.45

ECV – Environmental Coefficient of Variation, GCV – Genotypic Coefficient of Variation, PCV – Phenotypic Coefficient of Variation, h^2(bs) – Heritability (broad sense), GA – Genetic advancement at 5% selection intensity,

**, * Significant at 5 % and 1 % probability

Table 2: Genotypic correlation coefficient between different fatty acids in *G hirsutum* genotypes

Variables	Myristic Acid (14:0)	Palmitic Acid (16:0)	Palmetoeic Acid (16:1)	Stearic Acid (18:0)	Oleic Acid (18:1)	Linoleic Acid (18:2)	Linolenic Acid (18:3)	Arachidic Acid (20:0)	Behenic Acid (22:0)	Lignoceric Acid (24:0)
Myristic Acid (14:0)	**1**	**0.611**	0.245	0.114	**-0.426**	-0.179	-0.014	-0.045	-0.063	0.162
Palmitic Acid (16:0)		**1**	**0.535**	0.008	**-0.378**	**-0.459**	**-0.336**	0.017	0.057	0.123
Palmetoeic Acid (16:1)			**1**	-0.034	-0.088	**-0.354**	-0.200	0.110	0.052	0.156
Stearic Acid (18:0)				**1**	**0.453**	**-0.621**	0.146	**0.812**	**0.379**	0.255
Oleic Acid (18:1)					**1**	**-0.621**	0.085	**0.540**	0.007	-0.153
Linoleic Acid (18:2)						**1**	0.121	**-0.652**	-0.159	-0.065
Linolenic Acid (18:3)							**1**	-0.116	-0.048	0.241
Arachidic Acid (20:0)								**1**	**0.379**	0.238
Behenic Acid (22:0)									**1**	0.290
Lignoceric Acid (24:0)										**1**

Values in bold are different from 0 with a significance level at 0.05

Statistical analysis

The replication-wise data on fatty acid profile were analyzed statistically (ANOVA) and comparison of means using WINDOSTAT Ver. 7.5 statistical package (www.windostat.org), and results were tabulated. Results were compared for fatty acid profile. The Pearson correlation was used to determine relationship between different fatty acids.

RESULTS AND DISCUSSION

Variability for fatty acid profile

Availability of sufficient variability in the working collection of cotton can help in formulating breeding programmes for the development of any specific character. The ANOVA for all characters demonstrated significant variation for fatty acids due to genotypes as indicated by highly significant mean squares (Table 1) except Lignoceric acid. Good range was observed for all the fatty acid studied among the genotypes i.e.myristic acid (0.537 to 0.918), plamitic acid (21.16 to 26.12), palmetoeic acid (0.432 to 0.638), stearic acid (1.925 to 3.405), oleic acid (15.09 to 20.83), linoleic acid (51.30 to 57.93), linolenic acid (0.27 to 0.47), arachidic acid (0.17 to 0.32) and for other two i.e. Behenic acid and Lignoceric acid the range was negligible. The environmental coefficient of variation (ECV) only for Lignoceric acid was high (42.16%) as compared to Genotypic coefficient of variation (GCV), while for remaining fatty acids GCV was higher than ECV indicating the importance of genetic contribution towards these characters and scope for genetic improvement of these characters through selection.

Heritability and Genetic advance

Genotypic coefficient of variation does not give the idea of total variation that is heritable. The relative amount of heritable portion of variation can be assessed through heritability estimates. Heritability estimates give an idea about the effectiveness with which selection can be practiced for genetic improvement of a particular character based on phenotypic performance. High heritability coupled with high genetic advance was observed for Stearic acid (95.9 & 27.71%), Arachidic acid (76.3 & 27.65%), Myristic acid (87.3 & 2 2.14%), Palmetoeic acid (83.6&19.21) and Linolenic acid (68.0 & 18.83), indicating the possibility of improvement of these traits through selection. High heritability accompanied with high genetic gain indicate that these traits are under the control of additive gene action and directional selection for these traits in the genetically diverse material could be effective for desired genetic improvement.

Genotypic Correlation between different fatty acids studied

Palmitic acid was significantly positively correlated with Myristic acid (0.611) and Palmetoeic acid was found positively correlated with Palmitic acid (0.535) which indicated that selection for one character will also improve the another character at the same time. Oleic acid was significantly negatively correlated with the Myristic acid (-0.426) and Palmitic acid (-0.378), while positively correlated with Stearic acid (0.453). Linoleic acid was negatively correlated with Palmitic acid(-0.459), Palmetoeic acid (-0.354), Stearic acid and Oleic acid (-0.621). The Linolenic acid was found negatively correlated with the Palmitic acid (-0.336), while Arachidic acid showed significant positive correlation with Stearic acid (0.812), oleic acid (0.540) and negative correlation with Linoleic acid (-0.652). Behenic acid showed significant positive correlation with Stearic acid (0.379) and Arachidic acid (0.379). Positive correlation between them helps in the simultaneous improvement of these characters while negative correlation decreases the other character. Hence, breeder should select characters in combination with each other to improve the desired fatty acids. These results are in confirmation with the Lukonge *et. al.* (2007).

The genetic improvement in cotton for fatty acids is possible through selection exercised for those characters which showed high values of GCV, PCV, heritability and genetic advance. The characters such as Myristic acid, Palmetoeic acid, Stearic acid, Oleic acid, Linolenic acid and Arachidic acid indicated high heritability and high genetic advance shows that improvement is possible by selection itself while characters like Linoleic acid, Palmitic acid having high heritability with low genetic advance can be improved through heterosis breeding.

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Response of Foliar Application of Gibberellic Acid and NAA on Growth, Quality and Flower Yield in African Marigold

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ABSTRACT

A field experiment was conducted at farm of Horticulture Section, College of Agriculture, Nagpur during winter season of 2013-2014 with view to study the effect of different concentrations of GA_3 (100, 200, 300 and 400 ppm) and NAA (50,100, 150 and 200 ppm) on growth, quality and flower yield in African marigold. The result revealed that, vegetative growth *viz.,* height of plant (43.56 cm), number of branches (10.83), spread of plant at 50 per cent flowering stage E-W (24.77) and N-S (24.92) was recorded significantly maximum with treatment of GA_3 at 400 ppm, whereas, stem diameter (1.27 cm) of plant were found maximum with the treatment NAA 50 ppm. In respect of quality parameters, *viz.,* length of pedicel (7.05 cm), shelf life (4.68 days) was found maximum with the treatment of GA_3 400 ppm whereas, treatment NAA 50 ppm had produced significantly maximum weight (6.10 g) and diameter of fully opened flower (6.51 cm). Regarding yield contributing characters *viz..,* number of flowers plant^{-1}(48.66), flower yield plant^{-1} (254.00 g) and ha^{-1}(187.96 q) were recorded maximum at GA_3 400 ppm.

Marigold is mostly grown for cut flowers as well as loose flowers for making garlands or grown as bedding flowering plant in garden display. The globular shaped flowers with long stalks are used for cut flower purpose.

Now a days the use of growth regulators play an important role by increasing, reducing or modifying the physiological process within plant and which ultimately affect the growth, flowering and yield. Gibberellins and NAA fall in growth promote group of plant hormones. Gibberellic acid and NAA plays a vital role in improving the vegetative growth characters of the plants as it enhances the elongation and cell division by promoting the DNA synthesis in the cell. It reduced the juvenile phase due to increase in photosynthesis and respiration with enhanced co_2 fixation in the plant. Gibberellic acid helps to produce the good quality flower and increased flower yield in marigold. Therefore, present experiment was undertaken in order to study the effect of GA_3, NAA on growth and yield of African marigold.

MATERIAL AND METHODS

A field experiment was carried out at farm of Horticulture Section, College of Agriculture, Nagpur during *Rabi* season of the year 2013-2014.The experiment was laid out in a Randomized Block Design with three replications. The experiment comprised with nine treatment *viz.* T_1 - GA_3 100 ppm, T_2 - GA_3 200 ppm, T_3 - GA_3 300 ppm, T_4 - GA_3 400 ppm, T_5 - NAA 50 ppm, T_6 - NAA 100 ppm, NAA T_7 - 150 ppm and T_8 - NAA 200 ppm and T_9 - Control.

The African marigold variety F_1 hybrid seed was procured from local source. The seeds were sown after filling the mixture of 70 per cent cocopeat, 15 per cent l^{-1} and 15 per cent soil in protray under control condition. The seed was sown on 27 September 2013. Four week old seedlings were used by transplanting. The transplanting was done at a spacing of 45×30cm distance. A recommended dose of fertilizers *viz*., 100 kg nitrogen, 50 kg phosphorus and 25 kg potassium ha^{-1} was applied through urea, single super phosphate and muriate of potash. Half dose of nitrogen and full dose of phosphorus and potash was applied at the time of transplanting in all treatment plots and the remaining half of nitrogen was applied as top dressing after 30 days of transplanting.

Regarding treatments of GA_3 at 100, 200, 300 and 400 ppm and NAA at 50,100,150,200 ppm was prepared as per treatment concentration with distilled water just before their use. Foliar application of GA_3 and NAA was applied twice at 15 and 30 days after transplanting as per treatment. Spraying was done in the morning hours on both the surface of the leaves and apical meristem. Various observations were recorded on five randomly selected plants in each treatment plot and in each replication on various growth parameters like, height of plant, Stem diameter (cm) and branches plant^{-1} was recorded at 90 days of transplanting, spread of plant was recorded at 50 per cent flowering stage, and yield parameters like number of flower, yield of flower plant^{-1} and ha^{-1} were recorded at the time of harvesting.

RESULTS AND DISCUSSION

Growth parameters

Data from Table 1 revealed that, foliar application of gibbarllic acid, plant height (43.56 cm), number of branches plant^{-1} (10.83), spread of plant E-W (24.77 cm)

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and N-S (24.92 cm) were recorded significantly maximum under the treatment GA_3 400 ppm which was statistically at par with the treatments GA_3 300 ppm and followed by the treatments GA_3 200 ppm and GA_3 100 ppm.

As regard foliar application of NAA, plant height (38.68 cm), number of branches plant^{-1} (9.43), spread of plant E-W (22.34 cm) and N-S (22.76 cm) were recorded significantly maximum under the treatment NAA 50 ppm which was statistically at par with the treatments NAA 100 ppm and followed by the treatments NAA 150 ppm and NAA 200 ppm. However, minimum plant height (31.69 cm), number of branches plant^{-1} (8.34) and spread of plant E-W (31.69 cm) and N-S (24.68 and 24.71 cm) were recorded in control treatment.

From above results, it is showed that gibberellic acid 400 ppm and NAA 50 ppm had significantly increased vegetative parameters in African marigold. This might be due to the fact that, an application of gibberellic acid at different concentrations the growth of plant increased by increasing intermodal length and due to cell division and cell enlargement and enhancement the apical dominance. Similar results were recorded Swaroop *et al*. (2007) and Yadav *et al.* (2013) in African marigold. They reported that, GA_3 300 ppm was recorded maximum vegetative growth parameters.

Similarly, NAA plays a vital role in improving the vegetative growth characters of the plants might be due to the fact that NAA, being a member of auxin group promotes vegetatives growth by active cell division and cell elongation. Similar results were recorded by Kanwar and Khandelwal (2013) in African marigold. They reported that, NAA 200 ppm was recorded maximum vegetative growth parameters.

Yield parameters

The data from table 2 revealed that, treatment GA_3 400 ppm recorded maximum number of flowers plant^{-1} (48.66), yield of flower plant^{-1} (254.00 g) and ha^{-1} (187.96 q) which was found to be at par with the treatment GA_3 300 ppm number of flowers plant^{-1} NAA 50 ppm yield of flowers plant^{-1} and NAA 50 ppm yield of flowers ha^{-1}. However significantly minimum number of flowers plant^{-1}, yield of flower plant^{-1} and ha^{-1} were recorded in control treatment.

From above results, it is showed that gibberellic acid 400 ppm and NAA 50 ppm. This might be due to the fact that, the increase in yield and yield parameters with GA_3 spary may be due to better crop growth, more number of braches thus increased higher number of flowers plant^{-1}. Similar results were recorded Sunitha *et al*. (2007) and Kumar *et al.* (2010) in African marigold. They reported that, GA_3 200 ppm was recorded maximum yield parameters.

Quality parameters

Data from table 2 revealed that, foliar application of NAA 50 ppm recorded significantly maximum weight of flower (6.10 g), diameter of fully opened flower (6.51 cm) which was statistically at par with the treatments NAA 100 ppm and NAA 150 ppm Whereas, significantly minimum weight of flower and diameter of fully opened flower was recorded under control treatment. Application of naphthalene acetic acid noted maximum weight of flower and diameter of flower in African marigold. The increase in these floral characters might be due to the fact that NAA enhanced rate of respiration resulting in production of metabolic energy which would have been utilized by plants for cellular expansion and tissue growth resulting in the improvement on weight of flowers and diameter of flower. The results obtained in this investigation are in close agreement with the findings of Pandey and Chandra (2008) in French marigold and Kanwar and Khandelwal (2013) in African marigold. They reported that, NAA 200 ppm was recorded maximum vegetative growth parameters.

As regard foliar application of GA_3, length of pedicel (7.05 cm) and more shelf life (4.68 days) were recorded significantly maximum under the treatment 400 ppm which was statistically at par with the treatments GA3 300 ppm, GA_3 200 ppm and followed by GA_3 100 ppm and NAA 50 ppm. However, significantly minimum length of pedicel and minimum shelf life was recorded with the control treatment.

The favorable effect of GA_3 might be attributed due to that GA_3 promotes cell division and cell elongation resulting in longer pedicel length. Girisha *et al.* (2012) reported that GA_3 150 ppm recorded maximum spike length in Daisy.

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Table 1. Response of foliar application of GA_3 and NAA on vegetative growth parameters in African marigold

Treatments	Height of plant (cm)	Stem diameter (cm)	Branches plant^{-1}	Spread of plant at 50 % flowering (cm)	
				E-W	N-S
T_1 – GA_3 100 ppm	38.73	1.17	9.45	22.68	23.19
T_2 – GA_3 200 ppm	39.10	1.18	9.49	24.19	24.66
T_3 – GA_3 300 ppm	41.85	1.19	9.81	24.68	24.71
T_4 – GA_3 400 ppm	43.56	1.20	10.83	24.77	24.92
T_5 – NAA 50 ppm	38.68	1.27	9.43	22.34	22.76
T_6 – NAA 100 ppm	34.62	1.26	9.41	21.41	22.24
T_7 – NAA 150 ppm	33.56	1.21	9.26	21.22	21.42
T_8 – NAA 200 ppm	32.82	1.21	9.20	20.95	21.20
T_9 – Control (Water spray)	31.69	1.13	8.34	19.32	20.61
SE (m) ±	1.46	0.01	0.27	0.68	0.44
CD at 5%	4.39	0.05	0.82	2.05	1.32

Table 2. Response of foliar application of GA_3 and NAA on flower yield and quality in African marigold

Treatments	Number of flowers plant^{-1}	Yield of flowers plant^{-1} (g)	Yield of flowers ha^{-1} (q)	Weight of flower (g)	Diameter of fully opened flower (cm)	
Length of pedicel (cm)						
T_1 – GA_3 100 ppm	42.33	180.45	133.64	4.23	5.36	6.16
T_2 – GA_3 200 ppm	43.00	180.34	133.33	4.38	5.53	6.30
T_3 – GA_3 300 ppm	46.66	214.63	158.95	4.60	5.56	6.84
T_4 – GA_3 400 ppm	48.66	254.00	187.96	5.22	5.64	7.05
T_5 – NAA 50 ppm	41.33	252.11	186.72	6.10	6.51	6.19
T_6 – NAA 100 ppm	39.33	210.80	155.86	5.36	6.31	6.17
T_7 – NAA 150 ppm	37.33	195.60	144.75	5.24	6.20	5.84
T_8 – NAA 200 ppm	35.33	157.57	116.66	4.46	5.63	5.72
T_9 – Control (Water spray)	29.33	110.86	82.09	3.78	4.58	4.52
SE (m) ±	1.58	11.38	6.86	0.28	0.28	0.25
CD at 5%	4.76	34.13	20.57	0.84	0.85	0.75

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Significance of Herbal Garden in Conservation of Biodiversity of Medicinal and Aromatic Plants and its Utilization

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ABSTRACT

In India, there are more than 10,000 medium to large drug manufacturing units , which utilize several drug plants both from cultivation as well as wild sources as raw materials. Whereas, bulk of this raw material is obtained from forest and less than 40 medicinal plants species are under systematic cultivation. Due to extensive deforestation and over exploitation of our rich forestlands, the availability of valuable species has dwindled. Looking to the present deteriorating conditions of medicinal plants in natural forest, preservation/ conservation and propagation of left out plants have become an important task. *Ex-situ* conservation facilitates to conserve the species of high importance in controlled conditions, its reintroduction in the wild and an insight in to the basic biology of the species to work out new strategies for its conservations.

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra) has taken right initiative by establishing a herbal garden in the name of Nagarjuna (a sage at ancient times) in the year 1976 on 8.00 hectares land. At present Nagarjun Medicinal Plants Garden possesses more than 450 medicinal and aromatic plant species out of which 340 species have been registered under IC numbers allotted by NBPGR, New Delhi comprising of 84 trees, 79 perennial/shrubs, 38 creepers/ climbers, 31 bulbs/rhizomes and 76 annual/seasonal. The research work on commercial viable medicinal plant species was also under taken to develop the agro technologies and up till now 30 recommendations have been released on Periwinkle, Babchi, Khasikateri, Muskdana, Safed musli, Kalmegh, Ashwagandha, Isabgol , Shatavar, Mucuna, Aloe vera and Long pepper Palmarosa, and Lemongrass

India has one of the oldest, richest and most diverse cultural traditions associated with the use of medicinal plants. There are millions of women and elders who have traditional knowledge of herbal home remedies. Therefore, medicinal and aromatic plants ought to be given the status of a 'National Resource', because their sustained availability is essential to sustain one of the oldest medical traditions, a priceless legacy of the Indian people. Over a million practitioners of the Indian system of medicine, in the oral and codified streams use around 7500 species of plants in preventative, promotive and curative applications. There are over 10,000 herbal products and processes documented in medicinal literature. During modern times there is a tremendous resurgence of interest into "Ayurveda" and as such medicinal plants have gained new ground. Considerable information about these Medicinal plants and their active principles has accumulated over the years. The international interest in 'Alternative Medicine' has opened up new vistas in not only exploiting the already known medicinal plants but also in identifying newer active principles from plants and herbs for medicinal use.

In India, there are more than 10,000 medium to large drug manufacturing units , which utilize several drug plants both from cultivation as well as wild sources as raw materials (Anonymous, 2003). Whereas, bulk of this raw material is obtained from forest and less than 40 medicinal plants species are under systematic cultivation. Due to extensive deforestation and over exploitation of our rich forestlands, the availability of valuable species has dwindled. Looking to the present deteriorating conditions of medicinal plants in natural forest, preservation/ conservation and propagation of left out plants have become an important task.

Present Status

India with its varied soil and climatic conditions possesses rich flora that include about 2500 species accredited with virtues. Of these, about 500 to 600 plants find regular use in ayurvedic and unani system of medicine. India ranks good position in the supply of medicinal plants to the industrialized countries of the West, where demand for natural drugs/herbal products has been on the increase in recent years. Despite a diverse nature of crops grown in the country and existence of a fast growing pharmaceutical industrial sector, the share of India in world trade at present is quite insignificant considering the large geographical area. This is bound to rise with improved research input in cultivation and progressively efficient management of farm sector through

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opening of the economy. Apart from requirement of medicinal plants for internal consumption, India exports crude drugs to developed countries, viz USA, Germany, France, Switzerland, UK and Japan. The principal herbal drugs that have been finding a good market in foreign countries are Ashwagandha, Acorus, Cassia tora, Dioscorea, Isabgol, Senna, and essential oils, etc.

With ever increasing demand of natural food, pharmaceutical perfumery, flavours and cosmetic products, the cultivation of Medicinal and Aromatic Plants has now become a popular and economically viable proposition. The availability of medicinal plants is already under serious threats due to habitat degradation. It is estimated that over 500 species are being used for drug preparation by the pharmaceutical industries and around 70 per cent of plant collection involve destructive harvesting from the forest areas (Anonymous, 2000).

The plant parts used by these industries are:

1)	Roots - 29.6%	6)	Leaves	-	5.8%
2)	Whole plant - 16.3%	7)	Stem	-	5.5%
3)	Bark - 13.5%	8)	Flowers	-	5.2%
4)	Fruits - 10.3%	9)	Rhizomes	-	4.4%
5)	Seeds - 6.6%	10)	Wood	-	2.8%

The data indicating severe deforestation and over exploitation of our forest lands. In the present context of "Back to nature" in health care it is relevant that these valuable plant species are not only preserved but also their cultivation must be adopted to meet the entire demand of the domestic industries and also to exploit the bright prospects for export.

Historical perspective

There is an urgent need to understand clearly the meaning of conservation. It is defined as "The management of Human use of the biodiversity so that it may yield the greatest sustainable benefit to present generation while maintaining its potential to meet the needs and aspirations of future generations". *Ex-situ* conservation facilitates to conserve the species of high importance in controlled conditions, its reintroduction in the wild and an insight in to the basic biology of the species to work out new strategies for its conservations. It can be implemented through various techniques. (Shrivastava and Kumar, 2010). Herbal or Botanical Garden maintained by ancient herbal Doctors, healers, sages and the Royal families supported the conservation efforts where beauty of display was fully justified with the medicinal aspects. Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra) has taken right initiative by establishing a herbal garden in the name of Nagarjuna (a sage at ancient times) in the year 1976 on 8.00 hectares land. Centuries ago, Nagarjuna and his team had made possible the advent of Ayurveda Chemical era and then started the process of complete Ras preparation through tests of mercury, sulphur. Vastnabh, Hingul, Tankan, Phitkari, Kuchala (Strychinine), opium (Afim), Bhang, Dhatura and Jaiphal. Even Today, Ras medicines with less quantity are used for fast and maximum effects.

At present **Nagarjun Medicinal Plants Garden** possesses more than **450** medicinal and aromatic plant species out of which 340 species have been registered under IC numbers allotted by NBPGR, New Delhi comprising of 84 trees, 79 perennial shrubs^{-1}, 38 creepers climbers^{-1}, 31 bulbs rhizomes^{-1} and 76 annual seasonal^{-1}. The research work on commercial viable medicinal plant species was also under taken to develop the agro technologies and up till now 30 recommendations have been released on Periwinkle, Babchi, Khasikateri, Muskdana, Safed musli, Kalmegh, Ashwagandha, Isabgol , Shatavar, Mucuna, Aloe vera and Long pepper Palmarosa, and Lemongrass

All India Coordinated Research Project on Medicinal and Aromatic Plants has been implemented in the University from January 1997. Since its inception the research work on Periwinkle, Khasikateri, Babchi, Safed Musli, Ashwagandha, Muskdana, Kalmegh, Isabgol Shatavar, Mucuna, Aloe vera and Long pepper has been carried out under the technical research programmes on crop improvement, crop production and phyto chemistry. The centre has undertaken the work of overall development of Medicinal and Aromatic Plants on the following objectives.

Objectives:

1. Collection and Conservation of medicinal and aromatic plants in the garden
2. To test the possibilities of growing medicinal and aromatic plants on plains and to develop the agro technologies for their beneficial cultivation.
3. Processing technologies of Medicinal and Aromatic Plants for adoption at rural level.
4. To make awareness among farming community for non-traditional cropping in dry land agriculture, in context of diversification in agriculture.

Current Status of Research and Development

Under Maharashtra Agro climatic and soil conditions, certain medicinal plant species can

successfully be cultivated with their economic viability. Some important economic viable medicinal and aromatic plants are

1. Aswagandha (*Withania somnifera*)
2. Sonamukhi (*Cassia angustifolia)*
3. Kalmegh (*Andrographis paniculata*)
4. Isabgol (*Plantago ovata*)
5. Aloe vera (*Aloe barbadensis*)
6. Safed musli (*Chlorophytum borivilianum*)
7. Kawach bij (*Mukuna pruriens*)
8. Palma rosa (*Cymbopogan martinii*)
9. Lemon grass (*Cymbopogan flexuosus*)
10. Citronella (*Cymbopogan winterianus*)

Some of the agro technologies of medicinal and aromatic plants developed are as under

I) Ashwagandha (*Withania somnifera.* Dunal)

- Seed requirement
- Time of Harvest
- Nutritional management

II) Safed musli (*Chlorophytum borivilianum*)

- Seed Germination Studies
- Yield potential as influenced by planting material:
- Plant Geometry and Nutritional management
- Control of chlorosis
- Harvesting Period studies
- Post harvest studies
- Processing for market

III) Kalmegh (*Andrographis paniculata*)

- Planting and harvesting time
- Post harvest deterioration studies

IV) Shatavar (*Asparagus racemosus*)

- Plant Geometry and Duration
- Post harvest deterioration studies

V) Isabgol (*Plantago ovata*)

- Sowing time and seed rates
- Crop rotation
- Nutritional management

VI) Periwinkle (*Catharanthus roseosus*)

- Intercropping studies
- Feasibility of growing under partial shade of fruit orchards.

VII) Musk Dana/Musk mallow (*Abelmoschus moschatus* Medic.)

- Nutritional management

VIII) Kawach beej (*Mucuna pruriens*)

- Organic cultivation

IX) Long pepper (*Piper longum*)

- Nutritional management

X) Aloe vera (*Aloe barbedensis*)

- Crop geometry
- Nutritional Management

Major Constraints:

Proper identification of the genuine plant species and their conservation is very important, as their allies are sure to bring down the efficiency of formulations. The new interest among the drug companies in herbal preparation has precipitate greater attention and has resulted into commercial exploitation of important medicinal and aromatic plant and therefore it is also necessary to cultivate those plant species having medicinal value with such technical know how so as to maximize the production. The production technologies should emphasized on suitable cropping system, utilization of bio fertilizers, efficient management of non monetary inputs, inter cropping, crop rotation and sequence so that these crops become an integral part of the cropping system.

The major constraints experienced by the farmers are non availability of quality planting material of improved varieties, lack of development and extension support in the cultivation, processing, unorganized marketing and wide fluctuations in the market price. Research so far conducted in the various medicinal plant research centers have developed / evolved good number of high yielding varieties with better quality attributes, however, no mass production programme is being implemented which resulted into non availability of good and genuine planting material. At present, there is no regulated, controlled market available in the State and development in this regard is very important. In view of above, it is suggested to take-up cultivation on group basis, which will facilitate for assured market.

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Diversity and Abundance of Scarab Beetles from Akola Vicinity

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ABSTRACT

A survey was conducted by Department of Entomology, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola to study the occurrence and distribution of scarabaeoidea beetles in three different locations of Akola vicinity of Maharashtra during *Kharif* 2013. Scarab beetles were collected through light traps, by using net, hand picking and were preserved for further study. In Scarabaeoidea superfamily, composed of low families viz; Scarabaeidae, Hybosoridae, Trogidae and Geotrupidae were registered. Family Scarabaeidae (72.85%) added affluent fauna to the Akola vicinity followed by Hybosoridae (20.2%) and Trogidae (4.44%) while Geotrupidae (2.45%) distributed least. Amongst the subfamilies, Scarabaeinae (36.96%) found dominant, followed by Rutelinae (25.61%) and Hybosorinae (20.24%). Subfamily Geotrupinae showed least faunal contribution about 2.45%. The Shannon biodiversity index data supports the present finding. Diversity index of Scarabaeinae recored abundance in population (0.36788), followed by Rutelinae (0.34886) and Hybosorinae (0.32334). Whereas, Melolonthinae (0.1599), Cetoniinae (0.14473) and Troginae (0.13828) had moderate abundance. Geotrupinae subfamily showed lower population. However, moderate to rich Shannon biodiversity index (H|=1.57386) was noticed in terms of subfamilies of scarabs in Akola vicinity.

Coleoptera is the largest order in animal kingdom including 40 per cent of all insects and nearly 30 per centof all animal species comprises of 166 families. The members of this order are commonly known as 'beetles' include about 3, 50,000 species among which about 15,088 species are known from Indian region (Parvez and Srivastava, 2010).

The superfamily Scarabaeoidea is one of the largest superfamilyin the order Coleoptera and includes approximately 31,000 species worldwide, of which the family Scarabaeidae composed of about 91per cent of all scarabaeoids and includes about 27,800 species throughout the world. The family Scarabaeidae possesses both beneficial (Dung beetles) and harmful beetles (Thakare *et al.* 2012). Dung beetle is a common name applied to beetles in the subfamilies Scarabaeinae and Aphodiinae while most species in the subfamilies Melolonthinae, Dynastinae, Rutelinae and Cetoniinae feed on plant products and are agricultural pests of various commercial crops. The dung beetles as a whole performs a series of ecological functions such as nutrient cycling, soil aeration, seed dispersal and regulation of enteric parasites and dung breeding dipterans pests. (Chandra *et al.,*2012). Some scarabs are known to inflict considerable losses in cane yield as well as sugar output. The grubs of *Holotrichia serrata* feed on the roots and cause losses up to 40 to 70 per cent. Availability of abundant roots and adequate moisture for a longer time in sugarcane, groundnut and pea crop tend to increase the white grub build up remarkable. This is further facilitated by prevalence of host trees for adult feeding on borders of commercial crop (Theurkar *et al.,* 2013). Scarabs causes economic loss to the crops like Jowar, Bajra, Maize, Cotton, Sugarcane, Mung bean, Udid, Groundnut, Sesamum, Rala (finger millet), Bhendi, Brinjal, Pumpkin and Soybean etc. Biodiversity of insects could be summarizing with two of its components, species richness and evenness. The richness indicates the number of species present in a designated area. The information regarding the biodiversity of scarabs in Vidharbha, which too in agriculture sector is scanty. To enhance the production, new technologies developed by breeder faces the challenge of new emerging pests. Therefore, correct identification based on morphological characters of pests at least up to family and sub family level is necessary and taxonomy play an important role in this regard. The information on the activity of the specific fauna in particular agro-ecosystem is needed to generate the information on level of active fauna and its predominance in that ecosystem. With this hypothesis present investigation was carried out.

MATERIAL AND METHODS

Scarabs were collected through light traps installed at various locations of Dr. Panjabrao Deshmukh Krishi Vidhyapeeth, Akola and nearby places in study area and from field crops by using net and hand picking. These fauna were sorted out and categorized under family and subfamily level.

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A nylon mesh was fixed below the light trap for the collection of the trapped insects. Light trapped insects in the nylon mesh were collected each day, beetles were killed by Potassium cyanide or Ethyl acetate in a killing jar; pinned and dried in hot air oven, labeled appropriately and stored in the insect collection wooden showcases. For studying the distinguishing morphological characters of different specimens, stereo zoom microscope (Nikon SMZ 800) with attached Nikon camera was used. The collected fauna then categorized under different families and subfamilies with the help of taxonomic key given by Ratcliffe and Jameson, (2002). Shannon biodiversity index was calculated to analyze the abundance and diversity richness of Scarabaeids fauna. Shannon biodiversity index was worked out by the formula as below.

Pi= ni/N —— (equation-1)

***H*= - Σpi Ln pi** —— (equation-2)

n*i*= number of individuals of species "*i*"

N = total number of individuals of all species

p*i*= relative abundance of species "*i*"

S = total number of species

H' = The Shannon Diversity Index

RESULTS AND DISCUSSION

1. Collection of scarabaeid fauna

Specimens of Scarabaeoid fauna were collected from the study area of Dr. P.D.K.V., Akola during *Kharif* 2013 and Categorized into families and different sub families (Table 1). The collected Scarabaeoid fauna was composed of four families i.e. scarabaeidae, Hybosoridae, Trogidae, Geotrupidae. The members of Scarabaeidae family were further classified into Scarabaeinae, Rutelinae, Melolonthinae and Cetoniinae. Remaining three families i.e. Hybosoridae, Trogidae, Geotrupidae encontinued the members of only one subfamily each i.e. Hybosoridae, Trogidae, Geotrupidae, respectively.

Table 1. Categorization of collected Scarabaeoid fauna in Akola vicinity (2013)

Superfamily	Family	Subfamily
Scarabaeoidea	Scarabaeidae	Scarabaeinae
		Rutelinae
		Melolonthinae
		Cetoniinae
	Hybosoridae	Hybosorinae
	Trogidae	Troginae
	Geotrupidae	Geotrupinae

Table 2. Subfamily and Family wise per cent composition of Scarabaeoid fauna in Akola vicinity

S.N.	family	subfamily	Percentage (%)
1.	Scarabaeidae (72.84%)	Scarabaeinae	36.96
		Rutelinae	25.61
		Melolonthinae	5.52
		Cetoniinae	4.75
2.	Hybosoridae (20.24%)	Hybosorinae	20.24
3.	Trogidae (4.44%)	Troginae	4.44
4.	Geotrupidae (2.45%)	Geotrupinae	2.45
	Total (100%)		100

Family wise composition of scarabaeoid fauna collected from Akola vicinity

Scarabaeidae

Scarabaeidae emerged as largest family of superfamily scarabaeoidea contributing 72.85 per cent of the total Scarabaeoid fauna (Table 2). Similar results have also been reported earlier by Thakare *et al.* (2012) from Melghat Tiger Reserve. Bhawane *et al*. (2012) reported 29 species during their study under 22 genera distributed in 4 subfamilies of family Scarabaeidae. They further reported that, Scarabaeidae family i.e. grubs of *Leucopholis lepidophora*, *Holotrichia fissa, Holotrichia karschi, Holotrichia serrata, Adoretus versutus, Adoretus lasiopygus, Anomala bengale*nsis were polyphagus feeders and serious pests of Agricultural, Horticultural and Silvicultural crops. Chandra (2007 & 2012) studied faunistic records of 29 species under Scarabaeidae from Jabalpur, M.P.(India) supporting the present findings.

Hybosoridae

With 20.24 per cent of the total Scarabaeoid fauna this family found to be the second largest family of superfamily scarabaeoidea in Akola vicinity. Chandra *et al*. (2012) also studied new 29 species of two families viz. Scarabaeidae and Hybosoridae from Jabalpur, Madhya Pradesh (India) conformed the availability of Hybosoridae fauna in Central India condition.

Trogidae

Trogidae family contribute about 4.44per cent (Table 2) of total scarabaeoid fauna in study area. Earlier Grebennikov and Scholtz (2004) studied families and subfamilies of Scarabaeoidea including Trogidae and carried out morphological characterization.

Geotrupidae

2.45per cent of the total Scarabaeid fauna was represented by this family. It was reported to be the smallest family of superfamily scarabaeoidea in Akola vicinity. Similar, results were reported by Ziani and Sama (2013) from Turkey.

Family: Scarabaeidae (Plate: 1a &Plate: 1b)

Subfamily: Scarabaeinae

Maximum number of insects collected during the present study belongs to Scarabaeinae subfamily contributing to 36.96 per cent of the total Scarabaeoid fauna (Table 2) emerging as the largest subfamily of family scarabaeidae (Table 2). Similar results have been reported by Thakare *et al.* (2011) with 26 species of scarab beetles belonging to 14 genera and 8 subfamilies from Melghat area of Amravati district of Vidarbha. Scarabaeinae was the dominant subfamily with respect to species diversity (15 species).

Subfamily: Rutelinae

Subfamily Rutelinae contributed to 25.61per cent of the total Scarabaeoid fauna (Table 2). Rutelinae ranked as second largest subfamily of family scarabaeidae. More or less similar results were reported by Kumar *et al.* (2006) with thirteen species of scarabaeids on rose from different parts of Bangalore. They reported four genera under sub family Melolonthinae, three under Rutelinae and three under Cetoniinae.

Subfamily: Melolonthinae

Of the total Scarabaeoid fauna 5.52 per cent was represented by subfamily Melolonthinae (Table-2). Similar results were reported by Theurkar *et al.* (2013) from Khed Taluka (Pune) a part of Northern Western Ghats of Maharashtra, India with five major species of white grubs namely *Holotrichia consaguinea*, *H .serrata*, *H fissa*, *Leucopholis lepidophora* (Melolonthinae) and *Anomola* sp. (Rutelinae). Dadmal *et al.* (2013) reported five species of Melolonthinae from Maharashtra.

Subfamily: Cetoninae

Cetoniinae subfamily contributes about 4.75 per cent (Table 2) of total scarabaeoid fauna. These beetles were hand-picked on okra and cotton crops being typically diurnal. Taggar *et al.* (2012) reported the occurrence of chafer beetle *Oxycetonia versicolor* damaging important grain legumes such as Pigeon pea (*Cajanus cajan*) and Mung bean (*Vigna radiata*) from Punjab, India. Heavy infestation of these flower beetles at flowering stage caused considerable damage to crops. Adult beetles devour the flower, buds and reduces the number of pods that were set. Similar results were also reported by Bhatnagar (2012) who carried out survey of cetoniid pests in Rajasthan, India. He observed that adults of *Chilo lobaacuta* were found damaging the leaves of rose, the ears of sorghum (jowar), maize and the flowers and seedling of cabbage and cauliflower. Adults of *Oxycetonia versicolor* were found to be feeding on flowers of citrus, cotton, *bhendi,* ear head of sorghum, maize and flower and shoot of groundnut. Thus the present findings are in tune to the previous findings in terms of Cetoniids as a foliage and flower feeders on different field crops.

Family: Hybosoridae

Subfamily: Hybosorinae

Of the total Scarabaeoid fauna 20.24 per cent was represented by this subfamily and represents the third

largest subfamily in this vicinity. Similar results reported by Thakare *et al.* (2012). They collected thirty two species of scarab beetles belonging to twenty genera, eight subfamilies including Hybosorinae and three families under superfamily Scarabaeoidea from Melghat Tiger Reserve, Vidarbha, Maharashtra (India). Chandra *et al.* (2012) also recorded Hybosorinae from Jabalpur.

Family: Trogidae
Subfamily:Troginae

4.44 per cent of the total Scarabaeid fauna was represented by this subfamily (Table 2). Grebennikov and Scholtz (2004) studied families and subfamilies of Scarabaeoidea including Troginae and carried out morphological characterization.

Family: Geotrupidae
Subfamily: Geotrupinae

Geotrupinae subfamily contributing about 2.45per cent (Table 2) of total scarabaeid fauna in Akola vicinity found to be the least dominant group. Similar result were reported by Nuria and Fransisco (2010) who described Geotrupinae species from North and Central America (NCA), representing an average of 0.41 species per year.

3. Shannon Biodiversity Index

Shannon biodiversity index was worked out for the total collection. Calculated diversity index supports the quantitative data collection. Moderate to rich Shannon biodiversity index (H^{l}=1.57386) was noticed in terms of subfamilies of scarabs in Akola vicinity (Table 3).

Table 3. Subfamily wise Shannon Biodiversity Index of Scarabaeid Fauna in Akola Vicinity

Subfamily	pi(ln(pi))
Scarabaeinae	-0.36788
Rutelinae	-0.34886
Melolonthinae	-0.1599
Cetoniinae	-0.14473
Hybosorinae	-0.32334
Troginae	-0.13828
Geotrupinae	-0.09087
H'	**1.57386**

The data (Table 3) indicates that Scarabaeinae subfamily fauna showed abundance in population (0.36788), followed by Rutelinae (0.34886) and Hybosorinae(0.32334). Whereas, subfamily Melolonthinae (0.1599), Cetoniinae (0.14473) and Troginae (0.13828) had moderate abundance of Scarabaeid fauna. Geotrupinae subfamily showed lower population of scarabaeoid fauna. However, moderate to rich Shannon biodiversity index (H^{l}=1.57386) was noticed in terms of subfamilies of scarabs in Akola vicinity.

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Genetic Variability Created Through Biparental Mating in Early Segregating Generation of Rice

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ABSTRACT

Biparental mating was attempted in the F_2 of SYE-2001 x PKV HMT of rice (*Oryza sativa* L.). The biparental population (BIP) had higher mean performance than the F_3 self's for all the characters under study. The lower limit of range was, in general smaller for all the characters in the *biparental* population. The upper limit has also increased in the desired direction for all the characters. Sufficient high genetic variations as maintained in the BIP, for most of the characters. Biparental population also exhibited improved estimates of heritability and genetic advance.

Genetic variability is the most important pre-requisites for any successful crop improvement programme. It has been aurged that one of the reasons for failure to achieve a major breakthrough in productivity of self pollinated crops like rice is the lack of sufficient variability. The presence of large linkage blocks and inverse relations among the correlated characters are most common. Under such circumstances, conventional breeding methods such as pedigree, bulk and back cross methods again impose restriction on the chance of better recombination are also associated with the weakness of causing rapid homozygosity and low genetic variability (Cleggy *et al.* 1972). On the other hand biparental mating is expected to break linkage blocks and provide better opportunities for recombination's than the selfing series (Gill *et al.* 1973). It is also a useful system of mating for generation of increase variability and may appropriately be applied where lack of desired variation is the immediate need in the breeding programme. Though sharply differing views have been expressed on the effectiveness of biparental mating approach in self pollinated crops, it has been successfully employed in some self pollinated crops like in basmati rice. The present investigation was therefore, planned to compare the performance of biparental progenies with selfed ones with respect to creating genetic variability for yield and its contributing traits.

MATERIAL AND METHODS

Two rice genotypes SYE-2001 and PKV HMT were selected on the basis of their contrasting characteristics for productivity related features as well as reaction to blast and bacterial blight. The F_2 generation of the cross between these two lines was thus an ideal material to effect biparental mating and hence about 200 F_2 plants were selected for selective intermating on the visual basis of vigour, plant type, earliness and resistant to blast and bacterial blight. These F_2 plants used in biparental intermating were also selfed to generate F_3 progenies. The experiment was conducted at the experimental field of Agricultural Research Station, Sindewahi, during wet season, 2013. The biparental population (BIP) and their corresponding F_3 population were sown in 10 rows each in 5 meter length with 20 cm. spacing between rows and 15 cm between plants within the rows. The data were recorded on all the plants in BIP and F_3 for days to 50 % flowering, plant height (cm.), no. of panicles m^{-2}, spikelets $panicle^{-1}$, panicle length (cm.), days to maturity, 1000 seed weight (g) and yields $plant^{-1}$ (g). The mean, range and various components of variance were worked out in the biparental as well as F_3 progenies. The phenotypic and genetic coefficients of variances were computed considering the variances of non-segregating generations to be an indicative of environmental variance (V_e). Assuming the variance in segregating population (V_p) to be equal to the sum of variance due to genotype (V_g) and variance due to environment (V_e), the parameter V_g was computed by substracing mean variance of non-segregating generations from the variance of F_2. The phenotypic and genotypic co-efficient of variation (Burton and Devane 1953), heritability in broad sense (Hanson *et al*. 1956) and genetic advance (Eobinson *et al.* 1949) were also computed.

RESULTS AND DISCUSSION

The results indicated that the mean and range values of biparental progenies for all the traits were found higher than the F_3 population (Table 1). Upper limit of

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range was especially higher in BIP than the F_3 populations indicating that, the intermating has helped in releasing more variability than selfing generations by expecting breakage of linkage blocks. It may also be due to accumulation of favourable genes as BIP progenies were developed by crossing between the segregants selected on the basis of better performance. The general shifts in the value of range of expression of characters by biparental approach were also reported in chick pea by Nagaraj *et al.* (2002) and Narendra Singh (2004). It is also interesting to note that the mean performance improved considerably in respect of panicle m^{-2}, spikelets $panicle^{-1}$ and seed yield $plant^{-1}$. Superior mean performance of biparental progenies appeared to be due to better exploitation of additive and non-additive gene effects. The non-additive gene effects contributing to the expression of characters is a function of an interaction of alleles which influencing the characters. In BIP, which provide a better scope for the reshuffling of the alleles concerned would certainly help in the better exploitation of the non additive gene effect and hence results in the increase in mean performance. It also attributed to the creation of more genetic variability by breakage of undesirable linkage which otherwise conceal the genetic variation in the small size F_2 generations (*Gill et al.* 1973).The results of the present investigation are in agreement with the earlier reports on wheat (Yunus and Paroda 1983; Namatullah and Jha 1993) and chick pea (Nagaraj *et al.* 2002 and Narendra singh, 2004).

In general, the variability parameters are higher for biparental progenies than the F_3 population in respect of all the traits studied (Table 2). Higher GCV and PCV in the BIP as compared to F3 were also reported in wheat by Nanda *et. al.,* (1990) and in Chickpea by Narendra Singh (2004) and Nagarajan *et al* (2002). The phenotypic coefficient of variation (PCV) was the maximum for grain yield (34.61 and 35.21) followed by no. of spikelets $panicle^{-1}$ (22.44 and 23.26) and panicles m^{-2} (13.82 and 16.62) for F_3 and BIP population, respectively. On the other hand, 1000 grain weight, plant height, and panicle length had moderate estimates of PCV for both the populations. Similar trends were observed for genotypic coefficient of variation (GCV) for almost all the traits, though they were slightly low to PCV. Similar finding also reported in cauliflower (Kanwar and Korla 2002). The higher magnitude of GCV and PCV in BIP populations indicating more scope for selecting better segregants for the traits like grain yield, No. of spikelets $panicle^{-1}$ and panicles m^{-2}. The heritability estimates was the highest for 1000 grain weight (96.04 and 97.14), followed by grain yield $plant^{-1}$ (92.80 and 93.12), Panicle length (87.63 and 91.63), No. of spikelets $panicle^{-1}$ (86.19 and 89.89) and panicles m^{-2} (76.35 and 90.28) for F_3 and BIP population, respectively. This suggested that the variation due to environment played a relatively limited role in influencing the inheritance of these characters and thus the expected response to selection is higher in BIP. High heritability in case of BIP over F_3 has also been reported in bread wheat by Nanda *et al* (1990) and in Chickpea by Narendra singh (2004) and Nagarajan *et al* (2002).

Among the characters studied, panicles m^{-2} and spikelets $plant^{-1}$ (109.14 and 72.01, respectively) showed higher genetic advance, indicating that, the gain from selection based on these two traits would be higher in biparental progenies than in their corresponding selfed progenies. This is further supported by the wider range of expression and that too in the desirable direction in BIP as mentioned earlier. High heritability accompanied with

Table 1. Mean and Range of expression in respect of various quantitative traits in intermated (BIP) and selfed (F_3) population of rice

Characters	Mean ± SE		Range	
	F_3	Biparental population	F_3	Biparental population
Days to 50%flowering	103 ±1.89	110.68 ± 4.02	99-112	96-114
Plant height (cm.)	106.21 ± 4.56	110.68 ± 4.02	98.33-115.0	95.33-118.67
Panicles m^{-2}	246.72 ± 9.53	275.40 ± 8.23	201-279.67	197.0-324.67
No. of spikelets $panicle^{-1}$	114.17 ± 5.84	130.45 ± 5.56	90.0-145.67	84.67-156.33
Panicle length (cm)	28.19 ± 0.44	29.10 ± 0.65	24.87-30.40	24.30-32.03
Days to maturity	137 ± 0.93	139 ± 1.01	134-139	133-142
1000 grain weight (g)	17.84 ± 0.30	21.54 ± 0.32	17.40-22.93	17.0-24.1
Grain yield (g) $plant^{-1}$	14.65 ± 0.78	17.62 ± 0.93	9.75-20.64	8.70-22.07

Table 2. Estimates of genetic variability parameters of eight quantitative traits in F_3 and BIP population of rice

Character	Population	GCV (%)	PCV (%)	h2 (bs) (%)	GA (% as mean)	Genetic gainas % of mean
Days to 50% flowering	F_3	5.50	6.34	75.26	13.12	11.38
	BIP	7.08	7.81	82.20	17.98	16.30
Plant height (cm.)	F_3	7.04	10.19	47.78	3.78	9.53
	BIP	9.15	11.12	67.82	22.03	18.14
Panicles m^{-2}	F_3	12.08	13.82	76.35	68.47	59.83
	BIP	15.79	16.62	90.28	109.14	103.28
No. of spikelets $panicle^{-1}$	F_3	20.64	22.44	86.19	62.02	57.58
	BIP	22.05	23.26	89.89	72.01	68.28
Panicle length (cm)	F_3	9.11	9.51	87.63	6.49	6.21
	BIP	10.41	11.12	91.63	7.48	7.00
Days to maturity	F_3	1.77	2.13	68.79	5.28	4.38
	BIP	2.03	2.39	72.16	6.35	5.39
1000 grain weight (g)	F_3	12.92	13.19	96.04	6.63	6.50
	BIP	15.42	15.65	97.14	8.64	8.52
Grain yield (g) $plant^{-1}$	F_3	33.40	34.61	92.80	12.42	11.97
	BIP	34.00	35.21	93.12	15.25	14.72

low genetic gain was found for panicle length and days to maturity, indicating that, these traits is more likely under the control on non-additive gene action and selection for these traits would be less effective. Rest of the traits had moderate to high heritability with low genetic gain, indicating the influence of environment on these traits. The comparison of biparental mating and selfing shows that, additional variability realized with biparental mating in the early segregating generation is probably brought about by rare recombination between linked loci. In addition to this, it is also expected to help in maintaining a greater variability for selection to be effective for longer period in crops like rice where lack of variability has been implicated as one of the important causes for limited progress. Hence, the use of biparental mating in early segregating generation (F_2) of an appropriate cross could be of much use in widening variability and consequently in making considerable gains in improving productivity.

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Genetics of Fertility Restoration of "Wild Abortive" Cytoplasmic Male Sterility in Rice

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ABSTRACT

The availability of stable cytoplasmic male sterility and fertility restoring system is vital for commercial exploitation of heterosis in rice. Inheritance study using two effective fertility restorers (IR-72 and VDN-12-12) and one cytosterile source (IR58025A), their F_2 and BC_1 populations revealed that the fertility restoration was governed by two independent genes, one of which appeared to be stronger in action than other. Cross IR58025A x IR72 showed segregating ratio of 9:6:1 and 1:2:1 in F_2 and BC_1 generations, respectively, for spikelet fertility indicating two major genes with epistasis and incomplete dominance. While, cross, IR58025A x VDN-12-12, exhibited the restoration pattern fitted well in a segregation ratio of 12:3:1 and 2:1:1 in F_2 and BC_1 generations, respectively, for spikelet fertility indicating two major genes with dominant epistasis. Change in fertility restoration by different restorer lines with the same CMS line could either due to cytoplasmic genetic interactions of CMS line and fertility restoring genes or may be affected by modifier genes.

Hybrid rice technology offers a potentially viable option for increasing rice (*Oryza sativa* L) yield potential beyond the level of inbred high-yielding varieties by exploiting heterosis, or hybrid vigor, on a commercial scale. Hybrid rice varieties have clearly shown a 1–1.5 t/ha (20–30%) yield advantage over conventionally bred modern varieties in farmers' fields in China (Lin and Yuan 1980) and outside China (Yuan and Virmani, 1988). Cytoplasmic male sterility (CMS) combined with a fertility restoration system has been found to be the most efficient genetic tool in commercializing this technology in rice (Lin and Yuan 1980; Virmani and Wan 1988). CMS is a maternally inherited trait characterized by the inability of a plant to produce functional pollen that is associated with abnormal open reading frames (ORFs) found in mitochondrial genomes and, in many cases, male fertility can be restored by fertility restorer (*Rf*) genes associated with nuclear genes encoding pentatricopeptide repeat (PPR) proteins (Chase and Babay-Laughnan 2004; Hanson and Bentolila 2004). The discovery of cytoplasmic male sterility (CMS) not only facilitates hybrid seed production, but also provides an excellent system for the study of nucleus cytoplasm interaction. High yield potential of CMS derived F1 hybrids depends upon their high pollen fertility and spikelet fertility, which determined by the number and mode of action of restorer genes present in their restorer parent. The inheritance of fertility restoration in the wukd abirtuve (WA) CMS system has been extensively investigated. A majority of studies reported digenic inheritance with two independent genes (Zhou, 1983; Young and Virmani, 1984; Virmani *et al*., 1986; Govinda Raj and Virmani, 1988; Bharaj *et al*., 1991; Teng and Shen, 1994) and the chromosomal locations of the two *Rf* genes (*Rf3* and *Rf4*) have also been determined. Zhang *et al*. (1997) mapped the *Rf3* gene using restriction fragment length polymorphism (RFLP) on chromosome 1. Yao *et al*. (1997) identified two *Rf* loci on chromosomes 1 (*Rf3*) and 10 (*Rf4*) and showed that the effect of *Rf4* is larger than that of *Rf3*.

Knowledge of the genetic control of male fertility restoration and extent of fertility restoration facilitates, transfer of fertility restorer genes to promising breeding lines and undertake improved restorer breeding programme and ultimately their deployment in hybrid breeding programme. In the present investigation, involving two crosses *viz*., IR58025A x IR72 and IR58025A x VDN12-12 was undertaken to understand the genetics of fertility restoration of CMS line of WA cytoplasm.

MATERIAL AND METHODS

In the present investigation, one CMS line, IR58025 A and two restorer lines, IR72 and VDN-12-12 were used in the study. The CMS line, IR58025A inherited "WA" cytoplasm imparting male sterility. The restorer lines, IR 72 and VDN-12-12 were crossed with the cytoplasmic male sterile line IR58025A during Kharif 2011. The two fertile F_1s *viz*., IR58025A x IR72 and IR58025A x VDN-12-12

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were selfed as well as backcrossed to female parent (IR58025A) to generate F_2 and BC_1 populations. Twenty five grams of F_2 seed each of the entire two cross combinations were sown and more than 250 population of F_2 was raised. Seedlings of the parental, $F_1$and F_2 were transplanted 20 x15 cm apart using single seedling hill^{-1}. Two panicles of each plant in parental, $F_1$and F_2 were bagged at panicle emergence to avoid out crossing. The bagged panicles of individual plants were separately harvested at maturity and fertile and sterile spikelets were counted and percent spikelet fertility was worked out. The F_2 progeny of two cross combinations *viz*., IR58025A x IR72 and IR58025A x VDN-12-12, along with their parents, F_1^s and BC_1 were evaluated during Kharif 2012 at Agriculture Research station, Vadgaon Maval, District Pune. Spikelet fertility per cent was used as the main criteria for the evaluation of fertile and sterile plants.

For spikelet fertility, plants were classified into fully fertile, partial fertile, partial sterile and complete sterile groups according to the classification proposed by Virmani *et al.* (1997). The plants showing > 75 per cent seed setting were grouped under complete fertile, 50.1 to 75 per cent under partial fertile, 0.1 to 50 per cent under partial sterile and 0 per cent seed setting under complete sterile group.

To enable Chi-square analysis, partially fertile and partially sterile plants were pooled together to make a single category as semi- fertile which is then fitted to different types of interactions (Govinda Raj and Virmani, 1988). The data, thus generated, were subjected to chi-square test. Chi-square is a test of significance to test the goodness of fit between observed values and expected values based on hypothesis.

RESULTS AND DISCUSSION

The spikelet fertility data on the parents and hybrids indicated that all the F_1 plants were completely fertile and identical to the restorer lines (male parent. The spikelet fertility of male parents, hybrids and their F_2^s is given in Table 1. Both the cross combinations showed more than 80 per cent spikelet fertility (Table 1).This indicated that restoration of fertility in the F_1^s was inherited as a dominant trait.

In the present study, both F_2 and backcross plants derived from respective crosses were grouped into fully fertile (FF: 76-100% fertility), partially fertile (PF: 50.1–75%), partially sterile (PS: 0.1–50%) and completely sterile (CS: 0 %) based on their spikelet fertility. The segregation pattern in both the F_2 populations showed continuous variation in spikelet fertility ranging from 0 to 100 per cent.

In F_2 progenies of cross IR58025A x IR72 as suggested in earlier reports (Govinda Raj and Virmani 1988), partially fertile and partially sterile plants were pooled together to make a single category as semi fertile which is then fitted to 9:6:1 and 1:2:1 for F_2 and BC_1 populations respectively. The observed ratio (137:98:15) of fertile [includes fully fertile (FF); partial fertile (PF); partial sterile (PS)] to completely sterile (CS) individuals did not differ significantly from 9(fertile):6(semi fertile):1(sterile) ratio ($\div^2$=0.310) revealing the role of two dominant independent genes in the inheritance of fertility restoration and displayed epistasis with incomplete dominance interaction. This was also confirmed from the segregation behaviour of the test-cross (BC_1) progenies (1:2:1) (Table 2).It seems that the restoration ability of IR72 is governed by two independent major genes.

The cross IR58025A x VDN-12-12 segregated in F_2 generation in the ratio of 12 fertile: 3 (partially fertile + partially sterile): 1completely sterile plants. The test cross (BC_1) data also confirmed the above results showing the segregation of fertile, partial fertile/sterile and completely sterile in the ratio of 2:1:1 (Table 2). Thus, the results indicated the involvement of two dominant genes in the inheritance of fertility restoration, which exhibited epistasis with dominant interaction.

Segregation behaviour for number and nature of genes controlling the fertility restoration using spikelet fertility analysis in F_2 and BC_1 showed that the fertility restoration in these two genotypes are governed by two independent dominant genes, one of which is stronger in action than the other. The effect of one of the two genes in restoring fertility appears to be stronger than the other, because the presence of one of the genes alone conferred partial fertility (Bharaj *et al*., 1991; Bharaj *et al*., 1995; Virmani *et al*. 1997; Yograj *et al*., 2002 and Sharma and Singh, 2003). But the mode of interaction of the genes, however, varied among crosses (Table 3). The presence of one of them conferred semi-sterility, although the two genes appeared to have additive effects in imparting the fertility restoration. Similar results were reported earlier using different restorer lines (Sohu and Phul, 1995; Ramalingam *et al*., 1992). It could be assumed that *Rf3* and *Rf4* were the dominant alleles of the two restorer genes

Table 1. Percent of spikelet fertility in male parents, hybrids and their F_2 populations of rice

Crosses	Spikelet fertility %		
	Male parent	Hybrids	F_2
IR58025A/IR72	88.60	84.65	70.13
IR58025A/VDN-12-12	88.64	84.25	65.45

Table 2. Segregation pattern for fertility restoration (spikelet fertility) in different populations (F_2 and BC_1)

S.N.	Cross combinatons	Generation	Total no. of plants	Segregation pattern				(FF): (PF+PS) :CS	Genetic ratio	X^2	X^2 table value
				FF	PF	PS	S				
1	IR58025A/IR72	F_2	250	137	67	31	15	137:98:15	**9:6:1**	0.310	5.991
		BC_1	145	37	32	43	33	37:75:33	**1:2:1**	0.379	5.991
2	IR58025A/VDN-12-12	F_2	250	178	42	16	14	178:57:15	**12:3:1**	3.290	5.991
		BC_1	150	83	20	18	40	83:38:40	**2:1:1**	1.025	5.991

FF = fully fertile, PF = partially fertile, PS = partially sterile, CS = completely sterile
Spikelet fertility reaction: CS = 0 %; PS = 0.1 to 50 %; PF = 50.1 to 75 %; FF = 76 – 100 %
(PF and PS were merged in to one group (semi fertile) to enable Chi-square analysis)

Table3. Proposed genetic constitution of F_2 segregants in different crosses

S.N.	Crosscombinations	Segregation pattern		
		FF	SF	CS
1	**IR58025A/IR72**	**9** *Rf3— Rf4—*	**3** *Rf3— rf4rf4* **3** *rf3rf3 Rf4—*	**1***rf3rf3 rf4rf4*
2	**IR58025A/VDN-12-12**	**9** *Rf3— Rf4—* **3** *Rf3— rf4rf4*	**3** *rf3rf3 Rf4—*	**1** *rf3rf3 rf4rf4*

Table 4. Gene interactions shown by F_2 segregants in different crosses

S.N.	Crosscombinations	Gen.	(FF):(PF+PS):CS	Genetic ratio	Gene interaction
1	IR58025A/IR72	F_2	137:98:15	**9:6:1**	Epistasis with incomplete dominance
2	IR58025A/VDN-12-12	F_2	178:58:14	**12:3:1**	Epistasis with dominance

and the plants having dominant alleles of the genes in homozygous or heterozygous condition (*Rf3-Rf4*) were fully fertile. The plants having dominant alleles of one of the two genes in homozygous or heterozygous condition but homozygous recessive alleles of the other gene (*Rf3_Rf4Rf4* or *Rf3Rf3Rf4_*) were partially sterile or partially fertile, and vice versa. The plants homozygous for the recessive alleles of both the genes (*rf3f3rf4rf4)* were completely sterile (Table 3). Zhang *et al*. (1997) and Yao *et al*. (1997) designated the fertility restoration locus in chromosome 1 as *Rf3*. The second *Rf* locus in chromosome 10 was designated as *Rf4* for WA-CMS system by Yao *et al*. (1997) and Jing *et al*. (2001).

The results revealed that F_2 population of the first two crosses *viz*., IR58025A x IR72 and IR58025Ax VDN-12-12 exhibited a segregating ratios of 9 (fertile) : 6 (partially fertile + partially sterile): 1(completely sterile

plants) and 1 (fertile) : 2 (partial sterile/fertile) : 1 (sterile) and 12 (fertile) : 3 (partially fertile + partially sterile): 1 (completely sterile plants) and 2(fertile): 1(partial sterile/ fertile) : 1 (sterile)in F_2 and BC_1 generations respectively, for spikelet fertility indicating two major genes displaying epistasis with incomplete dominance and dominant epistasis gene interaction governing the fertility restoration in these two crosses.

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Stability Analsis in Local Lines of Lathyrus for Yield and its Components

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ABSTRACT

Evaluation of five lathyrus genotypes NLK-40, NLK-48, NLK-73, NLK-36 and NLK-5 along with three checks Ratan, Mahateora and Pratik was carried out over three seasons in the experimental farm of Botany Section of *Rabi* 2010-12, College of Agriculture, Nagpur with the objective to now the existence of genotype x environment (Gx E) interactions for seed yield plant^{-1} and their component traits. Mean squares due to genotypes differed significantly for days to 50 per cent flowering, days to maturity, plant height, no. of pods plant^{-1} and seed yield plant^{-1}. Environments in which the genotypes were grown also differed significantly for no. of pods plant^{-1} and seed yield plant^{-1}. Variance due to G x E interactions was highly significant for days to 50 per cent flowering, no. of pods plant^{-1} and seed yield plant^{-1} indicating the differential response of genotypes in expression of the characters to varying environments. Predictable component of environmental variations prevailed for no. of pods plant^{-1} and seed yield plant^{-1}. Stability analysis revealed that NLK-5 and NLK-40 were identified as the stable genotypes other than the check Ratan, Mahateora, Pratik which were identified to be suitable for growing over all the environment.

Lathyrus is an important pulse crop and considered as a model crop for sustainable agriculture. The cultivation as a model crop for sustainable agriculture. The cultivation of lathyrus is predominant in India, Bangladesh, Ethiopia and Nepal. In India, its cultivation is mainly confined to states of U.P, Bihar, West Bengal, Madhya Pradesh, Chattisgarh, Maharashtra and also in small pockets of other states. It is a very sturdy crop with a deep penetrating root system and can be grown on a wide range of soil types. The importance of this crop as a pulse is due to its high seed protein content (28%) as reported by Mehta, 1991. Sharma and Padmanabhan (1969) analyzed and reported that the protein quality of lathyrus seed is better than any other pulse crop. When other crops fail, lathyrus often becomes the principal food source for the poor. Indeed, it may be the only source of food available during drought and famine. However, eating large amount of lathyrus can cause "neurolathyrism" an irreversible paralysis of the lower limbs. Lathyrus varieties generally have low yield potential, poor plant type and high neurotoxin content which is unstable over environment (Ramanujam *et al.* 1980).

As cultivation of lathyrus in India is predominately in paddy track under utera condition, both biotic and abiotic stresses determine the yield and also expression of component traits like no. of pods plant^{-1}. The information pertaining to the role of genotype x environmental interactions (G x E) in the inheritance of pod yield and its related traits is almost negligible in lathyrus. In view of this there is need to identify genotypes having stable yield across the environments with desirable characteristics. Therefore, an attempt has been made in the present study to evaluate different local lines of lathyrus along with the cultivated varieties across the seasons to know the role of G x E interactions and also to analyze the stability of genotypes for different traits.

MATERIAL AND METHODS

The experimental material consisted of five local lines of lathyrus (NLK-40, NLK-48, NLK-73, NLK-36 and NLK-5) along with three cultivated varieties (Ratan, Mahateora and Pratik). A field experiment involving all the genotypes was laid out in a Randomized Complete Block Design with three replication during three different seasons viz., *Rabi* 2010, 2011 and 2012 at experimental farm of Botany Section, College of Agriculture, Nagpur. The experimental crop was raised by adopting a suitable spacing of 30cm x 10cm and normal dose of fertilizers ie. 20:40:20 NPK and all agronomic practices were followed. Observations were recorded on five randomly selected plants for days to 50 per cent flowering, days to maturity, plant height (cm), no. of branches plant^{-1}, no. of pods plant^{-1} and seed yield plant^{-1} (g). Data collected was subjected to a two-way analysis of variance and the stability parameters were computed following the model proposed by Eberhart and Russell (1966).

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RESULTS AND DISCUSSION

Analysis of variance (Table 1) for seed yield and its component traits revealed that the genotypes differed significantly for all the characters except no. of branches plant^{-1} indicating the presence of variability in the material. Similarly environments in which the genotypes were grown were also differing significantly for no. of pods plant^{-1} and seed yield plant^{-1}. Variance due to G x E interactions was highly significant for days to 50 per cent flowering, no. of pods plant^{-1} and seed yield plant^{-1} indicating the differential response of genotypes in expression of the characters to varying environments. The existence of G x E interactions for pod yield and its important component traits has also been reported by Verma *et al*. (2011), Kamaluddin *et al*. (2012) in soybean and Nath *et al*.(2013) in mungbean.

The mean square for genotypes x environments (linear) is found to be significant for all the traits except for no. of branches plant^{-1} which indicates that variation in the performance of genotypes is due to the regression of genotypes on environments and hence the performance is predictable in nature. Considering the stability of performance of genotypes for different characters across the environments, it was observed that the variances due to non linear component of environments (pooled deviations) was non significant for seed yield and its components indicating the role of predictable portion of environment influencing this trait. In contrary to this result the importance of predictable and unpredictable components were involved in determining interaction of the genotypes with environment were reported by Nath *et al*. (2013) in mung bean.

According to Eberhant and Russell (1966), an ideally adopted variety would be the one having high mean value, unit regression coefficient (b = 1.0), and a deviation from regression as small as possible. Mean values, regression coefficient and deviation from regression S^2di for eight genotypes are given in Table 2. The deviation of each genotype from its regression when tested by an appropriate F test were found to be non significant for all the eight genotypes for all the traits studied. S^2d is non significant for all the genotypes and for all the traits studied. Seed yield plant^{-1} and no. of pods plant^{-1} were considered for selecting stable genotypes as these two traits recorded G x E as compared to other traits. The three check varieties Ratan, Mahateora, Pratik and

Table 1. Pooled analysis of variance for stability of seed yield plant^{-1} and their components

Source of variance	d.f	Mean sum of squares					
		Days to 50% flowering	Days to maturity	Plant height	No. of branches plant^{-1}	No. of pods plant^{-1}	Seed yield plant^{-1}
Genotypes	7	29.4583**	4.0503**	22.8247*	0.1739	40.6455**	1.9918**
Environment	2	18.0556	11.1667	61.5741	0.2269	229.4074**	3.3084**
GxE	14	8.7857**	1.2566	9.0767	0.1898	11.4550**	0.3598*
Environment (Linear)	1	12.0370	22.3333	123.1481	0.4537	458.8148	6.6168
G x E (Linear)	7	5.6325**	2.1991**	14.9490*	0.2099	20.2446*	0.6853**
Pooled deviation	8	0.1966	0.2749	2.8039	0.1485	2.3322	0.0300
Ratan	2	0.3077	0.0597	0.3511	0.0000	0.3588	0.0010
Mahateora	2	0.0534	0.1659	0.2707	0.0142	0.1066	0.0058
Pratik	2	0.1047	0.0203	0.1105	0.1639	1.7762	0.0108
NLK-40	2	0.0193	0.1497	0.0301	0.1276	0.1357	0.0238
NLK-48	2	0.1368	0.0701	4.4520	0.0363	0.7133	0.0038
NLK-73	2	0.0086	0.3732	2.2158	0.0000	0.4341	0.0027
NLK-36	2	0.1368	0.0017	2.7621	0.1837	2.3789	0.0049
NLK-5	2	0.0193	0.2591	1.0234	0.0686	3.4256	0.0677
Pooled Error	48	1.0972	0.6713	4.8981	0.1296	3.8426	0.1482

* and ** indicates significance at 5% and 1% probability levels, respectively

Table 2. Stability parameters for seed yield plant^{-1} and their components in lathyrus

S.N.	Genotypes	Days to 50% flowering			Days to maturity			Plant height		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	Ratan	49.00	2.2154**	0.48	87.67	0.9552**	-0.5519	37.00	1.9218**	-4.1960
2	Mahateora	45.55	4.276**	-0.99	87.89	1.5920**	-0.3396	37.44	0.2045	-4.3568
3	Pratik	50.00	0.0923	-0.88	89.22	-0.1095	-0.6307	40.22	2.6195**	-4.6772
4	NLK-40	50.77	-0.9538**	-1.05	86.56	0.4876	-0.3720	44.44	0.9985**	-4.8380
5	NLK-48	51.22	0.1231	-0.82	87.22	0.9652**	-0.5312	39.33	0.4150	4.0058
6	NLK-73	49.77	1.1692**	-1.80	89.00	1.6119**	0.0750	41.00	0.4962	-0.4667
7	NLK-36	51.00	-1.4769**	-0.82	89.33	2.5075**	-0.6680	36.00	-0.2977	0.6261
8	NLK-5	49.44	2.5538 **	-1.058	86.44	-0.0100	-0.1531	41.33	1.6421**	-2.8514
	Mean	**49.59**	**0.9998**		**87.91**	**0.9999**		**39.59**	**0.9999**	

Table 2. continued ...

SN.	Genotypes	No. of branches plant^{-1}			No. of pods plant^{-1}			Seed yield plant^{-1}		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
1	Ratan	4.67	0.0000	-0.1296	28.33	1.2399**	-3.1251	5.35	1.1350**	**-0.1464**
2	Mahateora	4.22	0.8980	-0.1013	35.33	1.2758**	3.6295	6.32	0.6523**	**-0.1367**
3	Pratik	4.33	4.6531*	0.1980	27.11	1.7588**	-0.2903	4.96	2.6334**	**-0.1267**
4	NLK-40	4.33	2.6939	0.1255	32.66	1.0375**	-3.5712	4.73	0.4839*	-0.1008
5	NLK-48	4.22	0.1633	-0.0571	23.66	0.5483*	-2.4161	3.66	0.1564*	-0.1407
6	NLK-73	4.00	0.0000	-0.1296	27.00	1.3639**	-2.9744	4.84	1.5213**	-0.1428
7	NLK-36	4.11	-1.6327	0.2377	26.66	-0.1928	0.9151	4.13	-0.1781	-0.1384
8	NLK-5	4.67	1.2245	0.0076	29.00	0.9687**	3.0086	5.42	1.5957**	**-0.0129**
	Mean	**4.31**	**1.0000**		28.71	1.0000		4.92	0.9999	

one local selection NLK-5 had mean seed yield higher than the over all mean, and b significantly deviating from zero and non significantly deviating from one, thus has unit regression coefficient and S^2d ie. deviation from regression was non-significant. These genotype could be regarded as stable and widely adapted. NLK-40 can also be considered stable for yield as its mean seed yield though not higher but at par with the over all mean and has unit regression coefficient and S^2d non-significant.

Similarly for no. pods plant^{-1}, Mahateora, NLK 40 and NLK 5 recorded higher no. of pods than the over all mean, and b significantly deviating from zero and non significantly deviating from one, thus has unit regression coefficient and S^2d ie. deviation from regression was non-significant. These three genotypes were regarded as stable and widely adapted for no. of pods plant^{-1}. The other two check varieties Ratan and Pratik recorded low no. of pods plant^{-1} but were at par with average and unit bi values and non-significant S^2d, hence can be considered as stable.

The genotypes NLK-36 and NLK-48 were poorly adapted to unfavorable environments in view of bi values less than the unity and low seed yield plant^{-1} and no. of pods plant^{-1}. The genotype NLK-73 was poorly adopted to all the environments as mean performance was less

than the average and unit bi values and non-significant S^2d.

Thus, from this study it can be concluded that NLK-5 and NLK-40 were identified as the stable genotypes other than the check Ratan, Mahateora and Pratik which funded suitable for growing over all the environment.

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Correlation Study for Seed Yield and Yield Contributing Traits in Safflower

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ABSTRACT

Estimation of Correlation coefficient analysis was taken up for eleven attributes in safflower (*Carthamus tinctorious L.)* to understand the association of different characters on seed yield in the present investigation, seed yield exhibited high positive correlation on plant stand, number of effective capsules and 100 seed weight. However the correlation coefficient showed negative with the trait days to maturity (-0.5734**) but highly significant.

Safflower (*Carthamus tinctorious* L.) is a member of the family Asteraceae (Compositae), cultivated mainly for the high quality edible oil extracted from the seeds. The crop has been grown in India since ancient times initially for the dye extracted from its florets and later as an oilseed crop. Safflower oil is rich in polyunsaturated fatty acids (linoleic acid 78%) which play an important role in reducing blood cholesterol levels and is considered to be a healthy cooking medium. Breeding initiatives in India have resulted in the development of many improved varieties and a few hybrids (Anjani and Mukta, 2008). It has been cultivated locally for its oil and flower. Normal types of its whole seed contents 27 -32 per cent oil, 5-8 per cent moisture,14-15 per cent protein and 32-34 per cent crude fiber (Golkar *et.al.,2011*)

Selection is the one of the principle tools of crop improvement. The effectiveness of selection for particular trait depends upon the extent of direct or indirect effects of the trait on seed yield. Therefore, knowledge of interaction among the characters is very essential to determine the extent and nature of relationship between yield and its contributing characters. the present study was undertaken to measure degree to which characters are associated with yield or among themselves. This help the plant breeder to build selection criterion for selecting and developing high yielding genotypes in safflower (*Carthamus tinctorious L.).*

MATERIAL AND METHODS

The material for the present study consisted of thirty eight accessions and two cultivated check varieties the experimental material were grown in a Randomized Block Design with three replications in rabi season 2014 under irrigated condition at the experimental farm of Oilseed Research Station, Latur, VNMKV,Parbhani (M.S.). The single row of 5 m length was sown following 45 and 20 cm spacing between and within rows respectively. Recommended agronomic practices and prophylactic measures were adopted for growing of good crop.

Data were recorded for 11 quantitative traits over three replication and mean values were used for analysis. The phenotypic correlation coefficients were calculated by working out the variance components of each character and the covariance components for each pair of character. The direct and indirect effects were estimated by taking seed yield as the dependent variable using correlation coefficient following Fisher and Yates (1967)

RESULTS AND DISCUSSION

Positive significant relationship were found between seed yield and plant stand, number of effective capsule, 100 seed weight (similar results were reported by Shivani D and Sameer Kumar, 2012).The result revealed that in the most of the cases genotypic correlation were higher than corresponding phenotypic correlation which indicate that the traits were inherently associated with among themselves .However a few traits showed higher phenotypic correlation than genotypic correlation indicating that though the traits were inherently associated among themselves they were also affected by the environment the effects of plant stand, number of effective capsule and 100 seed weight were positively associated with one another and with seed yield per plant (Table 1).

The correlation coefficient shows highly significant with the trait number of effective capsule (0.4296**,0.7284**, respectively). These findings are in agreement with the findings of Fisher and Yates (1967).The traits which showed highest correlation with seed yield plant^{-1} were number of effective capsule (0.7284**), 100 seed weight (0.1895) and plant stand (0.1197). However it

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Table. 1 Phenotypic (P) and Genotypic (G) correlation coefficients of seed yield and yield components in Safflower

Characters		Days to 50% flowering	Days to maturity	Plant stand	No of seed/capsule	No of effective capsule	100 seed weight	Volume weight	Hull content	Harvest index	Oil content	Seed yield/plant
Days to 50% flowering	PG	1.0000	0.3265	-0.2211	0.1454	-0.0416	-0.2197*	0.1067	0.0610	-0.0166	0.2298*	-0.1742
		1.0000	1.7712	-0.0939	0.5747	-0.6950	-0.7607	0.5969	0.2612	0.1973	0.9389	-0.3084**
Days to maturity	PG		1.0000	-0.1186	0.0714	-0.2377**	-0.1878*	0.3898***	0.1849*	0.0869	0.3577***	-0.3609**
			1.0000	-0.3819	0.4111	-0.8053	-0.1896	0.9244	0.2634	0.1829	1.1833	-0.5734**
Plant stand	PG			1.0000	0.0263	-0.0307	0.0240	-0.0195	-0.1556	0.0020	0.0330	0.0589
				1.0000	0.0489	0.0979	0.1410	-0.1494	0.0985	0.2861	-0.3547	0.1197
No of seed/ capsule	PG				1.0000	-0.2005*	-0.2885**	-0.0990	-0.2685**	-0.0218	0.1126	-0.0682
					1.0000	-0.2237	-0.5507	-0.2038	-0.2438	0.2001	0.1562	-0.1367
No of effective capsule	PG					1.0000	-0.1228	-0.2624**	0.0314	-0.0252	-0.1292	0.4296**
						1.0000	-0.1339	-0.4715	0.0152	-0.0362	-0.3869	0.7284**
100 seed weight	PG						1.0000	0.1283	0.1368	-0.1158	-0.1450	0.1636
							1.0000	0.2037	0.1461	-0.2442	-0.1908	0.1895
Volume weight gm	PG							1.0000	0.1745	-0.1048	0.3431***	-0.1676
								1.0000	0.3071	-0.0198	0.5354	-0.2415*
Hull content	PG								1.0000	-0.0035	0.1062	-0.1600
									1.0000	-0.1156	0.2124	-0.1127
Harvest index	PG									1.0000	0.0952	-0.0853
										1.0000	0.3557	-0.2044*
Oil content	PG										1.0000	-0.2091*
											1.0000	-0.2512**
Seed yield/plant	PG											1.0000
												1.0000

*.** significant at 5% and 1% level respectively

Table 2. Mean performance of safflower genotypes for different characters.

S.N.	Entry Name	Days to 50% Flowering	Days to Maturity	Plant Stand	Number of Seeds/ Capitulum	Number of Effective Capitulum plant^{-1}	100-Seed Weight (gm)	Volume Weight (gm)	Hull Content (%)	Harvest Index (%)	Oil Content (%)	Seed Yield plant^{-1} (gm)
1	PBNS-128	83.33	110.66	57.33	9.66	20.00	4.49	52.50	52.89	26.59	23.32	12.31
2	PBNS-129	83.33	111.66	62.00	11.00	17.33	3.93	47.67	46.86	28.41	22.79	9.61
3	PBNS-130	85.33	112.66	69.33	13.33	21.00	3.82	53.60	47.90	30.89	22.27	10.51
4	SHARDA-1	84.66	112.66	58.00	10.66	21.66	3.38	48.90	44.94	26.39	21.38	10.91
5	PBNS-131	85.33	112.66	68.66	18.33	12.33	4.18	47.97	41.25	27.54	21.14	8.20
6	PBNS-132	82.66	111.00	71.66	12.66	21.66	4.32	50.72	39.58	26.64	22.28	16.47
7	PBNS-135	82.66	111.00	61.66	15.33	24.00	2.87	45.06	50.41	28.21	23.96	10.07
8	PBNS-136	83.00	111.33	65.66	14.00	18.66	3.45	51.79	40.98	30.50	23.17	11.35
9	PBNS-86	85.00	112.66	64.00	12.33	20.66	3.36	44.49	47.64	25.39	20.55	8.92
10	PBNS-12-1	83.66	111.33	63.33	13.33	21.00	3.81	45.19	51.85	25.55	21.92	11.05
11	PBNS-120	82.66	110.66	63.66	16.33	21.00	3.08	50.22	36.10	27.62	21.88	11.57
12	PBNS-121	82.00	110.66	67.00	13.33	22.00	4.20	55.61	43.97	23.45	22.81	13.25
13	JSI-120	82.33	112.00	65.66	12.00	19.33	4.69	45.61	47.82	30.61	24.14	5.26
14	PBNS-125	85.33	114.00	67.33	12.33	20.66	4.17	59.62	48.92	28.86	27.50	9.89
15	SSF-1109	82.00	114.00	62.33	11.66	17.00	4.70	58.49	48.58	26.16	25.42	8.03
16	NARI-98	85.00	114.33	68.33	15.33	16.00	3.64	54.63	38.83	29.28	25.93	5.82
17	PBNS-12(ch)	83.66	113.66	64.33	11.00	18.00	5.00	60.69	46.49	25.60	22.95	8.56
18	DSI-118	83.33	113.66	65.00	14.66	14.33	5.03	60.89	47.65	28.32	23.13	6.23
19	AKS/GMU-4576	83.66	113.66	62.66	13.33	18.66	4.22	57.67	50.76	29.97	23.54	9.00
20	JSI-118	81.33	112.00	65.00	13.00	17.33	5.09	53.32	50.01	24.18	25.65	9.50
21	PBNS-124	85.00	112.66	64.66	13.33	18.66	3.90	43.91	42.50	29.78	26.01	9.54
23	DSI-117	82.66	113.33	66.66	13.66	15.00	3.47	52.96	43.13	32.31	27.90	7.10
24	NARI-97	86.66	116.33	60.33	13.00	20.33	3.22	60.90	48.28	31.20	29.02	6.50
25	ASF-1301	86.33	115.33	59.33	15.66	18.66	2.90	60.67	47.17	29.13	26.44	9.27
26	JSI-119	82.00	112.33	53.66	11.66	17.00	5.05	52.26	38.88	27.29	24.78	10.32
27	DSI-116	89.00	116.66	61.33	16.66	14.66	3.96	59.82	50.56	24.44	27.78	6.64
28	PBNS-123	86.00	115.33	62.33	13.00	20.00	4.83	58.87	54.53	30.94	28.48	15.90

Table 2. continued....

S.N.	Entry Name	Days to 50% Flowering	Days to Maturity	Plant Stand	Number of Seeds/ Capitulum	Number of Effective Capitulum plant^{-1}	100-Seed Weight (gm)	Volume Weight (gm)	Hull Content (%)	Harvest Index (%)	Oil Content (%)	Seed Yield plant^{-1} (gm)
29	SSF-1215	84.33	113.33	55.66	13.66	18.33	4.09	57.98	46.58	28.47	23.45	7.09
30	NARI-96	86.33	114.66	63.00	20.66	15.66	2.93	48.20	48.06	29.54	27.88	5.65
31	AKS-327	84.33	113.00	63.33	11.33	19.33	4.00	53.35	51.47	23.54	25.32	8.80
32	DSI-115	88.66	116.33	57.33	16.66	13.00	2.77	60.18	45.62	26.84	29.68	6.14
33	PBNS-112	84.33	114.33	64.66	16.66	16.33	3.44	60.42	50.90	24.38	25.59	7.80
34	DSI-113	86.66	115.66	65.33	9.66	19.00	3.45	57.71	45.56	27.18	28.43	6.80
35	A1	84.33	113.00	67.33	10.00	17.00	4.08	61.11	48.99	28.43	29.21	10.44
36	JSI-117	82.66	113.00	65.66	10.00	16.00	3.84	60.72	50.00	27.43	22.20	5.67
37	DSI-114	86.00	114.00	64.33	10.33	15.00	4.10	59.67	51.93	27.48	23.87	9.51
38	SSF-1201	84.33	113.66	63.00	9.00	13.00	4.27	59.21	51.00	28.62	24.21	3.88
39	ASF-1302	83.66	112.33	64.66	11.33	19.33	3.90	56.45	47.68	26.56	25.69	6.27
40	SHARDA(ch)	85.00	114.00	60.66	13.00	18.33	4.00	53.19	45.26	26.06	26.53	10.39
	GM	**84.36**	**113.25**	**63.45**	**13.16**	**18.10**	**3.94**	**54.54**	**46.77**	**27.60**	**24.84**	**9.02**
	SE±	**1.28**	**1.10**	**2.42**	**1.16**	**1.46**	**0.30**	**2.05**	**2.17**	**1.47**	**1.18**	**0.64**
	CD at 5%	**3.67**	**3.15**	**6.90**	**3.32**	**4.18**	**0.87**	**5.85**	**6.20**	**4.19**	**3.37**	**1.84**

reported that the days to 50 per cent flowering, days to maturity, number of seed capsule^{-1}, volume weight, hull content (%), harvest index and oil content (%) have negative correlation with yield. The possible reason for deviation may be due to different material used in the present study and also due to very low direct and indirect effect.

The correlation coefficient showed negative with the trait days to maturity (-0.5734**) but highly significant (similar results were reported by Deshpande V.S., Choudhary M.B.(2004). Oil content had negative phenotypic and genotypic direct effect on seed yield, their correlation with yield was positive. (similar results were reported by Jawanjal S.S, Choulwar S.B and Patil S.R (2006).

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Hybrid AKPHM 11303: A Ray of Hope for Breaking Yield Plateau in Pigeonpea

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ABSTRACT

The productivity of pigeonpea has been low and stagnant for last five decades and it is hovering about 600 to 700 kg ha^{-1}. Exploitation of heterosis has emerged as one of the potential option for breaking yield plateau in pigeonpea after the identification of GMS. However, the technology suffers from a major technical bottleneck when it comes to a large scale seed production. To overcome the inherent problems associated with GMS system, CGMS system were developed using various wild relatives of pigeonpea. CGMS based hybrid recombination's using A2 source were developed during last four years and tested in preliminary yield trials. In Central zone pigeonpea hybrid AKPHM 11303 recorded 1642 kg ha^{-1} average yield. It gave 30.35 per cent, 41.83 per cent, 33.80 per cent and 25.89 per cent increased yield over the ruling varieties BSMR-736, ICPL-87119 (Asha), Maruti and CO-6 respectively Fertility restoration is the crucial requirement for hybrid breeding programme in pigeonpea. Hybrid AKPHM 11303 showed 94.5 per cent plant fertility over all the locations. This hybrid matures in 165 days with good grain size compare to the ruling verities of pigeonpea. (100 seed weight 11.5 g) This hybrid also exhibited moderate reaction to the *Fusarim* wilt. Therefore the medium duration pigeonpea hybrid AKPHM-11303 showed ray of hope for breaking yield plateau in pigeonpea.

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is a short lived perennial shrub belonging to the economically most important tribe Phaseoleae and the *subtribe Cajaninae*. In India it is one of the very important grain legume and occupies second position in area and production next to chickpea Commercial exploitation of heterosis has been possible in crops like sorghum and cotton either through male sterility systems or through hand pollination. Until recently, hybrid vigour in pigeonpea could not be used to enhance its genetic yield potential due to lack of stable male sterility systems. A successful search for easily identifiable and stable genetic male sterility at different institutions in India has paved the way for commercial exploitation of hybrid vigour in pigeonpea and six hybrids *viz.,* ICPH 8, COPH 1, COPH 2, PPH 4, AKPH 4104 and AKPH 2022 have been released for cultivation (Bajpai *et al.,* 2003).

In GMS system, it is an obligate practice to rogue out 50 per cent of fertile plants. This is laborious and time consuming job, adding to the production cost of seeds. Due to the limitation of large-scale hybrid seed production in GMS-based hybrids, the development of cytoplasmic-nuclear male-sterility (CMS) became imperative. So far, seven different such CMS systems have been identified in pigeonpea with varying degrees of success. Of these, A2 and A4 systems derived from crosses involving wild relatives of pigeonpea and cultivated types have shown promise because of their stability under various agro-climatic-ecological conditions and availability of good maintainers and fertility restorers. To overcome these bottlenecks, breeding of a stable cytoplasmic–genetic male-sterility (CGMS) system was required (Ariyanayagam *et al.*1995; Tikka et al. 1997; Wanjari *et al.* 2001; Saxena and Kumar 2003; Saxena *et al.* 2005). The male-sterile genotype selected by Ariyanayagam *et al*. (1995) from the cross involving *Cajanus sericeus* Benth. ex Bak., a wild relative of pigeonpea and a cultivar, looked promising but the expression of male sterility was not stable from one season to another (Saxena *et al*. 1996). This paper reports the development of CGMS hybrid AKPHM 11303 based on A2 cytoplasm (*Cajanus. scarabaeoides*), its performance at national level, fertility restoration, and discusses the prospects for breeding commercial pigeonpea hybrids.

MATERIAL AND METHODS

The hybrid AKPHM 11303 has been evolved from a cross of AKCMS 11A x AKPR 303 at Pulses Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (M.S). Among the several CGMS based hybrid recombination's using A2 source were developed during last four years and tested in preliminary yield trials, a promising hybrid AKPHM 11303 was evaluated in coordinated trials (IHT (Medium), AHT-1 (Medium) and AHT-2 (Medium) at the national levels at various locations during the year 2010-11 to 2013-14 along with the national checks *viz.,* BSMR 736, ICPL 87119, Maruti and Co 6. The

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Fig.1. Plant and seed of pigeonpea hybrid AKPHM 11303

Fig. 2. Parental lines of pigeonpea hybrid AKPHM 11303

stability performance of pigeonpea hybrid was also carried out. The characters of male and female parents were recorded as per DUS guidelines and different biochemical parameters and dal character was carried out. Subsequently, this hybrid (AKPHM 11303) was tested for sterility mosaic and wilt in coordinated programme at hot spots along with susceptible checks.

RESULTS AND DISCUSSION

In Coordinated programme, Initial Hybrid Trial (IHT) under Central zone, pigeonpea Hybrid AKPHM 11303 recorded 1176 kg ha^{-1} grain yield which was higher than the checks *viz.,* BSMR 736 (876 kg ha^{-1}), ICPL–87119 (760 kg ha^{-1}) Maruti (1019 kg ha^{-1}) and Co-6 (925 kg ha^{-1}) during the year 2010-11(Annual Progress Report 2010-11). In Advance Hybrid Trial-1 (AHT-1), pigeonpea Hybrid AKPHM 11303 recorded 1618 kg ha^{-1} grain yield which was higher than the checks *viz.,* BSMR 736 (1195 kg ha^{-1}), ICPL–87119 (1087 kg ha^{-1}) Maruti (1136 kg ha^{-1}) and Co-6 (1078 kg ha^{-1}) during the year 2011-12 (Annual Progress Report 2011-12). During the year 2012-13, in Advance hybrid trail 2, the pigeonpea Hybrid AKPHM 11303

Table 1. Yield performance (Kg/ha) of medium duration pigeonpea hybrid AKPHM 11303 in Coordinated trial in Central Zone (2010-11 to 2013-14)

Location	AKPHM 11303	BSMR 736 (Ch)	ICPL 87119 (Ch)	Maruti (Ch)	Maruti Co-6 (Ch)
2010-11(IHT Med)					
Mean (4)	1176	876	760	1019	925
% Increase over		34.24	54.73	15.44	27.13
2011-12 (AHT1 Med)					
Mean (4)	1618	1195	1087	—	—
Mean (3)	1535	—	—	1136	1078
% Increase over		35.39	48.85	35.08	42.39
2012-13 (AHT 2 Med)					
Mean (5)	1737	1382	1333	1218	1536
% Increase over		25.71	30.33	42.56	13.09
2013-14 (AHT 2 Med)					
Mean (4)	2014	1556	1408	1473	1519
% Increase over		29.48	43.09	36.73	32.57
Weighted Mean(17)	1642	1260	1158		
% Increase over		30.35	41.83		
Weighted mean(16)	1628	—	—	1217	1293
% Increase over				33.80	25.89

Table 2. Percent fertility of medium duration pigeonpea hybrid AKPHM 11303 in Coordinated trial in Central Zone (2010-11 to 2013-14)

Location	AKPHM 11303	BSMR 736 (Ch)	ICPL 87119 (Ch)	Maruti (Ch)	Co-6 (Ch)
Per cent plant fertility.					
2010-11(IHT)					
Akola	83	100	100	100	100
SK Nagar	97	100	100	100	100
2011-12 (AHT1)					
Badnapur	100	100	100	100	100
SK Nagar	100	100	100	100	100
2012-13 (AHT2)					
Akola	100	100	100	100	100
SK Nagar	73.30	100	100	100	100
Krishi Dhan	98.86	100	100	100	100
2013-14 (AHT2)					
Badnapur	100	100	100	100	100
SK Nagar	98.2	100	100	100	100
Mean (9)	**94.5**	**100.0**	**100.0**	**100.0**	**100.0**

recorded 1737 kg ha^{-1} grain yield which was higher than the checks *viz.,* BSMR 736 (1382 kg ha^{-1}), ICPL–87119 (1333 kg ha-1) Maruti (1218 kg ha^{-1}) and Co-6 (1536 kg ha^{-1}) (Annual Progress Report 2012-13) however the hybrid again repeated in the next year 2013-14 where also it gave 2014 kg ha^{-1} grain yield over the checks BSMR 736 (1556 kg ha^{-1}), ICPL–87119 (1408 kg ha^{-1}) Maruti (1473 kg ha^{-1}) and Co-6 (1519 kg ha^{-1}) (Annual Progress Report 2013-14).

In overall performance of four years trials during 2010-11 to 2013-14, this hybrid AKPHM 11303 was superior for yield (1642 kg ha^{-1}) than check varieties recorded 30.35, 41.83, 33.80 and 25.89 per cent increase in yield over BSMR 736, ICPL–87119 Maruti and Co-6 respectively in coordinated programme (Table 1a).

Fertility Restoration: Fertility restoration is a crucial requirement for successful hybrid synthesis using CGMS system in pigeonpea. Hybrid AKPHM 11303 was tested for fertility restoration over nine locations during 2010-11 to 2013-14 in central zone (Table 2). This hybrid showed 94.5 per cent plant fertility.

Reaction to diseases: The genotype AKPHM 11303 was tested during the year 2011-12 for reaction to fusarium wilt and sterility mosaic disease under coordinated programme at ICRISAT, Patencheru, Hyderabad (A.P.) location. The AKPHM 11303 showed moderate resistant reaction to wilt disease. Similarly, the same genotype exhibited moderate resistant reaction to sterility mosaic disease at ICRISAT against the susceptible checks (Table 3).

Table 3. Disease reactions of AKPHM 11303 in Coordinated trial during 2011-12

S N.	Entry	% SMD ICRISAT	% PB ICRISAT	% Wilt ICRISAT
1	AKPHM 11303	29.4	5.9	64.7
2	Maruti (ch)	100.0	0.0	0.0
3	Asha (ch)	0.0	0.0	0.0
4	BSMR 736 (ch)	0.0	0.0	21.4
5	Co 6 (ch)	0.0	0.0	100.0
6	VIPULA (ch)	25.0	0.0	75.0
7	ICP 2376 (ch)	0.0	11.1	88.9

Table 4a. Quality parameters : cooking time, protein and carbohydrate content of AKPHM 11303 and various checks.

S.N.	Particular	Genotype				
		AKPHM 11303	PKVTARA	ICPL-87119 (Ch)	BSMR-736 (Ch)	BSMR-853 (Ch)
1	Cooking time (min)	**25.00**	24.00	25.00	26.00	26.00
2	Protein per cent (Whole grain)	**22.00**	21.50	19.90	19.20	19.60
3	Protein per cent (*dal*)	**23.80**	23.60	21.10	21.60	21.90
4	Carbohydrate per cent	**58.40**	58.00	57.30	57.50	57.40

Table-4b. Quality parameter : *per cent dal* recovery of AKPHM 11303 and various checks using PKV mini *dal* mill.

S. N.	Components	AKPHM 11303	PKVTARA	ICPL-87119(Ch)	BSMR-736 (Ch)
1	Grade I (*Phatka*) *dal* (%)	**50.20**	59.17	50.85	55.22
2	Grade II *dal* (%)	**24.40**	16.37	23.83	20.30
3	Total *dal* recovery (%)	**74.60**	75.54	74.68	75.52
4	Broken *dal* (%)	**1.20**	1.13	1.11	1.12
5	Powder and Husk (%)	**24.20**	19.70	19.73	19.00

Table 5: Ancillary observations of AKPHM 11303 in Coordinated trial 2010-11 to 2013-14

Location 11303	AKPHM 736 (Ch)	BSMR 87119 (Ch)	ICPL (Ch)	Maruti (Ch)	Co-6 (Ch)	PKV Tara
a) Days to 50% flowering						
Mean (17)	111	119	120	113	118 (16)	113(1)
b) Days to maturity						
Mean (16)	165	166	171	160	166 (15)	165(1)
c) Plant height (cms).						
Mean(5)	168.6	163.54	159.64	150.96	179.4	157.3(1)
d) 100 seed weight (g).						
Mean (17)	11.5	10.4	10.7	9.9	9.0	9.3

Quality parameters: The hybrid AKPHM 11303 required 25 minutes for cooking, 22 per cent protein in whole grain whereas 23.80 per cent in dal and 58.40 per cent carbohydrate which is at par with the all the checks (Table 4a). The dhal recovery (74.60 %) was also similar with the checks PKV TARA, ICPL 87119 and BSMR 736 (Table 4b.)

Ancillary characters: Pigeonpea hybrid AKPHM 11303 is a medium duration (165 days maturity) hybrid with height of 11.5 cm. It has bold seed size with red seed colour (11.5 g per 100 seed weight) which is commercially preferred**.** (Table 5)

DUS Characteristics: Male and female parents of hybrid AKPHM 11303 are morphologically distinct which suited for easy rouguing during commercial seed production. The female parent has flowers with yellow petals without red streaks whereas male has flowers with red streaks and both the parents showed plane green pods but hybrid AKPHM 11303 showed green pod colour with brown edge. (Fig. 2)

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Molecular Characterization of Different Variants and Restorer Lines in Hybrid Pigeonpea Through SSR Markers

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ABSTRACT

The present investigation was carried out with the objective to assess genetic diversity among 28 parental lines consisting 8 CMS, 8 maintainer and 12 restorer lines of pigeonpea using SSR markers. Nearly 21 SSR markers have been used, of which 12 primers were found monomorphic and 9 were polymorphic. Amongst all SSR primers used, a total of 63 alleles were amplified. The PIC values for 21 SSR markers varied from 0.138 (CCB-5) to 0.994 (CCB-3). The present study revealed that molecular characterization using SSR markers can be efficient tool for genotyping the varieties with reasonable accuracy. Therefore the present study was conducted with the objective of characterization and documentation of pigeonpea genotypes using SSR markers.

Pulses constitute an important ingredient in predominantly vegetarian diet and are important as source of protein that nutritionally balances the proteins from cereal grains. Among the pulses pigeonpea is a most important grain legume crop of rain-fed agriculture in the semi-arid tropics.

Characterization at molecular level will provide robust information regarding genotype diversity. Genotypic difference relation to heterosis will provide preliminary information about involvement of various loci in different recombination of hybrids developed from diverse set of parents. SSR microsatellites are mostly related to the specific locus on chromosomes. Molecular markers are DNA sequence variants that can readily be detected and whose inheritance can be monitored (Newbury and Ford-Lloyd 1999). Molecular marker technology can facilitate the precise determination of the number, chromosomal location and individual and interactive effects of genes that control traits (Ariyanayagam*et al.* 1993). Microsatellites offer several advantages compared to other molecular markers: they are highly reproducible, highly polymorphic, PCR-based and readily portable within a species (Edwards *et al*., 1996). Despite the reported high informative nature of SSRs, the high cost and time required for their development is a major limitation. This is especially the case in crops such as pigeonpea, for which no sequences exist in databases that could be directly searched for SSRs. In such species, microsatellites can only be isolated *de novo*. In case of CGMS system most of the CMS lines were unstable for sterility, also good combinations of A x R were not identified and fertility restoration is one of the major problem associated with this system.

MATERIAL AND METHODS

Plant Material

In the present investigation 28 parental lines of pigeonpea including 8 CMS, 8 maintainer and 12 restorer were used to study genetic diversity using 21 SSR markers. All the genotypes were collected from SRS, Pulses Dr. PDKV, Akola.

Table 1 : List of genotypes used in present study

S.N.	Cms lines	Maintainer lines	Restore lines
1	Oval leaf-A	Oval leaf-B	AKPR-249
2	Sesamum leaf-A	Sesamum leaf-B	AKPR-178 (E)
3	Obcordifoliate Leaf-A	Obcordifoliate Leaf-B	AKPR-12
4	Small Leaf-A	Small Leaf-B	AKPR-178(M)
5	Dwarf 30 cm-A	Dwarf 30 cm-B	AKPR-344
6	Dwarf 45 cm-A	Dwarf 45 cm-B	AKPR-8
7	Dwarf. 60 cm-A	Dwarf 60 cm-B	AKPR-210
8	Dwarf 90 cm-A	Dwarf 90 cm-B	AKPR-325
9			AKPR-364
10			AKPR-319
11			AKPR-359
12			AKPR-292

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DNA Extraction and SSR analysis

DNA was extracted from 2 gm fresh leaves of two week old seedlings by the Cetyl Trimethyl Ammonium Bromide method (Anonymous, 2006) with minor modifications. The contamination of RNA was removed by addition of 90 mg ml^{-1} Ribonuclease A to the DNA sample of 100 mg ml^{-1} and incubated at 37^0C for 1 hr. The quality of DNA was confirmed on 0.08 per cent agarose gel electrophoresis.

For SSR analysis, 21 SSR primers were procured from Axygen Biosciences and used for PCR amplification which spread across different chromosomes of pigeonpea. Each polymerase chain reaction was carried out in 20 ml reaction volume containing 50 ng of DNA, 10 x polymerase buffer (10 x tris with 20 mM $Mgcl_2$), 25 mM dNTPs, 0.05 ml of each promer (10Pmol), 1 unit of taq polymerase (fermentas), 0.5ml of 5 per cent formaide and 1 ml of 5 mM spermidine using eppendorf and applied biosystem thermal cyclers. Thermal cycler programme for PCR comprised 95^0C for 5 min. for initial denaturation followed by 36 cycles of 95^0C for 45 seconds, 55 to 65^0C for 45 seconds, 72^0C for 45 seconds and ending up with 7 minute at 72^0C for the final extension. The annealing temperature was adjusted based on the specific requirements of different primer combinations. The PCR products were separated electrophoretically using 3 per cent agarose gel and also by polyacrylamide gel. The ethidium bromide (0.5 mg ml^{-1}) was used to stain the gel for about 30 min. A 100 bp DNA ladder was spotted on first well with an amount of 5ml as a fragment length standard and in the remaining wells, about 10ml of each sample was loaded and photographed.

Statistical Analysis:

1. DNA bands were scored which were formed in the range of expected amplified product size given for each particular primer (Table 2).
2. Amplified bands were numbered according to their migration within the gel.
3. For each genotype, the presence or absence of each bands was determined and scored '1' if present and '0' if absent.
4. Polymorphic information content (PIC) refers to the value of a SSR marker for detecting polymorphism within a population. PIC depends on the number of detectable alleles and the distribution of their frequency (Botstein *et al*., 1980). The value was calculated as,

$$PICi=1-\sum_{j=1}^{n} P_{ij}^{2}$$

Where,

PICi is the polymorphic information content of a marker i, P_{ij} is the frequency of the j^{th} pattern for markeri and the summation extent over n pattern.

RESULTS AND DISCUSSION

Out of 21 SSR primers screened, 12 primers *viz.*,CCB-10,CCttc001, CCtta001, CCtta002, CCtta003, CCcat001, ICPM1A08, ICPM1B04_a, ICPM1C02, ICPM1D10, ICPM1F11, ICPM1G04 were found monomorphic and nine primers *viz.*, CCB-2, CCB-3, CCB-4, CCB-5, CCB-6, CCB-7, CCB-8, CCB-9 and CCttat001 were found polymorphic for the set of selected genotypes. The polymorphic information content (PIC) value of 9 SSR loci were calculated across 28 pigeonpea genotypes and is presented in Table 2.

As a result, 9 markers showed polymorphism in 28 parental lines analyzed. These polymorphic markers amplified a total of 28 alleles (in expected range of band size) with an average of 3.1 alleles per marker. Eleven markers (11) amplified 3 alleles, six primers amplified 2 alleles while a maximum of 5 alleles were amplified by one marker (CCttc001). Bands were considered under expected base pair size only. The PIC values calculated for these 9 polymorphic primers were in the range of 0.138 (CCB-6) to 0.994(CCB-3) with an average of 0.563 per marker (Table 2).

The highest PIC value was found in primer CCB-3 (0.994) followed by CCB-7 (0.968). High PIC value indicates high degree of polymorphism among the genotypes which helps to estimate genetic distance with more and more precision. In present study four primers *viz.*, CCB-3 (0.994), CCB-7 (0.968), CCB-8 (0.897), CCB-9 (0.897) showed high PIC values indicating their utility for assessment of genetic diversity. Thus it is necessary to obtained information about genetic diversity from polymorphic primers only so that genetically divergent genotypes can be effectively identified. Odeny *et al*. (2009) recorded 0.72 highest PIC value and similarly, 0.658 PIC value were recorded by Songok *et al*. (2010) for CCB-4 primer of SSR markers in pigeonpea.

The banding pattern observed in case of primer CCB-2 is presented in plate 5. The primer CCB-2 amplified four types of SSR allelic bands among 28 genotypes the size of bands amplified ranged from 131 to 182 bp which is

Table 2. SSR polymorphism among male sterile (A), maintainer (B) and restorer (R) lines

SSR markers	A- lines	B- lines	R- lines	PIC	All lines	Band Size (bp)	
	No. ofalleles	No. ofalleles	No. ofalleles	value	No. ofalleles	Observed	Expected
CCB-2	3	3	3	0.325	3	131-182	154-165
CCB-3	3	3	3	0.994	3	245-288	117-121
CCB-4	3	3	3	0.382	4	231-264	216-236
CCB-5	3	3	3	0.138	3	192-226	185-207
CCB-6	4	4	4	0.202	4	193-240	202-208
CCB-7	3	3	3	0.968	3	151-187	152-160
CCB-8	3	3	3	0.897	3	118-145	138-148
CCB-9	4	4	4	0.897	4	159-208	148-174
CCB-10	3	3	3	-	3	240-292	244-250
CCttc001	5	5	5	-	5	152-204	185–220
CCtta001	4	4	4	-	4	224-320	220
CCtta002	2	2	2	-	2	234-251	240–320
CCtta003	2	2	2	-	2	147-172	180–190
CCcat001	3	3	3	-	3	153-243	155–185
CCttat001	3	3	3	0.265	3	208-249	210–250
ICPM1A08	2	2	2	-	2	295-330	290–294
ICPM1B04_a	2	2	2	-	2	139-160	108-178
ICPM1C02	3	3	3	-	3	246-289	272–294
ICPM1D10	2	2	2	-	2	306-332	294–330
ICPM1F11	2	2	2	-	2	238-275	243–265
ICPM1G04	3	3	3	-	3	100-171	133–158

same as expected. The polymorphic information content calculated for primer CCB-2 was 0.325. Type I and type II allelic bands of CCB-2 were common in all the genotypes. Type III band were absent in Obcordifoliate leaf B, AKPR-178 (E), AKPR-12, AKPR-319 and AKPR-356.

In case of CCB-3 primer three types of allelic bands were produced in range of 245-288. Type III band of CCB-3 primer was present only in Oval leaf A and Oval leaf B. presented in plate 5. Other bands were common in all genotypes. Range of amplified banding pattern for CCB-3 is from 245 to 288 bp. Primer CCB-4 amplified four bands in 28 genotypes with rage from 231 to 264. PIC value for CCB-4 primer was 0.382. Type I band were present in 24 genotypes and absent in four *viz.,* Oval leaf A, Oval leaf B, Sesamum leaf A and Sesamum leaf B. Type II band were present in all genotypes. Type III band was present in 22 genotypes and absent in 6 genotypes *viz.*, Small leaf A, Small leaf B, Dwarf 30 cm A, Dwarf 30 cm B, Dwarf 45 cm A and Dwarf 45 cm B. (Fig.1)

The banding pattern observed in SSR primer CCB-5 presented in plate 6 the primer CCB-5 amplified four types of SSR bands. The size of bands amplified with primer CCB-5 ranged from 192 to 226 bp. The polymorphic information content (PIC) value for CCB-5 was 0.138. Type I band of primer CCB-5 was absent in all genotype except Dwarf 90 cm B. Type II and type IV bands were present in all except Dwarf 90 cm B and AKPR-249. Whereas type III band was monomorphic in all 28 genotypes (Fig. 2).

The banding pattern observed by SSR primer CCB-6 is presented in plate.6. The primer CCB-6 amplified 4 types of bands were ranged from 193 to 240 bp. The polymorphic information content (PIC) value for primer CCB-6 was 0.202. Type I and type II bands were present in all the genotypes except AKPR-12 and AKPR-359. Type III and type IV bands were monomorphic in all genotypes.

The banding pattern observed in SSR primer CCB-7 is presented in plate.6. The primer CCB-7 amplified

3 types of bands ranged from 193 to 240 bp. The polymorphic information content (PIC) value for primer CCB-6 was 0.202. Type I band was present in AKPR-249, AKPR-178 (E), AKPR-12, AKPR-178 (M) and AKPR-344 genotypes. Type II and type III bands were common for all 28 genotypes (Fig. 2)

. The banding pattern observed in SSR primer CCB-8 is presented in plate.7. The primer CCB-8 amplified 4 types of bands ranged from 118 to 145 bp. The polymorphic information content (PIC) value for primer CCB-8 was observed 0.897. Type I band was present in Dwarf 45 cm A, Dwarf 45 cm B, AKPR-249, AKPR-178 (E), AKPR-210, AKPR-325, AKPR-364, AKPR-319 and AKPR-292. Type II band was common in all genotypes and type III was present all genotypes except AKPR-249 and AKPR-210 (Fig. 3).

The banding pattern observed in SSR primer CCB-9 is presented in plate.7. This primer amplified 4 types of bands ranged from 159 to 208 bp. The polymorphic information content (PIC) value for primer was 0.897. Type I band was present in Dwarf 30 cm A, Dwarf 30 cm B, Dwarf 45 cm A, Dwarf 45 cm B, Dwarf 60 cm A, Dwarf 60 cm B, Dwarf 90 cm A, Dwarf 90 cm B, AKPR-249, AKPR-178 (E), AKPR-210 and AKPR-364. Type II, type III and type IV bands were common in all genotypes.

Twelve primers; CCB-10, CCttc001, CCtta001, CCtta002, CCtta003, CCttc001, ICPM1A08, ICPM1B04_a, ICPM1C02, ICPM1D10, ICPM1F11 and ICPM1G04 were found monomorphic in all 28 genotypes. Information regarding the amplifications of respective primers was given in the Table 2.

Primer CCttat001 was able to amplify three allelic bands in between the range of 208 to 249 bp presented in plate 7. Polymeric information content (PIC) value 0.265 was found for CCttat001. Type I and type III bands were found polymorphic (Fig. 3). Type I band was absent in

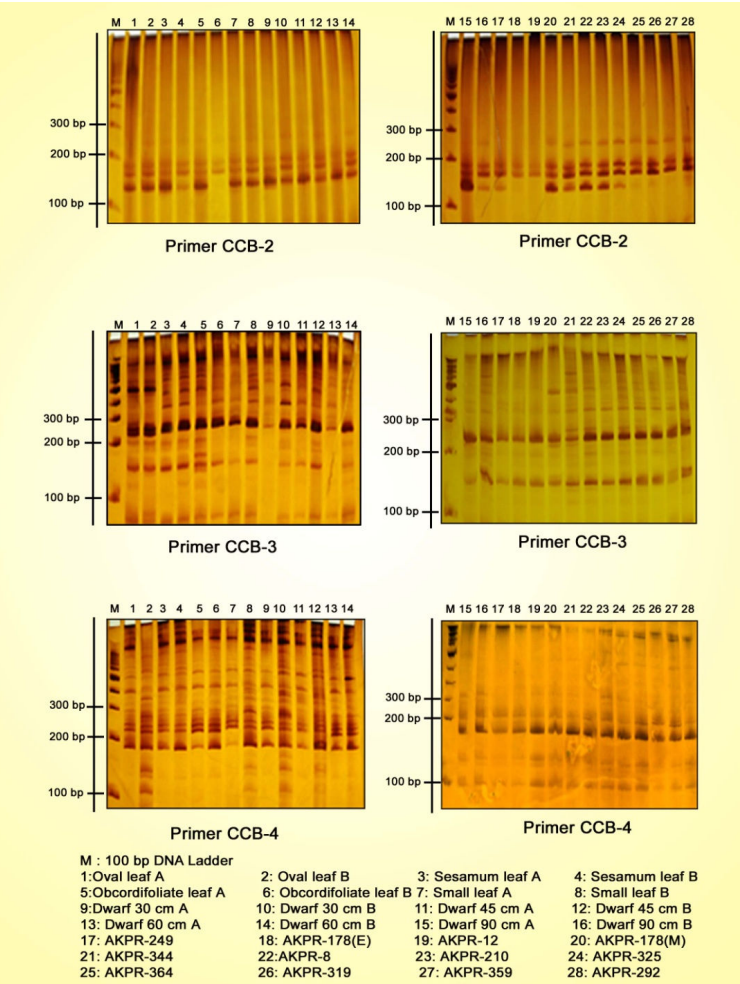

Fig.1 SSR banding profile of pigeonpea genotypes amplified with primers CCB-2, CCB-3 and CCB-4

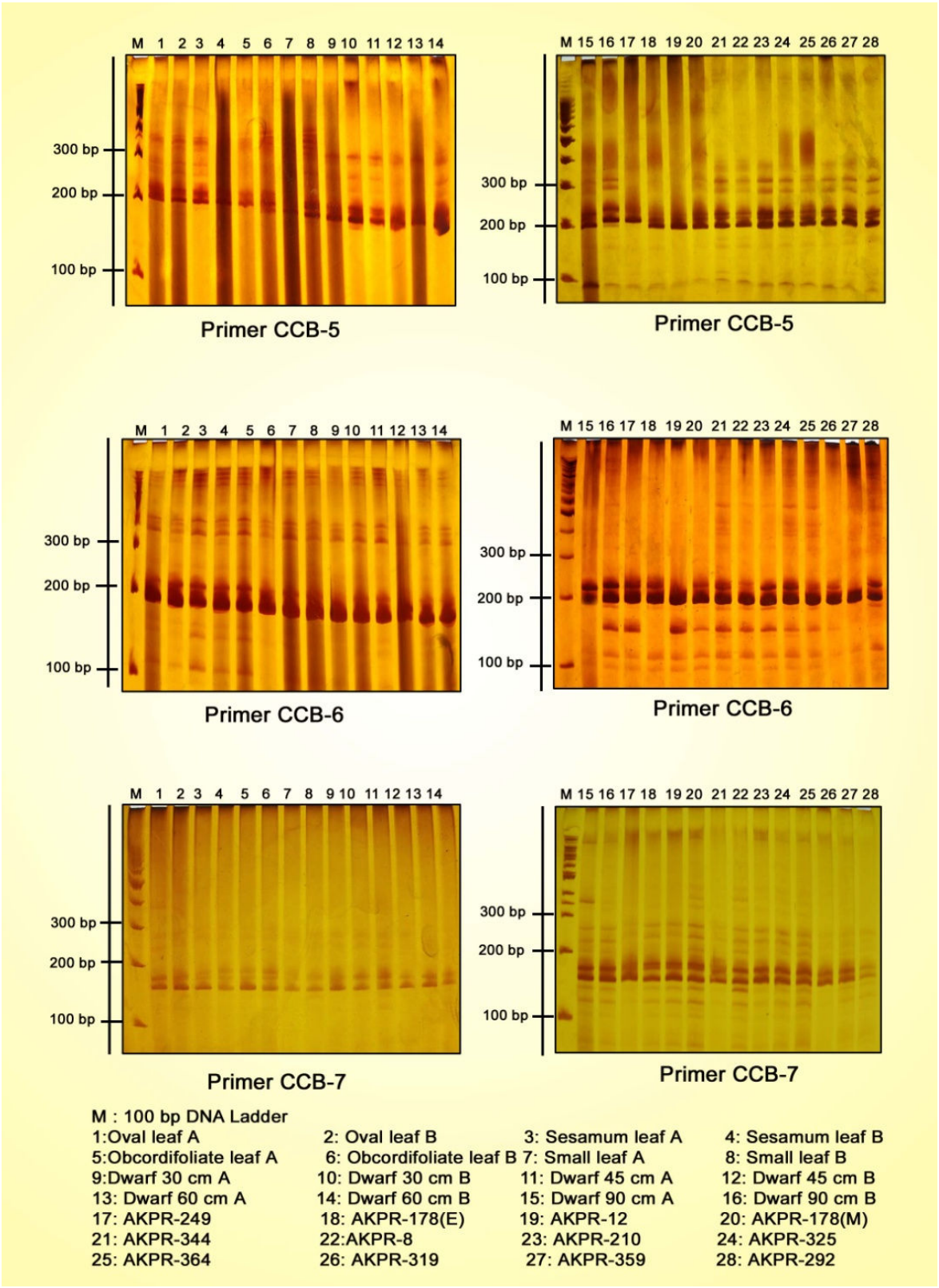

Fig.2 SSR banding profile of pigeonpea genotypes amplified with primers CCB-5, CCB-6 and CCB-7

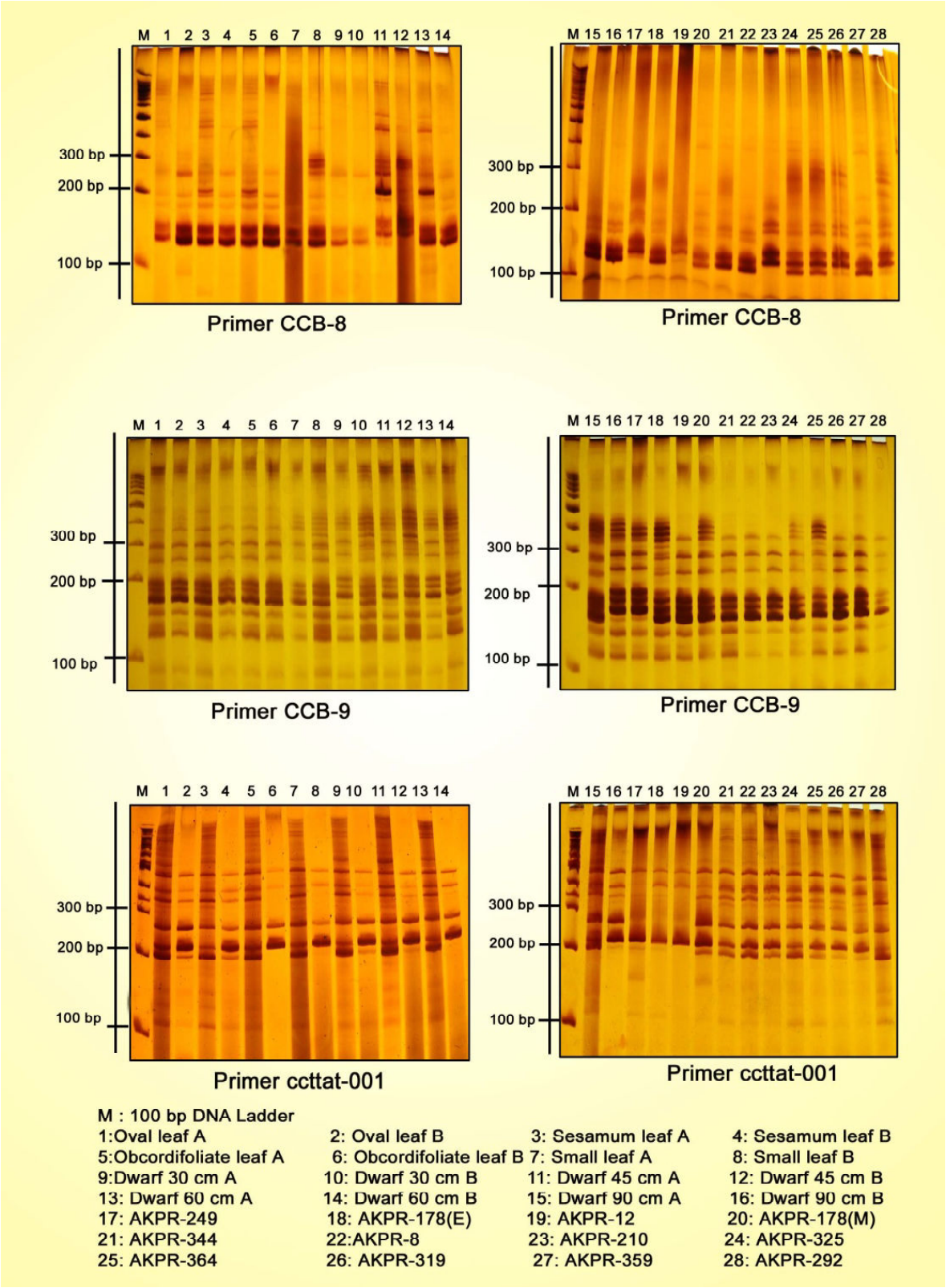

Fig.3 SSR banding profile of pigeonpea genotypes amplified with primers CCB-8, CCB-9 and ccttat-001

AKPR-249, AKPR-12, AKPR-178 (E) and type III was absent in Obcordifoliate leaf B, small leaf B, Dwarf 60 cm B and AKPR-12 genotypes.

The size of the bands amplified with selected primers was found in between 118 and 320 bp when compared with DNA molecular weight 100 bp ladder. A total of 63 alleles were obtained with an average of 3.1 alleles per locus. Similar results in expected size were observed by Burns *et al*. (2001), Odeny *et al*. (2007), Songok *et al*. (2010), Saxena *et al*. (2010). The average number of alleles locus^{-1} was 3.14 found by Odoney *et al*. (2009). Previous diversity analysis of cultivated pigeonpea species reported an average of 3.10 for 10 polymorphic loci (Burn *et al*. 2001) and 3.4 for 9 polymorphic loci (Odoney *et al*. 2007) which are similar to the present results in expected range.

In fact, some factors that are responsible for hiding the association between genetic divergence and heterosis which include the use of smaller set of SSR markers. If markers linked with heterotic components are used for such analysis, there is a high possibility of observing the association between genetic divergence and hybrid vigour. (Bohn et.al. 1999)

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Assessment of Genetic Divergence for Seed Related Characters in Selected Germplasm of Safflower

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ABSTRACT

The set of 150 genotypes along with five checks 'A-1, Bhima, Manjira, JSF-1 and HUS-305' were evaluated in augemented block design with five blocks at the field of Oilseed Research Unit, Dr. PDKV, Akola during rabi 2012-2013. The average inter cluster distance is maximum between clusters IX and XII (3635.208), followed by clusters VI and XII (3615.87), clusters VIII and XII (3542.073), clusters I and XII (2924.360), clusters XII and XIII (2892.245). The seed yield per plant, number of capitula per plant, days to maturity, seeds per capitulum,days to 50 per cent flowering, volume weight, oil content contribute significantly towards genetic divergence. The present study projected the importance of GMU-3439, GMU-3482, GMU-3475 as parents for higher heterosis in F_1 and potential transgrants in subsequent generations as they have least mean days to 50 per cent flowering, days to maturity, hull content and high mean of GMU-3590, GMU-3490, GMU-3433, A-1 and GMU-3522 for number of capitula per plant, number of seeds per capitula, 100 seed weight, ,volume weight, seed yield per plant and oil content respectively for the further improvement in respect to these seed characters.

Safflower (*Carthamus tinctorius* L.), is one of the important oilseed crop grown in winter season on residual soil moisture.The genetic diversity which is the basis of crop improvement is produced due to inherent genetic differences in plant species and hence, it is necessary to evaluate extent of genetic divergance in breeding lines. The selection of the parents for hybridization determines the success of breeding programme. There are many approaches for selection of parents for hybridization viz. multivariate analysis, ecographic diversity, regression analysis, selection of parents may also based on *per se* performance and combining ability analysis (Verma and Kumar, 1974). The importance of genetic diversity of crop improvement has long been appreciated by breeders but the basic difficulty was recognizing and estimating such diversity. The genetic diversity is the basis of plant breeding programme created due to inherent genetic differences in the plant species and is of major interest to plant breeder. The more diverse parent, the greater are the chances of obtaining higher amount of heterotic expression in F1 and broad spectrum of variability in segregating generations. So, there is an urgent need of detailed genetic evaluation for variability and genetic diversity in safflower germplasm collections. The present investigation was undertaken to measure the genetic diversity among the germplasm accessions of safflower and to select diverse genotypes which will be further utilize for the further genetic improvement of safflower.

MATERIAL ND METHODS

The experiment was conducted with 155 elite safflower genotypes which include five released varieties (HUS-305, A-1, JSF-1, MANJIRA and Bhima) at the field of Oilseeds Research Unit Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola. All the experiment was conducted during *Rabi* season of 2012-13 in a augmented blocked design, in a single row plot of four meter length. The experimental design consists of five block design with each block containing 30 germplasm and five checks. Check were comman for all recommendation cultural practices were followed to grow good crop. The observations were recorded on five randomly selected plants for nine quantitative traits *viz*., days to 50 per cent flowering, days to maturity, No. of capitula per plant, No. of seeds per capitulum, 100 seed weight, hull content per cent, volume weight (gm 100 ml^{-1}), seed yield per plant and oil content. The data were subjected to D^2 statistics as described by Rao (1952) and genotypes were grouped into different clusters by following Tochers method using Windstat statistical software.

RESULTS AND DISCUSSION

The analysis of variance and covariance to study the genetic differences among set of 150 germplasm lines and 5 checks for 9 traits under the study and the results are presented in Table 1. D^2 analysis was carried out to analyze genetic divergence among these genotypes. The

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variation among the genotypes were significant for days to 50 per cent flowering, days to maturity, number of capitula per plant, number of seeds per capitulum, 100 seed weight, hull content, volume weight, seed yield plant^{-1} and oil content indicating the presence of wide genetic variability for these characters.

The D^2 analysis resulted in the grouping of 150 genotypes and 5 checks were grouped into fourteen clusters by Tocher's method. Grouping pattern of different clusters is given in Table 2. Cluster IV was the largest involving 45 genotypes from different geographic origin. In this cluster IV check HUS-305 and cluster II check JSF-1 cluster V check Manjira, A-1, Bhima were included. The next largest cluster was cluster V (44 genotypes) and cluster II (29 genotypes) respectively. Cluster I and III having 14 genotypes each. VI,VII,VIII,IX,X,XI,XII,XIII involves only 1 number of genotype in each cluster.

Average intra and inter cluster statistical distance among 9 characters was calculated by Tocher's method and were presented in the Table 3. Maximum intra cluster value was observed for cluster V (308.713) and minimum cluster I (61.179). The average inter cluster distance was maximum between clusters IX and XII (3635.208), followed by clusters VI and XII (3615.87), clusters VIII and XII (3542.073), clusters I and XII (2924.360), clusters XII and XIII (2892.245).

The clusters having maximum distance were genetically divergent and hence genotypes in these clusters can be used as parent for breeding programme to obtain maximum segregation. The seed yield per plant, days to maturity, seeds per capitulum, days to 50 per cent flowering, volume weight, Oil content contribute Significantly towards genetic divergence overall study of cluster mean for all nine characters indicated that cluster XII showed maximum mean for character viz. Seeds per capitulum, number of capitula per plant, seed yield. The cluster IX exhibit highest cluster mean for oil contend, hull content while cluster VII showed highest cluster mean for days to maturity.

The contribution of each character towards genetic divergence has been presented in the Table 4. The contribution to the total divergence was maximum by seed yield per plant (32.39 %), number of capitula per plant (26.98 %), days to maturity (19.19 %), seeds per capitulum (10.83 %), days to 50 per cent flowering (8.36 %), volume weight (1.80 g lit^{-1}) and oil content (0.39 %). While hull content does not shown any contribution towards genetic divergence in the present study.

They analysis has helped to identify to diverse parents for hybridization progaramme on the basis of mean performance and cluster formed genotypes for different characters have been selected for used in further breeding programme in Table 5. GMU-3439, GMU-3482 and GMU-3475 having last mean for days to 50 per cent flowering, days to maturity and hull content. This genotype can be utilized as parents for getting higher heterosis in F_1 and potential transgrants in subsequent generalrous. Similarly GMU-3590, GMU-3490, GMU-3433, A-1 and GMU-3522 having high mean for number of capitula and seed capitilum^{-1}, 100 seed weight, volume weight, seed yield plant^{-1} and oil content respectively. These results are in conformity with that of Agarwal *et al*. (1982), Patil *et al*. (1991), Rao *et al* (1980), Diwaker *et al* (2006), Murkute (2010) and Sirisha *et al*. (2012). This genotype can be

Table 1: Analysis of variance for augmented design

Source of error	Df	Days to 50% flowerig	Days to maturnity	No. of capitula plant^{-1}	Number of seeds capitulum^{-1}	100 seed wt (gm)	Hull content (g)	Volume wt (g/100ml)	Seed yield plant^{-1}	Oil content (%)
Blocks	4	8.48	22.15	798.87**	700.89**	1.89**	0.19**	3.52 **	191.55	2.24 **
Entries	154	15.25**	32.56**	88.95	82.94	0.99**	0.07**	6.14***	80.73	2.47**
Checks	4	22.76**	134.94**	399.14**	341.96**	1.69**	0.12**	28.14 **	564.56**	2.13**
Germplasm	149	14.83**	29.94 **	79.82	74.82	0.87**	0.07*	5.56***	55.54	2.49 **
Germplasm with check	1	46.94 **	14.18	207.70	256.53*	16.32**	1.01 **	5.83 **	1897.81**	1.17 *
Error	16	3.23	8.74	56.42	56.54	0.29	0.02	0.63	108.63	0.23

Note- * significance at 5% level, ** significance at 1% level

Table 2. Grouping of genotypes into different clusters

Cluster	No. of genotypes	Name of genotypes
I	14	GMU-3470, GMU-3444,GMU-3491, GMU-3436, GMU-3472, GMU-3475,GMU-3495, GMU-3522, GMU-3512, GMU-3517, GMU-3527, GMU-3589, GMU-3567, GMU-3573
II	29	GMU-3455, GMU-3448, GMU-3441, GMU-3450, GMU-3445, GMU-3488, GMU-3460, GMU-3509, GMU-3503, GMU-3502, GMU-3508, GMU-3524, GMU-3525, GMU-3523, GMU-3532, GMU-3514, GMU-3544, GMU-3507, GMU-3551, GMU-3552, GMU-3597, GMU-3561, GMU-3618, GMU-3616, GMU-3607, GMU-3585, GMU-3547, GMU-3620,JSF-1.
III	14	GMU-3469, GMU-3474, GMU-3442, GMU-3454, GMU-3499, GMU-3501, GMU-3504, GMU-3579, GMU-3614, GMU-3603, GMU-3594, GMU-3595, GMU-3600, GMU-3605.
IV	45	GMU-3478, GMU-3468, GMU-3481, GMU-3438, GMU-3452, GMU-3435, GMU-3447, GMU-3458, GMU-3467, GMU-3476, GMU-3462, GMU-3433, GMU-3548, GMU-3533, GMU-3541, GMU-3521, GMU-3516, GMU-3519, GMU-3505, GMU-3530, GMU-3492, GMU-3511, GMU-3518, GMU-3535, GMU-3549, GMU-3494, GMU-3539, GMU-3513, GMU-3558, , GMU-3562, GMU-3617, GMU-3583, GMU-3596, GMU-3577, GMU-3601, GMU-3586, GMU-3587, GMU-3598, GMU-3581, GMU-3593, GMU-3619, GMU-3571, GMU-3612, GMU-3599,HUS-305.
V	44	GMU-3451, GMU-3465, GMU-3446, GMU-3449, GMU-3473, GMU-3545, GMU-3490, GMU-3477, GMU-3432, GMU-3434, GMU-3443, GMU-3480, GMU-3485, GMU-3431, GMU-3459, GMU-3528, GMU-3537, GMU-3506, GMU-3510, GMU-3515, GMU-3526, GMU-3556, GMU-3553, GMU-3547, GMU-3531, GMU-3550, GMU-3496, GMU-3534, GMU-3543, GMU-3572, GMU-3575,MANJIRA, , GMU-3564,BHIMA, GMU-3557, GMU-3563, GMU-3578, GMU-3560, GMU-3610, GMU-3565, GMU-3568, GMU-3569, GMU-3602,A-1.
VI	1	3463
VII	1	3486
VIII	1	3493
IX	1	3615
X	1	3439
XI	1	3456
XII	1	3590
XIII	1	3482
XIV	1	3484

Table 3. Ave rage Intra and Inter cluster distances

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**	**Cluster XI**	**Cluster XII**	**Cluster XIII**	**Cluster XIV**
Cluster I	**61.179**	471.682	859.416	211.842	1146.304	100.312	379.479	146.339	159.539	383.827	495.350	2924.360	529.682	1665.067
Cluster II		**94.839**	215.711	286.043	352.376	775.858	317.034	716.169	775.478	238.675	192.767	1261.576	710.517	618.495
Cluster III			**152.704**	558.858	441.246	1273.339	418.611	1072.276	1133.767	509.922	287.916	1078.193	1135.760	451.968
Cluster IV				**212.678**	781.428	353.318	359.036	380.316	418.844	350.152	373.988	2151.634	636.824	1241.423
Cluster V					**308.713**	1560.905	876.641	1552.793	1653.966	573.866	564.889	733.467	1185.858	607.969
Cluster VI						**0.000**	565.613	227.830	215.957	659.054	797.540	3615.870	560.791	2178.259
Cluster VII							**0.000**	523.237	485.477	325.654	149.505	2307.010	391.047	736.857
Cluster VIII								**0.000**	82.140	513.930	683.582	3542.073	858.254	2015.801
Cluster IX									**0.000**	640.192	659.954	3635.208	728.469	2058.607
Cluster X										**0.000**	210.249	1922.125	451.792	831.207
Cluster XI											**0.000**	1667.733	508.571	685.004
Cluster XII												**0.000**	2892.245	978.070
Cluster XIII													**0.000**	1276.098
Cluster XIV														**0.000**

Table 4. Contribution of each character towards genetic divergence

S. N.	Source	Times rank first	% Contribution
1	Days to 50 % Flowering	998	8.36
2	Days to Maturity	2290	19.19
3	No. of Capitula Per Plant	3220	26.98
4	No.of Seeds/ Capitulum	1293	10.83
5	100 Seed Weight (g)	6	0.05
6	Hull content (%)	0	0.00
7	Volume wt (g/100ml)	215	1.80
8	Seed Yield/ Plant (g)	3866	32.39
9	Oil Content (%)	47	0.39

Table 5. Cluster means for nine characters

Character/ Cluster	Days to 50 % Flowering	Days to Maturity	No. of Capitula Plant^{-1}	No.of Seeds Capitulum	100 Seed Weight (g)	Hull content (g)	Volume wt (g l^{-1})	Seed Yield Plant^{-1} (g)	Oil Content (%)
Cluster I	66.249	140.360	13.326	13.420	4.087	0.659	26.253	8.426	23.869
Cluster II	66.585	139.941	26.349	26.454	4.543	0.693	26.725	15.993	23.728
Cluster III	66.391	136.260	32.683	32.177	4.477	0.675	26.870	12.453	23.818
Cluster IV	68.060	141.228	18.901	19.415	4.658	0.784	27.249	10.865	22.811
Cluster V	67.412	143.640	31.605	31.798	4.805	0.809	27.481	25.185	23.511
Cluster VI	68.920	139.960	8.240	8.720	4.424	0.725	30.145	7.630	22.999
Cluster VII	63.920	126.360	21.840	21.320	4.944	0.831	29.143	10.798	23.781
Cluster VIII	59.920	140.360	12.840	12.320	4.744	0.581	21.713	1.398	21.421
Cluster IX	65.720	135.560	11.840	10.920	3.544	0.525	18.441	2.294	24.511
Cluster X	55.920	138.960	20.240	21.720	3.624	0.895	24.825	19.730	23.819
Cluster XI	63.920	130.960	20.240	29.720	2.624	0.965	24.055	15.670	24.229
Cluster XII	75.720	147.560	46.840	45.920	3.144	0.825	24.541	32.134	20.861
Cluster XIII	65.920	126.360	12.840	12.320	5.744	1.391	27.713	25.638	22.431
Cluster XIV	61.920	127.360	43.840	29.320	4.344	0.531	29.713	24.318	23.241

utilized for the further improvement of these characters in safflower breeding programme.

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Analysis of Genetic Variability and Correlation in F_2 Populations of Linseed

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ABSTRACT

The genetic variability and nature of character association were studied in seven F_2 crosses along with six parents of linseed. A wide range of genetic variability was observed in yield and yield contributing traits. Seed yield plant^{-1} (g) and number of capsules plant^{-1} recorded high genotypic coefficient of variation. All of the characters evaluated, exhibited high magnitude of heritability in broad sense and genetic advance. Number of capsules plant^{-1} had significant positive correlation with seed yield plant^{-1} indicating the significance at this trait for indirect selection for high yielding crosses.

Linseed (*Linum usitatissimum* L.) is an important oilseed crop of the world grown during *rabi* season. It plays a major role in catering edible oil as well as industrial demand of the century. In India, production of edible oil is grossly short of the requirements. Consequently, large quantities have to be imported for making up the shortfall, which is turn, is a drain on foreign exchange resources.

India ranks first in area in the world, but is at fifth place in terms of productivity. However, there is considerable scope for improving the yield potential of this crop. Vigorous efforts, therefore, are needed to increase the yield levels and to achieve self sufficiency. Yield is one of the most important economic character and is the product of multiplicative interaction of contributing characters. Designing efficient and desirable plant type requires the existence of genetic variability in the material. In order to incorporate desirable characters to maximize economic yields, the information on the nature and extent of genetic variability present in a population for desirable characters, their association and relative contribution to yield constitutes the basic requirement. F_2 generation provides an active breeding material from which desirable plants may be selected (Cavalli, 1952 and Jain *et al.,* 1988). Knowledge of the magnitude and type of association between yield and its components themselves greatly help in evaluating the contribution of different yield components towards yield. Correlation between yield and its components have been immense importance in selecting suitable plant type.

The area under linseed in world and in India is decreasing from last five decades. The future prospects for increasing area under linseed seem to be limited. Therefore, this study was undertaken with an objective to estimate the genetic parameters in F_2 population for further selection.

MATERIAL AND METHODS

The present experiment was conducted during *Rabi* 2013- 14 in Agriculture Botany Section, College of Agriculture, Nagpur. The experimental material included Seven F_2 populations derived from F_1's raised during *Rabi* 2011- 12.

Six linseed genotypes of diverse origin were crossed in a line x tester design. The resultant 7 crosses along with their six parents were sown in F_1 generation during rabi 2012. The six parents and their 7 crosses were grown during rabi 2013-14 in randomized complete block design with two replications. Three rows for each F_2 cross and parent were allotted. Each row consisted of 24 plants. Sowing was taken up with a spacing of 45x3 cm. The recommended cultural practices and plant protection measures were undertaken as per schedule to raise a healthy crop. The observations were recorded on 100 plants in each F_2 population and five randomly selected plant in each parent for the following eight characters *viz.,* days to 50 per cent flowering, days to maturity, plant height at maturity (cm), number of primary branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsules^{-1}, seed yield plant^{-1} (g) and oil content (%).

The data were subjected to the following statistical and biometrical analysis and genetic parameters in each F_2 variance (V_{F2}) , Genotypic variance (V_G), Environmental variance (V_E), Phenotypic and Genotypic coefficient of variation, Heritability (broad sense) (%) and Genetic advance were estimated using standard formulae. Genotypic correlation were computed according to Burton and Devane (1953).

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RESULTS AND DISCUSSION

Significant genotypic differences were observed for five out of eight characters studied viz., days to 50 per cent flowering, plant height at maturity (cm), number of primary branches plant^{-1}, number of capsules plant^{-1} and seed yield plant^{-1} (g) indicating substantial genetic variability for these characters among the genotypes (Table-1).

The mean performance, range, variance, coefficient of variation and heritability and genetic advance of each F_2 population are presented in Table 2.

The maximum number of primary branches plant^{-1} and number of capsules plant^{-1} were produced in cross EC-1392 x NL-97 while cross EC-1392 x Padmini produced maximum seed plant^{-1}. The magnitude of coefficient of variation among the different population was high for seed yield plant^{-1} and number of capsules plant^{-1}. Moderated coefficient of variation was observed for primary branches plant^{-1}. The coefficient of variation was low for plant height at maturity and not estimated in days to 50 per cent flowering and days to maturity indicating uniformity among the F_2 population for these traits.

Estimates of heritability in broad sense were high ranging from 67.15 to 98.31 for characters viz., number of capsules plant^{-1} (75.25 to 98.17) and seed yield plant^{-1} (67.15 to 98.31). The significance of number of capsules plant^{-1} in F_2 crosses with high heritability for making selection also observed by Savita *et al* (2007) and Kumar *et al* (2012). Estimates of heritability revealed that the selection can effectively be made on phenotypic basis by means of selection for high estimates of heritability.

The crosses EC-1392 x NL-97 and EC-1392 x Padmini had high heritability and genetic advance for primary branches plant^{-1} and number of capsules plant^{-1} indicates the predominance of additive gene action for these traits, there by suggesting amenability of these characters through selection. The significance of primary branches plant^{-1} and number of capsules plant^{-1} in F_2 populations with high heritability and high genetic advance for making selection also observed by Reddy et al (2013).

High heritability with lower values of genetic advance and high genetic coefficient of variation estimates observed in crosses JRF-4 x Padmini and EC-1392 x Padmini for seed yield plant^{-1} indicated the presence of non additive gene action so that selection of superior plants in F_2 population for seed yield would not be rewarding. Similar results were also observed by Bibi et al (2011) and Reddy *et. al.,* (2013).

Correlation of favourable genes and break up of linkages associated with mating system causes a change and direction of character association as a result of recombination (Vinayan and Govindarasu, 2010). These associations are best measured in correlation co-efficient. The knowledge of interrelationship of plant characters with seed yield plant^{-1} helps the breeder in improvement of complex characters like seed yield plant^{-1} for which direct selection is not much effective. Recombination in segregating generations leads to formation of new pattern of association of linked characters, hence the genotypic correlation co-efficient of different characters with seed yield plant^{-1} were estimated and presented in Table 3. Plant height at maturity exhibit significant positive correlation with days to 50 per cent flowering (r_g = 0.7256**) and negative correlation with seed yield plant^{-1} (r_g = -0.1984). Primary branches plant^{-1} exhibit significant positive correlation with oil content (r_g = 0.8348**) and capsule plant^{-1} (r_g = 0.5611*) and positive correlation with seed yield plant^{-1} (r_g = 0.3406). Capsule plant^{-1} was found to exhibit high significantly correlated with days to maturity positive correlation with all the character study except for days to 50 per cent flowering and seed capsules^{-1}. Days to maturity exhibited positive correlation with oil content (r_g = 0.4367), yield plant^{-1} (r_g = 0.3704), seed capsules^{-1} (r_g = 0.2082) and days to 50 per cent flowering (r_g = 0.1770). Oil content also exhibited positive correlation with yield plant^{-1} (r_g = 0.1782), seed capsules^{-1} (r_g = 0.0891) and days to 50% flowering (r_g = 0.0057). Days to 50 per cent flowering exhibited negative correlation with yield plant^{-1} (r_g = -0.3828) and positively correlated with seed capsules^{-1} (r_g = 0.2529). Seed capsules^{-1} exhibited positive correlation with yield plant^{-1} (r_g = 0.0832).

The correlation coefficient of seed yield plant^{-1} with different traits revealed that primary branches plant^{-1}, days to maturity, oil content and seed capsule^{-1} were positively associated with yield plant^{-1} but negatively association with plant height and days to 50 per cent flowering. Usually quality characters like oil content were found to be positively correlated with yield parameter. It can be concluded from the correlation studies that capsule plant^{-1} exhibited the maximum significant correlation coefficient with seed yield plant^{-1}. This trait can be used

Table 1. Analysis of variance for seven characters in linseed

Source of variation	d.f.	Mean Square						
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches plant^{-1}	Number of capsules plant^{-1}	Number of seed capsule^{-1}	Seed Yield plant^{-1} (g)
Replications	1	12.461	26	81.738	2.117	7.399	0.111	0.0008
Genotypes	12	21.801*	2.833	336.513**	2.950**	45.200**	0.822	0.140**
Error	12	3.878	4.333	42.169	0.381	12.28	0.402	0.018

** Significant at 1%,* Significant at 5%.

Table 2. Estimation of genetic parameters in each F_2 population

S.N.	F_2 crosses/	Number of primary branches plant^{-1}						Number of capsules plant^{-1}						Seed yield plant^{-1}					
	Parents	Mean	Range	VF_2	GCV (%)	h^2 (%)	Genetic Advance	Mean	Range	VF_2	GCV (%)	h^2 (%)	Genetic Advance	Mean	Range	VF_2	GCV (%)	h^2 (%)	Genetic Advance
1	JRF-4 X Padmini	07.06	19.00 (4-23)	06.79	31.58	73.22	03.93	27.98	76.9 (1.6-78.5)	176.88	45.31	90.94	24.91	01.16	14.8 (0.2-15)	1.61	108.56	98.31	2.57
2	JRF-4 X NL-97	7.16 16.00	07.25 (3-19)	32.42	74.31	04.12	20.09	78.0	124.78 (06-84)	48.22	75.25	17.31	00.60	2.3	0.11 (0.2-2.5)	046.49	67.15	0.47	
3	JRF-4 X PKVNL-260	08.07	12.00 (5-17)	03.41	17.65	59.51	02.26	28.66	4.00 (09-73)	159.03	42.78	94.60	24.57	01.16	3.70 (0.3-4)	0.31	046.21	92.30	1.06
4	EC-1392 X Padmini	08.29	18.00 (4-22)	09.61	32.38	75.02	04.79	30.52	3.00 (10-93)	360.30	61.62	98.17	38.38	01.43	3.80 (0.2-4)	0.70	057.73	97.89	1.68
5	EC-1392 X NL-97	08.35	17.00 (4-21)	10.47	33.92	76.63	05.10	27.38	00.0 (8-108)	377.37	68.18	92.35	36.95	00.96	2.8 (0.1-2.9)	0.30	053.86	90.41	1.02
6	GS-234 X NL-97	07.10	14.00 (3-17)	04.94	25.62	66.94	03.06	24.99	95.5 (4-99.5)	231.29	59.36	95.21	29.82	00.79	3.3 (0.1-3.4)	0.26	060.63	86.09	0.91
7	GS-234 X PKVNL-260	07.88	19.00 (4-23)	06.12	28.40	81.92	04.17	22.02	51.5 (9-60.5)	107.23	45.17	92.26	19.68	01.13	2.7 (0.3-3.0)	0.35	050.13	90.91	1.11

Table 3. Estimation of correlation coefficient for different characters with seed yield plant^{-1}

No.	Characters	Primary branches plant^{-1}	Capsules plant^{-1}	Days to maturity	Oil content	Days to 50% Flowering	Seed capsule	Yield plant^{-1}
1	Plant height at maturity	-0.1351	0.1456	-0.5062	0.3401	0.7259**	-0.0198	-0.1984
2	Primary branches plant^{-1}		0.5611*	0.4944	0.8348**	-0.0010	0.5031	0.3406
3	Capsules plant^{-1}			0.9154**	0.5408*	0.0067	0.1451	0.6204*
4	Days to maturity				0.4367	0.1770	0.2082	0.3704
5	Oil content					0.0057	0.0891	0.1782
6	Days to 50% maturity						0.2529	-0.3828
7	Seed capsule^{-1}							0.0832

Note:- ** Significant at 1% and * significant at 5%.

for genetic analysis in F_2 population to improve seed yield plant^{-1} in linseed. Akbar *et al*. (2001) observed number of capsules plant^{-1} had highly significant positive genotypic correlation coefficient with seed yield plant^{-1}.

On the basis of high mean, genotypic coefficient of variation, heritability and genetic advance for economic traits like number of capsules plant^{-1} and seed yield plant^{-1}, five crosses *viz.,* EC-1392 × Padmini, EC-1392 × NL-97, GS-234 × NL-97, JRF-4 × Padmini, JRF-4 × PKVNL-260 were identified as the potential crosses for obtaining segregants and hence were subjected to individual plant selection. The study revealed scope for early generation selection owing to high genetic variability, heritability and genetic advance for number of capsules plant^{-1} and seed yield plant^{-1} in five crosses *viz.,* EC-1392 × NL-97, EC-1392 × Padmini, GS-234 × NL-97, JRF-4 × PKVNL-260, JRF-4 × Padmini in which individual plant selection were effected. Capsule plant^{-1} exhibited the maximum significant correlation coefficient with seed yield plant^{-1}. This trait can be used for genetic analysis in F_2 population to improve seed yield plant^{-1} in linseed.

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Germplasm Evaluation in Medicinal Plants for Crop Improvement

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ABSTRACT

The extent of variability in plant, determines the limits of selection for its improvement. Therefore a systematic work on germplasm characterization and evaluation including agro-morphological and quality parameters to assess the genetic variability and utilization in developing varieties has been carried out in important medicinal plants like Safed musli (*Chlorophytum borivilianum*),Aloe vera (*Aloe barbadensis*) and Ashwagandha(*Withania somnifera*) . The results revealed that the genotype AKSM –13 of Safed musli produced higher root weight per plant followed by AKSM–12.The highest saponin content was observed in AKSM-12.Among the eleven genotypes under PYT, the genotype AKSM – 08 and AKSM – 07 recorded significantly higher root yield. Significantly higher saponin content was observed in AKSM-08

In Aloe vera the genotype IC 112532 recorded significantly highest leaf length, leaf thickness, and leaf weight as well as mucilage per cent and in Ashwagandha the genotype AKA- 13 and check JA -134 recoded highest root yield (3.80g) plant^{-1}.

The genetic variability in medicinal plants is due to prolonged changes in the habitat and environment like other plants in nature. It is essential to enrich the genetic diversity by evaluating them for agro-morphological and quality parameters including active compounds and identification of value rich germplasm to develop an improved cultivar for their utilization. After agro-morphological and chemical, the promising germplasm will be harnessed for commercial production of raw material as well as to find out the newer source of drugs. The extent of variability in plant, determines the limits of selection for its improvement. Therefore a systematic work on germplasm characterization and evaluation including agro-morphological and quality parameters to assess the genetic variability and utilization in developing varieties has been carried out in important medicinal plants like Safed musli (*Chlorophytum borivilianum*),Aloe vera (*Aloe barbadensis*) and Ashwagandha(*Withania somnifera*).

MATERIAL AND METHODS

Safed Musli (*Chlorophytum borvilianum*) is an important Ayurvedic medicinal herb belongs to family Liliaceae. The roots of this herb are mainly used to treat general debility and male sterility. It is also advised as a supplementary therapy for blood purification, nervous disorder and some gynecological problems. The dried fasciculated roots are reputed to have aphrodisiac properties and from an important ingredient of herbal tonics prescribed in Ayurvedic system of medicine in India.

Thirteen genotypes collected from the forest area of Melghat and one check viz MCB 405 (variety released by Mansoor centre, MP) were planted in *Kharif* 2013-14 in a plot size of 2.10 x 3.0 m with seven lines of each genotypes under study The morphological characters viz., Number of leaves per plant, Length of leaves, Width of leaves, Number of root plant^{-1}, Root length, Root girth and Fresh weight of root were recorded. Being a non replicated trial only standard deviation was worked out. A preliminary yield trial of Safed musli to assess the yield potential and quality of different genotypes was also conducted with eleven genotypes including one check MCB-405 tried in RBD with three replications.

Aloe barbadensis (2n = 14) is an important medicinal plant of India belongs to the family Liliaceae. Because of its huge demand and vast utility, it is widely collected indiscriminately from the wild source and thus this species is becoming commercially threatened due to over and destructive harvesting from natural sources. The commercial cultivation is not popular among the farming community due to lack of technical know-how on geunine type of *Aloe vera* and its package of practices. Though there is much diversity in Aloe vera, the cultivators are unable to choose the best ecotype genetically differentiated subpopulation that is restricted to a specific habitat for commercial cultivation.

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Nine genotypes were collected from throughout Maharashtra region and eight genotypes from National Research Centre, Boriavi (Anand), Gujrat. In all seventeen genotypes were planted in *Kharif* season 2013-14 for evaluation.

Ashwagandha(*Withania somnifera*) a medicinal plants belongs to Soalnaceae family found throughout drier parts of India. The roots are compact and light brown in colour , contain alkaloids (Withanin, somniferin, etc.) and steroidal lactones (Withanolides).The roots are being used for rheumatic pain, general debility, mental disorders and gynecological problems. Also used as tonic for hiccup, cough, female disorders, as a sedative, in care of sensile debility and ulcers etc. The leaves and seeds are also having medicinal property to cure carbuncles, inflammation and swellings and seed as diuretic.

Thirteen genotypes of Ashwagandha along with two varieties (developed by JNKKV, Mandsoor) were evaluated under Akola condition in late kharif season of 2013-14

RESULTS AND DISCUSSION

In evaluation trial of Safed musli conducted during the kharif season of year 2013-14. out of thirteen genotypes and one check viz MCB 405, genotype AKSM -13 exhibited its superiority for number of root per plant, root length and fresh root weight per plant (20.00 g).However, highest saponin content was observed in AKSM-12(Table 1).

Out of eleven genotypes including one check MCB-405 tested under PYT , two genotypes AKSM -08 and AKSM – 07 recorded significantly higher root yield (44.05 and 40.86 q ha^{-1}) over the check MCB - 405 (37.22 q ha^{-1}). As regarding the other characters AKSM – 07 and AKSM – 08 recorded at par performance with the check MCB – 405. However, significantly higher saponin content was observed in AKSM-08 as compared other genotypes tested (Table 2). Data recorded for number of leaves, length of leaves and width of leaves was found non- significant. Similar results were also observed by Anonymous, 2014 a.

Table 1. Morphological characters of Safed musli

Genotype	No. of Leaves Plant^{-1}	Length of the Leaves (cm)	Width of Leaves (cm)	No. of Root Plant^{-1}	Root Length (cm)	Root Girth (mm)	Fresh weight of Root (g Plant^{-1})	Sapo-nin (%)
AKSM-01	10.00	18.52	1.56	9.00	7.77	5.92	16.80	7.05
AKSM-02	10.80	19.23	1.78	9.20	4.81	6.66	17.00	7.15
AKSM-03	11.00	20.09	1.73	9.80	4.75	6.81	18.00	7.28
AKSM-04	10.00	20.97	1.74	12.20	2.57	6.72	12.60	6.75
AKSM-05	9.80	23.35	1.72	10.00	4.81	6.59	17.00	7.10
AKSM-06	10.00	21.45	1.80	9.80	4.76	6.60	16.80	6.90
AKSM-07	11.80	20.36	1.78	10.20	5.02	7.17	18.60	7.45
AKSM-08	10.00	21.57	1.83	10.20	5.06	7.11	19.00	8.53
AKSM-09	10.20	21.35	1.74	9.00	6.00	6.64	16.60	7.41
AKSM-10	9.20	20.65	1.78	9.00	5.50	6.60	18.00	7.53
AKSM-11	10.20	20.49	1.82	10.00	4.85	5.75	17.20	11.03
AKSM-12	12.60	22.75	1.89	11.00	6.41	6.86	**19.20**	**12.01**
AKSM-13	**12.40**	18.75	1.79	**11.20**	**6.51**	6.71	**20.00**	6.88
MCB-405	10.40	18.64	1.76	10.40	5.81	5.81	18.40	7.10
Mean	**10.60**	**20.58**	**1.77**	**10.07**	**5.33**	**6.57**	**17.51**	**7.87**
SD ±	**1.01**	**1.48**	**0.07**	**0.93**	**1.25**	**0.44**	**1.76**	**1.62**

Table 2. Yield contributing characters and yield of various genotypes of Safed Musli under PYT

Genotype	No. of Roots Plant^{-1}	Length of roots (cm)	Girth of roots (mm)	Fasciculated root weight (g Plant^{-1})	Fasciculated root yield (q ha^{-1})	Saponin (%)
AKSM-01	21.80	7.27	5.37	16.73	31.93	6.93
AKSM-02	27.20	5.02	6.23	17.93	34.96	6.95
AKSM-03	27.20	5.12	6.49	16.60	34.98	6.71
AKSM-04	37.40	2.76	6.33	13.33	29.01	6.59
AKSM-05	27.60	5.31	6.97	16.40	33.06	6.34
AKSM-06	27.00	5.12	6.71	18.33	35.95	7.00
AKSM-07	29.20	5.40	7.00	19.00	40.86	6.68
AKSM-08	30.20	5.58	6.95	19.47	44.05	7.33
AKSM-09	24.00	5.92	6.33	16.60	33.69	6.53
AKSM-10	27.00	4.82	6.28	17.13	31.40	6.68
MCB-405	28.80	5.79	6.25	18.80	37.22	7.00
SE (M)±	0.50	0.18	0.29	0.87	1.53	0.07
CD (0.5%)	1.48	0.52	0.85	2.55	4.48	0.20
CV%	10.20	6.32	8.52	9.50	8.20	1.86

Table 3. Yield contributing characters of Aloevera of Aolevera

SN	Genotype	Plant height (cm)	No. of suckers Plant^{-1}	No. of Leaves Plant^{-1}	Leaf Length (cm)	Leaf width (cm)	Leaf thickness (mm)	Leaf weight (g/Plant)	Mucillege (%)
1	AKAv 09-01	**60.85**	4.50	**15.00**	**55.45**	**7.03**	14.54	277.40	51.40
2	AKAv 09-03	48.30	6.40	12.10	45.55	6.02	16.90	227.10	63.74
3	AKAv 09-04	46.60	4.80	11.70	43.32	5.24	16.95	196.40	63.31
4	AKAv 09-05	48.90	4.20	11.70	46.10	6.28	17.09	240.70	65.21
5	AKAv 09-06	46.00	5.80	12.10	43.20	5.84	16.81	212.20	59.71
6	AKAv 09-07	47.10	5.60	12.00	43.00	5.76	17.00	230.80	62.89
7	AKAv 09-08	48.40	6.00	12.10	45.80	6.76	16.22	257.70	64.81
8	AKAv 09-09	43.60	4.10	11.60	41.50	5.78	17.15	216.60	64.90
9	AKAv 09-10	47.90	5.40	12.10	44.30	5.77	17.09	241.10	60.50
10	IC 285626	51.21	7.20	12.20	45.25	6.52	16.62	219.00	64.96
11	IC 285629	52.17	4.70	11.80	47.26	6.68	16.07	247.30	65.75
12	IC 285630	53.10	5.70	12.50	47.50	6.47	17.42	290.70	71.07
13	IC 310619	47.55	7.20	11.90	44.35	6.00	15.72	233.70	61.43
14	IC 112521	51.40	5.80	12.30	47.40	6.84	15.86	261.60	63.43
15	IC 112527	52.90	5.60	11.50	50.10	6.34	16.22	271.90	59.28
16	IC 112531	50.10	4.30	11.90	47.20	6.46	17.41	257.40	62.09
17	IC 112532	55.20	4.50	13.20	52.20	6.70	18.29	325.70	70.63
	SE (M)±	2.10	0.78	0.33	1.84	0.38	0.87	16.98	1.58
	CD (0.5%)	6.30	N.S.	0.98	5.52	N.S.	2.61	50.89	4.74
	CV%	5.94	20.55	3.77	5.61	8.69	7.37	9.70	3.54

Table 4. Morphological character of Aloe Vera

S. N.	Genotypes	Leaf orientation	Leaf color	Blotches on young Leaves	Spine color
1	AKAv 09-01	Whorled	Pale	Medium	**Light red**
2	AKAv 09-03	Whorled	Pale	**Heavy**	Pale
3	AKAv 09-04	Whorled	Pale	Medium	Pale
4	AKAv 09-05	Whorled	Pale	Medium	Pale
5	AKAv 09-06	Whorled	Pale	Medium	Pale
6	AKAv 09-07	Whorled	Pale	Medium	Pale
7	AKAv 09-08	Whorled	Pale	Medium	Pale
8	AKAv 09-09	Whorled	Pale	Medium	Pale
9	AKAv 09-10	Whorled	Pale	Medium	Pale
10	IC 285626	Whorled	Pale	Medium	Pale
11	IC 285629	Whorled	Pale	Medium	Pale
12	IC 285630	Whorled	Pale	Medium	Pale
13	IC 310619	Whorled	Pale	Medium	Pale
14	IC 112521	Whorled	Pale	Medium	Pale
15	IC 112527	Whorled	Pale	Medium	Pale
16	IC 112531	Whorled	Pale	Medium	Pale
17	IC 112532	Whorled	Pale	Light	Pale

Table 5. Morphological character and root yield of Ashwagandha (*Withania somnifera*)

SN	Genotype	Plant height (cm)	No. of main branches	Berries Plant^{-1}	Root Length (cm)	Root Diameter (mm)	No. of Secondary root	Seed yield (g Plant^{-1})	Dry Root yield (g Plant^{-1})	Berry colour	Matu rity duration
1	AKA-01	50.80	2.60	166.20	18.30	8.32	2.00	5.80	3.40	Y	E
2	AKA-02	39.40	2.20	162.00	17.90	8.95	2.40	5.20	1.80	Y	E
3	AKA-03	38.60	2.00	149.40	18.70	8.65	2.40	3.60	2.00	Y	E
4	AKA-04	37.48	2.40	172.20	18.10	8.40	2.20	4.60	1.60	Y	E
5	AKA-05	43.40	2.40	164.20	18.80	8.59	2.00	5.20	1.60	Y	E
6	AKA-06	37.90	2.20	129.40	18.76	8.76	2.20	3.00	1.80	Y	E
7	AKA-07	42.50	2.60	157.20	18.44	8.68	2.20	4.80	2.20	Y	E
8	AKA-08	37.30	1.80	124.80	16.40	7.42	2.40	4.40	1.80	Y	E
9	AKA-09	42.20	2.20	132.80	18.30	8.11	2.00	3.40	1.40	**R**	**M**
10	AKA-10	53.80	2.40	140.40	19.00	8.47	2.40	3.60	3.40	**R**	**M**
11	AKA-11	56.80	2.40	141.60	19.00	8.71	2.40	3.40	3.20	Y	E
12	AKA-12	44.50	2.20	121.80	18.00	8.38	2.20	2.80	1.40	Y	E
13	AKA-13	48.00	1.80	131.20	**19.60**	**9.89**	**2.60**	3.40	**3.80**	Y	E
14	JA-134	41.00	2.40	143.80	19.30	8.87	2.40	3.60	3.80	Y	E
15	JA-20	47.80	2.80	178.40	18.60	9.36	2.40	6.00	2.80	Y	E
	Mean	**44.10**	**2.29**	**147.69**	**18.85**	**8.64**	**2.28**	**4.19**	**2.40**		
	SD ±	**6.13**	**0.28**	**18.10**	**1.42**	**0.55**	**0.18**	**1.03**	**0.90**		

Y= Yellow, R=Red. E= Early M= Medium

Out of 17 genotypes of Aloe vera evaluated for morphological parameters revealed that IC 112532 exhibits its significance for plant height, number of leaves per plant, leaf length, leaf width, leaf thickness and leaf weight along with higher mucilage (pulp) per cent, followed by the local collected genotype AKAv 09-01 and IC 285630 (Table-3). Similar results were also observed by Anonymous, 2013.

The study on collection, maintenance and evaluation of germplasm of Ashwagandha (*Withania somnifera Dunal*) revealed that genotype AKA- 13 recorded higher root length (19.60cm), root diameter (9.89 mm), number of secondary roots and dry root yield per plant (3.80). Similarly the check variety JA – 134 recorded the equal dry root yield, followed by AKA -01 and AKA -10. As regard the berry colour AKA -09 and AKA -10 exhibited red colour are having medium maturity (Anonymous, 2014b).

CONCLUSION

Genotype AKSM –13 of Safed musali produced higher root weight per plant followed by AKSM–12. The highest saponin content was observed in AKSM-12.

Among the eleven genotypes of Safed musali under PYT. Genotype AKSM – 08 and AKSM – 07 recorded significantly higher root yield (q ha^{-1}).Significantly higher saponin content was observed in AKSM-08

The genotype IC 112532 of Aloevera recorded significantly highest leaf length, leaf thickness, and leaf weight as well as mucilage per cent. In terms of qualitative attributes light spine color in AKAv 09-01, heavy blotches on young leaves in AKAv 09-03 and light blotches on young leaves of IC 112532 were identified as a marker characters.

The genotype AKA-13 and check JA -134 of Ashwagandha recorded highest root yield (3.80g) $plant^{-1}$.

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AKU 10-1: High Yielding, Early, Medium Bold Seeded Genotype of Blackgram for Maharashtra

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ABSTRACT

AKU 10-1 high yielding genotype of urdbean (*Vigna mungo (L)* Hepper) derived through hybridization followed by pedigree selection method from a cross of TAU-1 x AKU-18-1. It has early (70 days) and synchronous maturity with medium bold grain size (4.5 g 100 seed^{-1}). The variety has shown tolerance to *Macrophomina* blight and moderately resistant to powdery mildew. In Vidarbha region it was found to be superior by 19.59 per cent, 21.57 per cent, 17.96 per cent and 29.49 per cent over the existing checks i.e. TAU-1, AKU-15, TPU-4 and BDU-1, respectively whereas in Maharashtra it showed superiority by 16.88 per cent, 17.42 per cent, 12.58 per cent and 20.66 per cent over the existing checks TAU-1, AKU-15, TPU-4 and BDU-1, respectively Therefore the genotype was recommended for release during *Kharif* season in Maharashtra.

Blackgram (*Vigna mungo* (L.) Hepper), also known as urad, urd bean, urd, urid, black gram. It is the most important pulse crop grown in India. In agriculture, legumes have been important from the ancient times. White *et al.* (1953) reported that legumes are being grown as economic crops since the 6000 year. Legumes represent the third largest family of higher plants and comprise more than 650 genera and 18,500 species. Mungbean and Urdbean are two important legumes in Phaseloid clade within Papillionidae and occupy pivotal position in Indian Agriculture.

The productivity of pulses is very low as compared to cereals, which have been selected for high grain yield under high input conditions, while the selection pressure in case of pulses have been focused on the adaptation to both biotic and abiotic stresses.

Among the pulses, productivity of blackgram is very low as compared to other pulse crops, because of lack of improved, high yielding and disease resistant varieties. Considering these, efforts were made to develop high yielding, early maturing, disease and pest resistant variety of blackgram. This paper reports the development of promising genotype of blackgarm AKU 10-1, its performance at Maharashtra level and discuss the prospects for breeding commercial blakcgram variety.

MATERIAL AND METHODS

The blackgram genotype AKU 10-1 has been evolved from a cross of TAU-1 x AKU-18-1 at Pulses Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (M.S). Among the several selections made in segregating population, a promising strain AKU 10-1 was evaluated in state multilocation varietal trials at various locations during the year 2011-12 to 2013-14 along with the standard and ruling state level and national checks *viz.,* TAU 1, AKU 15, BDU 1 and TPU 4. The stability performance of pigeonpea hybrid was also carried out. The characters of AKU 10-1 were recorded as per DUS guidelines and different biochemical parameters and dal character was carried out. Subsequently, this starin was also tested for disease and pest reactions in state programme along with susceptible checks.

RESULTS AND DISCUSSION

In State Multilocation Varietal Trial, urdbean strain AKU 10-1 recorded 1222 kg ha^{-1} grain yield which was 20.87, 26.63, 16.27 and 21.35 per cent higher than the checks *viz.,* TAU 1 (1011 kg ha^{-1}), AKU 15 (965 kg ha^{-1}), TPU 4 (1051 kg ha^{-1}) and BDU 1 (1007 kg ha^{-1}) respectively during the year 2011-12 over nine locations. During 2012-13, AKU 10-1 recorded 1025 kg ha^{-1} grain yield which was 13.13, 9.27, 9.27 and 27.97 per cent higher than the checks *viz.,* TAU 1 (906 kg ha^{-1}), AKU 15 (938 kg ha^{-1}), TPU 4 (938 kg ha^{-1}) and BDU 1 (801 kg ha^{-1}), respectively whereas in 2013-14 this genotype recorded 814 kg ha^{-1} grain yield which was 16.14, 15.84, 11.73 and 23.00 per cent higher than the checks *viz.,* TAU 1 (701 kg ha^{-1}), AKU 15 (703 kg ha^{-1}), TPU 4 (729 kg ha^{-1}) and BDU 1 (728 kg ha^{-1}), respectively over nine locations of Maharashtra. In overall performance of three year trials during 2011-12 to 2013-14, this genotype was superior for

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Table 1 A. Yield performance of AKU-10-1 in State Multilocation Varietal Trial of Urdbean (SMVT-*Urdbean*) conducted in Vidarbha (Grain yield kg/ha)

Year/ Location	AKU-10-1	TAU-1 (Ch)	AKU-15 (Ch)	TPU-4(Ch)	BDU-1 (Ch)	CD	CV (%)
2011-12							
Akola	1718	1117	1276	1293	1233	133	10.35
Yavatmal	2485	2010	2120	2259	1779	71	15.02
Buldana	1316	1213	814	1067	1252	74	10.42
Mean (3)	**1840**	**1447**	**1403**	**1540**	**1421**		
% increase over		**27.15**	**31.14**	**19.48**	**29.46**		
2012-13							
Akola	1484	1170	1140	1069	838	120	11.07
Yavatmal	2048	1472	1524	1560	1479	213	14.13
Buldana	1316	1199	1184	1299	1053	46	4.07
Mean (3)	**1616**	**1280**	**1283**	**1309**	**1123**		
% increase over		**26.25**	**25.95**	**23.45**	**43.86**		
2013-14							
Akola	961	731	718	768	686	76	10.82
Yavatmal	1536	1194	1365	1341	1495	222	18.26
Buldana	1203	1658	1430	1268	1048	145	11.41
Mean (3)	**1233**	**1194**	**1171**	**1126**	**1076**		
% increase over		**3.24**	**5.29**	**9.54**	**14.56**		
Weighted mean (9)	**1563**	**1307**	**1286**	**1325**	**1207**		
% increase over		**19.59**	**21.57**	**17.96**	**29.49**		

Table 1 B. Yield performance (Kg/ha) of AKU-10-1 in AICRP trials in Central Zone of India (2011-12)

Location	AKU-10-1	KU-96-3 (Ch)	NUL-7 (Ch)	CD	C.V. (%)	Days to 50 % flowering	Days to maturity	100 Seed wt. (g)
2011-12 (IVT)								
Badnapur	962	567	877	183	15	35	65	3.3
Navsari	774	642	789	154	13	45	89	3.5
Sehore	1244	1235	1169	169	18	41	83	3.8
Jalgaon	1271	638	1423	104	8	44	68	4.0
Kota	556	652	520	111	10	48	81	3.9
Raipur	633	767	604	168	16	47	78	4.6
Akola	1579	1273	1376	231	12	35	78	4.5
Pachora	857	899	1037	79	5	36	74	3.9
Mean (8)	**985**	**834**	**974**			**42**	**76**	**3.9**
% Increase		**18.09**	**1.09**					

Table 2 . Disease reaction of AKU 10-1 recorded at Akola

S.N.	Variety	2010-11		2011-12		2012-13		2013-14		Mean	
		MB	PM	MB	PM	MB	PM	MB	PM	MB	PM
1	**AKU 10-1**	**6.2**	**7.0**	**10.0**	**30.5**	**1.6**	**21.9**	**3.7**	**31.9**	**5.38**	**22.83**
2	TAU-1	6.2	15.5	10.1	27.4	0	19.8	4.3	30.5	5.15	23.30
3	AKU-15	3.2	8.5	7.1	32.6	1.1	9.6	3.6	25.4	3.75	19.03
4	TPU-4	9.4	15.5	10.3	38.8	0	11.6	6.3	22.5	6.50	22.10
	Susceptible check (Kopergaon)	24.2	54.0	36.4	69.5	4.8	36.9	22.7	86.9	22.03	61.83

yield (1020 kg ha^{-1}) than check varieties and recorded 16.88, 17.42, 12.58 and 20.66 per cent increase in yield over TAU 1, AKU 15, TPU 4 and BDU 1, respectively in state programme (Table 1a).

The genotype AKU 10-1 also tested in AICRP trial of MULLaRP in Central Zone of India during 2011-12, where this genotype recorded 985 kg ha^{-1} grain yield which was 18.09 and 1.09 per cent higher than the national checks *viz.,* KU 96-2 (834 kg ha^{-1}) and NUL 7 (974 kg ha^{-1}), respectively (Table 1B)

Reaction to diseases: The genotype AKU 10-1 was tested from the year 2010-11 to 2013-14 for reaction to Macrophomina Blight and Powdery at Akola location. The genotype AKU 10-1 consistantatly showed resistant reaction to Macrophomina Blight whereas moderately resistant reaction to powdery mildew against the susceptible checks (Table 2).

Reaction to pest: The urdbean genotype AKU 10-1 was screened for Etiella pod damage and helicoverpa at Pulses Research Unit, Dr. PDKV, Akola during the year 2011-12 to 2013-14. According to pest resistance /susceptibility ratings (PS/SR), this genotype exhibited at par reaction for both the pests. The per cent pod damage was 1.6 due to *Helicovarpa armigera* which was less than the checks, TAU 1 (2.2 %) and AKU 15 (1.9 %) whereas pod damage due to Etiella was similar with the checks. (Table 3)

Quality parameters: The genotype AKU 10-1 required 20 minutes for cooking and 21.3 per cent protein which is similar with the all the checks. The dhal recovery (76.7 %) was also similar with the checks AKU 15, TAU 1and TPU 4 (Table 4.)

Table 3. Pest reaction of AKU 10-1 recorded at Akola

Entry	% Etiella pod damage				% Helicoverpa pod damage			
	2013-14	2012-13	2011-12	Mean	2013-14	2012-13	2011-12	Mean
AKU 10-1	1.7	1.1	3.4	2.1	1.7	1.1	2.0	1.6
TAU 1	2.3	1.4	2.1	1.9	1.2	1.8	3.7	2.2
AKU 15	1.5	0.4	4.9	2.3	2.9	1.8	0.9	1.9
TPU 4	2.2	1.4	5.9	3.2	1.1	1.4	2.1	1.5

Table 4. Quality parameters of AKU-10-1

S. N.	Variety	Dal recovery	Protein (%)	Cooking time (min.)
1.	AKU 10-1	76.7	21.3	20
2.	AKU-15 (Ch)	75.2	21.4	20
3.	TAU-1 (ch)	74.0	21.0	20
4.	TPU-4 (ch)	74.5	21.3	20

Table 5. Ancillary characters of AKU-10-1 and checks from SMVT-*Urdbean*

Characters/Location	AKU-10-1	TAU-1 (Ch)	AKU-15 (Ch)
a) Days to 50 % flowering			
Mean (9)	38	40	40
b) Days to maturity			
Mean (9)	70	73	72
c) Plant height (cm)			
Mean (9)	44.20	47.77	43.14
d) 100 Seed wt. in gms.			
Mean (9)	4.5	4.9	5.0

Ancillary parameters

Urdbean genotype AKU 10-1 is early (70 days) and synchronous maturity with height of 44.20 cm. It has medium bold seed size (4.5 g per 100 seed weight) which is commercially preferred**.** (Table 5)

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Relationship Between Heterosis and Genetic Divergence for Yield and Quality Traits in Sesame

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ABSTRACT

The parents and 45 F_1 crosses of sesame (*Sesamum indicum* L.) were assessed for rank correlation to generate the information on relationship between heterosis and genetic divergence for yield and quality traits in sesame (*Sesamum indicum* L.) during *Kharif* 2011-12 at Department of Agricultural Botany, Dr. PDKV, Akola in RBD with three replications. Rank correlation between heterosis and genetic divergence was found significant for number of seeds capsule^{-1} and seed yield plant^{-1}. Rank correlation between useful heterosis and genetic divergence was found significant for seed yield plant^{-1}, days to 50 per cent flowering and plant height. The characters which showed significant relationship among heterosis, useful heterosis and genetic divergence, preference should be given to those genotypes which perform better for the characters *viz*., days to 50 per cent flowering, plant height, number of seeds capsule^{-1} and seed yield plant^{-1}. The present study projected the importance of NIC-12607, SP-1162-B, TKG-21, Shekhar, Swetha Til, Hima, JCSC-8, SI-7-2, RT-46 as one of the parents and AKT-64, JLT-7 and Phule Til-1 as another parent for getting high heterotic cross in F_1.

Sesame (*Sesamum indicum* L.) is known to be the most ancient indigenous oilseed crop with the highest area, production and export in the world. Sesame oil has precious uses in industrial and culinary purposes. However, the productivity of this crop is a prime need. To improve the quantity and quality of sesame seed yield and oil, development of high yielding sesame variety/ hybrid with high oil content and quality is of great importance. Genetic divergence and heterosis are of great interest to the plant breeder as they play a vital role in framing a successful breeding programme. The nature and magnitude of genetic divergence in a population is essential for selection of diverse parents which upon hybridization leads to a wide spectrum of gene recombination for quantitatively as well as qualitatively inherited traits (Sharma, 1985).

Selection of parents for crossing is the first and the most important task to evolve superior hybrids or strains. It is increasingly realized that crosses between divergent parents usually produce greater heterosis than those between closely related ones. But when divergent parents are crossed, heterosis is not found to occur always. It is therefore, essential to explore the possible limits to parental divergence within which there are reasonably high chances for the occurrence of heterosis. According to Bhatt (1970), the mean statistical distance may be considered as a guideline and crosses between parents belonging to different clusters having same or higher inter-cluster distance than the mean statistical distance may be attempted. The crosses should be chosen from widely separated clusters. Then the question arises which of the genotypes from more diverse clusters may be used for crossing. In that case preference should be given for those genotypes which perform better for the characters which contributed much towards divergence. In the present study an attempt have been made to know the relationship among the heterosis, useful heterosis and genetic divergence for yield and quality traits in sesame so that it helps to project the importance of parents for getting high heterotic cross in F_1.

MATERIAL AND METHODS

Experimental material for the present study consisted of eighteen sesame genotypes involving three female parents, AKT-64, Phule Til-1, JLT-7 and fifteen male parent viz; T-13, Tarun, Shekhar, RT-46, Hima, Swetha Til, GT-1, TKG-21, SI-7-2, SI-11, JCSC-8, SP-1162-B, NIC-16207, NIC-16205, IC-14329 were crossed in line x tester mating design during *Kharif* 2010-11. The resulting 45 hybrids along with their parents were raised during *Kharif* 2011-12 at Head, Department of Botany, Dr. Panjabrao Deshmukh Krushi Vidyapeeth, Akola in a randomized block design with three replications. One row of fifteen plants of each genotype was sown at the spacing of 45

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cm between rows and 15 cm between plants. Normal recommended cultural practices and plant protection measures ware followed. Five competitive plants were randomly selected for recording biometrical measurements on days to 50 per cent flowering, days to maturity, plant height (cm), number of branches plant^{-1}, number of capsules plant^{-1}, number of seeds capsules^{-1}, seed yield plant^{-1} (g), 1000 seed weight (g), oil content (%) and fatty acid profile (%). The statistical and biometrical analysis was performed as per the methodology suggested by Mahalanobis (1936) for Genetic diversity analysis, grouping of genotypes by Tocher's method describer by Rao (1952), heterosis and useful heterosis were computed by standard foumulae. Spearman's Rank Correlation Coefficient was estimated by following Snedecor and Cochran, 1980.

RESULTS AND DISCUSSION

In the present study, rank correlation between heterosis (H), useful heterosis (UH) and genetic divergence for different characters have been studied in Table 1 to 12. Rank correlation between heterosis and genetic divergence was significant for the characters, number of seed capsule^{-1} and seed yield plant^{-1} whereas non-significant for the characters *viz.*, days to 50 % flowering, plant hight, number of branches plant^{-1} and number of capsules plant^{-1}.

However, rank correlation between useful heterosis and genetic divergence was significant for seed yield plant^{-1}, days to 50 % flowering, plant hight. Rank correlation between useful heterosis and genetic divergence was non-significant for the characters *viz.*, number of branches plant^{-1}, number of capsules plant^{-1} and number of seeds capsules^{-1} under study.

Characters which showed significant relationship among heterosis, useful heterosis and genetic divergence, preference should be given to those genotypes which perform better for these characters showing significant relationship among heterosis, useful heterosis and genetic divergence. In the present investigation the characters, days to 50 per cent flowering, plant hight, number of seeds capsules^{-1}, seed yield plant^{-1} were also taken into account while chosing the genotypes from significant relationships.

The present study projected the importance of NIC-12607, SP-1162-B, TKG-21, Shekhar, Swetah Til, Hima, JCSC-8, SI-7-2 and RT-46 as one the parent and AKT-64, JLT-7 and Phule Til-1 as another parent for getting high heterotic cross in F_1 as these parents perform better for exploitation of heterosis for the traits showing significant relationship. These results are in agreement with those given by Tripathi *et al.* (2013); Narayan and Murugan (2013) for genetic divergence and Jatothu *et al.* (2013) for heterosis .

Table 1. Relationship between Heterosis (H) and genetic divergence for days to 50 per cent flowering.

S.N.	Heterotic crosses for days to 50% flowering	H (%)	Cluster combination	Intra & Intercluster distance
1.	AKT-64 x TKG-21	-4.88**	I x I	26.701
2.	JLT-7 x SP-1162-B	-5.00*	I x I	26.701
3.	AKT-64 x SP-1162-B	-5.26**	I x I	26.701
4.	AKT-64 x T-13	-6.02**	I x I	26.701
5.	AKT-64 x Tarun	-6.45**	I x I	26.701
6.	Phule Til-1 x Hima	-6.52**	I x IV	448.602
7.	AKT-64 x IC-14329	-6.67**	I x I	26.701
8.	AKT-64 x NIC-16207	-7.14**	I x I	26.701
9.	Phule Til-1 x Swetha Til	-7.47**	I x IV	448.602
10.	AKT-64 x Swetha Til	-7.90**	I x IV	448.602
	Rank Correlation (r_s) at 8 df	**-0.0666^{ns}**		

*, **: Significant at 5% and 1% level, respectively; (-) Indicates negative heterosis

Table 2. Relationship between Heterosis (H) and genetic divergence for Plant height (cm).

S.N.	Heterotic crosses for Plant height (cm)	H (%)	Cluster combination	Intra & Intercluster distance
1.	AKT-64 x NIC-16207	44.79**	I x I	26.701
2.	JLT-7 x TKG-21	44.08**	I x I	26.701
3.	AKT-64 x JCSC-8	43.12.**	I x I	26.701
4.	Phule Til-1 x SP-1162-B	39.55**	I x I	26.701
5.	AKT-64 x NIC-16205	35.20**	I x I	26.701
6.	Phule Til-1 x Shekhar	33.63**	I x II	82.350
7.	JLT-7 x Shekhar	31.03**	I x II	82.350
8.	Phule Til-1 x NIC-16207	29.68**	I x I	26.701
	Rank Correlation (r_s) at 6 df	**0.1667^{ns}**		

*, ** Significant at 5% and 1% level, respectively

Table 3. Relationship between Heterosis (H) and genetic divergence for number of branches plant^{-1}.

S. N.	Heterotic crosses for number of branches plant^{-1}	H (%)	Cluster combination	Intra & Intercluster distance
1.	Phule Til-1 x NIC-16207	33.68**	I x I	26.701
2.	AKT-64 x NIC-16207	26.00**	I x I	26.701
3.	Phul Til-1 x SI-7-2	25.26**	I x I	26.701
4.	Phule Til-1 x JCSC-8	23.00**	I x I	26.701
5.	Phule Til-1 x SP-1162-B	22.89**	I x I	26.701
6.	JLT-7 x Hima	20.40**	I x IV	448.602
7.	AKT-64 x JCSC-8	17.14**	I x I	26.701
8.	JLT-7 x SP-1162-B	15.91**	I x I	26.701
9.	Phule Til-1 x T-13	15.90**	I x I	26.701
10.	JLT-7 x NIC-16205	12.44**	I x I	26.701
	Rank Correlation (r_s) at 8 df	**0.4787^{ns}**		

*, ** Significant at 5% and 1% level respectively

Table 4. Relationship between Heterosis (H) and genetic divergence for number of capsules plant^{-1}.

S. N.	Heterotic crosses for number of capsules plant^{-1}	H (%)	Cluster combination	Intra & Intercluster distance
1.	JLT-7 x Swetha Til	115.74**	I x IV	448.602
2.	Phul Til-1 x Swetha til	92.18**	I x IV	448.602
3.	JLT-7 x Hima	86.11**	I x IV	448.602
4.	JLT-7 X RT-46	66.80**	I x I	26.701
5.	AKT-64 x NIC-16207	61.58**	I x I	26.701
6.	JLT-7 x Shekhar	54.86**	I x II	82.350
7.	Phule Til-1 x RT-46	51.32**	I x I	26.701
8.	JLT-7 x NIC-16205	48.43**	I x I	26.701
9.	Phule Til-1 x Shekhar	48.33	I x II	82.350
10.	AKT-64 x Hima	45.14**	I x IV	448.602
	Rank Correlation (r_s) at 8 df	**0.3333^{ns}**		

*, ** Significant at 5% and 1% level respectively

Table 5. Relationship between Heterosis (H) and genetic divergence for number of seeds capsule^{-1}.

S.N.	Heterotic crosses for number of seeds capsule^{-1}	H (%)	Cluster combination	Intra & Intercluster distance
1.	Phule Til-1 x Swetha Til	80.57**	I x IV	448.602
2.	JLT-7 x Swetha Til	74.30**	I x IV	448.602
3.	JLT-7 x Hima	69.23**	I x IV	448.602
4.	Phule Til-1 x Hima	59.55**	I x IV	448.602
5.	Phule Til-1 x T-13	52.83**	I x I	26.701
6.	JLT-7 x Shekhar	43.35**	I x II	82.350
7.	AKT-64 x Swetha Til	36.96**	I x IV	448.602
8.	JLT-7 x GT-1	34.61**	I x I	26.701
9.	JLT-7 x NIC-16205	31.47**	I x I	26.701
10.	JLT-7 x JCSC-8	30.21**	I x I	26.701
	Rank Correlation (r_s) at 8 df	**0.9515****		

*, ** Significant at 5% and 1% level respectively

Table 6. Relationship between Heterosis (H) and genetic divergence for seed yield plant^{-1}.

S. N.	Heterotic crosses for seed yield plant^{-1}	H (%)	Cluster combination	Intra & Intercluster distance
1.	JLT-7 x Swetha Til	78.54**	I x IV	448.602
2.	AKT-64 x IC-14329	62.15**	I x I	26.701
3.	Phule Til-1 x Shekhar	61.37**	I x II	82.350
4.	AKT-64 x SI-7-2	56.74**	I x I	26.701
5.	AKT-64 x SP-1162-B	50.72**	I x I	26.701
6.	Phule Til-1 x RT-46	50.13**	I x I	26.701
7.	AKT-64 x NIC-16207	49.43**	I x I	26.701
8.	JLT-7 x NIC-16205	49.13**	I x I	26.701
9.	AKT-64 x Swetha Til	47.06*	I x IV	448.602
10.	Phule Til-1 x SI-7-2	43.45**	I x I	26.701
	Rank Correlation (r_s) at 8 df	**0.6484***		

*, ** Significant at 5% and 1% level respectively

Table 7. Relationship between Heterosis (UH) and genetic divergence for days to 50% flowering.

S. N.	Heterotic crosses for days to 50% flowering	UH (%)	Cluster combination	Intra & Intercluster distance
1.	AKT-64 x IC-14329	-5.56*	I x I	26.701
2.	AKT-64 x NIC-16207	-7.14**	I x I	26.701
3.	AKT-64 x T-13	-7.14**	I x I	26.701
4.	AKT-64 x SP-1162-B	-7.14**	I x I	26.701
5.	AKT-64 x TKG-21	-7.14**	I x I	26.701
6.	JLT-7 x Shekhar	-7.14**	I x II	82.350
7.	JLT-7 x Tarun	-7.14**	I x I	26.701
8.	Phule Til-1 x Tarun	-7.14**	I x I	26.701
9.	AKT-64 x Tarun	-7.94**	I x I	26.701
10.	JLT-7 x GT-1	-7.94**	I x I	26.701
	Rank Correlation (r_s) at 8 df	**0.8181****		

*, ** Significant at 5% and 1% level, respectively; (-) Indicates negative useful heterosis

Table 8. Relationship between Heterosis (UH) and genetic divergence for Plant height (cm).

S. N.	Heterotic crosses for Plant height (cm)	UH (%)	Cluster combination	Intra & Intercluster distance
1.	JLT-7 x Swetha Til	74.30**	I x IV	448.602
2.	JLT-7 x Hima	53.25**	I x IV	448.602
3.	Phule Til-1 x SP-1162-B	52.94**	I x I	26.701
4.	AKT-64 x NIC-16207	52.63**	I x I	26.701
5.	JLT-7 x TKG-21	50.77**	I x I	26.701
6.	AKT-64 x Hima	48.92**	I x IV	448.602
7.	Phule Til-1 x Swetha Til	47.68**	I x IV	448.602
8.	AKT-64 x JCSC-8	46.44**	I x I	26.701
9.	Phule Til-1 x NIC-16207	42.72**	I x I	26.701
10	AKT-64 x NIC-16205	42.11**	I x I	26.701
	Rank Correlation (r_s) at 8 df	**0.7090***		

* & **: significant at 5% and 1% level respectively; (-) Indicates negative useful heterosis

Table 9. Relationship between Heterosis (UH) and genetic divergence for number of branches plant^{-1}.

S. N.	Heterotic crosses for number of branches plant^{-1}	UH (%)	Cluster combination	Intra & Intercluster distance
1.	Phule Til-1 x NIC-16207	20.95**	I x I	26.701
2.	AKT-64 x NIC-16207	20.00**	I x I	26.701
3.	Phul Til-1 x SI-7-2	13.33**	I x I	26.701
4.	Phule Til-1 x JCSC-8	17.14**	I x I	26.701
7.	AKT-64 x JCSC-8	17.14**	I x I	26.701
6.	JLT-7 x Hima	15.24**	I x IV	448.602
	Rank Correlation (r_s) at 4 df	**0.4285^{ns}**		

* & **: significant at 5% and 1% level respectively; (-) Indicates negative useful heterosis

Table 10. Relationship between Heterosis (UH) and genetic divergence for number of capsules plant^{-1}.

S.N.	Heterotic crosses for number of capsules plant^{-1}	UH (%)	Cluster combination	Intra & Intercluster distance
1.	JLT-7 X RT-46	79.52**	I x I	26.701
2.	JLT-7 x Swetha Til	77.64**	I x IV	448.602
3.	Phule Til-1 x RT-46	67.61**	I x I	26.701
4.	AKT-64 x NIC-16207	66.56**	I x I	26.701
5.	Phule Til-1 x JCSC-8	65.94**	I x I	26.701
6.	Phule Tit-1 x SI-7-2	65.52**	I x I	26.701
7.	Phule Til-1 x Swetha til	64.26**	I x IV	448.602
8.	JLT-7 x Shekhar	59.87**	I x II	82.350
9.	JLT-7 x NIC-16205	58.20**	I x I	26.701
10.	AKT-64 x IC- 14329	58.20**	I x I	26.701
	Rank Correlation (r_s) at 8 df	**0.5393^{ns}**		

* & **: significant at 5% and 1% level respectively; (-) Indicates negative useful heterosis

Table 11. Relationship between Heterosis (UH) and genetic divergence for number of seeds capsule^{-1}.

S. N.	Heterotic crosses for number of seeds capsule^{-1}	UH (%)	Cluster combination	Intra & Intercluster distance
1.	JLT-7 x Shekhar	36.89**	I x II	82.350
2.	JLT-7 x NIC-16205	35.25**	I x I	26.701
3.	Phule Til-1 x T-13	32.79**	I x I	26.701
4.	Phule Til-1 x SI-7-2	32.79**	I x I	26.701
5.	JLT-7 x GT-1	31.97**	I x I	26.701
6.	Phule Til-1 x Swetha Til	29.51**	I x IV	448.602
	Rank Correlation (r_s) at 4 df	**0.14285^{ns}**		

* & ** Significant at 5% and 1% level, respectively; (-) Indicates negative useful heterosis

Table 12. Relationship between Heterosis (UH) and genetic divergence for seed yield plant^{-1}.

S. N.	Heterotic crosses for seed yield plant^{-1}	UH (%)	Cluster combination	Intra & Intercluster distance
1.	Phule Til-1 x RT-46	75.00**	I x I	26.701
2.	JLT-7 x RT-46	65.00**	I x I	26.701
3.	AKT-64 x SP-1162-B	64.38**	I x I	26.701
4.	AKT-64 x NIC-16207	62.50**	I x I	26.701
5.	Phule Til-1 x Shekhar	61.88**	I x II	82.350
6.	JLT-7 x NIC-16205	61.25**	I x I	26.701
7.	AKT-64 x IC-14329	60.63**	I x I	26.701
8.	JLT-7 x GT-1	57.50**	I x I	26.701
9.	AKT-64 x SI-7-2	56.25**	I x I	26.701
10.	Phule Til-1 x NIC-16207	53.13**	I x I	26.701
	Rank Correlation (r_s) at 8 df	**0.8787****		

* & ** Significant at 5% and 1% level, respectively; (-) Indicates negative useful heterosis

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Inheritance Study for Grain Number and Grain Weight in Wheat

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ABSTRACT

Inheritance study for grain number and grain weight in Wheat (*Triticum aestivum* L.) was undertaken to estimate the additive, dominance and epistatic components. The experimental material comprised of six generations (P_1, P_2, F_1, F_2, BC_1, BC_2) of four crosses was evaluated Rabi 2008-09. Results revealed the preponderance of dom x dom effect for grain number and grain weight per spike. Duplicate type of epistasis was also noticed for these characters. The preponderance of non-fixable gene effects (non-add) than fixable components (add) and presence of add x add (i) and dom x dom (l) interactions indicated the employment of bi-parental mating or reciprocal recurrent selection would be more realistic for further improvement in wheat grain yield vide selection of grain number and grain weight per spike.

Wheat *(Triticum aestivum* L.) is an important cereal crop widely cultivated in the World providing ample food calories and protein to the human population. It is the second most important cereal crop after rice grown under diverse agro-climatic conditions contributing about 32 per cent of total food grain production in India (Singh *et al.,* 2004) and staple food crop in at least 43 countries. Estimation of various genetic components of variances are used as measure of gene action, which is essential to the breeder for starting a judicious crop breeding program. The concept of generation mean analysis was used by Hayman (1958) for estimation of genetic components of variation. Since this technique involves six different generation's viz. parents (P_1 and P_2), filial generations (F_1 and $F_{2)}$ and their backcrosses (BC_1 and BC_2) and the analysis is based on mean values over replications, it is known as generation mean analysis. Metric traits assessed in wheat usually are plant height (cm), effective tillers per plant, grains per spike, grain weight per spike (g) and grain yield per plant (g).

Testing of epistasis is necessary before estimation of genetic variation because it helps in deciding the method of analysis for estimation of components of variation. The estimates of gene effects have a direct bearing on the method of hybridization and selections, which should be adopted in specific breeding program. The magnitude of additive effects is particularly useful to the breeder in developing pure line varieties, whereas information on dominance and perhaps epistatic gene effects can be valuable in the development of hybrids. The present investigation was planned with an aim to determine the relative importance of additive, dominance and epistasis using analysis of generation mean for various quantitative traits in wheat.

MATERIAL AND METHODS

The present investigation was carried out at Wheat Research Unit, Dr. PDKV, Akola during *Rabi* 2006-07, 2007-08 and 2008-09. Seven diverse wheat genotypes viz. LOK-58, AKAW-2956, MP-1210, NIAW-301, UAS-304, HI–1454 and MACS–2496 were selected as parents on the basis of their origin and yield potential. Crosses were attempted during Rabi 2006-07 to generate the F_1's and F_1's were advanced in F_2's and backcrosses were also attempted during 2007-08.

Final experimental trial, comprising of seven parents with their 4 F_1s, 4F_2s and 8 back cross generations were evaluated during Rabi 2008-09 in a randomized block design with three replications. Parent's, F_1s and back cross generations were grown in double rows, while F_2s in five rows. Sowing was done by dibbling the seeds at a distance of 10 cm in rows of 2m length with row to row spacing of 25cm. Non experimental rows were planted around the layout to eliminate the border effects. Fertilizer dose @ 60kg N, 60kg P_2O_5 and 60kg K_2O ha^{-1} was applied at the time of sowing and 60kg N ha^{-1} was top dressed 21 DAS coinciding with the crown root initiation stage. Six irrigations were applied during the entire crop period and recommended agronomic practices were adopted to raise healthy crop.

Data recorded on plot basis for days to spike emergence and 100 grain weight, while rest of the quantitative characters viz. plant height (cm), tillers per

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plant, grains per spike, grain weight per spike (g) and grain yield plant^{-1} (g) were recorded on randomly selected 5 plants for parent's, F_1s and back crosses, while 25 plants for F_2s. The generation means for each character were subjected to standard statistical analysis to test the difference among various generations studied as per the standard procedure (Panse and Sukhatme, 1985). Scaling test was used to check the adequacy of additive-dominance model for various characters in each cross (Hayman and Mather, 1955). The significance of anyone of these scales was taken to indicate the presence of epistasis i.e. non-allelic interaction. In the presence of non-allelic interactions, various gene effects were estimated using 6-parameter model (Hayman, 1958).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes and crosses for all the characters. The general mean for days to spike emergence were depicted as 57 days , 100 grain weight 39.38g, plant height (80.95cm), tillers plant^{-1} (3.80), grains spike^{-1} (53.83), grain weight spike^{-1} (2.05g) and grain yield plant^{-1} (13.29g) due to the different generations

The results scaling tests for assessing the validity of additive-dominance models are given in Table 2. All four scales (A, B, C and D) were non-significant for any cross, however, at least one or more than one scales were found significant in some crosses for five quantitative characters viz. plant height (cm), tillers plant^{-1}, grains spike^{-1}, grain weight spike^{-1} (g) and grain yield plant^{-1} (g). Scale A was found significant in cross NIAW 301/UAS304 (plant height, tillers plant^{-1} and grains spike^{-1}) and in cross HI 1454/MACS 2496 (grains and grain weight spike^{-1}) while B was found significant in cross AKAW2956/LOK58 (grains spike^{-1}) indicates the presence of all three kinds of interactions. While scale C was found significant in cross AKAW2956/LOK58 (plant height), in cross AKAW2956/ LOK58 and AKAW2956/MP1210 (grains spike^{-1}) and in cross AKAW2956/MP1210 (grain weight spike^{-1}), which thereby indicated the inadequacy of simple additive-dominance model and the presence of epistasis. The D scales were non- significant in all the crosses except AKAW2956/MP1210 and HI 1454/MACS 2496 (grains spike^{-1}), in cross AKAW2956/MP1210 (grain weight spike^{-1} and grain yield plant^{-1}) indicating the presence of non-allelic interactions for these characters in mentioned crosses.

In general, the A, B, C and D scaling tests depicted the adequacy of additive-dominance model for most of the characters. However C and D scaling tests were found significant in some crosses for days to spike emergence, grains spike^{-1}, grain weight spike^{-1} and grain yield plant^{-1} indicating the presence of add x add (D) and dom x dom (C) interactions, respectively. Significance of scales C and D both in cross AKAW2956/MP1210 (grains spike^{-1} and grain weight spike^{-1}) indicated the presence of add x add as well as dom x dom type of interactions. These results are in agreement with those obtained by Verma and Yunus, 1988 and Ahmad *et al*, 2007.

The 3 and 6 parameters of gene effect conducted by using the population means revealed that mean effect [m] was highly significant for all characters in all crosses except in crosses AKAW2956/LOK58 and NIAW 301/ UAS304 for the characters tillers and grain yield per plant. In general, magnitude of the dominance effect were high for all the characters, except days to spike emergence in cross NIAW 301/UAS304, 1000 grain weight, tillers plant^{-1} and grain weight spike^{-1} in cross HI 1454/MACS 2496 and grain yield plant^{-1} in cross AKAW2956/LOK58. However in the present study the magnitude of add x add (i) and dom x dom (l) gene effects were quite high in comparison of add x dom (j) gene effects (Table 3) except in case of cross HI 1454/MACS 2496 for grains and grain weight spike^{-1}. Similar results were found by Ahmad *et al.* 2007; Singh *et al.* 1986; Sharma *et al.* 1986 and Fatechi *et al.* 2004

The presence of dominance component (h) with

Table 1. Analysis of variance

Source	df	Days to spike emer	1000-gr wt. (g)	Plant height (cm)	Effective Tillers pl^{-1}	Grain spike^{-1}	Grain wt. pl^{-1} (g)	Grain yield pl^{-1} (g)
Replications	2	1.96	1.77	2.46	3.56	1.25	1.62	1.14
Treatments	23	32.14**	10.83**	10.46**	4.74**	10.54**	4.33**	5.56**
Error	46	0.65	0.82	2.20	0.76	3.18	0.14	0.49

* Significant of 5% level ** Significant of 1% level

Table 2. Scaling tests for different characters in three crosses of bread wheat

Character/ Cross	Scaling tests			
	A	B	C	D
Plant height (cm)				
AKAW2956/LOK58	1.43±0.67	0.62±0.15	-0.56±0.67	-1.50±0.20
AKAW2956/MP1210	1.26±0.64	0.64±0.50	0.07±0.58	-0.50±0.21
NIAW 301/UAS304	7.24**±1.55	0.17±0.67	1.39±0.74	-0.64±0.96
HI 1454/MACS 2496	-1.34±0.30	-0.40±0.12	4.18**±1.92	-2.66±0.52
Tillers per plant				
AKAW2956/LOK58	-2.61±0.81	-0.26±0.45	-1.99±0.10	-0.76±0.42
AKAW2956/MP1210	-0.67±0.68	-1.40±0.61	-0.64±0.25	0.20±0.12
NIAW 301/UAS304	2.87**±1.46	-0.83±0.08	-1.11±0.85	-1.67±0.35
HI 1454/MACS 2496	-2.45±0.55	-0.68±0.22	-2.08±2.71	0.62±0.57
Grains per spike				
AKAW2956/LOK58	1.62±0.32	3.60**±1.66	3.56**±1.61	-0.25±0.37
AKAW2956/MP1210	-3.22±0.43	-0.65±0.42	2.52*±0.98	7.05**±1.87
NIAW 301/UAS304	2.60*±1.04	-0.39±0.25	-0.30±0.21	-0.82±0.59
HI 1454/MACS 2496	2.14*±1.53	-3.86±0.42	-0.68±0.59	2.41*±0.14
Grain wt. per spike (g)				
AKAW2956/LOK58	0.19±0.06	0.48±0.32	0.74±0.44	-0.10±0.08
AKAW2956/MP1210	-1.21±0.32	0.53±0.23	3.20**±0.50	5.31**±0.17
NIAW 301/UAS304	1.20±0.20	-0.57±0.29	-0.53±0.46	-0.53±0.24
HI 1454/MACS 2496	2.40*±0.20	-3.10±0.29	-1.77±0.42	-1.27±0.12
Grain yield per plant (g)				
AKAW2956/LOK58	-0.89±0.23	1.19±0.53	-1.51±0.68	-1.53±1.03
AKAW2956/MP1210	0.27±0.17	-0.23±0.21	1.81±0.79	1.98*±1.33
NIAW 301/UAS304	1.54±0.65	-0.59±0.26	-0.93±0.54	-1.22±0.75
HI 1454/MACS 2496	-0.68±0.87	-1.84±1.60	-1.60±1.19	0.20±0.36

add x add (i) gene effects were significant in the crosses AKAW2956/MP1210 and HI 1454/MACS 2496 for grains per spike and grain weight per spike. Estimates of digenic interactions revealed that add x add (i) and dom x dom (l) gene interactions were found significant in the crosses AKAW2956/MP1210 and HI 1454/MACS 2496 for grains per spike and grain weight spike^{-1}. Similar findings are reported by various researchers Singh and Rai, 1987; Chatrath *et al,* 1986 and Pawar *et al.,* 1988 In respect of days to spike emergence and 1000 grain weight the dominance effect (h) were high with preponderance. Thus hybridization, reciprocal recurrent selection and bi-parental mating would be quite useful for improvement in 1000 grain weight.

Grain yield per plant predominantly controlled by additive gene in crosses AKAW2956/LOK58 and NIAW 301/UAS304 and controlled by dominant gene in cross HI 1454/MACS 2496. Prepondrance of dominance effect and suggestation for reciprocal recurrent selection and bi-parental mating for improvement in various generations was reported by Shekhawat et al. (2006). The presence of dominance component (h) with add x add (i) and dom x dom (l) gene effects were significant in cross AKAW2956/MP1210 for grain number and grain weight per spike. These findings are in accordance with previous studies by Chatrath *et al,* 1986.

Opposite sign of dominance component (h) and dom x dom (l) type of gene effect were recorded for grains spike^{-1} in crosses AKAW2956/LOK58, AKAW2956/MP1210 and HI 1454/MACS 2496 which revealed that a

Table 3. Estimates of gene effects for different characters in bread wheat

Character/ cross	m	d	h	I	j	l
Days to spike emergence						
AKAW2956/LOK58	54.80**+0.48	0.67+0.47	4.13**+1.03	-	-	-
AKAW2956/MP1210	53.45**+0.52	0.58+0.47	9.97**+1.10	-	-	-
NIAW 301/UAS304	59.16**+0.42	2.07*+0.41	1.84+0.78	-	-	-
HI 1454/MACS 2496	52.59**+0.33	6.02**+0.35	8.10**+6.37	-	-	-
1000 grain weight (g)						
AKAW2956/LOK58	35.99**+0.60	0.42+0.64	4.53**+1.46	-	-	-
AKAW2956/MP1210	37.55**+0.34	1.15+0.52	1.77+0.62	-	-	-
NIAW 301/UAS304	37.77**+0.49	2.11*+0.81	5.30**+0.77	-	-	-
HI 1454/MACS 2496	42.87**+0.34	8.32**+0.42	1.06+0.62	-	-	-
Plant height (cm)						
AKAW2956/LOK58	8.69**±1.16	-0.72±0.41	1.56±0.53	1.50±1.03	0.36±0.04	-1.60±0.68
AKAW2956/MP1210	4.54**±0.47	-3.18**±1.17	0.52±0.35	0.50±0.43	0.75±0.24	-0.89±0.74
NIAW 301/UAS304	8.02**±1.02	0.75±0.31	0.88±0.09	0.64±0.03	0.99±0.84	-1.00±0.26
HI 1454/MACS 2496	5.18**±1.44	-2.15*±0.75	1.55±0.65	2.66**±1.04	-0.27±0.23	-0.90±0.57
Tillers per plant						
AKAW2956/LOK58	1.45±1.01	0.96±0.06	-0.10±0.09	0.76±0.85	-1.56±1.33	0.44±0.23
AKAW2956/MP1210	2.30*±1.88	-1.45±0.48	-0.80±0.70	-0.20±0.35	0.58±0.27	0.79±0.26
NIAW 301/UAS304	0.04±0.02	-0.48±0.75	1.65±1.44	1.67±0.70	-1.79±0.99	2.56*±1.15
HI 1454/MACS 2496	3.95**±1.41	6.26**±0.35	-2.57*±0.56	-0.62±0.39	-1.54±1.53	1.51±0.54
Grains per spike						
AKAW2956/LOK58	7..35**±1.84	-0.29±0.14	2.01*±1.64	0.25±0.74	-1.25±0.81	-2.69**±1.33
AKAW2956/MP1210	11.90**±0.93	1.62±1.43	-4.82**±2.32	-7.05**±1.75	-1.65±1.55	5.04**±1.68
NIAW 301/UAS304	3.42**±1.30	-0.51±0.56	0.93±1.13	0.82±0.19	1.43±0.97	-0.78±0.44
HI 1454/MACS 2496	9.01**±1.61	-3.98** ±2.03	-2.66**±1.24	-2.45*±1.29	5.78**±3.31	2.40*±1.19
Grain wt. per spike (g)						
AKAW2956/LOK58	2.46**±0.82	-0.18±0.16	0.42±0.24	0.10±0.80	-0.23±0.41	-0.31±0.59
AKAW2956/MP1210	9.56**±0.39	1.36±0.17	3.79**±0.94	5.31**±0.35	-1.37±0.18	3.65**±0.58
NIAW 301/UAS304	3.06**±0.49	1.10±0.10	0.81±0.17	0.53±0.48	1.06±0.16	-0.38±0.69
HI 1454/MACS 2496	5.45**±0.26	3.36**±0.06	0.65±0.71	1.27±0.25	5.78**±0.12	0.16±0.58
Grain yield per plant (g)						
AKAW2956/LOK58	0.27±0.12	2.74* ±1.17	1.28±1.17	1.53±0.76	-1.49±1.38	-1.20±0.64
AKAW2956/MP1210	3.46**±1.41	0.30±0.24	-1.90±1.99	2.05*±0.72	0.39±0.16	2.57**±1.18
NIAW 301/UAS304	0.15±0..09	2.99**±1.09	1.31±1.04	1.22±0.51	1.57±0..91	-1.14±0.87
HI 1454/MACS 2496	2.96**±0.76	0.56±0.64	3.12**±1.25	-0.20±0.12	0.93±0.13	1.06±0.64

duplicate type of epistatic gene action was important in the inheritance of character. However cross AKAW2956/ MP1210 exhibited complementary type of gene action in the inheritance of grain weight spike^{-1} character. Hence, on the basis of significant estimates of gene effect above results suggested that grain number and grain weight spike^{-1} were predominantly under the control of dominance gene effects (h). Gene interactions add x add (i) and dom x dom (l) were also found for character grain number and grain weight spike^{-1}.

Grain yield is complex character, dependent upon the contribution of a large number of components affecting directly or indirectly. The preponderance of dominance x dominance effect was depicted for grain number and grain weight spike^{-1}. Duplicate type of epistasis was also

noticed for these characters. The preponderance of non-fixable gene effects (non-additive) than fixable components (additive) and presence of add x add (i) and dom x dom (l) interactions indicated employment of bi-parental mating or reciprocal recurrent selection would be more realistic for further improvement in grain yield through grain number and grain weight per spike. However, reciprocal recurrent selection deployment would not be easy for applicability in wheat, thus the hybridization followed by selection and some cyclic crosses in segregating generations would be more useful to set positive and favorable gene constellations.

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Studies on Heterosis for Seed Yield Oil content and Fatty Acid Profile in Safflower

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ABSTRACT

Heterobeltiosis and standard heterosis for seed yield, oil content and fatty acid profile was studied in 45 crosses developed through half diallel mating design involving 10 parents. The range of standard heterosis and heterobeltiosis for seed yield per plant was from -16.38 per cent to 43.34 per cent and -22.24 per cent to 105.32 per cent, respectively. The cross combination JSF1 x A2 (45.34) and AKS/S41 x JSF1 (42.40) recorded significant positive standard heterosis over check AKS 207 for seed yield plant^{-1}. For character like oil content, oleic acid, linoleic acid and palmitic acid moderately low to low amount of heterosis was recorded for oil content. JSI 99 x NARI 34 (13.48) recorded highest standard heterosis while JSI 97 x A2 (19.54) and AKS/GMU 2724 x JSF1 (9.04) with highest standard heterosis for oleic and linoleic acid respectively. Parents JSF1 and AKS/41 were associated for developing top heterotic crosses for seed yield plant^{-1} and these can be utilized in hybrid development programme. High heterotic crosses expected to produce transgressive segregant in subsequent generation.

Safflower (*Carthamus tinctorious* L.) is an important oilseeds crop of India. In recent year Safflower has gained importance as a source of healthy edible oil because of its high percentage of polyunsaturated fatty acid (Linoleic acid 70 %). For utilizing potential for yield and oil content heterosis breeding can prove to be better option. *Per se* performance of potential lines gives closes but information on magnitudes of haterosis and Combining ability of parents for yield, oil and other quality traits and are more useful. Gouda *et al.* (1997) reviewed heterosis for yield and other character and reported considerable amount of heterosis over standard check for seed yield and other traits. The present study was undertaken to determine magnitude of heterobeltiosis and standard heterosis in safflower and to identify most heterosis crosses.

MATERIAL AND METHODS

The experimental material composed of 10 safflower genotypes viz. AKS/S41, AKS/GMU22724, PBNS 12, JSI 97, Bhima, Sagarmuthiyalu, JSF1, JSI99, NARI 34, and A2 were crossed in diallel fashion excluding reciprocal to obtained 45 crosses during *Rabi* 2007-08. The crosses (F_1) along with their parents were grown in Randomized Block Design in three replications during *Rabi* 2008-09 at Oilseed Research Unit, Dr. PDKV, Akola. Each entry was sown in two rows of three meter length. Distance between rows was 45 cm and sowing was done with hand dibbling 20 cm apart within the row. Recommended package of practices were followed for raising healthy crop and maintained standard population.

The yield was recorded on five random but competitive plants. Oil content was determined by following NMR (Nuclear Magnetic Resonance) technique at Oilseed Research Unit, Dr. PDKV, Akola. The fatty acid composition in seed of each treatment were estimated by Gas liquid Chromatography (GLC) on a sample of 10 seeds/ treatment and percentage of palmitic acid, stearic acid, oleic acid and linoleic acid were estimated. Each character was analysed separately using analysis of variance technique suggested by Panse and Sukhatme (1967) and heterosis was calculated in F_1 crosses over better parent and standard check AKS-207.

RESULTS AND DISCUSSION

The analysis of variance for parents and crosses for different character revealed that significant difference for all the traits suggesting the presence of considerable amount of genetic variance for these traits under study. Parents vs. crosses comparison were significant for all the traits expect for Palmitic acid indicated presence of overall heterosis for all the traits.

For seed yield 26 crosses showed significant positive heterobeltiosis (Table 1). Top ranking cross was JSF1 x A2 (105.32) followed by AKS/S 41 x JSF1 (91.11). Significant positive standard heterosis were recorded in 20 crosses and highest significant standard heterosis was recorded by JSF1 x A2 (45.34).

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Table 1. Range of Heterobeltiosis (BH) and Standard heterosis (SH) it's best heterotic crosses and Number of significant crosses in desired direction for various character.

S. N.	Characters	Heterosis over	Range of Heterosis	Best heterotic Cross	Number of Significant Crosses in desirable direction
1.	Seed yield / plant (g)	BH	-22.24 to 105.32	JSF1 x A2	26
		SH	-16.38 to 45.34	JSF1 x A2	20
2.	Oil content (%)	BH	-27.72 to 10.80	AKS/GMU 2724 x PBNS 12	7
		SH	-23.37to13.48	JSI 99 x NARI 34	12
3.	Palmitic acid (%) (16:0)	BH	-34.18 to 14.29	JSI 97 x JSI 99	-
		SH	-14.75 to31.15	AKS/GMU 2724 x Sagarmathiyalu	8
4.	Stearic acid (%) (18:0)	BH	-59.42 to 42.86	JSF1 x NARI 34	4
		SH	-50.00 to 41.67	JSI 97 x Bhima	5
5.	Oleic acid (%) (18:1)	BH	-32.97 to 20.93	JSI 97 x A2	8
		SH	-35.63 to 19.54	JSI 97 x A2	15
6.	Linoleic acid (%) (18:2)	BH	-10.78 to 6.85	Sagarmathiyalu x A2	2
		SH	-5.53 to 9.04	AKS/GMU 2724 x JSF1	12

Table 2. Heterobeltiosis (BH) and Standard heterosis (SH) of superior crosses for seed yield, oil content and fatty acid profile in Safflower

S.N.	Crosses	Mean Yield plant^{-1}	Heterosis over	Oil content (%)	Palmitic acid (16:0)	Stearic acid (18:0)	Oleic acid (18:1)	Linoleic acid (18:2)
1.	JSF1 x A2	35.11	BH	-24.46**	1.39	-32.00**	3.49	-8.27**
			SH	-19.90**	19.67*	-29.17**	2.30	-1.21
2.	AKS/S 41 x JSF1	34.40	BH	-17.58**	-28.95**	-21.74*	0.60	-4.64**
			SH	-15.73**	-11.48	-25.00*	-2.87	-2.70*
3.	AKS/S 41 x A2	32.62	BH	-13.09**	-18.042*	-20.00*	3.49	1.09
			SH	-8.99**	1.64	-16.67	2.30	-0.13
4.	AKS/S 41 x PBNS 12	32.20	BH	-17.15**	-10.53	-47.83**	1.08	-1.08
			SH	-16.40**	11.48	-50.00**	8.05*	-1.21
5.	JSF 1 x NARI 34	32.19	BH	-27.72**	-25.00**	-48.00**	0.58	-30.88**
			SH	-13.26**	-6.56	-45.83**	-0.57	2.02
6.	PBNS 12 x NARI 34	30.64	BH	-20.04**	-31.58**	31.25*	-24.73**	1.28
			SH	-4.04**	-14.75	-12.50	-19.54**	6.61**
7.	Bhima x JSI 99	29.94	BH	-24.56**	5.08	-13.79	16.09**	-6.56**
			SH	-22.70**	1.64	4.17	16.09**	-3.91**
8.	JSI 99 x A2	29.92	BH	-18.88**	6.94	-10.34	-14.37**	0.81
			SH	-15.06**	23.23**	8.33	1.63	0.94

Note:- * Significant at 1 % and **Significant at 5 %

For oil content 7 crosses recorded significant positive heterobeltiosis whereas 12 crosses recorded significant positive standard heterosis. AKS/GMU 2724 x PBNS 12 (10.80) recorded highest positive heterobeltiosis followed by JSI 97 x JSF1. For standard heterosis JSI99 x NARI 34 (13.48) ranked 1st followed by Bhima x NARI 34 (13.26). For Palmitic acid not a single cross recorded significant positive heterobeltiosis but 8 crosses recorded significant positive standard heterosis with AKS/GMU 2724 x Sagarmathiyalu (31.15) ranked 1st followed by AKS/ GMU 2724 x JSI 97 (29.51). For stearic acid 4 crosses showed significant positive heterobeltiosis while 5 crosses registered significant positive standard heterosis JSF 1 x NARI 34 (42.86) and JSI 97 x Bhima (41.67) recorded highest heterobeltiosis and standard heterosis for the trait.

For oleic acid 8 crosses recorded significant positive heterobeltiosis while 15 crosses recorded significant positive standard heterosis. JSI97 x A2 ranked 1st with 20.93 and 19.34 per cent heterobeltiosis and standard heterosis respectively. For linoleic acid Sagarmathiyalu x A2 (6.85) recorded highest significant positive heterobeltiosis followed by AKS/S 41 x NARI 34 (2.56) and highest standard heterosis recorded by AKS/ GMU 2724 x JSF1 (9.04) followed by Bhima x JSF1 (8.50). Two crosses showed significant positive heterobeltiosis while 12 cross with significant positive standard heterosis for the said trait.

Similar results for yield and oil content was reported by Parde *et. al*. (2010) and for fatty acid profile by Ragab and Friedt (1992).

Comparison of top eight crosses (Table 2) based on *per se* performance for yield reveled that top ranking crossers showed negative heterosis for oil content while Bhima x JSI 99 showed significant positive heterosis for oleic acid PBNS 12 x NARI 34 showed significant positive standard heterosis for linoleic acid. From the above it can be seen that for yield heterobeltiosis and standard heterosis was moderate to high and can be exploited through heterosis breeding howere for traits like oil content, linoleic acid, Oleic acid and Palmitic acid moderately low to low amount of heterosis was recorded. Hence can be improved by recombination breeding. JSF 1 and AKS/S 41 associated for developing high heterotic crosses for yield and can be utilizing in hybrid breeding programme. High heterotic crosses expected to produce transressive segregant in subsequent generation.

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Heterosis for Yield Contributing Traits and Oil Content in Sunflower

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ABSTRACT

The fifty five sunflower hybrids along sixteen parents (five lines & eleven testers) and standard check (PKVSH-952) were evaluated in randomized block design with three replications at Oilseed Research Unit, Dr. PDKV, Akola during *Kharif*-2013 to estimate the extent of heterosis in sunflower hybrids. The highest and significant average heterosis and standard heterosis for seed yield per plant was recorded by cross combination CMS 10A X AKSF 6R (115.73% & 34.90%) followed by CMS 21A X RHA 138-2R (114.96% & 28.67%). These cross combinations also recorded maximum standard heterosis for most of the yield contributing traits. The crosses AKSF-12A x DOR-R-2-1(10.26%) recorded highest standard heterosis for oil content followed by CMS 21A x PKV 105R (10.22%) and AKSF-1A x 298R (9.64%). On the basis of per cent heterosis, heterobeltiosis and standard heterosis five cross combinations *viz*., CMS 10A X AKSF 6R, CMS 21A X RHA 138-2, AKSF-1A X RHA 138-2, AKSF-1A X AKSF 6R and CMS 21A x 856 R were identified as promising crosses.

Sunflower (*Helianthus annuus* L.) is one of the most important oilseed crop in the world. Sunflower is originated in the South-West United States-Mexico area (Heifer, 1955; Vranceanu and Stoenescu, 1979). Sunflower was introduced for commercial cultivation in India in 1969 from former USSR. Low yielding genotypes and hybrids of sunflower are the major constraints of sunflower productivity due to which the area and production of sunflower is decreasing in past few years. To conquer this constraint breeders have center of attention towards production of hybrids through heterosis breeding, which become possible due to discovery of cytoplasmic male sterility by Leclercq (1969) and fertility restoration system by Kinman (1970).

The present investigation revealed extent of heterosis (average heterosis, heterobeltiosis and standard heterosis) observed within the available genetic variability of crosses for various characters studied. The main purpose of this study is to identify superior cross combination for seed yield as well as for oil content, which would be certainly helpful for evolving superior hybrids in future.

MATERIAL AND METHODS

The experimental material was consist of 5 CMS lines *viz*., CMS 21A, CMS 10A, AKSF-1A, AKSF-12A, MSSR-1A and 11 testers *viz*., AK 1R, AKSF 6R, AKSF 12R, 856 R, PKV 105R, PKV 110R, 189/1R, 298 R, 178–2R, RHA 138–2, and DOR–R–2–1 and their 55 F_1's. The five CMS lines were crossed with the eleven restorers/testers in Line x Tester fashion during *rabi* 2012-13 and obtained sufficient crossed seeds. The 55 F_1's crosses along with their 16 parents and one check (PKVSH-952) were evaluated in Randomized Block Design (RBD) with three replications at the farm of Oilseeds Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra state, India) during *Kharif*- 2013. Each entry was sown in one row of 4.5 m length in each replication. The inter and intra-row spacing was 60 cm and 30 cm, respectively. All the standard agronomic and plant protection measures were used. The data was recorded on plant basis, from each genotype in each replication on 5 randomly selected plants and their average value was computed for head diameter (cm), hundred seed weight (g), seed filling percentage, hull content (%), seed yield per plant (g) and oil content (%). Oil contends of all genotypes were determined by using NMR (nuclear magnetic resonance) machine. Heterosis was calculated over mid parent, better parent and standard check (PKVSH-952) for seed yield, its components and oil content.

RESULTS AND DISCUSSION

The analysis of variance for various characters under study is presented in Table 1. The variation among treatments was highly significant for all of the characters. This indicates presence of substantial genetic variability for the characters studied. The parents revealed highly significant variation for head diameter, 100 seed weight and oil content. The hybrids revealed highly significant variation for all the characters under study.

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The percentage of average heterosis (H_1), heterobeltiosis (H_2) and standard heterosis (H_3) for the characters studied is given in Table 2. In sunflower, positive heterosis is desirable for all the characters studied except hull content, where negative heterosis is desirable.

The present estimation of heterosis for different characters is study under Table 2. Average heterosis for head diameter ranged from 15.38 to 170.87 per cent. Out of 55 crosses the cross i.e. AKSF-1A X RHA 138-2 (170.87%) followed by CMS 21A X RHA 138-2 (138.26%), AKSF 1A x 189/1R (126.24%) and CMS 10A x AKSF 6R (124.51%) show the maximum significant average heterosis. Out of 55 hybrids, maximum significant positive heterobeltiosis was exhibited by AKSF-1A X RHA 138-2 (146.73%) followed by AKSF-1A X 856 R (116.19%) and CMS 10A x AKSF 6R (111.22%). Standard heterosis ranged from -31.13 to 42.66 per cent over check PKVSH 952. Cross CMS 10A x AKSF 6R (42.66 %) exhibited maximum positive standard heterosis. Radhika *et al.* (2001), Habib *et al.* (2006) and Patil *et al*. (2007) reported positive heterosis for head diameter.

The CMS 10A X AK 1R (108.81%) exhibited maximum positive average heterosis for 100 seed weight followed by CMS 10A x 856R (107.02%). The maximum significant positive heterobeltiosis is recorded by cross CMS 10A X AK 1R (104.81%) followed by CMS 21A x 856R (100.00%). Standard heterosis over best check PKVSH 952 ranged from -36.66 to 20.92 per cent. The cross CMS 10A x AKSF 12R (20.92%) exhibited highest significant positive standard heterosis followed by CMS 21A x RHA 138-2 (19.00%). Gangappa *et al.* (1997), and Halaswamy *et al*. (2003) reported a highly significant genetic difference among inbred lines for 100 seed weight, which are comparable with present experimental findings. For the percentage of filled seeds per head having maximum significant positive average heterosis recorded in CMS 21A X RHA 138-2 (30.17%) then after the maximum positive heterobeltiosis observed in hybrid 21A x PKV 104 R AKSF-1A X RHA 138-2 (26.64%), CMS 21A x RHA 138-2 (26.53%) and AKSF-12A X RHA 138-2 (26.37%). The results are inconformity with the earlier reports of Madrap and Makne (1993) recorded high level of heterosis in cross CMS 234A x RHA 273 for seed filled percent. The hull content highest significant negative in average heterosis for the cross CMS 10A X AKSF 6R (-30.41%). Then the Cross AKSF-12A X PKV 110R (-33.00%), CMS 10A x AKSF 6R (-32.28%) reported highest significant negative heterobeltiosis for hull content. The cross CMS 10A x AKSF 6R (-13.4%) exhibited highest negative standard heterosis. Most of the crosses showed significant negative heterosis for this trait.

Oil content is also an equally important character along with seed yield per plant in sunflower. In pooled analysis, the observed average heterosis range of hybrid was from 4.99 to 40.16 per cent and from -1.06 to 36.36 per cent for heterobeltiosis. The cross AKSF-12A X DOR-R-2-1 (40.16%) exhibited highest significant average heterosis followed by AKSF-1A X DOR-R-2-1(38.13%). The cross AKSF-12A X DOR-R-2-1 (36.36%), AKSF-1A X DOR-R-2-1 (33.36%) exhibited highest significant positive heterobeltiosis. Standard heterosis over best check i. e. PKVSH-952 ranged from -9.58 to 10.26 per cent. Five crosses viz., AKSF –12A x DOR–R–2–1 (10.26%), CMS 21A x PKV 105R (10.22%), AKSF 1A x 298R (9.64%), AKSF 1A x DOR-R-2-1 (9.55%), CMS 21A x AKSF 12R (9.20%) recorded the significant positive standard heterosis over PKVSH-952. Nehru *et al*. (2000) noted highest heterosis and heterobeltiosis for seed yield and oil content per cent.

For seed yield (kg plant^{-1}), the range of average heterosis from 12.75 to 115.73 per cent. Out of 55 crosses, the highest positive average heterosis was recorded the cross CMS 10A x AKSF 6R (115.73%), CMS 21A x RHA 138-2 (114.96%) and AKSF 12A x PKV 110R (107.66%). The Heterobeltiosis for this trait was ranged from 7.77 to 101.01 per cent. Maximum significant positive heterobeltiosis was found in hybrid CMS 10A X AK 1R (101.01%), AKSF 12A x PKV 110R (98.12%), CMS 21A X RHA 138-2 (96.19%) and CMS 10A x AKSF 6R (95.64%). The range of standard heterosis over PKVSH 952 was found to be -34.24 to 34.90 per cent. Cross CMS 10A x AKSF 6R (34.90%) exhibited highest positive standard heterosis followed by CMS 21A x RHA 138-2 (28.67%). Comparable types of results were reported by Nehru e*t al.* (2000), Singh and Singh (2003), Patil *et al.* (2007), and Dutta *et al.* (2011).

In this study cytoplasmic male sterile lines and restorer were used as parents and line x tester analysis was used as an appropriate method for the estimation of average heterosis, heterobeltiosis and standard heterosis.

The significant average heterosis, heterobeltiosis and standard heterosis has been observed for yield and yield contributing characters in many crosses. Six crosses viz., CMS 10A x AKSF 6R, CMS –21A

Table 1. Analysis of variance for Heterosis.

Sources of variation	d.f.	Head diameter (cm) 1	100 seed weight (g) 2	Seed filling (%) 3	Hull content (%) 4	Oil content (%) 5	Seed yield plant^{-1} (g) 6
Replications	2	1.301	0.060	35.666	1.788	7.897	11.207
Treatments	70	38.795**	3.065**	109.35**	15.457**	26.749**	193.291**
Parents	15	20.109**	0.569**	37.361	6.219	20.029**	16.692
Crosses	54	16.97**	1.970**	84.749**	12.017**	8.676**	102.780**
Parents vs Crosses	1	1497.269**	99.6053**	2517.9812**	339.791**	1103.491**	7729.887**
Male XFemale	40	9.994**	1.3842**	32.761	8.904**	6.333**	55.668**
Error	140	1.9234	0.106	31.230	4.635	2.276	11.076

Note: * Significant at 5% level of significance, ** Significant at 1% level of significance

Table 2. Heterosis (%) over mid-parent (H_1), better-parent (H_2) and standard check(H_3) for different characters in sunflower

S.N.	Crosses	Headdiameter (cm)			100 seed weight (g)			Seed filling (%)		
		H_1	H_2	H_3	H_1	H_2	H_3	H_1	H_2	H_3
1	CMS 21A x AK 1R	15.38	7.58	-25.91 **	41.04 **	31.56 **	-24.25 **	-2.17	-4.94	-10.51
2	CMS 21A x AKSF 6R	23.13 *	21.94	-16.02	32.00 **	20.00 *	-15.55 **	15.59 *	13.71	0.97
3	CMS 21A x AKSF 12R	28.13 *	0.00	-31.13 **	21.84 *	17.78	-32.18 **	5.33	4.47	-7.23
4	CMS 21A x 856 R	105.51 **	68.39 **	15.97	100.00 **	100.00 **	15.16 **	20.54 **	18.08 *	4.85
5	CMS 21A x PKV 105R	57.28 **	28.39 *	-11.58	25.56 **	25.56 **	-27.70 **	4.56	4.20	-7.48
6	CMS 21A x PKV 110R	60.34 **	20.00	-17.35 *	34.46 **	32.22 **	-23.86 **	11.18	5.61	-6.22
7	CMS 21A x 189/1R	100.88 **	47.74 **	1.76	62.69 **	54.56 **	-11.00	6.31	2.97	-2.45
8	CMS 21A x 298 R	72.29 **	38.39 **	-4.69	71.43 **	63.64 **	3.65	19.40 **	13.74	1.00
9	CMS 21A x 178–2R	41.93 **	29.63 **	8.00	60.44 **	37.12 **	11.32 *	17.97 **	17.54*	5.15
10	CMS 21A x RHA 138–2	138.26 **	93.65 **	33.37 **	90.77 **	77.14 **	19.00 **	30.17 **	26.53**	12.36
11	CMS 21A x DOR–R–2–1	55.04 **	42.29 **	-2.00	26.55 **	22.33 *	-29.56 **	8.01	5.43	-6.38
12	CMS 10A x AK 1R	82.09 **	82.06 **	8.44	108.81 **	104.81 **	6.14	-2.06	-3.65	-9.3
13	CMS 10A x AKSF 6R	124.51**	111.22**	42.66**	97.91**	71.82**	20.92**	26.80**	23.20**	12.21
14	CMS 10A x AKSF 12R	46.37 **	20.67	-28.15 **	49.09 **	46.43 **	-21.31 **	5.45	3.29	-5.93
15	CMS 10A x 856 R	116.31 **	88.06 **	11.98	107.02 **	96.67 **	13.0….24 *	21.92 **	17.96 *	7.44
16	CMS 10A x PKV 105R	89.66 **	64.22 **	-2.22	55.56 **	47.78 **	-14.91 **	1.05	-0.56	-9.43
17	CMS 10A x PKV 110R	107.58 **	63.43 **	-2.69	60.71 **	55.17 **	-13.63 *	10.88	4.07	-5.22
18	CMS 10A x 189/1R	97.05 **	52.20 **	-9.38	74.07 **	74.07 **	-9.79	-4.62	-6.46	-11.38
19	CMS 10A x 298 R	109.21 **	77.99 **	5.98	70.11 **	54.65 **	-2.05	18.93 **	11.94	1.96
20	CMS 10A x 178–2R	41.28 **	21.12 *	0.91	26.02 **	3.23	-16.19 **	11.46	10.47	0.62
21	CMS 10A x RHA 138–2	89.65 **	63.43 **	-2.69	64.52 **	45.71 **	-2.11	14.89 *	10.32	0.48
22	CMS 10A x DOR–R–2–1	73.09 **	70.19 **	1.33	43.03 **	40.48 **	-24.50 **	8.26	4.38	-4.93
23	AKSF–1A x AK 1R	61.11 **	51.44 **	-9.80	42.77 **	31.18 **	-21.94 **	2.82	-1.94	-7.68
24	AKSF–1A x AKSF 6R	100.04 **	77.63 **	19.97 *	80.30 **	66.36 **	17.08 **	24.55 **	24.20 **	6.70

25	AKSF–1A x AKSF 12R	56.17 **	35.65 *	-28.90 **	45.76 **	38.71 **	-17.47 **	4.86	3.71	-9.42
26	AKSF–1A x 856 R	135.08 **	116.19 **	13.31	90.16 **	87.10 **	11.32 *	21.58 **	21.39 **	3.70
27	AKSF–1A x PKV 105R	95.97 **	79.44 **	-5.95	76.94 **	74.09 **	3.58	1.97	0.37	-11.49
28	AKSF–1A x PKV 110R	95.02 **	61.17 **	-15.53	22.33 **	18.39	-29.56 **	12.43	8.79	-7.07
29	AKSF–1A x 189/1R	126.24 **	83.13 **	-4.02	54.02 **	44.09 **	-14.27 *	-1.30	-6.15	-11.09
30	AKSF–1A x 298 R	72.68 **	55.15 **	-18.68 *	44.79 **	40.40 **	-11.07 *	8.21	5.01	-10.29
31	AKSF–1A x 178–2R	47.39 **	20.05 *	0.02	14.69 *	-0.63	-19.32 **	7.52	5.10	-5.98
32	AKSF–1A x RHA 138–2	170.87 **	146.76 **	29.33 **	84.85 **	74.29 **	17.08 **	27.83 **	26.64 **	8.18
33	AKSF–1A x DOR–R–2–1	64.07 **	56.76 **	-9.80	23.16 **	17.20	-30.26 **	0.19	-0.32	-14.85 *
34	AKSF –12A x AK 1R	27.25 **	4.83	-3.58	48.69 **	31.68 **	-14.91 **	-3.13	-7.16	-12.6
35	AKSF –12A x AKSF 6R	32.87 **	15.22	5.98	56.40 **	50.00 **	5.57	19.54 **	19.28 *	2.93
36	AKSF –12A x AKSF 12R	53.77 **	9.18	0.42	42.81 **	30.79 **	-15.48 **	14.05 *	13.36	-0.99
37	AKSF –12A x 856 R	53.59 **	13.53	4.42	69.63 **	60.40 **	3.65	19.42 **	18.63 *	2.38
38	AKSF –12A x PKV 105R	46.53 **	7.97	-0.69	62.30 **	53.47 **	-0.83	15.35 *	14.11	0.63
39	AKSF –12A x PKV 110R	70.60 **	17.03	7.64	81.91 **	69.31 **	9.40	26.90 **	22.19 **	5.45
40	AKSF –12A x 189/1R	56.43 **	5.80	-2.69	39.56 **	25.74 **	-18.75 **	13.49 *	8.43	2.73
41	AKSF –12A x 298 R	53.49 **	11.59	2.64	59.00 **	57.43 **	1.73	20.09 **	15.98 *	0.09
42	AKSF –12A x 178–2R	4.71	-0.22	-8.22	-13.12 *	-21.99 **	-36.66 **	12.19	10.20	-1.41
43	AKSF –12A x RHA 138–2	97.40 **	44.93 **	33.30 **	77.67 **	74.29 **	17.08 **	28.20 **	26.37 **	9.05
44	AKSF –12A x DOR–R–2–1	31.68 **	7.03	-1.56	50.27 **	37.62 **	-11.07 *	20.98 **	19.77 **	3.35
45	MSSR 1A x AK 1R	12.02	6.72	-29.79 **	71.18 **	67.90 **	-12.99 *	3.24	-4.98	-10.55
46	MSSR 1A x AKSF 6R	40.01 **	38.19 **	-6.67	10.99	-3.64	-32.18 **	21.76 **	16.97 *	0.50
47	MSSR 1A x AKSF 12R	37.83 **	9.39	-28.04 **	52.85 **	50.12 **	-19.32 **	5.68	0.73	-12.02
48	MSSR 1A x 856 R	44.10 **	20.23	-20.91 *	47.37 **	40.00 **	-19.39 **	20.56 **	16.31 *	-0.95
49	MSSR 1A x PKV 105R	88.09 **	56.33 **	2.84	54.27 **	46.56 **	-15.61 **	15.25 *	9.35	-3.57
50	MSSR 1A x PKV 110R	62.63 **	23.61	-18.68 *	35.71 **	31.03 **	-27.06 **	17.08 *	16.54 *	-6.90
51	MSSR 1A x 189/1R	104.48 **	52.65 **	0.42	80.25 **	80.25 **	-6.59	1.15	-7.17	-12.06
52	MSSR 1A x 298 R	81.99 **	48.77 **	-2.13	36.67 **	24.24 **	-21.31 **	14.19 *	13.31	-8.92
53	MSSR 1A x 178 2R	23.98 *	10.93	-7.58	31.70 **	7.88	-12.41 *	16.15 *	9.45	-2.08
54	MSSR 1A x RHA 138-2	89.84 **	57.08 **	3.33	67.74 **	48.57 **	-0.19	21.32 **	17.93 *	-1.13
55	MSSR 1A x DOR-R–2–1	44.01 **	34.99 **	-8.91	62.55 **	59.64 **	-14.20 *	10.34	6.81	-9.68
	RANGE	15.38 to 170.87	-0.22 to 146.76	-31.13 to 42.66	-13.12 to 108.81	-21.99 to 104.81	-36.66 to 20.92	-4.62 to 30.17	-7.17 to 26.64	-14.85 to 12.36
	SE(D)±	1.09	1.26	1.26	0.25	0.29	0.29	4.27	4.93	4.93
	CD 5%	2.166	2.50	2.50	0.49	0.57	0.57	8.47	9.78	9.78
	CD 1%	2.865	3.30	3.30	0.65	0.76	0.76	11.21	12.94	12.94

Note : H_1- Average Heterosis, H_2- Heterobeltosis, H_3- Standard Heterosis,

* Significant at 5% level of significance

** Significant at 1% level of significance

Significance of H_1 was tested on the deviation of F_1 mean values from mid parental value i.e. F_1 – MP

Significance of H_2 was tested on the deviation of F_1 mean values from better parent i.e.F_1 – BP

Significance of H_3 was tested on the deviation of F_1 mean values from check i.e. F_1 – check

Cont. Table 2

S.N.	Crosses	Hull content (%)			Oil content (%)			Seed yield per plant (g)		
		H_1	H_2	H_3	H_1	H_2	H_3	H_1	H_2	H_3
1	CMS 21A x AK 1R	-23.95 **	-25.10 **	6.69	17.21 **	10.97 **	1.41	45.72 **	45.19 **	-20.83 *
2	CMS 21A x AKSF 6R	-17.98 **	-23.08 **	6.26	14.90 **	5.57	2.91	68.91 **	50.76 **	3.95
3	CMS 21A x AKSF 12R	-13.16 *	-14.05	18.73	25.21 **	17.69 **	9.20 **	60.30 **	59.75 **	-12.92
4	CMS 21A x 856 R	-15.20 *	-17.52 *	13.94	18.23 **	10.34 **	3.96	102.15 **	83.03 **	22.20 **
5	CMS 21A x PKV 105R	-9.64	-9.83	24.56 *	28.02 **	21.74 **	10.22 **	74.16 **	62.21 **	1.77
6	CMS 21A x PKV 110R	-18.55 **	-19.14 **	13.35	18.84 **	13.54 **	1.77	70.15 **	69.85 **	-8.06
7	CMS 21A x 189/1R	-22.85 **	-25.28 **	3.22	24.05 **	17.44 **	7.32 *	69.57 **	67.39 **	-6.99
8	CMS 21A x 298 R	-9.72	-13.60	19.36	24.07 **	16.97 **	7.84 *	93.69 **	83.44 **	11.05
9	CMS 21A x 178–2R	8.37	-0.43	37.55 **	22.81 **	15.78 **	6.75 *	91.17 **	73.26 **	15.41
10	CMS 21A x RHA 138–2	-11.25	-17.12 *	14.49	31.13 **	30.46 **	7.61 *	114.96 **	96.19 **	28.67 **
11	CMS 21A x DOR–R–2–1	-6.35	-9.79	24.62 *	30.79 **	26.65 **	3.40	62.72 **	62.47 **	-12.05
12	CMS 10A x AK 1R	-27.22 **	-30.94 **	-1.63	16.71 **	5.19	-3.87	103.89 **	101.01 **	12.79
13	CMS 10A x AKSF 6R	-30.41 **	-32.28 **	-13.40	13.01 **	-0.98	-3.48	115.73 **	95.64 **	34.90 **
14	CMS 10A x AKSF 12R	-17.58 **	-19.83 **	8.46	18.61 **	6.18	-1.48	65.69 **	63.32 **	-8.36
15	CMS 10A x 856 R	-20.22 **	-21.04 **	3.09	19.16 **	5.96	-0.16	95.87 **	80.25 **	20.34 *
16	CMS 10A x PKV 105R	-23.22 **	-25.92 **	1.90	17.24 **	6.11	-3.93	66.17 **	57.39 **	-1.26
17	CMS 10A x PKV 110R	-27.01 **	-30.21 **	-2.16	20.11 **	9.20 *	-2.12	86.31 **	82.70 **	2.52
18	CMS 10A x 189/1R	-19.79 **	-20.27 *	3.20	16.65 **	5.14	-3.92	74.74 **	73.89 **	-2.43
19	CMS 10A x 298 R	-14.90 *	-15.44	8.14	30.02 **	16.73 **	7.62 *	73.93 **	67.57 **	1.45
20	CMS 10A x 178–2R	-8.97	-13.30	10.88	14.50 **	2.79	-5.22	66.55 **	53.42 **	2.20
21	CMS 10A x RHA 138–2	-19.68 **	-22.20 **	-0.50	27.42 **	20.36 **	-0.72	73.77 **	61.21 **	5.74
22	CMS 10A x DOR–R–2–1	-6.67	-6.71	19.41	31.94 **	29.24 **	-1.16	90.91 **	87.26 **	5.08
23	AKSF–1A x AK 1R	-23.97 **	-26.72 **	4.38	21.99 **	15.83 **	5.85	43.50 **	30.67 *	-13.23
24	AKSF–1A x AKSF 6R	-3.09	-7.18	22.65 *	11.21 **	2.46	-0.12	80.88**	77.54**	22.42**
25	AKSF–1A x AKSF 12R	-11.22	-12.26	18.71	17.36 **	10.64 **	2.65	56.74 **	42.70 **	-5.24
26	AKSF–1A x 856 R	-16.45 *	-16.94 *	9.75	11.49 **	4.34	-1.68	74.18 **	73.71 **	15.97
27	AKSF–1A x PKV 105R	-6.27	-8.12	26.39 *	25.01 **	19.22 **	7.94 *	47.72 **	43.64 **	-4.62
28	AKSF–1A x PKV 110R	1.01	-1.89	37.53 **	16.77 **	11.90 **	0.29	28.82 *	16.73	-22.49**
29	AKSF–1A x 189/1R	-11.63	-12.52	15.58	15.65 **	9.81 **	0.35	62.52 **	49.25 **	-0.89
30	AKSF–1A x 298 R	-6.29	-8.37	21.07 *	25.77 **	18.91 **	9.64 **	12.75	7.77	-28.44**
31	AKSF–1A x 178–2R	-16.85 *	-22.01 **	3.04	18.20 **	11.76 **	3.04	36.27 **	36.06 **	-9.37
32	AKSF–1A x RHA 138–2	-10.04	-14.22	13.35	27.06 **	26.80 **	4.60	87.75 **	86.60 **	23.91 **
33	AKSF–1A x DOR–R–2–1	-4.23	-5.73	24.56 *	38.13 **	33.36 **	9.55 **	48.63 **	34.71 **	-10.55
34	AKSF –12A x AK 1R	-8.41	-14.28 *	22.11 *	10.76 **	4.39	-4.61	63.14 **	56.45 **	-7.07
35	AKSF –12A x AKSF 6R	-1.28	-2.55	21.02 *	21.25 **	10.92 **	8.12 *	79.07 **	66.67 **	14.92
36	AKSF –12A x AKSF 12R	-6.68	-10.51	21.07 *	10.20 **	3.12	-4.32	76.32 **	69.05 **	0.42
37	AKSF –12A x 856 R	-18.98 **	-20.96 **	3.20	22.94 **	14.22 **	7.62 *	71.58 **	62.13 **	8.24
38	AKSF-12A x PKV105R	-22.70 **	-26.45 **	1.16	19.76 **	13.36 **	2.63	63.46 **	59.11 **	-0.17
39	AKSF –12A x PKV 110R	-28.95 **	-33.00 **	-6.08	21.43 **	15.49 **	3.51	107.66 **	98.12 **	17.69 *

S.N.	Crosses	Hull content (%)			Oil content (%)			Seed yield per plant (g)		
		H_1	H_2	H_3	H_1	H_2	H_3	H_1	H_2	H_3
40	AKSF –12A x 189/1R	-8.76	-10.61	15.71	4.99	-1.06	-9.58 **	60.11 **	54.94 **	-7.96
41	AKSF –12A x 298 R	-3.79	-4.58	20.48 *	21.43 **	13.96 **	5.08	90.25 **	88.47 **	14.09
42	AKSF –12A x 178–2R	9.01	5.29	30.75 **	18.55 **	11.26 **	2.58	32.64 **	25.46 *	-16.42
43	AKSF –12A x RHA 138–2	1.77	0.00	24.19 *	20.30 **	19.11 **	-1.75	98.09 **	88.75 **	23.80 **
44	AKSF –12A x DOR–R–2–1	-5.30	-6.71	19.41	40.16 **	36.36 **	10.26 **	65.53 **	57.96 **	-6.17
45	MSSR 1A x AK 1R	-18.12 **	-19.94 **	14.04	11.49 **	9.68 **	3.59	62.77 **	50.32 **	-18.04 *
46	MSSR 1A x AKSF 6R	-1.64	-7.10	26.44 *	9.25 **	7.55 *	4.84	40.16 **	17.03	-19.31 *
47	MSSR 1A x AKSF 12R	-16.04 *	-16.29 *	13.94	12.95 **	11.96 **	5.74	78.14 **	64.54 **	-10.31
48	MSSR 1A x 856 R	-21.33 **	-22.92 **	4.90	14.54 **	14.40 **	8.05 *	38.77 **	17.39	-21.63 *
49	MSSR 1A x PKV 105R	-15.87 *	-16.31 *	15.12	14.67 **	12.30 **	6.06	77.59 **	54.16 **	-3.28
50	MSSR 1A x PKV 110R	-12.51	-13.78	20.86 *	7.95 *	5.20	-0.64	34.69 *	25.01	-32.57 **
51	MSSR 1A x 189/1R	-11.67	-13.83	17.28	13.22 **	11.38 **	5.20	29.26 *	18.36	-34.24 **
52	MSSR 1A x 298 R	-12.37	-15.54 *	14.96	9.77 **	8.46 *	2.44	86.14 **	64.08 **	-0.67
53	MSSR 1A x 178 2R	-5.20	-12.3	19.36	12.72 **	11.38 **	5.20	29.90 *	9.99	-26.73 **
54	MSSR 1A x RHA 138-2	-17.68 *	-22.59 **	5.35	19.10 **	11.56 **	5.36	101.48 **	71.68 **	12.60
55	MSSR 1A x DOR-R–2–1	-0.35	-3.31	31.59 **	15.62 **	4.63	-1.19	63.77 **	51.96 **	-17.99 *
	Range	-30.41 to 9.01	-33.00 to 5.29	-13.4 to 37.55	4.99 to 40.16	-1.06 to 36.36	-9.58 to 10.26	12.75 to 115.73	7.77 to 101.01	-34.24 to 34.90
	SE(D)±	1.6316	1.884	1.884	1.0563	1.2197	1.2197	1.0563	3.0424	3.0424
	CD 5%	3.2341	3.7344	3.7344	2.0937	2.4176	2.4176	2.0937	6.0306	6.0306
	CD 1%	4.2782	4.94	4.94	2.7697	3.1982	3.1982	2.7697	7.9775	7.9775

Note : H_1 - Average Heterosis, H_2- Heterobeltosis, H_3- Standard Heterosis,

* Significant at 5% level of significance

** Significant at 1% level of significance

Significance of H_1 was tested on the deviation of F_1 mean values from mid parental value i.e. F_1 – MP

Significance of H_2 was tested on the deviation of F_1 mean values from better parent i.e.F_1 – BP

Significance of H_3 was tested on the deviation of F_1 mean values from check i.e. F_1 – check

x RHA 138–2, AKSF–1A x RHA 138–2, AKSF –12A x RHA 138–2, AKSF–1A x AKSF 6R and CMS 21A x 856R recorded the highly significant standard heterosis over best check PKVSH 952 for yield and most of the yield contributing traits. The cross CMS 10A X AKSF 6R showed significant highest standard heterosis for head diameter, hundred seed weight and seed yield per plant. Five crosses viz., AKSF –12A x DOR–R–2–1, CMS 21A x PKV 105R, AKSF–1A x 298 R, AKSF–1A x DOR–R–2–1 and CMS 21A x AKSF 12R recorded the significant positive standard heterosis for oil content over check PKVSH-952.

Considering the of average heterosis, heterobeltiosis and standard heterosis of crosses, five crosses viz., CMS 10A X AKSF 6R, CMS 21A X RHA 138-2, AKSF-1A X RHA 138-2, AKSF-1A X AKSF 6R and CMS 21A x 856 R are identified as promising crosses and these crosses may be need to further evaluation for commercial exploitation.

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Quadrialiel Analysis in Indian Mustard

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ABSTRACT

Genetic analysis of various quantitative characters was undertaken on 45 double crosses obtained from six diverse genotypes in quadriallel mating design. The characters viz., days to 50 per cent flowering, days to maturity , plant height, number of siliqua plant $^{-1}$ and seed yield plant $^{-1}$ were predominantly governed by dominance x dominance non allelic interaction followed by additive x additive x additive type. Parents Varuna, Laxmi and Seeta were found better general combiners for seed yield plant $^{-1}$ and number of siliqua plant $^{-1}$ whereas, Varuna and Kranti for days to maturity. Four double crosses viz., (Varuna x Laxmi) x (Seeta x Ashirwad), (Vardhan x Ashirwad) x (Seeta x Laxmi), (Varuna x Kranti) x (Vardhan x Ashirwad) and (Varuna x Laxmi) x (Vardhan x Kranti) were selected for seed yield plant $^{-1}$ and number of siliqua plant $^{-1}$. It is suggested to perform diallel selective mating or biparental mating among F_2 population of these crosses and resulting material is advised to carry forward by single seed descent method to break undesirable linkages.

The main object of mustard breeding is to increase its yield and oil content. Many of the yield contributing characters quantitatively inherited. Quantitative characters display continuous variation and in general are controlled by polygenes showing Mendelian inheritance, modified by environment. To study inheritance of such continuously varying characters different biometrical approaches are used. These biometrical approaches have their basis on the usage of statistical procedure such as mean, variances and covariances. Basic requirement for the breeder before they initiate the sensible breeding programme is to partition the variation into components which measured the different types of gene action.

Quadriallel analysis is one of the important biometrical tools that provide information on gene action on different quantitative characters, partitioning epistasis in different components and also useful for estimating general combining ability and specific combining ability effects for evaluation of potential breeding lines.

With above views in mind this research work was planned with objectives of determinining nature of gene action in different quantitative characters and to estimate the general and specific combining ability effect for evaluation of potential breeding lines and crosses under study.

MATERIAL AND METHODS

The experimental material consisted of six diverse genotypes crossed in diallel fashion to secure 15 F_1 's. These F_1 's were crossed in four way to get 45 double crosses taking care that no parent was repeated in double cross. These 45 double crosses were sown in randomized complete block design, replicated thrice during *rabi* 2009-2010. Data were recorded for days to 50% flowering, days to maturity, number of primary branches plant $^{-1}$, plant height at maturity (cm) , number of siliqua plant $^{-1}$, 1000 seed weight (g), seed yield plant $^{-1}$ (g) and oil content in percentage.

The *per se* performance of crosses give only some indication of usefulness in selecting potential crosses but their long term potentialities are not known. Hence, selection of superior parents which has potential to produce superior cross combination and identifying best cross combination on the basis of combining ability which give required information in the absence of knowledge of genetic base of continuously varying characters. In most mating designs available, it is assumed that non allelic interaction are absent, whereas fact is often contrary assumption. In the presence of non allelic interaction estimates of additive and dominance are biased towards great extent. Use of genetic models where detection and estimation of epistasis is a great value to breeder. One of the method available for detection of additive, dominance and epistatic variation is quadriallel analysis of Rawlings and Cockerhams (1962). Therefore present investigation was conducted on mustard to determine role of epistasis and the nature of gene action for various quantitative characters and to estimates general and specific line effects for selection of potential breeding lines and crosses under study.

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Analysis of variance (Table 1) for two line specific, two, three and four line arrangement effects were significant for number of siliqua plant $^{-1}$ and seed yield plant $^{-1}$. Two line specific effects were also significant for days to maturity and plant height, two line arrangement effects were also significant for days to 50 per cent flowering and days to maturity. Three line and four line arrangement effect were significant for days to maturity and plant height. The effects arising owing to the arrangement of lines are exclusively results of dominance and interaction involving dominance components (Rawlings and Cockerhams, 1962). Obviously, there seems to be predominance of non additive gene effects in the present material. Similar results of non additive gene effects were also observed by Singh and Chaudhary (1977) in barley.

Considering general effect of set of any four parents in various combinations, irrespective of the order, it is obvious that the parents (Varuna, Vardhan, Seeta and Laxmi) formed the best combination for number of siliqua plant $^{-1}$, seed yield plant $^{-1}$ and plant height. The specific combination (Varuna x Kranti) x(Vardhan x Ashirwad) and (Varuna x Kranti) x (Seeta x Laxmi) exhibited highest value for number of siliqua plant $^{-1}$ and seed yield plant $^{-1}$.

Estimates of components of variance are presented in Table 2. These estimates indicated the magnitude of dominance x dominance (σ^2DD) component were maximum for all the characters namely viz days to 50% flowering, days to maturity, plant height, number of siliqua plant $^{-1}$, seed yield plant $^{-1}$ followed by additive x additive x additive (σ^2AAA). The estimates of additive (σ^2A) and additive x dominance (σ^2AD) were found to be negative and considered as non significant estimates.

Importance of dominance x dominance interaction for plant height and oil content were reported by Sachan and Singh (1988). Predominance of non additive gene effects were reported by Singh *et al.*(1985) for all characters.

Varuna, Laxmi and Seeta can be used in hybridization programme to improve seed yield plant $^{-1}$ and number of siliqua plant $^{-1}$. Dixit *et al.*(1983) , Thakral *et al.*(2000), Yadav *et al.*(1992) and Aghao *et al.*(2010). Also identified Varuna as good general combiner.

Table 1. Analysis of variance for general and pecific line effects

Source	df	Mean squares				
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of siliqua plant^{-1}	Seed yield plant^{-1} (g)
Double crosses	44	17.45**	40.33**	96.03**	7716.54**	4.45**
1- line general	5	31.86**	80.48**	47.95	7634.13**	5.17**
2- line specific	9	8.22	69.51**	148.44**	6191.71**	4.77**
2- line arrangement	9	33.89**	27.41**	46.06	11578.03**	3.77**
3- line arrangement	16	10.97	25.96**	100.52**	4976.20**	4.80**
4- line arrangement	5	10.79	16.89**	125.30*	12362.07**	3.27*
Error	88	5.75	3.71	35.44	581.73	1.08

Note : * Significant level at 5%, ** Significant level at 1%

Table 2: Components of genetic variance for different characters

Component	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of siliqua Plant $^{-1}$	Seed yield Plant $^{-1}$ (g)
σ^2A	_	_	_	_	_
σ^2D	29.89	4.58	389.81	87735.93	_
σ^2AA	_	225.42	32.72	_	15.18
σ^2AD	_	_	_	_	_
σ^2DD	66.40	254.72	1665.21	247177.24	39.11
σ^2AAA	42.53	83.82	1345.10	234813.89	11.53

Blank space indicate negative genetic variance

Table 3 .: Crosses selected on the basis of per se performance, general line effects and 2, 3 and 4 line specific effects

Crosses			(Varuna X Laxmi) X (Seeta X Ashirwad)			(Vardhan X Ashirwad) X (Seeta X Laxmi)			(Varuna X Kranti) X (Vardhan X Ashirwad)			(Varuna X Laxmi) X (Vardhan X Kranti)		
Characters			Seed yield plant^{-1} (g)	No. of siliqua plant^{-1}	Days to maturity	Seed yield plant^{-1} (g)	No. of siliqua plant^{-1}	Days to maturity	Seed yield plant^{-1} (g)	No. of siliqua plant^{-1}	Days to maturity	Seed yield plant^{-1} (g)	No. of siliqua plant^{-1}	Days to maturity
	Mean performance		8.33	372.33	94.33	8.15	370.07	87.66	6.92	278.13	97.00	6.28	243.80	96.00
1	line	1	0.18	2.59	0.89	-	-	-	0.18	2.59	0.89	0.18	2.59	0.89
	generaleffect	2	0.13	5.33	-	-	-	0.16	-	-	0.22	0.13	5.33	-
		3	0.07	7.02	-	0.07	7.02	-	-	-	-	-	-	-
		4	-	-	0.16	0.13	5.33	-	-	-	0.16	-	-	0.22
2	Line	1 x 2	0.15	4.30	0.44	-	-	0.50	0.08	-	0.40	0.15	4.30	0.44
	effect	1 x 3	0.10	2.74	-	0.40	2.27	-	-	-	-	-	-	-
	irrespective	1 x 4	-	-	0.61	0.06	5.57	-	-	-	0.61	0.08	-	0.40
	of	2 x 3	0.07	4.45	0.17	0.02	0.05	0.06	-	-	0.11	0.06	5.57	-
	arrangement	2 x 4	0.02	0.05	-	0.02	-	-	0.11	4.9	-	-	-	0.39
2	linespecific	(I j) (. .)	0.80	49.97	0.22	0.42	20.81	-	0.12	-	-	0.80	49.97	0.22
	arrangement	(i .)(j .)	0.17	11.04	0.70	0.08	0.95	-	0.16	-	-	0.16	-	-
3	line effect	123	0.18	6.52	0.12	-	-	0.50	0.02	-	0.19	0.50	4.98	-
	Irrespective	124	0.05	-	0.19	-	-	-	0.16	6.85	0.10	0.01	-	0.86
	of arrangement	134	0.02	-	0.12	-	-	0.50	-	-	0.81	0.02	-	0.19
		234	0.07	-	-	0.07	-	-	0.06	1.53	0.13	-	-	0.07
	Particular arrangement	0.03	0.95	-	o.10	1.31	-	0.01	20.45	0.30	-	-	-	
4	line effect	Irrespective	0.32	2.21	0.49	0.19	4.74	0.08	-	1.00	1.40	0.05	-	0.90
		Particular	0.31	21.03	-	0.68	37.45	-	0.68	37.44	-	0.31	21.03	-

Note : 1,2,3 and 4 represent the order of arrangement of parents in double cross and – indicates negative values

Genetic analysis of different quantitative characters revealed the predominant role of dominance x dominance type of epistatic gene action in the material. Selection like diallel selective mating or biparental mating may be effective to break undesirable linkages and resulting material must be carried by single seed descent method to overcome masking effect of non allelic interactions.

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Genetics of Glossy and Trichome Characters and its Association with Shoot Fly Resistance in Sorghum

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ABSTRACT

A diallel analysis of 36 F_1 and 36 F_2 progenies along with nine divergent parents were assessed in F_1 and F_2 generations to study inheritance of trichome characters and its association with shoot fly resistance segregating generations in sorghum during *Rabi* 2011-12. The study indicated that IS 18551, IS 2312, SPV 504, Ringni and AKSV 13R showed desirable gca effect for trichome density, leaf glossiness at 14 DAE, seedling vigour at 14 DAE and dead heart percentage at 14 & 28 DAE in F_1 and F_2 diallel progenies. Crosses exhibiting highest positive significant sca effects for almost all the shoot fly resistance traits included CSV 18R X IS 18551, Ringni X AKR MS45B and IS 2312 X IS 18551 in F_1 and F_2 diallel progenies. So these crosses may be forwarded further to develop genotypes with shoot fly resistance. The inheritance of grain yield and shoot fly resistance traits viz., dead heart percentage at 14 and 28 DAE, trichome density, seedling vigour, leaf glossiness, were predominantly governed by non-additive gene action in both F_1 and F_2 diallel set. The improvement of shoot fly resistance and yield would be possible by the exploitation of non-additive genetic components. Therefore, heterosis breeding for improvement of these characters will be rewarding.

Sorghum in the subtropics has a hostile environment where unreliable rainfall poor soils, pests, diseases and weeds constantly exert a harsh selection pressure. Insect pests are the major biotic constraints for production and productivity of sorghum. Among insects, shoot fly (*Atherigonia soccata*) *is* a major grain yield limiting factor that causes damage when the sowings are delayed. The early sown crop escapes from shoot fly damage, but the late sown crop is most affected. Agronomic practices, natural enemies, synthetic insecticides and host plant resistance have been employed for shoot fly management to minimize the losses. Insecticide application is beyond the reach of resource poor farmers and further it is not practically possible on large area. Hence, host plant resistance can play major role in minimizing the extent of losses and is compatible with other tactics of pest management, including the use of natural enemies and chemical control. The present study based on F_1 and F_2 diallel involving diverse resistance source is an attempt to study combining ability for shoot fly resistance.

MATERIAL AND METHODS

The nine diverse parents Ringni, Maldandi (M-35-1) , SPV 504, AKSV 13R(PKV Kranti), MS 104B , MS 45B, CSV 18R, IS 2312 and IS 18551 (two of them resistant, two susceptible and rest elite) were crossed in diallel fashion to develop 36 F_1's. Few seeds of these crosses were used for advancing the generation in *kharif* 2011-12. The experimental material comprised of nine parents, 36 F_1's and 36 F_2 progenies in randomized block design with three replications during *rabi* 2011-12 at Sorghum Research Unit, Dr. P.D.K.V., Akola. This experimental material was deliberately planted late for inviting high and uniform shoot fly pressure and interlard-fishmeal technique was also used for creating shoot fly pressure. (Taneja and Leuschner, 1985 and Nwanze, 1985). Each F_1 and parent was raised in two rows, each F_2 was raised in four rows all of which of 3 m length with recommended inter and intra row spacing of 45 x 15 cm, respectively. The data were recorded for grain yield plant $^{-1}$ (g) seedling vigour at 14 DAE, leaf glossiness at 14 DAE, trichome density on 14 DAE, dead heart percentage at 14 and 28 DAE for five randomly selected plants in each F_1 and parents nf 15 randomly selected plants of each F_2. Seedling vigour and leaf glossiness were measured on scale 1-5 as suggested by Sharma *et al* (1997). Trichome density was calculated as per the procedure outlined by Sharma *et al* (1997). All the recommended cultural operations were carried out to raise a good crop. All the necessary data transformations were done for seedling vigour, leaf glossiness and dead heart percentage . Data were subjected to statistical analyses as per method-2, model-1.

RESULTS AND DISCUSSION

Treatment differences were highly significant for all the traits studied both in F_1 and F_2 diallel progenies

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(Table 1). Further, partitioning of treatment variance into components viz., parents, hybrids and parents vs hybrids revealed that parents significantly differed among themselves for all the characters. Similarly, hybrids also showed highly significant differences for all the traits. Whereas, the parents vs hybrids comparison was significant for all the characters except seedling vigour at 14 DAE and leaf glossiness at 14 DAE in F_1 crosses and seedling vigour in F_2 diallel progenies . It may, thus be concluded that the parents included in this investigation possessed sufficient variability for the characters studied.

Thus, the analysis of variances revealed that the parents included in the present investigation possess sufficient diversity for the characters studied. This indicated that there is a scope to improve upon all the characters by selection on making crosses among the lines under study. Nimbalkar and Bapat (1987) also found similar results who observed a wide diversity among parents as indicated by highly significant variances due to parents, F_1's and segregating generations.

Combining ability analysis was carried out for all characters of F_1 and F_2 diallel progenies and presented in table 2. Dabholkar *et al.* (1989) revealed significance of mean squares due to gca and sca for number of eggs laid and dead hearts at 14, 21 and 28 DAE.

For all the characters under study, both gca and sca estimates were found significant. Their ratio of less than unity demonstrated preponderance of non-additive type gene action in both F_1 and F_2 diallel set for all the characters under study. Variance due to general combining ability were smaller than variances of specific combining ability for all the characters in both F_1 and F_2 diallel progenies. Therefore, non-additive gene action was more predominant for these characters. Aruna and Padmaja (2009) also reported that non additive gene action played important role in governing glossiness, seedling vigour and proportion of plants with dead hearts. But, Starks *et al*. (1970) reported that additive gene action contributed to most of the variation which was against the present findings. Dhillon *et al.* (2006) indicated the predominance of additive gene effects for leaf glossiness, trichomes and plants with dead hearts. Bhadouriya and Saxena (1997), Aruna *et al.* (2011) indicated the presence of both types of gene action for all the characters studied. The improvement of shoot fly resistance and yield would be possible by the exploitation of non-additive genetic components. Therefore, heterosis breeding for improvement of these characters will be rewarding.

It is seen from the Table 3 that, four parents proved to be best general combiner for all the shoot fly resistance related traits under study. The parent IS 18551 has been found to possess desirable gca for all the shoot fly resistance characters such as dead heart percentage at 14 and 28 DAE, trichome density, seedling vigour and leaf glossiness in F_1 and F_2 diallel progenies.

Another parent IS 2312, transmitted favourable genes for almost all the shoot fly resistance related characters in F_1 diallel set. This parent has been found to possess desirable gca for all the shoot fly resistance characters such as dead heart percentage at 14 and 28 DAE, seedling vigour and leaf glossiness in F_1 and F_2 diallel progenies, while trichome density only in F_1 diallel progenies.

Another parent SPV 504 was identified to contribute favourable genes in F_1 diallel crosses for dead heart percentage at 28 DAE in F_1 diallel progenies and seed yield per plant in F_2 diallel progenies. The parent Ringni was found to be capable of transmitting favourable genes for dead heart percentage at 14 and 28 DAE, seedling vigour and grain yield per plant in F_2 progenies and further the same parent transmitted favourable genes for grain yield per plant in F_1 diallel progenies. The parent AKSV 13R also possessed favourable genes for dead heart percentage at 28 DAE, trichome density and grain yield per plant in F_1 diallel, while dead heart percentage at 14 DAE and trichome density in F_2 diallel progenies. In view of their high gca effects for shoot fly resistant characters, they can be utilized in hybridization breeding programme as potential donors for getting superior segregates with shoot fly resistance.

The superior parental combinations having significantly high specific combining ability effects for traits contributing to shoot fly resistance are presented in Table 4 .

First cross that exhibited significant desirable sca effects in both F_1 and F_2 diallel set for characters related to shoot fly resistance was CSV 18R X IS 18551. This cross exhibited significant desirable sca effects for dead heart percentage at 14 DAE, trichome density per mm^2, seedling vigour 14 DAE, leaf glossiness and grain yield per plant in F_1 and dead heart percentage at 14 DAE, trichome density, seedling vigour and leaf glossiness in F_2 diallel progenies.

The next cross, Ringni X AKRMS 45B, recorded significant desirable sca effects for most of the shoot fly resistance traits in F_1 and F_2 diallel. The characters in F_1 included trichome density, seedling vigour, leaf glossiness and grain yield per plant and those in F_2 diallel included dead heart percentage at 14 DAE, trichome density, seedling vigour and leaf glossiness.

The third cross which exhibited non significant but negative sca effect for dead heart percentage at 14 DAE, but exhibited negative significant sca effect for dead heart percentage at 28 DAE was IS 2312 X 1S 18551. The same cross also showed significant desirable sca effect for some of the shoot fly resistance traits in both F_1 and F_2 diallel set. The characters with desirable sca effects were trichome density per $mm^{2,}$ seedling vigour, leaf glossiness and and grain yield per plant in F_1 and dead heart percentage at 14 DAE, seedling vigour and leaf glossiness in F_2 diallel progenies.

Fourth cross with significant desirable sca effect in F_1 and non-significant negative sca effect in F_2 was AKSV 13R X MS 104B. This cross exhibited desirable sca effects for most of the component characters in F_1 and F_2 diallel.

AKRMS 45B X CSV 18R also showed negative non significant sca effect in F_1 and F_2 for dead heart percentage at 28 DAE. But, the same cross also showed desirable significant sca effects for dead heart percentage at 14 DAE in F_1 diallel and dead heart percentage at 14 DAE, trichome density, seedling vigour and leaf glossiness in F_2 diallel progenies.

Another cross, M-35-1X IS18551 registered significant desirable sca effects for dead heart per cent at 28 DAE in F_1 but undesirable effect in F_2. This cross also recorded significant sca effects in desirable direction for dead heart percentage at 14 DAE, trichome density, leaf glossiness and seed yield per plant in F_1 diallel progenies, and it recorded significant sca effects in desirable direction for trichome density in F_2 diallel.

MS 104B XAKRMS 45B also showed significant desirable sca effect for dead heart percent in F_1 diallel and undesirable sca effect in F_2 diallel. This cross also exhibited desirable sca effects for most of the component characters in F_1 and F_2 diallel progenies.

The cross SPV 504 X CSV 18R also recorded negative but non-significant sca effect only for dead heart at 28 DAE in F_1 diallel, but exhibited significant negative sca effect for not only for dead heart at 28 DAE, but also for trichome density and grain yield per plant.

The crosses SPV 504 X AKSV 13R and MS 104B X CSV 18R also showed significant sca effects in desirable direction in F_1 diallel, but undesirable sca effects in F_2 diallel progenies. These crosses also exhibited desirable sca effects for some of the component characters in F_1 and one character each in F_2 diallel progenies.

It could be concluded that sca variances were predominant for most of the studied characters i.e. seed yield per plant, dead heart percentage at 14 and 28 DAE, trichome density, seedling vigour and leaf glossiness.

Thus, it could be concluded that, three specific combinations viz., CSV 18R X IS 18551, Ringni X AKRMS 45B and IS 2312 X IS 18551 , were observed to be most desirable, since it had significant desirable sca effects in desirable direction in both F_1 and F_2 diallel set. The remaining specific combinations had significant desirable sca effects for shoot fly resistance characters either in F_1 or F_2 diallel crosses only. Hence, these crosses may be further studied for better segregates with shoot fly resistance using pedigree method.

Table 1. Analysis of variance of in 9 x 9 diallel set of sorghum

Generation	Characters / Degrees of freedom	Sources					
		Replication	Treatments	Parents	F_1 / F_2 Crosses	Parents Vs. F_1/F_2 Crosses	Error
		2	44	8	35	1	88
F_1	Grain yield per plant	0.77	1064.32**	66.56**	977.66	12079.66**	4.49
F_2		7.21	515.81**	476.08**	500.77**	1360.09**	27.31
F_1	Dead heart percentage at 14 DAE	1.24	143.07**	258.46**	119.29**	52.46*	11.39
F_2		20.15	197.39**	258.13**	126.13**	2202.69**	10.85
F_1	Dead heart percentage at 28 DAE	7.91	164.08**	294.14**	116.88**	775.68**	8.97
F_2		5.42	157.45**	294.14**	92.45**	1338.84**	10.41
F_1	Trichomes density	0.001	5.50**	9.79**	4.29**	13.28**	0.002
F_2		0.003	5.51**	9.79**	4.64**	1.52**	0.003
F_1	Seedling vigour	0.01	0.31**	0.53**	0.27**	0.0001	0.023
F_2		0.11*	0.38**	0.53**	0.36**	0.10	0.03
F_1	Leaf glossiness	0.113**	0.39**	0.58**	0.35**	0.002	0.020
F_2		0.48**	0.39**	0.58**	0.35**	0.12*	0.02

*Significant at 5% level and ** Significant at 1% level

Table 2. Analysis of variance for the combining ability in 9 x 9 diallel set

Generation	Characters / Degrees of freedom	Sources					
		GCA	SCA	Error	ó² gca	ó² sca	ó² gca / ó² sca
		8	36	88			
F_1	Grain yield per plant	208.17**	387.35**	1.496	18.789	385.857	0.049
F_2		215.29**	328.29**	1.381	19.446	327.462	0.059
F_1	Seedling vigour at 14 DAE	0.17**	0.09**	0.008	0.015	0.082	0.183
F_2		0.18**	0.17**	0.011	0.015	0.1060	0.143
F_1	Leaf glossiness at 14 DAE	0.20**	0.11**	0.007	0.018	0.105	0.17
F_2		0.23**	0.11**	0.008	0.02	0.098	0.209
F_1	Trichomes density	2.75**	1.63**	0.001	0.25	1.624	0.154
F_2		3.44**	1.48**	0.001	0.313	1.478	0.212
F_1	Dead heart percentage at 14 DAE	129.24**	29.57**	3.78	11.404	25.773	0.442
F_2		112.15**	55.49**	3.612	9.867	51.878	0.19
F_1	Dead heart percentage at 28 DAE	137.30**	36.34**	2.988	12.21	33.349	0.366
F_2		94.22**	43.21**	3.47	8.25	39.737	0.208

Significant at 1% level

Table 3. Estimates of general combining ability effects of parents from F_1 and F_2 crosses

S.N.	Parents	Grain yield per plant		Seedling vigour		Leaf glossiness		Trichome density		Dead heart percentage at 14 DAE		Dead heart percentage at 28 DAE	
		F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
1	Ringni	6.854 **	8.208 **	-0.013	-0.069 *	-0.009	-0.028	-0.032 **	0.363 **	-0.522	-2.571 **	0.150	-1.481 **
2	M-35-1	4.598 **	2.812 **	0.045	0.018	0.023	-0.008	-0.131 **	-0.234 **	-0.909	-0.109	1.032 *	0.261
3	SPV 504	1.631 **	2.933 **	0.028	0.036	-0.040	0.036	-0.084 **	0.013	-0.862	0.030	-1.267 *	-0.454
4	AKSV 13R	1.692 *	0.001	-0.004	0.017	0.042	0.036	0.137 **	0.452 **	-0.168	-1.154 *	-1.358 **	-0.651
5	MS 104-B	-0.176	0.020	.086 **	0.180 **	0.133 **	0.176 **	-0.193 **	-0.571 **	3.210 **	4.782 **	2.576 **	3.648 **
6	MS 45-B	-4.685 **	-3.485 **	0.120 **	0.186 **	0.137 **	0.205 **	-0.787 **	-0.758 **	4.672 **	4.835 **	3.189 **	4.731 **
7	CSV 18R	-4.178 **	-6.792 **	0.140 **	-0.049	0.136 **	-0.012	-0.344 **	0.022 *	3.923 **	0.462	5.416 **	1.135 *
8	IS 2312	2.962 **	-0.159	-0.210 **	-0.130 **	-0.221 **	-0.130 **	0.439 **	-0.334 **	-5.362 **	-1.209 **	-5.809 **	-2.410 **
9	IS 18551	-5.436 **	0.266	-0.192 **	-0.188 **	-0.201 **	-0.275 **	0.996 **	1.048 **	-3.982 **	-5.068 **	-3.930 **	-4.780 **
SE (m) (gi)		**0.348**	**0.334**	**0.025**	**0.030**	**0.023**	**0.026**	**0.008**	**0.009**	**0.554**	**0.541**	**0.491**	**0.529**
CD 5% (gi)		**0.691**	**0.664**	**0.049**	**0.059**	**0.046**	**0.051**	**0.016**	**0.018**	**1.100**	**1.074**	**0.976**	**1.051**
CD 1% (gi)		**0.916**	**0.879**	**0.066**	**0.078**	**0.061**	**0.067**	**0.021**	**0.024**	**1.459**	**1.424**	**1.293**	**1.393**
SE (m) (gi-gj)		**0.522**	**0.501**	**0.037**	**0.044**	**0.035**	**0.038**	**0.011**	**0.013**	**0.831**	**0.811**	**0.737**	**0.794**
CD 5% (gi-gj)		**1.037**	**0.995**	**0.074**	**0.088**	**0.069**	**0.076**	**0.022**	**0.026**	**1.651**	**1.611**	**1.464**	**1.578**
CD 1% (gi-gj)		**1.374**	**1.319**	**0.097**	**0.114**	**0.092**	**0.101**	**0.029**	**0.034**	**2.188**	**2.135**	**1.94**	**2.091**

Table 4. Estimates of specific combining ability effects for F_1 and F_2 in 9 x 9 diallel set

S.N.	Characters	Seedling vigour		Leaf glossiness		Trichome density		Dead heart percentage at 14 DAE		Dead heart percentage at 28 DAE		Grain yield plant^{-1}	
	Crosses	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
1	Ringni X M-35-1	-0.11	-0.189*	0.009	-0.01	-0.167 **	-13.567 **	-0.041	3.65*	-0.165	1.183	-13.567 **	-4.722 **
2	Ringni xSPV 504	0.014	-0.011	0.071	0.142	-0.188 **	9.285**	-0.157	3.3	0.201	3.108	9.285**	1.823
3	Ringni X AKSV 13R	-0.061	0.285**	-0.117	0.223**	-0.402 **	18.605**	-2.105	2.188	1.182	4.542**	18.605**	-4.930 **
4	Ringni X MS 104B	-0.151	-0.732 **	-0.208 **	-0.635 **	0.211**	12.653**	8.220**	-6.822**	0.185	-7.080 **	12.653**	-11.327 **
5	Ringni XAKRMS 45B	-0.291 **	-0.465**	-0.319 **	-0.633**	1.022**	14.315**	-0.298	-6.145**	-4.255*	-6.553 **	14.315**	-6.349 **
6	Ringni X CSV 18R	-0.205*	0.521**	-0.211 *	0.520**	0.121**	6.595**	-3.849*	11.058**	3.305*	6.526	6.595**	-5.121 **
7	Ringni X IS 2312	-0.068	0.065	-0.068	0.022	-0.055	29.965**	-0.368	3.353*	0.199	1.414	29.965**	42.562**
8	Ringni X IS 18551	0.584**	0.124	0.582**	0.167*	-2.261 **	-21.703 **	8.166**	4.455**	10.300**	4.294*	-21.703 **	45.967**
9	M-35-1 X SPV 504	0.136	-0.295**	0.309**	-0.407 **	-0.989**	24.360**	4.706**	-3.152	6.162**	0.332	24.360**	3.543**
10	M-35-1 X AKSV 13R	0.338**	0.118	0.308**	0.123	-1.32**	-19.080 **	1.519	6.579**	-3.244*	3.576*	-19.080 **	2.960**
11	M-35-1 X MS 104B	-0.423**	-0.225**	-0.590**	-0.108	1.846**	21.485**	-2.463	0.683	6.426**	-1.32	21.485**	34.399**
12	M-35-1 X AKRMS 45B	-0.046	0.198**	0.042	0.204*	0.321**	37.101**	-3.255	2.243	2.876	2.354	37.101**	7.604**
13	M-35-1 X CSV 18R	0.274**	-0.589 **	0.374**	-0.466 **	-1.32 **	-3.276*	11.801**	-4.234 **	5.882**	-6.576 **	-3.276*	13.208**
14	M-35-1 X IS 2312	-0.263**	0.175	-0.373**	0.289**	2.068**	7.604**	-5.251 **	10.268**	-4.046	7.755**	7.604**	-1.272
15	M-35-1 X IS 18551	-0.144	0.573**	-0.393 **	0.041	0.978**	8.943**	-5.148**	2.693	-5.182**	1.328	8.943**	-2.953*
16	SPV 504 X AKSV 13R	-0.208*	0.099	-0.437 **	0.329**	1.056**	4.506**	-7.141 **	10.050**	-4.621**	7.497**	4.506**	2.682*
17	SPV 504 X MS 104B	0.174*	0.106	0.109	-0.062	-0.188 **	3.654*	-2.526	-0.706	0.915	-1.788	3.654*	20.494**
18	SPV 504 X AKRMS 45B	0.151	-0.07	0.355**	0.080	-0.817**	13.430**	2.666	1.694	0.759	-0.447	13.430**	13.729**
19	SPV 504 X CSV 18R	-0.049	0.166	0.016	0.126	-0.044	-1.264	4.054*	-1.583	-1.661	-4.428*	-1.264	17.357**
20	SPV 504 X IS 2312	0.391**	0.326**	-0.037	0.245**	-0.740 **	-4.184*	5.036**	6.115**	8.710**	5.093**	-4.184*	-3.420 **
21	SPV 504 X IS 18551	-0.127	0.305**	0.049	0.39	-0.356**	-1.865	-0.951	7.204**	0.691	8.050**	-1.865	6.309**
22	AKSV 13R X MS 104B	-0.373 **	-0.135	0.277**	-0.151	0.488**	23.471**	2.300	1.075	-3.654*	-0.984	23.471**	-22.939**

Table 4. contnued.....

S.N.	Characters	Seedling vigour		Leaf glossiness		Trichome density		Dead heart percentage at 14 DAE		Dead heart percentage at 28 DAE		Grain yield plant^{-1}	
	Crosses	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**	**F_1**	**F_2**
23	AKSV 13RX AKRMS 45B	-0.300 **	-0.051	-0.370**	-0.090	0.859**	-16.847 **	1.018	-0.812	0.463	0.929	-16.847 **	0.946
24	AKSV 13R X CSV 18R	0.243**	-0.012	0.024	0.0370	-1.244 **	11.116**	5.320**	-1.145	6.552**	0.095	11.116**	12.154**
25	AKSV 13R X IS2312	-0.077	0.345**	0.201*	0.326**	-0.757 **	-8.247 **	1.025	9.526**	5.514**	7.093**	-8.247 **	7.317**
26	AKSV 13R X IS18551	0.575**	-0.313 **	0.451**	-0.383 **	-2.517 **	16.671**	10.542**	-5.262**	13.578**	-1.143	16.671**	21.572**
27	MS 104-B X AKRMS 45B	-0.284 **	0.036	-0.705 **	0.0190	0.669**	3.405	-6.477 **	0.506	-4.521 **	0.714	3.405	12.016**
28	MS 104-B X CSV 18R	-0.018	0.192*	0.183*	0.156	-0.125 **	-30.993 **	-5.735 **	1.892	-3.854*	1.797	-30.993 **	-0.33
29	MS 104-B X IS 2312	-0.061	0.182	0.200**	0.185*	0.416**	8.494**	-4.327*	5.966**	-2.243	7.275**	8.494**	-3.003 **
30	MS 104-B X IS18551	0.564**	0.491**	0.360**	0.500**	-2.194 **	-5.394 **	5.783**	12.136**	10.028**	11.965**	-5.394 **	-10.625 **
31	AKRMS 45-B X CSV 18R	-0.051	-0.378 **	-0.071	-0.500 **	-0.190 **	-2.657	-4.233*	-3.774*	-0.117	-1.433	-2.657	0.268
32	AKRMS 45-B X IS 2312	0.389**	0.266**	0.196**	0.246**	-0.973 **	-3.447*	3.522	4.710**	-0.309	4.272*	-3.447*	-5.355 **
33	AKRMS 45-B X IS 18551	-0.006	0.404**	0.356**	0.391**	-1.096 **	-24.468**	1.502	10.339**	6.072**	10.309**	-24.468**	-0.887
34	CSV 18R X IS 2312	0.279**	-0.198 *	0.287**	-0.237 **	-0.694 **	7.860**	0.224	-1.13	3.907*	-0.469	7.860**	-5.577 **
35	CSV 18R X IS 18551	-0.512 **	-0.383 **	-0.643 **	-0.336**	2.617**	39.448**	-12.446 **	-6.128 **	-11.245**	-6.859**	39.448**	-19.252 **
36	IS 2312 X IS 18551	-0.209 **	-0.439**	-0.149*	-0.353 **	0.321**	4.295*	0.589	-8.083**	-1.641	-5.737**	4.295*	-5.056**
	SE (m) Sij	**0.080**	**0.095**	**0.075**	**0.082**	**0.024**	**3.829**	**1.781**	**1.739**	**1.581**	**1.703**	**3.829**	**1.075**
	CD Sij at 5%	**0.158**	**0.188**	**0.148**	**0.163**	**0.048**	**7.608**	**3.539**	**3.455**	**3.141**	**3.384**	**7.608**	**2.136**

Table 5. Gene action governing inheritance of different characters in F_1 and F_2 diallel set

S.N.	Characters	Gene action in	
		F_1 diallel	F_2 diallel
1	Seed yield plant^{-1} (g)	Non-additive	Non-additive
2	Dead heart percentage 14 DAE	Non-additive	Non-additive
3	Dead heart percentage 28 DAE	Non-additive	Non-additive
4	Trichomes density per mm^2	Non-additive	Non-additive
5	Seedling vigour 14 DA E	Non-additive	Non-additive
6	Leaf glossiness 14 DAE	Non-additive	Non-additive
7	Recovery percentage	Non-additive	Non-additive

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New Promising Variety of Acid Lime : PDKV Bahar, a Prolific Bearer

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ABSTRACT

After sixteen years of constant nurturing of elite lime clones at AICRP (Fruits), Dr. PDKV, Akola was fruitful in the form of release of PDKV Bahar a prolific bearer. Followed by initial in-situ evaluation, total 11 elite clones were selected. Finally six most superior clones were evaluated (2009-14) along with commercially popular varieties viz. PDKV lime and Sai Sarbati as check in RBD replicated thrice for comparison. Study revealed PDKV Bahar (Clone-2) was superior over other clones as well as check varieties and recorded significantly maximum yield (124.92 kg plant^{-1} i.e.34.54 t ha^{-1}), no of fruits (1833 plant^{-1}), TSS(8.390B) and acidity (7.18) in all the fruiting seasons over the years compare to other clones and check varieties.

In India the important citrus fruits grown are mandarins, sweet oranges and acid lime sharing 41 per cent, 23 per cent and 23 per cent respectively of total citrus fruit production in country and the area area is under cultivation in Maharashtra is 37000 ha. Acid limes are grown mostly in Akola and Buldhana districts of Vidarbha region, area in the vicinity of Wadegaon (Patur- Dist. Akola) is famous belt of acid lime. High yielder, juicy, thin peeled less seedy/ seedless and diseases resistant particularly citrus canker and *Phytophthera* are the some of the characters having farmer's priority. Moreover painful harvesting of acid lime fruit is major concern of farmer which also retards harvesting efficiency.

Natural heterozygosity (Singh, 2012) and the spontaneous mutation is amply exist in acid lime, which form the base for the variability(Soost and Cameron,1975). Such desirable variant can selected if found fruitful conforming cherished goal, can be further utilized (Powell,1995, Waller,1995)

MATERIAL AND METHODS

PDKV Bahar : The intensive survey was conducted for selection of superior genotype in the year 1998 to 2002. . Initially plants were evaluated in situ. Acid lime trees having higher yield potential were selected from local acid lime orchard of Wadegaon area and planted at AICRP (Fruits), Dr. PDKV, Akola. A pedigree record of mother plants was also maintained for last 15 year. Selection was made for better fruit yield and quality (size of fruit, thin skin, less seeded, less thorny and resistant to canker) and more yield.

RESULTS AND DISCUSSION

The data recorded on height, spread and canopy volume of Acid lime revealed that treatment clone 2 (PDKV Bahar) was superior and recorded significantly highest growth parameters i.e. height (4.32 m), spread (4.92m) and canopy volume (55.460m^3) as compared to remaining clones and varieties.

The data recorded on number of fruits, fruit yield tree^{-1}, average weight of fruit revealed that clone 2 (PDKV Bahar) was superior and recorded significantly highest yield i.e. number of fruits i.e.1833 plant^{-1} year^{-1} (*ambia bahar* 1120, *mrug bahar* 427.6 and *hasta bahar* 285.8), fruit yield (124.92kg plant^{-1}year^{-1} i.e. 34.54 tonnes ha^{-1}) and average weight of fruit (*ambia bahar* 63.57 g, *mrug bahar* 65.37 g and *hasta Bahar* 54.31 g) as compared to remaining clones and varieties.

The data recorded on quality parameter of Acid lime revealed that variety PDKV lime recorded significantly highest percentage of juice (53.04 %) and Ascorbic acid (31.57 mg 100ml^{-1} of juice) and where as clone 2 (PDKV Bahar) recorded maximum TSS (7.66 %), acidity (7.18) and minimum peel thickness (1.62 mm).

The yield potential of PDKV Bahar lime was found higher compared to the other cultivated varieties of Kagji lime in Maharashtra(14.71 per cent and 21.32 per cent, respectively more than PDKV lime & Saisharbati), when evaluated together.

Reaction of acid lime genotypes to pest and disease

Least leaf infestation of leaf miner was onted on PDKV lime with 13.62 per cent followed by Clone2 and Chakradhar seedless.

The incidence of canker in acid lime was observed throughout the season in all clones and varieties. Clone No.2 recorded minimum disease incidence i.e. 40.52 per cent and intensity 8.03 percent which was significantly superior to all clones and varieties.

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Table 1: Vegetative growth and yield parameter of elite of Acid lime pooled mean (2009-14)

Clone	Plant Height (m)	Mean spread (m)	Plant volume (m^3)	No of fruits			Weight of fruit (Kg) plant^{-1}			Avg. Weight of fruit (g)			Av. Volume of fruits (ml)		
				Ambia	Mrug	Hasta	Ambia	Mrug	Hasta	Ambia	Mrug	Hasta	Ambia	Mrug	Hasta
1	3.74	4.35	37.28	1004	324	238.2	58.42	19.36	12.12	59.13	58.71	51.18	54.26	53.88	51.69
2	**4.32**	**4.92**	**55.46**	**1120**	**427.6**	**285.8**	**70.09**	**26.44**	**15.42**	**63.57**	**65.37**	**54.31**	**58.34**	**60.01**	**56.05**
3	3.85	4.5	41.79	1000	318.4	231.6	57.23	17.38	11.81	58.56	56.81	51.2	53.73	52.12	50.93
4	3.33	4.45	37.41	928.20	324.6	223.6	51.66	18.24	11.33	56.8	57.49	50.75	52.11	52.74	50.47
5	3.99	4.10	36.03	893.40	328.4	222.6	51	19.06	11.46	58.53	59.74	51.5	53.68	54.79	51.89
PDKV lime	4.04	4.28	39.54	1001	375.6	247.4	60.61	22.85	13.54	61.5	65.85	55.73	56.41	59.41	55.97
Saisarbati	3.89	4.04	33.63	935.80	331.4	236.2	58.34	21.22	12.56	60.18	63.19	53.95	58.35	57.98	55.5
CD at 5%	0.189	0.235	5.899	63.65	36.254	15.19	5.092	1.256	1.039	3.056	3.58	3.735	2.77	3.26	2.824

Table 2 : Yield and quality parameters of elite of Acid lime Clone pooled mean (2009-14)

Clone	No of fruits plant^{-1} year^{-1}	Total Yield (kg plant^{-1} plant^{-1})	Total Yield (tonnes ha^{-1})	Juice (%)	Ascorbic Acid mg/100 ml of juice	TSS	Acidity	No of seeds	Peel thicknes (mm)
1	1566.2	99.16	27.42	49.57	30.09	7.73	6.77	11.93	2.08
PDKV Bahar/ Clone-2	1833	124.92	34.54	52.41	31.47	**8.39**	**7.18**	11.60	1.62
3	1550.2	98.44	27.22	50.5	31.45	7.72	6.42	10.73	2.04
4	1476.4	91.96	25.43	51.52	30.65	7.77	6.40	10.47	2.15
5	1444.4	93.00	25.71	51.62	31.70	7.77	6.44	9.20	2.10
PDKV	1624.2	108.87	30.11	**53.04**	**31.57**	8.11	6.58	10.91	1.85
Saisarbati	1503.4	102.97	28.47	52.06	31.42	8.08	6.61	11.6	1.98
CD at 5%	72.354	6.127	1.695	1.536	2.016	0.073	0.083	0.966	0.174

Table 3. Incidence of leaf miner and canker on different clones and varieties from Pooled mean (2009-14)

Clones/ Varieties	Leaf infestation due to leaf miner (%)	Leaf infestation due to leaf miner (%)	Per cent Disease Incidence of Canker
Clone-1	16.76	16.76	46.14
	(24.17)	(24.17)	(42.78)
PDKV Bahar/ Clone-2	17.34	17.34	40.52
	(24.61)	(24.61)	(39.51)
Clone-3	15.11	15.11	44.70
	(22.87)	(22.87)	(41.94)
Clone-4	14.22	44.70	46.53
	(22.13)	x(22.13)	(43.00)
Clone-5	15.85	15.85	44.83
	(23.37)	(23.37)	(42.03)
PDKV-lime	**13.62**	**13.62**	45.59
	(21.63)	**(21.63)**	(42.46)
Sai Sharbati	14.68	14.68	46.04
	(22.52)	(22.52)	(42.73)
C.D. at 5%	2.25	5.49	1.27

Table 4: Performance Indicator

Clone	% more yield than						
	Yield t ha^{-1}	PDKV lime	Saisarbati	Plant character	No of seed $fruit^{-1}$	Peel thickness (mm)	Acidity %
1	27.42			Thorny	11.93	2.08	6.77
PDKV Bahar/ Clone-2	34.54	14.71	21.32	Thorny	11.6	1.62	7.18
3	27.22			Thorny	10.73	2.04	6.42
4	25.43			Thorny	10.47	2.15	6.4
5	25.71			Thorny	9.2	2.1	6.44
PDKV	30.11			Thorny	10.91	1.85	6.58
Saisarbati	**28.47**			**Thorny**	**11.6**	**1.98**	**6.61**

CONCLUSION

From the results, it can be concluded that, Clone 2 /PDKV Bahar of acid lime was found to be superior and recorded highest growth, yield and quality parameters (TSS and acidity) and given maximum return as compared to the other remaining genotypes and check varieties under Akola conditions.

The experiment is suggestive of emphasis could be given on clonal selection , since hetrozygosity and variant due to the spontaneous mutation can be very well exploited.

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DNA-Based Method for Detection and Identification of *Phytophthora* in *Citrus spp.*

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ABSTRACT

Phytophthora diseases cause major losses to agricultural and horticultural production in India and worldwide in citrus spp. Most *Phytophthora* diseases are soilborne and difficult to control, making disease prevention an important component of many disease management strategies. Detection and identification of the causal agent, therefore it's an essential part of effective disease management. Symptoms included slow decline, moderate leaf chlorosis, reduced growth, lack of tree vigor and dieback was found in citrus because of *phytopthora*. These symptoms were associated to extensive canker lesions and gummosis at the base of the trunk, and root rot, often extending from the main roots into the feeder roots. Among all the species of *phytophthora Phytophthora nicotianae* and *P. citrophthora* causes major losses in citrus orchard. The polymerase chain reaction (PCR) was used for the specific detection of diseases in citrus roots and soils. Primers were used in this study based on the nucleotide sequences of the internal transcribed space regions of different species of *Phytophthora*. From this primer its easy to diagnose the infestation of *phytophthora* in soil as well as infected part of plant. By using PCR-RFLP it's possible to discriminate *phytophthora* from other fungus samples. In this study specific primers were used for the detection of *phytophthora*. Molecular detection and identification strategies are much easier than conventional methods.

Phytophthora contains mostly plant pathogenic species that attack roots, stem bases, growing points, fruit and foliage of many plant species in natural communities and cropping systems. Its systematics has been based on morphologicaland physiological criteria (Tucker, 1931; Waterhouse, 1970; Newhook *et al.*, 1978). A tabular key devised by Newhook *et al*. (1978) and revised by Stamps *et al*. (1990) splits the genus into six groups, with the most important criteria for separation being the form and nature of the sporangium (papillate, semi-papillate and non-papillate) and the attachment of antheridium to oogonium (amphigynous or paragynous). *Phytophthora spp*. are the most damaging soil-borne pathogen in Vidarbha region of Maharashtra state that attack citrus plants right from damping off of seedlings in nursery beds to decay of fibrous roots, crown rot, collar rot, foot rotand gummosis in mature orchards. These diseases collectively is one of the major factors for the decline, low productivity and short life span of the famous Nagpur mandarin orange (*Citrus reticulata* Blanco) crop in Vidarbha region of Maharashtra state every year (Naqvi, 2000).

The most important *Phytophthora spp*. affecting citrus worldwide are *P. nicotianae* (syn. *P. palmivora,* and *P.citrophthora* (Bowman *et al.,* 2007). Identification of most fungi is based principally on morphology. For several genera of fungi, including *Phytophthora*, identification to species can be very difficult, because morphological features may vary significantly. For many *Phytophthora* species, this conventional tests is very sensitive and accurate method to determine the causal agent of diseases. However it is somewhat time-consuming and, therefore, are not wellsuited for routine screening of large number of samples. In addition, the limited number of evolutionarily relevant morphological characters available and the difficulties with inducing the production of informative structures inaxenic culture, may give rise to mis-identification of many *Phytophthora* species. Alternative method, such as the generation of protein profiles (Gill and Zentmyer 1978; Erselius and de Vallavielle1984; Erwin and Ribeiro 1996) have been developed for identification of *Phytophthora* species. Isozyme patterns have also been established for many species (Tooley *et al*. 1985; Oudemans and Coffey 1991; Erwin and Ribeiro 1996) and isozymes have been extensively used to determine variation within rather than between species.

Recent molecular analyses have substantially increase understanding of the phylogenetic relationships between *Phytophthora species* and provide anenormous source of data to develop molecular detection methods. These analyses were based on the ITS regions (Cooke *et al*., 2000) the mitochondrial encoded cytochrome oxidase II (CoxII) and I (CoxI) genes (Martin and Tooley, 2003) and the combinations of different coding genes of nuclear

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(transaction elongation factor 1α and β-Tubulin) and mitochondrial (CoxI; NADH dehydrogenase) genome (Kroon *et al.*,2004). As previously mentioned, ITS sequences in some circumstances fail to discriminate among closely related taxas. Similarly, phylogenetic analyses by Martin and Tooley (2003) and Kroon et al. (2004) were based on coding sequences with a relatively low mutation rates and therefore limited real target sites for diagnostic development. The elicitin gene (parA1) and the putative storageprotein genes (Lpv) proved to be effective targets for specific detection of *P. cinnamomi and P. nicotianae* respectively (Kong et al., 2003a,b) but neither genes contain introns and are unlikely to be variable enough todistinguish a broad range of species.

In this paper, we describe the development of PCR primers from internal transcribed space regions and their use in PCR assay to detect *Phytopthora spp.* in citrus spp., overall objective of the research described here was to develop a DNA-based diagnosticassay for detection and identification of a wide range of *Phytophthora* species of economic importance.

MATERIAL AND METHODS

Source of isolates and DNA extraction

In order to design species and genus-specific DNA-based diagnostictests, sequence information from the rRNA (rDNA) repeat was obtained from representative isolates of different *Phytophthora* species. Isolates within each species, as well as from species of the closely related genus. *Phytophthora spp.* isolates from root, fruit and soil samples were collected from various citrus orchards (Nagpur,Warud, Katol, Amravati, Achalpur and Akola district) of Vidarbha region.

Soil samples were collected from rhizosphere of eachplant at 5 to 30 cm depth along with feeder roots. Samples were diluted by adding 20 cc soil in 80ml of sterile distilled water and plated on a selective medium plate containing Pimaricin, Ampicilin, Rifamicin, penta-chloronitrobenzene and himexazol (PARPH) at concentration of each antibiotic into corn meal agar medium as shown in (Kannwischer and Michell, 1978). Typical muddy colonies of *Phytophthora* were observed on specific medium and those colonies were then purified on PARPH-CMA selective plate. *Phytophthora* colonies were maintained on corn meal agar.

For DNA extraction, the pathogen were grown in 20 ml culture of a sucrose/asparagine/mineral salts broth containing 30 $\mu g\ ml^{-1}$ β-sitosterol (Elliott *et al.*,1966). After vacuum filtration, the mycelium was freeze-dried for extended storage at "20 °C. To extract total DNA 10–20 mg of dry mycelia were crushed with liquid nitrogen and then suspended in 1:2 extraction buffer (200 mM Tri–HCl [pH 8],250 mM NaCl, 25 mM EDTA, 0.2% CTAB), vials were kept in water bath for 60min at 65p C and centrifuged with 13,000 rpm. The supernatant precipitated with 800 il of phenol/chloroform/isoamyl alcohol (25:24:1) and centrifuged at 13,000 rpm for 5 min. The aqueous phase was extracted twice with 800 il of phenol/chloroform/ isoamyl alcohol (25:24:1) and 700 µl of chloroform/isoamyl alcohol (24:1), respectively. DNA was precipitated with an equal volume of isopropanol for 1 h at 4 °C, then pellet was washed with 70 per cent cold ethanol (-20 °C), dried, resuspended in sterile distilled water and stored at -20°C. For routine amplifications, DNA was diluted to 50 ng/µl and maintained at 4 °C deep freeze.

PCR amplification

To ensure the quality of template DNA it was quantified using nanospectrophotometer, and then all extracts were amplified by PCR with universal primers as shown below. PCR reactions were performed in a total volume of 25 il containing 50 ng of genomic DNA, 10mM Tris–HCl (pH 9), 50Mm KCl, 0.1per cent Triton X-100, 100 µM dNTPs, 1mMMgCl2, 1 unit of *Taq* polymerase (Taq DNA polymerase, Promega Corporation, WI, USA) and 2 µM of ITS primers. The PCR reaction was incubated in a programmable thermal cycler starting with 5 min denaturation at 95 p C, followed by 35 cycles at 95p C for 30 sec, annealing at 56 ^{0}C for 45 sec, and extension at 72^{0}C for 1 min. A negative control (no template DNA present in PCR reaction) was included in all experiments. Amplicons were analysed by electrophoresis in 2 per cent agarose gels in TBE buffer (Sambrook *et al.*, 1989) and visualized by staining with ethidium bromide.

Polymerase chain reaction (PCR) amplification of the ITS region of the template DNA was performed using the primers. Primers used in this study are

ITSF-5;'TCCTCCGCTTATTGATATGC3' and ITS R-5'GAAGGTGAAGTCGTAACAAGG3' an universal primer designed to improve the amplification of a part of rDNA of Oomycota; it amplifies ~900 bp product in combination. The same primer was run with the other fungi as listed in fig.3 and The purified products were digested with

restriction enzyme *Alu-I*. The purified PCR products were sent for sequencing bi-directionally at the commercially available automated DNA sequencing facility (Chromus Biotech, Bangalore) for further genomic research work.

RESULTS AND DISCUSSION

Species identification in the genus *Phytophthora* is difficult and requires the use of taxonomic keys andknowledge of host range of the pathogen. The PCR method was describe in this research paper was found effective. PCR would definitely improve the diagnosis of *Phytophthora* species infecting citrus and in view of the wide host range of *P. nicotianae*, it could be applied to other host pathogen combinations as well. Considering the fact that *Phytophthora* diseases are related to soil inoculums of the pathogens, it could be interesting to develop a protocol that able to estimate the number of propagules of the pathogen in soil. Sporangia produced by sterile isolates of *P. citrophthora* and *P. nicotianae* are shown in (Fig. 1).

The PCR amplicons obtained from all the isolates were of expected size (~900 bp) (Fig. 2) as per similar result was found by (Das A. K *et al.*, 2011).On this basis its confirmed that *Phytophthora nicotianae* is the most prevalent species in citrus orchards of Vidarbha region with specific primers. From the infected samples of plant and soil its easy and rapid for detection of *phytophthora* using this primer i.e internal transcribed spacer (ITS) regions of ribosomal DNA as well as its easy to discriminate *phtpytophthora* from other fungi as shown in fig.3 using PCR-RFLP pattern using listed primers. The digested pattern shows discriminating result for identification of *phytophthora* from other fungi. From fig.4 concludes that the detection of disease in infected sample of plant with field soil. There was amplification found in diseased sample with *phytophthora* than other diseases.

Identification of representative isolates of each species and determining the evolutionary relationships among the different *Phytophthora* species based on the isolates usedin this study have been published previously (Crawford *et al*. 1996; Cooke *et al*. 2000). Since that time, additional studies have been conducted using ITS sequence information (F¨orster *et al*. 2000) and a combination of mitochondrial and nuclear gene sequences (Kroon *et al*. 2004; Martin and Tooley 2004) that all support the evolutionary relationships among an extensive set of *Phytophthora* species, as first putforward by Cooke *et al*. (2000). Sequencing of multiple isolates of the same species revealed that intra-specific variation in the rDNA ITS sequence is low and stable, but not absent. Sufficient sequence variation is present between species, allowing identificationof all *Phytophthora* species targeted in this study based onITS1 and ITS2 sequence alone (Cooke *et al*. 2000). It must be remembered that the PCR amplicons generated by the PCR process are *in vitro* amplification products from an rRNA multigene family, in which copies are arranged intandem repeats in the genomic template DNA. Concerted evolution acts to homogenise gene sequence composition in these tandem repeats, which are generally quite uniform, but mutation may also act to change nucleotide bases. There may be a propensity for mutations to accumulate with greaterfrequency at some sites in the gene sequence than at others.

This protocol would improve diagnosis considering the wide host range of the pathogens, particularly of *Phytopthora spp.* it could be applied to other host–pathogen combinations. Moreover, other *Phytophthora* diseases could be detected in a similar way, designing specific primers for the second round of PCR. Finally, considering that most *Phytophthora* diseases are related to soil inoculums of the pathogens it could be interesting to developa protocol able to estimate the propagule number of thepathogen. This approach is being actively pursued and new primers will be designed to apply Real time Scorpion-PCR. As well as by knowing the infestation in soil samples or in field its easy to follow an better management practices for the disease.

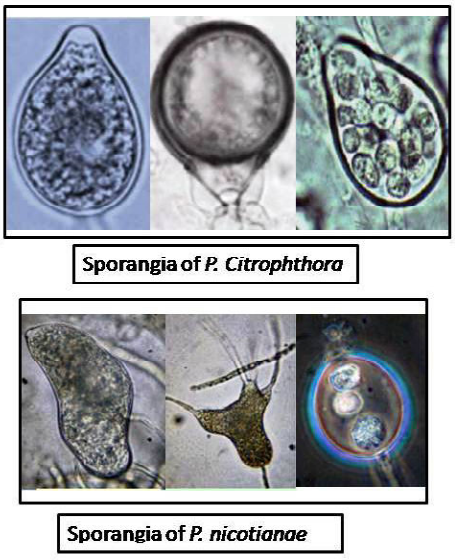

Fig.1. Sporangia of Phytopthora

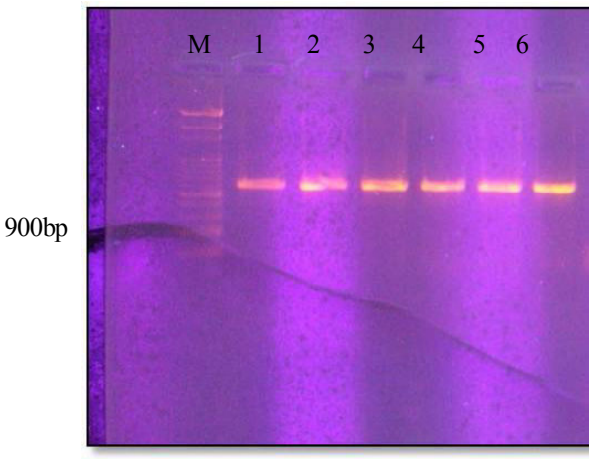

Fig. 2 Amplification of *Phytopthora spp.* of 6 locations. (M-Marker, 1-Akola, 2-Achalpur, 3-Amravati, 4-Varud, 5-Katol, 6-Nagpur) using ITS primer

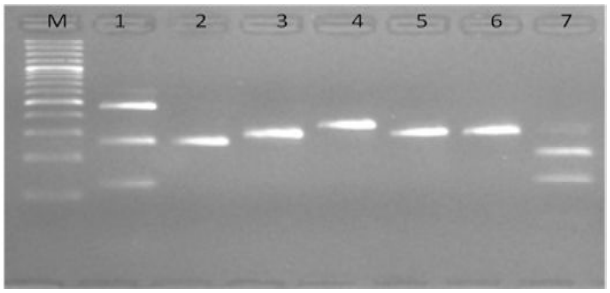

Fig.3 discrimination of *phytophthora spp*. from other fungal isolates (M-Marker, 1-*Phytophthora spp.*, 2- *Fusarium spp*., 3-*Rhizoctonia spp*., 4-*Apergillus spp*., 5- *Trichoderma spp.*, 6-*Alternaria spp.*, 7- *sclerotium spp*.) using PCR-RFLP pattern.

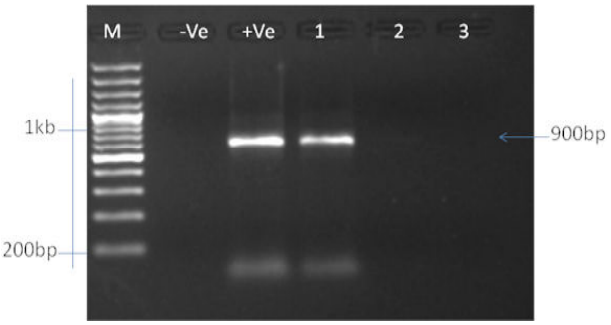

Fig-4. Detection of *phytophthora* disease in plant as well as soil sample (M-marker, -Ve- Negative control, +Ve- positive control, 1-DNA isolated from soil, 2-filed soil, 3- infected roots from other fungal disease.)

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Specific Leaf Weight : A Physiological Tool to Screen Drought Tolerance in Cotton Genotypes

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ABSTRACT

The investigation was conducted during *Kharif* season of 2010 and 2011 in RBD on the experimental field of Post Graduate Institute, Department of Agricultural Botany under non stress and water stress condition in pot culture. The seeds of 31 cotton genotypes (10 *G. arboreum* and 21 *G. hirsutum*) were sown in three replications. Experimental findings are based on two years pooled data under water stress and non stress conditions. Finding indicates significant superiority of *G. arboreum* over *G. hirsutum* which indicates tolerant towards water stress on the basis of morpho-physiological and seed cotton yield and its attributes. Result revealed that, at 120 DAS, under both stress and non stress condition, *G.arboreum* genotypes showed significantly more SLW than *G. hirsutum*. Specific leaf weight was found to be best indicator for drought tolerance and among *G. arboreum* AKA-8 (1.78 g/dm²) Garrohill (1.91 g/dm²), AKDH-1 (1.82 g/dm²), KWA-8 (1.53 g/dm²), HD-110-151 (1.50 g/dm²), AKA-7 (1.49 g/dm²) and among *G. hirsutum viz.,* PKV-Hy-4 (1.51 g/dm²), PKV Hy-5 (1.34 g/dm²), Yamuna (1.17 g/dm²) and PKV-Hy-2 (1.10 g/dm²) were found better tolerant genotypes for water stress condition. The correlation co-efficient revealed that, SLW (r=0.741) has positive correlations with seed cotton yield and this criteria may be useful for assessing genotypes for drought studies.

It is estimated that one third of world population has been in area where the water sources are poor. In Maharshtra, about 95 to 97 per cent area is under rainfed cultivation. Vidarbha is largest cotton growing region in Maharashtra state. It covers about 40 per cent area of Maharashtra state and occupies an area of 15.60 lakh ha, with production of 35.50 lakh bales and productivity is 312 lint kg ha^{-1} (Anonymous, 2013). The main reason of low productivity of cotton in Vidarbha is its dependence on the monsoon rains. Most of the times erratic rainfall with uneven distribution occurs.

Therefore cotton crop has to face the water stress at flowering and boll development stage. Plant response to drought is in two ways *viz*., susceptibility and tolerance, which depends on the species, genotypes and developmental age of the plant. A strategy that tolerant plant often uses to overcome water deficit is the accumulation of solutes (osmotic adjustment) in the cell to help or maintain plant water status, particularly under drought. Drought tolerance is the struggle of plants to survive in the drought condition with little or no injury. Drought tolerance is either acquired by mitigating drought or by showing high degree of drought tolerance. The progress in developing crop cultivars for tolerance to abiotic stress particularly drought has been slow, because of lack of knowledge of inheritance of tolerance, low heritability and lack of efficient techniques for screening germplasm (Kush, 1998). Efforts were made in identifying genotypes with higher yield coupled with relatively better drought tolerance by investigating physiological components causing performance difference in deficit of stress condition and evaluated different genotypes of cotton which are more productive and tolerant to stress condition with utilizing minimum water resources on the basis of physiological parameters.

MATERIAL AND METHODS

The experiment was carried out on the experimental field of Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during *Kharif* season of 2010 and 2011. The experimental material consisted of 31 diverse genotypes of *G. hirsutum* (21 genotypes) and *G. arborium* (10 genotypes) was sown in earthen pots. Ninty three pots for water stress conditions (31 genotypes with three replications) were kept in rainout shelter and 93 pots for water non stress conditions (31 genotypes with three replications) were kept in open place and adopting RBD with three replications. Pots were filled with 9 kg of black cotton soil which was mixed with 1000 g FYM. All the pots was fully saturated by water to the field capacity before planting of seeds. For stress condition pots were kept moistened with desired quantity of water up to initiation of bolls (up to 75 days). Water stress was imposed at initiation of bolls for 12 days to each genotypes

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replication wise and watered thereafter for life saving. Second stress was imposed for 12 days after recovering first stress. This situation was maintained in rain out shelter. For non-stress conditions irrigation were applied at different growth stages to each genotype (earthen pots) replication wise up to maturity. Major morpho-physiological observations were recorded before and after imposition of water stress. SLW was estimated as per procedure suggested by Wolf et.al.(1972) The mean data analyzed for analysis of variance as per Panse and Sukatme (1967).

RESULTS AND DISCUSSION

Morphological characters

Leaf area (cm^2)

At 120 DAS mean values of G. *hirsutum* showed more leaf area per plant than G. *arborium* under stress and non stress conditions. Under non stress condition, when genotypes of both species compared with general mean (1555.78 cm^2), the genotype PA-402 (3064.3 cm^2) recorded significantly more leaf area $plant^{-1}$ followed by AKA-53B (2422.5 cm^2), PA-255 (2272.0 cm^2), PKV Rajat (2248.2 cm^2), DHY286-1 2119.4 cm^2), PKV-Hy-2 (2108.4 cm^2), LRA-5166 (1950.6 cm^2). Under stress condition, when genotypes of both species compared with general mean (902.3 cm^2), the genotype PA-402 (1788.3 cm^2), PA-255 (1326.4 cm^2) of *G. arborium* and AKA-53B (1414.1 cm^2), PKV Rajat (1312.5 cm^2), DHY-286-1 (1237.3 cm^2), LRA-5166 (1138.8 cm^2) of *G. hirsutum* recorded significantly more leaf area per plant. In moisture stress condition, *G. arborium* gave higher leaf area $plant^{-1}$ as compared to *G. hirsutum* genotypes. The reduced leaf area, leaf growth and response to water stress may conserve water. These findings are in accordance with the findings of Ludlow and Muchow (1990). As water stress increases, older leaves senescence to various degrees, this reduces the leaf area of plants. Young *et al*. (2004) also reported loss of leaf function and premature onset of senescence of older leaves.

Specific Leaf Weight (g/dm^2/plant) (SLW)

SLW was found lower at initial stages of growth and increase steadily up to 120 DAS. It was ob served more under stress than non stress condition. At 120 DAS, under both stress and non stress condition, *G.arborium* genotypes showed significantly more SLW than *G. hirsutum*. Under non stress condition, when genotypes of both species compared with general mean (0.68 g/dm^2/plant), KWA-8 (1.33 g/dm^2/plant), AKA 7, AKDH-1 (1.26 g/dm^2/plant) each, HD-110-151, AKA-8 (1.19 g/dm^2/plant) each and, Garrohill (1.18 g/dm^2/plant) of *G. arborium* and only two genotypes of *G. hirsutum* AKH-9916 (0.89 g/dm^2/plant) and PKV Hy-4 (0.87 g/dm^2/plant) recorded significantly higher SLW/plant. Under stress condition, when genotypes of both species compared with general mean (0.93 g/dm^2/plant), then six *G. arborium* genotypes *viz.,* Garrohill (1.91 g/dm^2/plant), AKDH-1 (1.82 g/dm^2/plant), AKA-8 (1.78 g/dm^2/plant), KWA-8 (1.53 g/dm^2/plant), HD-110-151 (1.50 g/dm^2/plant), AKA-7 (1.49 g/dm^2/plant) and three of *G. hirsutum* genotypes PKV-Hy-4 (1.51 g/dm^2/plant), PKV-Hy-5 (1.34 g/dm^2/plant) and Yamuna (1.17 g/dm^2/plant) found statistically significant. From the data, it is clear that *G. arborium* varieties recorded more SLW than *G. hirsuaaatum* with exception of (PKV-Hy-4) and under moisture stress condition, SLW was found more than that under non stress condition.

Increase in SLW with age of the crop might be due to either enhanced layer of mesophyll cells and /or increased thickness of conducting vessels. Reduction in leaf size is also correlated with an increase in leaf thickness. Specific leaf weight (SLW) indicates the thickness of leaf and is known to have positive correlation with photosynthetic rate .

Total dry matter production (g/plant) TDM

Under non stress condition at 120DAS ,when all genotypes of both species compared with general mean (73.88 g/plant), six *G. arborium* genotypes recorded significantly higher TDM g $plant^{-1}$, viz. PA-255 (126.82 g $plant^{-1}$), AKA-8 (123.68 g $plant^{-1}$), PA-402 (119.75 g $plant^{-1}$) AKA-7 (119.22 g $plant^{-1}$), AKDH-1 (94.74 g $plant^{-1}$), KWA-8 (93.62 g $plant^{-1}$). Under water stress condition, when genotypes of both species compared with general mean (52.6 g $plant^{-1}$), six *G. arborium* genotypes *viz.,* AKA-8 (94.63 g $plant^{-1}$), AKA-7 (69.93 g $plant^{-1}$), AKDH-1 (66.21 g $plant^{-1}$), HD-110-151 (65.67 g $plant^{-1}$)), KWA-8 (65.39 g $plant^{-1}$), Garrohill (64.25 g $plant^{-1}$) and four genotypes of *G. hirsutum viz.,* LRA-5166 (75.18 g $plant^{-1}$), PKV-Hy-2 (68.18 g $plant^{-1}$), PKV-Hy-5 (61.83 g $plant^{-1}$), PKV-Hy-4 (61.76 g $plant^{-1}$) recorded significantly higher total dry matter. In present study it was observed that, the initial stages of growth (upto 60 DAS), most of the *G. hirsutum* genotypes recorded more total dry matter production per plant. This may be due to higher leaf area per plant which results in more

photosynthate production. Afterwards under irrigated as well as under water stress condition, there was reduction in leaf area in *G. hirsutum* varieties and opposite situation about *G. arborium* varieties. Initially *G. arborium* varieties were recorded lesser total dry matter production due to lower leaf area and afterwards it was increased. This may be due to the consistency in leaf area upto the time of harvest which was found more from 90 DAS upto the time of harvest. Krieg (1997) noted that the crop growth rate was reduced by water stress through reduction in size and number of leaves produced and in reduction of photosynthesis.

Yield and Yield Attributes

Seed cotton yield (SCY), g plant^{-1}

In non stress condition, when all genotypes of both species compared with general mean (59.41 g plant^{-1}), five *G. arborium* genotypes *viz.,* AKA-8 (102.81, g plant^{-1}), PA-255 (92.59 g plant^{-1}), AKDH-1 (91.23 g plant^{-1}), PA-402 (81.37, g plant^{-1}), AKDH-5 (79.74 g plant^{-1}) and two *G. hirsutum viz.,* PKV-Hy-2 (78.53, g plant^{-1}), PKV-Hy-5 (72.99, g plant^{-1}) recorded significantly higher seed cotton yield which showed in 73.05, 55.64, 53.56, 36.96, 34.22, 32.18 and 22.86 per cent higher over general mean respectively. Under water stress condition, five *G. arborium* genotypes *viz.,* AKA-8 (65.03 g plant^{-1}), AKDH-1 (62.30 g plant^{-1}), AKDH-5 (55-69 g plant^{-1}), Garrohill (55.15 g plant^{-1}), GAK-423 (54.97 g plant^{-1}) and three *G. hirsutum* genotypes *viz.,* PKV Hy-2 (58.22 g plant^{-1}), PKV-Hy-5 (57.87 g plant^{-1}), PKV-Hy-4 (52.43 g plant^{-1}) recorded significantly higher seed cotton yield and found 46.7, 40.54, 25.63, 24.41, 24.0, 31.33, 30.54 and 18.27 per cent more than general mean (44.33 g plant^{-1}) of both the species respectively. The seed cotton yield strongly influenced due to water stress condition. As water stress increases, older leaves senescence to various degrees. This reduces the leaf area of plants and ultimately reduced the photosynthetic area which may reduced yield of genotypes. Most of the *G. arborium* varieties were given better yield than *G. hirsutum* under water stress condition. These findings are in agreement with findings of Baig *et al.* (2009) who noted that *G. arborium* genotypes were suitable best under water stress condition of Maharashtra region. Similar findings also reported by Young *et al*. (2004) who also reported loss of leaf function and premature onset of senescence of older leaves. In present study the reduction in seed cotton yield by water stress may be mainly due to photosynthesis and translocation. Photosynthesis was more affected than translocation. This might be due to leaf water potential under water stress drastically reduced daily photosynthate in leaf area and in photosynthetic rate and then resulted in photosynthate transported from the leaves. Similar observations were also recorded by Sung (1982) under studies of source and sink relationship in cotton as affected by water stress. Stomatal closure in response to water stress results in decline in the rate of photosynthesis. Very severe drought condition results in limited photosynthesis due to decline in rubisco activity (Bota *et al*., 2004), Fuj and Huang (2001). Hoekstra *et al*. (2001) noted that dehydration results in cell shrinkage, a decline in cellular volume. This makes cellular content more viscous. Increased concentration of solutes leading to increased viscosity of cytoplasm may become toxic and may be harmful to the functioning of enzymes, including those of the photosynthetic machinery which ultimately reduced the yield.

Genotypic and phenotypic correlations

The seed cotton yield (g plant^{-1})showed significant positive correlation with dry matter production(r=0.886). It also showed significant phenotypic correlations with specific leaf weight (r=0.741), relative water content (r=0.292) and total dry matter production(r=0.902) at harvest under stress condition.

CONCLUSION

From this study it is concluded that the parameters like leaf area, dry matter accumulation, SLW, RWC and seed cotton yield differed significantly with respect of both stress and non stress condition in cotton. There was significant positive correlation with all these parameters. Among these, specific leaf weight is reliable, cheapest and simplest physiological tool to identify drought tolerant genotypes. In present study, AKA-8, Garrohill, AKDH-1, KWA-8, HD-110-151, AKA-7 from *G. arborium* and among *G. hirsutum viz.,* PKV-Hy-4, PKV Hy-5, Yamuna and PKV-Hy-2. As these genotypes has positive correlations with seed cotton yield, these may be useful for cotton breeders /researchers/biotechnologists for further improvement of cotton tolerant to drought. This criteria may be useful for assessing genotypes for drought studies.

Table 1. Effect of water stress and non stress condition on plant height (cm),Leaf area (cm^2 /plant), Total dry matter(g $plant^{-1}$) in different cotton genotypes at different growth stages (Pooled Mean)

S.N.	Cotton Genotypes	Plant height at harvest(cm)		Leaf area at 90DAS(cm)		Leaf area (cm^2/plant) at 120 DAS		at Harvest	
		Water stress	Non-water stress	Water stress	Non-water stress	Water stress	Non-water stress	Water stress	Non-water stress
1	AKA 7	166.7	102.4	1404.5	857.0	1189.0	694.3	119.22	69.93
2	AKA 8	148.7	120.5	1740.2	1133.6	1376.4	803.5	123.68	94.63
3	PA 255	152.7	125.8	2675.0	1888.3	2272.0	1326.4	126.82	56.47
4	PA 402	144.5	137.2	2924.7	1966.5	3064.3	1788.3	119.75	59.72
5	Garo hill	149.0	130.0	1090.5	664.9	778.3	454.4	72.17	64.25
6	AKDH-1(H)	135.0	112.2	995.7	627.1	968.2	506.8	95.74	66.21
7	GAK 423(F)	149.0	125.4	1219.8	859.3	1263.3	737.5	85.08	59.51
8	HD-110-151(M)	160.9	126.4	1345.2	723.1	937.7	547.4	84.63	65.67
9	AKDH-5(H)	86.1	72.8	1770.0	1132.5	1597.5	932.6	84.07	55.68
10	KWA 8(M)	139.8	130.4	1714.3	873.0	934.4	545.5	93.62	65.39
G. arborium (Mean)		143.2	118.3	1687.99	1072.53	1438.11	833.67	100.48	65.75
11	AKH-081	120.5	96.0	2248.8	1250.6	1504.7	878.4	63.72	40.26
12	PKV Rajat	89.8	96.5	2003.9	1384.8	2248.2	1312.5	75.56	50.18
13	AKH-8828	91.2	79.8	2474.5	1413.2	1884.9	1100.4	76.20	33.88
14	LRA-5166	84.7	93.6	1336.9	1512.3	1950.6	1138.8	76.37	75.18
15	AKH-0205	81.7	76.8	1342.8	1197.8	1472.3	859.5	54.56	45.26
16	AKH-9916	83.7	78.8	1614.0	838.5	1209.1	705.8	87.66	58.85
17	AKH-2006-1	74.8	77.6	1131.7	927.6	1576.8	920.5	54.44	38.09
18	AKH-2006-2	77.5	74.1	1720.5	1145.4	1649.8	964.7	55.60	38.88
19	NH-615	76.3	76.4	1941.9	1111.0	1491.6	870.8	49.16	36.87
20	MCU-5	86.0	89.4	2212.8	1415.8	1712.0	999.5	57.03	42.04
21	Ganga	112.4	77.5	2210.4	1271.4	1635.2	961.8	61.25	47.50
22	Yamuna	92.6	93.2	1459.0	938.6	1074.0	627.9	64.59	51.65
23	PKV-Hy-2(H)	77.9	79.5	2018.0	1353.4	2108.4	1094.1	82.30	68.18
24	AK-32(F)	91.9	97.8	2599.7	1454.3	1508.3	880.5	44.50	38.64
25	DHY-286-1(M)	76.2	76.8	3340.1	2064.9	2119.4	1237.3	44.02	37.22
26	PKV-Hy-4(H)	83.0	77.8	1207.8	728.9	981.8	573.3	65.71	61.76
27	CAK-23B(F)	69.0	73.5	1123.7	610.4	991.3	578.6	45.34	37.48
28	AKH-07R(M)	92.4	87.1	2208.0	1456.0	1544.3	901.6	40.00	35.05
29	PKV-Hy-5(H)	93.6	80.5	1600.5	858.8	1131.3	660.5	69.28	61.83
30	AKA-53B(F)	72.4	76.3	3494.5	2238.7	2422.5	1414.1	52.91	40.12
31	AKH-02 R(M)	94.6	81.5	1680.1	1181.7	1631.7	952.6	65.30	34.08
G. hirsutum (Mean)		86.8	82.9	1950.93	1254.96	1611.82	934.91	61.21	46.33
General Mean		105.0	94.3	1866.11	1196.11	1555.78	902.25	73.88	52.60
	S.E. (m±)	5.83	5.18	128.16	87.86	105.08	60.63	5.080	2.78
	C.D. at 5%	16.43	14.59	362.48	351.52	297.04	171.50	14.230	7.83

Note : H-Hybrid, F-Female parent, M-Male parent, V-Variety

Table 2 . Effect of water stress and non stress condition on specific leaf weight (g/dm^2) per plant in different cotton genotypes at different growth stages (Pooled Mean)

S.N.	Cotton Genotypes	60 DAS		90DAS		120DAS	
		Non Water Stress	Water Stress	Non Water Stress	Water Stress	Non Water Stress	Water Stress
1	AKA 7	0.82	0.44	0.99	1.00	1.26	1.49
2	AKA 8	0.57	0.22	0.83	0.96	1.19	1.78
3	PA 255	0.48	0.10	0.56	0.34	0.70	0.57
4	PA 402	0.36	0.21	0.48	0.39	0.51	0.51
5	Garo hill	0.84	0.48	0.70	1.05	1.18	1.91
6	AKDH-1(H)	1.25	0.65	1.17	1.25	1.26	1.82
7	GAK 423(F)	0.90	0.55	0.83	0.82	0.82	0.99
8	HD-110-151(M)	0.87	0.63	0.80	1.06	1.19	1.50
9	AKDH-5(H)	0.67	0.26	0.62	0.59	0.73	0.88
10	KWA 8(M)	0.75	0.37	0.71	0.83	1.33	1.53
	G. arborium (Mean)	0.75	0.39	**0.77**	**0.83**	**1.02**	**1.30**
11	AKH-081	0.44	0.23	0.38	0.42	0.58	0.70
12	PKV Rajat	0.53	0.28	0.47	0.47	0.42	0.52
13	AKH-8828	0.39	0.12	0.38	0.28	0.52	0.43
14	LRA-5166	0.79	0.36	0.75	0.65	0.53	0.98
15	AKH-0205	0.59	0.18	0.51	0.46	0.47	0.74
16	AKH-9916	0.71	0.41	0.64	0.78	0.89	1.07
17	AKH-2006-1	0.84	0.42	0.63	0.54	0.44	0.56
18	AKH-2006-2	0.51	0.19	0.41	0.41	0.43	0.59
19	NH-615	0.47	0.21	0.34	0.40	0.41	0.56
20	MCU-5	0.49	0.28	0.37	0.40	0.46	0.57
21	Ganga	0.41	0.21	0.35	0.43	0.47	0.63
22	Yamuna	0.64	0.38	0.55	0.67	0.75	1.17
23	PKV-Hy-2(H)	0.70	0.33	0.53	0.64	0.52	1.10
24	AK-32(F)	0.29	0.20	0.22	0.31	0.37	0.61
25	DHY-286-1(M)	0.20	0.11	0.16	0.22	0.25	0.37
26	PKV-Hy-4(H)	0.92	0.58	0.72	1.02	0.87	1.51
27	CAK-23B(F)	0.73	0.46	0.57	0.86	0.63	0.96
28	AKH-07R(M)	0.30	0.23	0.24	0.34	0.33	0.48
29	PKV-Hy-5(H)	0.70	0.45	0.58	0.90	0.81	1.34
30	AKA-53B(F)	0.23	0.10	0.20	0.22	0.29	0.38
31	AKH-02 R(M)	0.53	0.22	0.50	0.35	0.52	0.45
	G. hirsutum (Mean)	0.54	0.28	**0.45**	**0.51**	**0.52**	**0.75**
	General Mean	0.55	0.32	**0.55**	**0.61**	**0.68**	**0.93**
	S.E. m (±)	0.04	0.04	0.04	0.04	0.05	0.06
	C.D. at 5%	0.11	0.13	0.11	0.12	0.14	0.19

Note : H-Hybrid, F-Female parent, M-Male parent, V-Variety

Table 3. Effect of water stress and non stress condition on relative water content (%) per plant in different cotton genotypes at different growth stages (Pooled Mean).

S.N.	Cotton Genotypes	60 DAS		90DAS		120DAS		150 DAS	
		Non Water Stress	Water Stress	Non Water Stress	Water Stress	Non Water Stress	Water Stress	Non Water Stress	Water Stress
1	AKA 7	92.21	85.47	85.89	73.99	86.14	71.19	78.80	74.80
2	AKA 8	82.42	72.87	88.05	76.29	88.59	63.89	65.63	56.19
3	PA 255	75.87	70.80	83.91	74.34	83.57	67.16	65.94	56.24
4	PA 402	91.69	81.12	84.76	73.29	85.88	73.38	64.35	54.42
5	Garo hill	78.54	69.82	83.11	61.46	84.39	61.00	77.31	74.42
6	AKDH-1(H)	80.06	37.46	83.86	71.71	84.31	60.57	75.11	66.08
7	GAK 423(F)	75.93	66.21	86.94	64.34	87.20	59.85	69.32	60.03
8	HD-110-151(M)	82.63	72.02	89.45	76.71	89.45	59.75	70.98	63.61
9	AKDH-5(H)	81.29	70.67	87.12	69.47	86.93	59.46	69.61	71.23
10	KWA 8(M)	79.45	69.79	83.41	62.18	90.21	60.17	70.07	63.62
	G. arborium (Mean)	82.01	69.62	85.65	70.37	86.67	63.64	70.71	64.06
11	AKH-081	79.74	71.93	85.93	73.36	85.93	61.33	50.14	38.81
12	PKV Rajat	90.74	83.51	86.31	73.12	86.87	74.40	56.37	47.48
13	AKH-8828	82.14	70.89	84.83	75.53	84.05	62.71	71.13	62.75
14	LRA-5166	84.96	77.67	87.78	75.75	86.82	69.22	51.92	41.03
15	AKH-0205	84.90	80.89	88.86	79.81	88.39	67.34	64.24	54.16
16	AKH-9916	81.73	72.40	87.96	79.62	87.33	73.41	70.10	63.45
17	AKH-2006-1	91.08	82.68	83.82	77.77	84.74	74.90	56.34	45.34
18	AKH-2006-2	90.23	87.00	87.79	77.22	86.38	59.26	66.37	57.35
19	NH-615	79.01	70.53	88.91	80.56	90.67	72.36	76.47	73.66
20	MCU-5	87.83	82.64	88.50	75.17	88.21	69.49	70.38	57.78
21	Ganga	76.80	66.26	86.66	73.81	86.07	56.32	71.41	65.34
22	Yamuna	75.50	64.96	88.10	74.86	88.38	54.91	69.15	60.80
23	PKV-Hy-2(H)	86.35	82.04	81.92	70.28	83.10	68.00	72.35	61.07
24	AK-32(F)	91.94	84.02	85.11	78.32	82.21	58.90	70.32	63.47
25	DHY-286-1(M)	78.60	67.53	84.45	71.96	82.51	56.41	60.89	46.02
26	PKV-Hy-4(H)	85.08	78.77	84.04	72.47	80.93	73.47	66.56	56.95
27	CAK-23B(F)	78.61	67.22	87.19	69.10	86.41	60.91	60.94	45.14
28	AKH-07R(M)	80.26	71.81	87.43	62.69	86.69	62.58	62.84	53.63
29	PKV-Hy-5(H)	89.69	82.60	86.65	78.74	81.92	72.99	64.52	52.48
30	AKA-53B(F)	77.93	66.35	87.54	71.83	86.87	56.69	62.49	58.89
31	AKH-02 R(M)	83.24	70.94	85.79	63.74	85.69	62.19	65.40	52.91
	G. hirsutum (Mean)	83.64	75.36	86.46	74.08	85.72	65.13	64.78	55.17
	General Mean	83.11	73.51	86.20	72.88	86.03	64.65	66.69	58.04
	S.E. (m±)	NS	2.36	NS	2.81	NS	2.36	2.48	2.19
	C.D. at 5%	—	6.84	—	8.14	—	6.84	7.08	6.35

Table 4 Genotypic and Phenotypic correlation of different physiological parameters associated with yield under water stress condition

Traits		Boll retention	CSI 90 DAS	SLW 120 DAS	LA 120 DAS	Stomatal INDEX	RWC 120 DAS	DMP at harvest	Cell Membrane Injury 120 DAS	SCY plant^{-1}
Boll retention (%)	G	1	-0.190	-0.196	0.025	0.416 **	-0.342 **	-0.260 *	-0.109	0.143
	P	1	0.0119	-0.101	0.143	0.487 **	0.133	-0.084	0.053	0.051
CSI 90 DAS	G		1	-0.339 **	0.150	0.003	-0.460 **	-0.341 **	0.226 *	-0.332 *
	P		1	-0.204 *	0.269 **	0.149	0.146	-0.114	0.356 **	-0.058
SLW 120 DAS	G			1	-0.765 **	-0.031	-0.094	0.776 **	-0.139	0.745 **
	P			1	-0.647 **	0.037	0.109	0.779 **	-0.045	0.741 **
LA 120 DAS	G				1	-0.259 *	0.072	-0.288 **	0.154	-0.308 **
	P				1	-0.132	0.298 **	-0.139	0.256 *	-0.120
Stomatal Index	G					1	-0.475 **	-0.292 **	-0.020	-0.18
	P					1	0.008	-0.139	0.097	-0.009
RWC 120 DAS	G						1	0.069	-0.659 **	-0.149
	P						1	0.337 **	0.008	0.292 **
DMP at harvest	G							1	-0.192	0.886 **
	P							1	-0.008	0.902 **
Cell Membrane	G								1	-0.154
Injury 120 DAS	P								1	0.058
SCY/plant	G									1
	P									1

*Indicate significance at 5%, ** Indicates significance at 1%

CSI - Chlorophyll stability index, SLW- Specific leaf weight, LA – Lear area, RWC - Relative water content, DMP - Dry matter production, SCY - Seed Cotton Yield, G – Genotypic P - Phenotypic

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Influence of Pinching and Gibberellic Acid on Growth, Quality and Yield of African Marigold

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ABSTRACT

A field experiment was conducted at Main garden, Department of Horticulture, Dr. PDKV, Akola to study the influence of pinching and foliar application of gibberellic acid on growth, quality and flower yield in African marigold comprising four levels of pinching i.e. no pinching, pinching at 15 DAT, pinching at 22 DAT and pinching at 30 DAT and four levels of gibberellic acid i.e. 100 ppm, 200 ppm, 300 ppm and water spray (control) during summer season of the year 2010-11 and 2011-12. Among the pinching treatments, significantly more reduction in height of plant was recorded in the treatment pinching at 22 DAT whereas, pinching at 15 DAT was found to be best for improving other growth parameters *viz.,* number of branches plant^{-1}, diameter of main stem and leaf area at 50 per cent flowering stage and flower yield parameters viz., number of flower plant^{-1}, flower yield plant^{-1}.Whereas, quality parameters *viz.,* diameter of flower, longevity of intact flower was recorded maximum in the treatment no pinching. The foliar application of gibberellic acid, 300 ppm recorded significantly maximum vegetative growth parameters *viz*., height of plant, number of branches plant^{-1} , diameter of main stem and leaf area at 50% flowering stage, quality parameters like diameter of flower, longevity of intact flower on plant and flower yield parameters viz., number of flower plant^{-1}, flower yield plant^{-1}, plot^{-1} and ha^{-1}.

African marigold (*Tagetes erecta* Linn), a member of the family Asteraceae, is one of the most popular and commercial flowering annuals grown for its large sized attractive loose flowers. The demand of marigold as loose flowers is increasing constantly. It occupies special importance due to its hardiness and wider adoptability under wide range of Agro-climatic conditions. The pinching helps to emerge side branches and produce more number of good quality and uniform size flower. Gibberellin is helpful for transformation of dwarf plants in to tall ones by increasing cell elongation. Effect of pinching by manually and using gibberellic acid was ascertained for improving the growth and flower production of African marigold during summer month. But comparative studies involving the use of pinching and gibberellic acid are scarce. Therefore, the present experiment was undertaken to influence the effect of pinching and gibberellic acid on growth, quality and flower production in African marigold during summer season.

MATERIAL AND METHODS

Field experiment was conducted during summer season of the year 2010-11 and 2011-12 at main garden, University Department of Horticulture, Dr. P.D.K.V., Akola with the objective of staggering flower production and making flower available throughout the year in African marigold by pinching and gibberellic acid.

The experiment was laid out in Factorial randomized block design with sixteen treatment combinations replicated thrice. Treatment comprised of factor A with four pinching times viz., P_0 - no pinching, P_1 - pinching at 15 DAT, P_2 - pinching at 22 DAT and P_3 - pinching at 30 DAT and factor B with four concentrations of gibberellic acid viz., G_0 - control, G_1 – GA_3 100 ppm, G_2 - GA_3 200 ppm and G_3 - GA_3 300 ppm.

Transplanting of seedling were done in the month of January at the spacing of 45 cm x 30 cm. The recommended dose of fertilizers ($N:P_2O_5:K_2O$ @ 100:50:25 kg ha^{-1}) were applied in the form of urea, single supper phosphate and muriate of potash. Full dose of single supper phosphate and muriate of potash and half dose of urea was applied at the time of transplanting and remaining half dose of urea was applied one month after transplanting.

Regarding pinching treatments, 4-5 cm terminal portion of growing tip was nipped out as per treatment time i.e. 15, 22 and 30 DAT. The foliar application of gibberellic acid was done twice at 15 DAT and 30 DAT as per treatment concentration. The observations *viz*., number of branches plant^{-1}, plant spread, leaf area, initiation of first flower bud, and duration of flowering ,

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fresh weight of flower, diameter of flower, length of pedicel flower, longevity of flower, number of flower per plant, yield plant^{-1} and yield of flower ha^{-1} were recorded. Collected data was statistically analyzed as per Gomez and Gomez (1984).

RESULTS AND DISCUSSION

Effect of pinching:

Two years data presented in table 1 revealed that, pinching treatments reduced plant height during both the years of experiment. Significantly maximum reduction in plant height (75.46 cm & 75.52 cm, respectively) was recorded in pinching at 22 DAT followed by treatment pinching 15 DAT and 30 DAT during both the years of experiment. The reduction in the plant height in pinched plant is might be due to the removal of apical meristematic tissue which inhibits the apical dominance and diverts plant metabolites from vertical growth to horizontal growth. The similar results were quoted by and Pushkar and Singh (2012) in African marigold. They found that pinching at 20 DAT had recorded maximum reduction in plant height in African marigold.

Significantly maximum number of branches (18.65 and 18.70), diameter of stem (1.82 cm and 1.82cm, respectively) and leaf area (25.03 cm and 25.08 cm, respectively)was recorded with pinching at 15 DAT followed by pinching at 30 DAT and pinching at 22 DAT during the years of experiment. These results are also closed conformity with earlier studied quoted by Sharma *et al*. (2012) and Maharnor *et al*., (2012) who quoted that early pinching i.e. at 30 DAT had more effective for increasing number of branches stem diameter in African marigold.

Both year data (2010-11 and 2011-12) presented in Table 2 regarding quality parameters revealed that no pinching treatment recorded significantly maximum fresh weight of flower (7.40 g and 7.22g, respectively), diameter of flower (8.35 cm and 7.50 cm respectively), longevity of flower on plant (17.45 days and 17.58 days) followed by pinching at 15 and 22 DAT during both the year. These results are in line with the finding of Srivastava *et al*. (2002), Khandelwal *et al*. (2003) in marigold.

Both year data (2010-11 and 2011-12) presented in Table 2 regarding yield parameters, revealed that the maximum number of flower plant^{-1} (31.10 and 34.10 respectively), yield plant^{-1} (228.30g and 253.32 g , respectively), and yield of hectare^{-1} (16.90 t and 17.43 t, respectively) was registered under the treatment pinching at 15 DAT followed by pinching at 22 DAT and pinching at 30 DAT during both the year. This might be due to pinching remove the apical dominance which may help to produce large number of auxiliary shoot and vigorous branching which might have favoured production of maximum number of better quality flower. The results are in agreements with Pushkar and Singh (2012) in marigold who reported that pinching of marigold plant at 30 DAT was more effective for increasing yield of marigold flower.

Effect of Gibberellic acid

Data presented on table 1 during both year experiment (2010-11 and 2011-12) regarding growth parameters revealed that the height of plant (89.15 cm and 95.10 cm respectively), number of branches plant^{-1}(18.60 and 18.70 respectively), diameter of stem (1.79 cm and 1.82 cm, respectively,) and leaf area (25.03 and 25.08 cm^2 respectively) were recorded significantly maximum with foliar application of gibberellic acid 300 ppm followed by foliar application of gibberellic acid 200 and 100 ppm during both the year. Similar results were recorded by earlier workers Taygi and Kumar (2006), Swaroop *et al. (*2007) and Ramesh Kumar *et al.* (2010) in marigold. They found that GA_3 200 ppm had recorded maximum vegetative growth parameters in African marigold plant

Data presented on table 2 during both the year of experiment (2010-11 and 2011-12) revealed that, flower quality parameters such as fresh weight of flower (7.56 g and 7.09 g, respectively), diameter of flower (8.38 cm and 7.96 cm, respectively), and longevity of flower on plant(17.48 days and 18.85 days, respectively) were recorded significantly maximum in treatment 300 ppm gibberellic acid followed by treatments 200 and 100 ppm gibberellic acid during both the year. The results obtained in this study are in close agreement with the findings of Tripathi *et al.* (2003), Tyagi and Kumar (2006) in African marigold.

Data regarding yield parameters of both the year of experiment (2010-11 and 2011-12) presented in table 2 revealed that maximum number of flower plant^{-1} (31.74 and 33.17), flower yield plant^{-1}(239.94g and 235.16 g, respectively) and ha^{-1} (17.77 t and 17.41 t, respeactively) were registered under the treatment 300 ppm gibberellic acid followed 200 and 100 ppm gibberellic acid during both the year. An increase in the yield of flower of hectare^{-}

Table 1. Influenced of pinching and gibberellic acid on growth parameters in African marigold (Data over two year)

Treatments	Plant height (cm)		Number of branches plant^{-1}		Diameter of main stem (cm)		Leaf area (cm^2)	
	2010-11	2011-12	2010-11	2011-12	2010-11	2011-12	2010-11	2011-12
Pinching Time (P)								
P_0 – No pinching	89.15	95.10	16.33	16.70	1.70	1.74	21.07	21.40
P_1 – Pinching at 15 DAT	85.52	84.24	18.60	18.70	1.79	1.82	25.03	25.08
P_2 – Pinching at 22 DAT	75.46	75.52	17.19	17.03	1.74	1.75	22.98	23.26
P_3 - Pinching at 30 DAT	79.45	79.11	18.03	17.35	1.76	1.78	23.98	24.12
SE(m)±	0.913	1.195	0.266	0.108	0.008	0.006	0.405	0.349
CD at 5%	2.637	3.453	0.768	0.313	0.023	0.018	1.171	1.010
Gibberellic acid (G)								
G_0 – Control (Water spray)	73.99	75.01	15.73	16.61	1.69	1.72	17.83	18.14
G_1 – GA_3 100 ppm	81.11	82.75	17.14	17.16	1.73	1.76	24.02	24.18
G_2 – GA_3 200 ppm	84.68	86.33	17.98	17.68	1.76	1.78	25.25	25.33
G_3 – GA_3 300 ppm	88.40	89.88	19.30	18.33	1.81	1.84	25.95	26.31
SE(m)±	0.913	1.195	0.266	0.108	0.008	0.006	0.405	0.349
CD at 5%	2.637	3.453	0.768	0.313	0.023	0.018	1.171	1.010
Interaction effect (A X B)								
SE(m)±	1.826	2.391	0.532	0.216	0.016	0.013	0.811	0.699
CD at 5%	-	-	-	-	-	-	-	-

Table 2. Influenced of pinching and gibberellic acid on flower yield and quality parameters in summer African marigold (Data over two year)

Treatments	No. of flower plant^{-1}		Wt of flowers (g)		Flower yield plant^{-1}(kg)		Flower yield ha^{-1}(t)		Diameter of flower		Longevity of flower on plant (days)	
	2010-11	2011-12	2010-11	2011-12	2010-11	2011-12	2010-11	2011-12	2010-11	2011-12	2010-11	2011-12
Pinching Time (P)												
P_0 – No pinching	24.35	25.01	7.58	7.22	184.54	180.55	13.66	13.37	8.35	7.50	15 98	16.73
P_1 – Pinching at 15 DAT	31.10	34.10	7.35	6.90	228.30	253.32	16.90	17.43	7.91	7.00	17.45	17.58
P_2 – Pinching at 22 DAT	27.98	32.21	7.16	6.42	200.36	206.72	14.84	15.31	7.14	6.29	14.68	15.73
P_3 - Pinching at 30 DAT	29.69	32.96	6.44	6.05	192.05	197.33	14.22	14.61	6.42	5.69	13.93	14.83
SE(m)±	0.36	0.36	0.05	0.08	2.51	2.94	0.18	0.29	0.103	0.10	0.29	0.27
CD at 5%	1.04	1.03	0.16	0.25	7.24	8.48	0.54	0.84	0.298	0.28	0.88	0.78
Gibberellic acid (G)												
G_0 – Control (Water spray)	24.65	28.29	6.73	6.18	165.91	174.82	12.28	12.94	6.19	5.13	13.03	13.36
G_1 – GA_3 100 ppm	26.74	29.89	6.99	6.51	186.91	194.60	13.84	14.41	7.28	6.30	14.99	15.29
G_2 – GA_3 200 ppm	29.18	32.19	7.28	6.69	212.49	215.39	15.73	15.95	7.97	7.09	16.55	17.37
G_3 – GA_3 300 ppm	31.74	33.17	7.56	7.09	239.94	235.16	17.77	17.41	8.38	7.96	17.48	18.85
SE(m)±	0.36	0.36	0.05	0.08	2.51	2.94	0.18	0.29	0.103	0.10	0.29	0.27
CD at 5%	1.04	1.03	0.16	0.25	7.24	8.48	0.54	0.84	0.298	0.28	0.84	0.78
Interaction effect (A X B)												
SE(m)±	0.72	0.71	0.11	0.17	5.01	5.87	0.18	0.29	0.21	0.20	0.58	0.54
CD at 5%	-	-	-	-	-	-	0.54	0.84	0.59	0.57	-	-

^{1} might be due to the fact that, gibberellic acid treated plants produced more vegetative growth in terms of plant height and leaf area. This might have resulted into the production and accumulation of more photosynthates which would have diverted to the sink resulting into more yield of flower yield hectare^{-1} in African marigold. These results are in close conformity with the results of Ramdevputra *et al.* (2009) and Ramesh Kumar *et al.* (2010) in marigold.

Interaction effect:

The data presented in Table 1 and table 2 exhibited non-significant differences for all growth and yield parameters during both the years of experiment due to an interaction of the pinching and foliar treatment of gibberellic acid.

Data regarding yield parameters (Table 2) was found non significant. Whereas, diameter of flower (8.98 cm) was significantly maximum under the treatment combinations of no pinching along with foliar application of GA_3 300 ppm (P_0G_3) and it was followed by the treatment pinching at 15 DAT along with foliar application GA_3 300 ppm (P_1G_3) and no pinching along with GA_3 200 ppm (P_0G_2). Similar results are recorded by Rakesh *et al.* (2004) in chrysanthemum.

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Research Notes

Effect of Seed Size on Yield and Seed Quality Traits in Soybean

The experiment entitled "Effect of seed size on yield and seed quality traits in soybean (*Glycine max* L. Merrill.)" was conducted at experimental and research field of Seed Technology Research Unit and Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (M.S.) during *Kharif*, 2013-14 in Randomized Block Design with four replications . The experimental material comprised of six genotypes *viz.,* NRC 37, JS 97-52, JS 93-05, JS 335, TAMS 98-21 and TAMS 38 which were obtained from Soybean Research unit, Regional Research Center, Amravati. The seed lot of each genotype was further divided into three different seed sizes *i.e.* small, medium and bold. Thus, the 18 treatment combinations of genotypes were sown in separate plots with 8 rows spaced at 45 cm, distance. The observations were recorded on nine characters *viz.,* number of pods per plant, seed yield per ha (q ha^{-1}), test weight, seed germination, root length, shoot length, seedling fresh weight, seedling dry weight and vigour index and subjected to statistical analysis as per the standard procedure given by Panse and Sukhatme (1967).

The variety JS 335 recorded highest seed germination (94.95%) followed by JS 97-52 (93.18%), TAMS 98-21 (92.75%), NRC 37 (92.83%), JS 93-05(92.73%) and TAMS 38(92.58%). Medium seed size of variety JS-335 recorded significantly higher germination percentage (94.95%) followed by small and bold seed size. The bold seed size observed less germination percentage (92.58%) indicates that the germination is quick in medium and small sized seeds compared to bold seed. These findings are in agreement with those reported by Singh (2007), Anuradha *et al.* (2009) and Reddy *et al.*(2009). Mandanzi *et al.* (2010) . Vigour index in genotypes JS 335,TAMS 98-21 and JS 97-52 were found non significant . Medium seed size lot of variety JS 335 showed maximum vigour index (18.78) than the other seed sizes. It may be due to seed germination and vigour components are directly proportional to endosperm content of seed as the bold and medium seed size contains more amount of starch, lipid granules and protein globules as they showed best results for better germination and more vigour components.

These findings are in agreement with the report of Anuradha *et al.* (2009), Padua *et al.*, (2010) and Mandanzi *et al.*, (2010). The root length differed significantly due to different seed size lots of cultivars. The highest root length (cm) was recorded by bold seed size genotype TAMS 38 (12.53 cm) fallowed by JS 93-05 (12.40 cm), JS 335 (11.73 cm), NRC 37 (11.73 cm), JS 97-52 (9.78 cm) and TAMS 98-21 (9.60 cm). The maximum shoot length was observed in bold seed size cultivar TAMS 38 (16.45 cm) followed by TAMS 98-21 (15.88cm), JS 93-05 (15.15cm), JS 97-52 (13.35cm), NRC 37 (13.05cm) and JS 335 (13.03cm). However, Pereira *et al.*, (2009) and Tidke (1997) reported that root length and shoot length were higher in small seed grade cultivars in soybean. The highest seedling fresh weight was recorded by bold seed size the genotype TAMS 38 (7.28 g) followed by JS 93-05 (6.23 g), JS 97-52 (5.88 g), NRC 37 (5.23 g), TAMS 98-21 (5.10 g) and JS 335 (4.78 g). The seed crop harvested from bold seed size was found to be superior for seedling fresh weight than small and medium seed size. These findings are in agreement with reports of Charjan and Tarar (1997), Tidke (1997) . The highest seedling dry weight was recorded by bold seed size genotype TAMS 38 (0.53 g) followed by the genotypes JS 93-05 (0.52 g), TAMS 98-21 (0.52 g), JS 335 (0.45 g), NRC 37(0.44 g) and JS 97-52 (0.42 g). The similar observations were reported by Evans and Bhatt (1977), Charjan and Tarar (1997) and Tidke (1997).

Significantly highest number of pods per plant was found in medium seed size JS 335 (44.75), followed by JS 97-52 (42.35), TAMS 98-21 (41.13), TAMS 38 (40.33), NRC 37 (39.38) and JS 93-05 (38.23). Singh *et al.* (1972) reported t medium seed size has a significant influence on the number of pods per plant as compared to small and bold seed cultivar. However, EL- Zahab and Zahran (1976) concluded that the large seeds produced more number of pods per plant as compared with small and medium seeds. Significantly highest test weight is observed in bold seed size genotype TAMS 38 (12.55 g) and medium seed size genotype JS 93-05 (11.55 g), genotypes followed by TAMS 98-21 (10.50 g), JS 335(10.38 g), NRC 37 (9.40 g) and JS 97-52 (8.60 g). The similar results were obtained by Singh *et al.*(1972). Reddy *et al.* (2009) and Paul and Ramaswamy

(1979) reported that test weight were found to be increased with increase in seed size.

Overall, present study revealed that the medium seed size variety JS 335 performed better than all small (NRC 37 and JS 97-52) and bold (TAMS 98-21 and TAMS 38) seed variety in respect of yield and yield contributing characters. Medium seed size recorded significantly higher germination percentage (94.95%) followed by small and bold seed size. Vigour index in genotypes JS 335, TAMS 98-21 and JS 97-52 were found to be at par (around 18.50) and significantly superior compared to other genotypes. Medium seed size (JS 335) showed maximum vigour index (18.78) than the other seed sizes. The root length and shoot length was significantly superior in bold seed size as compared with small and medium seed size genotypes. The medium seed cultivar reported the highest number of pods per plant and test weight as compared to small and bold seed cultivar. The highest seedling fresh weight, highest seedling dry weight, higher root length (cm) and shoot length (cm) was recorded by bold seed size variety TAMS 38 than rest of the seed size.

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PKVSH 952 : A Promising Sunflower Hybrid for Vidarbha Region of Maharashtra

Sunflower (*Helianthus annuus* L.) emerged as a most important edible oil crop of Vidarbha region of Maharashtra. However, every year, both area and production has continuously exhibiting declining trend not only in Vidarbha or Maharashtra but at national level also. The major limitations in realizing higher production and profitability from sunflower crop are non availability of hybrid seed at sowing time and lack of irrigation facility to protect the crop during long dry spells at critical growth stages. In Vidarbha, currently sunflower is grown on 15000 ha. with production of 8000 q. and productivity 533 kg/ha (Anonymous, 2014). The urgent need of the region is to develop high yielding, medium duration hybrids and availability of hybrid seed at sowing time. Therefore the efforts were made in that direction and PKVSH 952, a high yielding and medium duration sunflower hybrid is pre-released for commercial cultivation in Vidarbha.

The Sunflower hybrid PKVSH 952 was tested in Preliminary Hybrid Trial (PHT) during *Kharif* 2011 at Akola location. On the basis of per se performance, it was promoted in Multilocaton Hybrid Trial (MHT) and also in State Hybrid Trial (SHT) during *Kharif* 2012. Multilocaton Hybrid Trial (MHT) was conducted at six locations and State Hybrid Trial (SHT) at eight locations along with other 10-12 entries. The net plot size adopted was 1.8 m x 3.9 m (3 Rows) and spacing of 60 cm x 30 cm. The experimental design was Randomized Block Design (RBD) with three replications. Every year at all locations the crop was sown in the 2nd fortnight of July under rainfed conditions and common dose of fertilizer 80:60:30 NPK kg ha^{-1} was applied. Recommended agronomic packages of practices were followed to raise healthy crop. Utilizing male sterile line CMS 302A as female and monohead population AKSF 6R as a male line PKVSH 952 was developed with an objectives of high yield and medium maturity duration.

Yield potential of PKVSH 952 was confirmed at Oilseeds Research Unit, Dr. PDKV, Akola in Preliminary Hybrid Trial (PHT) during *Kharif* 2011. It has proven superior performance for seed yield (1427 kg ha^{-1}) over checks PKVSH 27 (910 kg ha^{-1}) and SH-322 (872 kg ha^{-1}). Similarly, it has recorded 518 kg ha^{-1} oil yield (Table 1). On the basis of per se performance it was promoted to Multilocation Hybrid Trial (MHT) during *Kharif* 2012 conducted over six locations in Vidarbha. PKVSH 952 recorded average seed yield of 2088 kg ha^{-1}, which was 15.4 per cent and 6.8 per cent more than the yield of PKVSH 27 and LSFH 171, respectively. Oil yielding ability of PKVSH 952 was also more pronounced with mean oil yield of 799 kg ha^{-1} and the per cent increase over the checks was 13.3 per cent (PKVSH 27) and 19.3 per cent (LSFH

Table 1. Performance of PKVSH 952 in Preliminary Hybrid Trial (*Kharif* 2011)

Traits	PKVSH 952	PKVSH 27 (C)	SH 3322 (C)	S.E.m±	C.D.	C.V.
Seed yield (kg ha^{-1})	1427*	910	872	138.6	403.0	20.7
Oil yield (kg ha^{-1})	518	336	315			
Oil content (%)	36.3	36.9	36.1			

*Indicate significant superiority over best check hybrid

Table 2. Performance of PKVSH 952 in Multilocation Hybrid Trial (*Kharif* 2012)

Traits	PKVSH 952	PKVSH 27 (C)	LSFH 171(C)	S.E.m±	C.D.	C.V.
Seed yield (kg ha^{-1})	2088	1809	1955	103.7	318.5	12.4
Oil yield (kg ha^{-1})	799	705	670			
Oil content (%)	38.3	39.0	34.3			
Days to maturity	90	80	85			

Table 3. Performance of PKVSH 952 in State Hybrid Trial (*Kharif* 2012)

Traits	PKVSH 952	PKVSH 27 (C)	LSFH 171(C)	S.E.m±	C.D.	C.V.
Seed yield (kg ha^{-1})	1568	1439	1416	119.5	341.5	14.0
Oil yield (kg ha^{-1})	587	485	412			
Oil content (%)	37.4	33.7	29.1			

Table 4. Performance of PKVSH 952 in Initial Hybrid Trial (*Rabi* 2011-12) at Akola

Traits	PKVSH 952	KBSH 1 (C)	KBSH 44 (C)	S.E.m±	C.D.	C.V.
Seed yield (kg ha^{-1})	942*	729	637	43.1	128.0	13.7
Oil yield (kg ha^{-1})	339	265	217			
Oil content (%)	36.0	36.3	34.1			

*Indicate significant superiority over best check hybrid

171), respectively and PKVSH 952 matures in 90 days (seed to seed) as against check PKVSH 27 which matures in 80 days (Table 2).

PKVSH 952 was tested at State Level in State Hybrid Trial (SHT) at eight locations during *Kharif* 2012 and recorded average yield of 1568 kg ha^{-1}, which was 9.0 per cent and 10.7 per cent more than yield of PKVSH 27 and LSFH 171, respectively. Similarly, it was given 587 kg ha^{-1} oil yield, which was 21.0 per cent and 42.5 per cent more than the oil yield of PKVSH 27 and LSFH 171 respectively (Table 3). PKVSH 952 was also evaluated in AICRP's Initial Hybrid Trial (IHT) at Akola location during *Rabi* 2011-12 and exhibited significantly superior performance over best check KBSH-1 (Table 4).

Looking to the overall superior seed and oil yield performance of sunflower hybrid PKVSH 952 in different trials; this hybrid is considered as promising sunflower hybrid for cultivation in Vidarbha region of Maharashtra.

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Diversity of Pollinating Insect in Sunflower

Sunflower (*Helianthus annuus* L.) belongs to typical alogamic (cross pollinated) entomofilic plant, which requires pollinators for high quality fertilisation. Sunflower crop was foraged by numbers of pollinating bees. A frequently visited sunflower cultivar can produce significantly higher hybrid seed yield than a less visited cultivar (Skinner, 1987). Moreti *et al*. (1993) reported an increase in sunflower productivity about 98.4 per cent, due to the pollination made by honeybees. Insect pollinators play a crucial role in improving the productivity of cross pollinated crops. The availability of sufficient number of suitable pollinators during flowering time is essential for achieving optimum pollination. Little attention is paid to the need of conserving and enhancing the pollinator diversity in crop ecosystem (Jadhav et al. 2011). To maintain sustainable insect pollination services it is essential to conserve flower-rich natural habitats (Steffan -Dewenter and Tscharntke.1999).Considering the importance of pollinating insects for high quality fertilisation and to produce higher hybrid seed yield, present study was carried out to know the diversity pollinating insects in sunflower ecosystem.

Study was carried out at Oilseed Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during *Kharif* 2013 and 2014 to document the pollinators diversity and their abundance in sunflower agroecosystem. Sunflower KBSH 44 was raised with all recommended agronomic practices except insecticidal sprays. Randomly selected ten plants were observed daily during 10.00 to 12.00 hours and recorded the insects visited to sunflower capitulum and was expressed as mean number of pollinators plant^{-1} 5 min^{-1}. Species diversity was also documented by collecting insects visiting sunflower capitulum and get it identified from NPIB coordinating cell, IARI New Delhi through NPIB project, Department of Entomology, Dr. Panjabrao Deshmukh Krishi Vidyapeeth,Akola.

Sunflower crop foraged by numbers of pollinating insects is studied through present study and documented in Table 1. Wherein, ten diversified species of pollinating insects were observed visiting sunflower capitutlum belongs to order Hymenoptera and Diptera on hybrid sunflower KBSH 44. Four species viz., *Apis dorsata* Fabricius, *Xylocopa* sp., *Teragonula laeviceps* Smith, *Apis florea* Fabricius from Apidae, two species *viz., Scolia quadripustulata* Fabricius and *Megascolia* sp. from Scoliidae and one species i.e *Nomia* sp. from Halictidae were recorded under Hymenoptera. Dipteran foragers belonging to familiy Syrphidae, constituted *Eristalinus quinquelineatus* Fabricius, *Phytomia crassa* Fabricius and *Phytomia argyrocephala* Macquart. Amongst the pollinating insect visited sunflower during the flowering period, *Apis dorsata* Fabricius was the most dominant. Present findings are in the tune to the findings of Jadhav *et al*. (2011) who reported that *Apis dorsata* was the more frequently visiting insect pollinator in hybrid sunflower. Relative abundance of insect visitors to sunflower capitula revealed that *Apis* sp. constituted 88.85 per cent indicating the dominance of hymenopterans in sunflower ecosystem. Swaminathan and Bharadwaj (1982) recorded *Apis dorsata,* the most frequently visiting bee species on sunflower. Renganayaki *et al*. (2008) also reported that sunflower crop was foraged by sufficient number of four species of honey bees viz., *Apis dorsata, Apis cerana indica, Apis florea* and *Mellifera irridipennis.* An essential pollination service is performed by domesticated honeybees (*Apis mellifera*) and by wild bees (feral honeybees, 58 species of bumble bees, and hundreds of species of solitary bees) (Corbat *et al*. 1992). Kasina *et al*. (2007) found the diversity of pollinators associated with sunflower at Makueni district, a semi-arid area in Eastern Kenya and they were *Merylis flavipes* LeConte, Coleoptera (Melyridae: Melyrinae), *Phytomia incisa* Wiedemann, Diptera (Syrphidae: Syrphinae), *Rhynchomydaea* sp. Malloch Diptera (Muscidae: Muscinae), *Apis mellifera* Linnaeus Hymenoptera (Apidae: Apinae), *Plebeina denoiti* Vachal Hymenoptera (Apidae: Apinae), *Ceratina* sp. Latreille Hymenoptera (Apidae: Xylocopinae), *Heriades* sp. Cresson Hymenoptera (Megachilidae: Megachilinae), *Pseudoanthidium* sp. Fs Sandanski Hymenoptera (Megachilidae: Megachilinae), *Belenois aurota* Fabricius Lepidoptera (Nymphalidae: Pierinae), *Byblia ilithyia* Drury Lepidoptera (Nymphalidae: Nymphalinae), *Cephonodes hylas* Walker Lepidoptera (Sphingidae: Macroglossinae), *Danaus chrysippus* Linnaeus Lepidoptera (Nymphalidae: Danainae), *Junonia hierta* Trimen Lepidoptera (Nymphalidae: Nymphalinae), *Junonia oenone* Linnaeus Lepidoptera (Nymphalidae: Nymphalinae). *Andrena sp.* (2.40%) (Andrenidae: Hymenoptera). *Halictus* sp. (3.69 %) (Halictidae: Hymenoptera) and a Syrphid fly (0.46%) (Syrphidae: Diptera). Glaiim *et al*. (2008) found the spices

Table 1. Species of pollinating insects associated with Sunflower.

S. N.	Species	Family	Order
1.	*Apis dorsata* Fabricius	Apidae	Hymenoptera
2.	*Xylocopa* sp. Indent	Apidae	Hymenoptera
3.	*Teragonula laeviceps* Smith	Apidae	Hymenoptera
4.	*Eristalinus quinquelineatus* Fabricius	Syrphidae	Diptera
5.	*Scolia quadripustulata* Fabricius	Scoliidae	Hymenoptera
6.	*Nomia* sp. Indent	Halictidae	Hymenoptera
7.	*Phytomia crassa* Fabricius	Syrphidae	Diptera
8.	*Megascolia* sp. Indent	Scoliidae	Hymenoptera
9.	*Phytomia argyrocephala* Macquart	Syrphidae	Diptera
10.	*Apis florea* Fabricius	Apidae	Hymenoptera

associated with sunflower were *Apis mellifera* , *Megachile* sp. , *Nomia* sp. , *Xylocopa fenestrate* and *X. aestuans*. It is clear from the findings that the sunflower capitulum in bloom is highly attractive to multitude of insect species among them *Apis dorsata* Fabricus is dominant and, contributed more for pollination in sunflower at Akola conditions.

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Performance of Gladiolus Varieties Under Vidarbha Conditions

Gladiolus is one of the most important bulbous ornamental crops grown in many parts of the world either as cut flower or for garden display. The inflorescence is also used for making bouquets and for floral decorations. The crop is very rich in its varietal wealth and exhibits enormous variability. Hence, it is necessary to collect and evaluate the available varieties to find out the suitable varieties for the specific region. Keeping this in view, the present investigation was undertaken to evaluate the performance of gladiolus varieties for useful traits under Vidarbha conditions.

The experiment was carried out at Satpuda Botanic Garden, College of Agriculture, Nagpur (M.S.) during *rabi* season of the year 2010-11. Eight treatments as varieties of gladiolus such as 'T_1 American Beauty', 'T_2-Pisttacinus Hybrid', 'T_3-Nova Lux', 'T_4-Monte Alto', 'T_5-Pink Perfection', 'T_6-Phule Ganesh', 'T_7-Phule Tejas' and 'T_8-Phule Neelrekha' were tested in randomized block design with three replications. The disease free and uniform size corms of different varieties were selected for planting. The corms were dipped for 30 minutes in copper fungicide solution before planting and then planted in the field at the spacing of 45 x 15 cm. The cultural operations and plant protection measures were adopted as and when required. Manures and fertilizers were applied @ 20 t FYM + 400:200:200 kg nitrogen, phosphorus and potassium hectare^{-1}.

Flowering and flower yield

The data presented in Table. 1 revealed that, the variety Phule Tejas took significantly minimum period for first spike emergence, opening of first pair of florets and 50 per cent flowering (59.70, 71.60 and 76.00 days, respectively) as compared to other varieties, however, the maximum days were required for first spike emergence (83.40 days), opening of first pair of florets (94.20 days) and 50 per cent flowering (102.33 days), respectively for the variety Pink Perfection. As regards the yield of spikes, significantly the maximum spikes plant^{-1} (2.73) were harvested from the variety Psittacinus Hybrid and it was followed by the variety Phule Tejas (2.10), whereas, the variety Pink Perfection produced minimum spikes (1.00) plant^{-1} which was found to be at par with the varieties Monte Alto (1.13) and Nova Lux (1.27). The differential behavior might be due to the differential genetic make up of the varieties. Similar variations due to different gladiolus varieties was also documented by Neeraj *et al*. (2000), Rani *et al.* (2007) and Swaroop and Singh (2007).

Flower quality

In respect of quality parameters of gladiolus spikes length of spike was recorded significantly maximum (86.91 cm) with the variety Phule Ganesh which was found at par with the variety Pink Perfection (84.67 cm), while, minimum length of spike was observed with the variety Phule Tejas (57.10 cm). The diameter of spike was significantly the maximum (1.11 cm) with the variety Nova Lux and the variety Psittacinus Hybrid had produced the spike with minimum diameter (0.54 cm) which was at par with the variety Phule Tejas (0.59 cm).

Significantly the maximum length of rachis (44.76 cm) and florets spike^{-1} (14.40) were noted by variety Phule Ganesh which was found to be at par with the varieties Monte Alto, Pink Perfection and Phule Neelrekha, however, the varieties Phule Tejas and Psittacinus Hybrid produced minimum length of rachis (30.62 cm) and florets spike^{-1} (8.33), respectively. Longevity of flower on plant was found maximum (16.13 days) with the variety Phule Neelrekha which was at par with the varieties Pink Perfection, Phule Ganesh and Monte Alto, however, minimum longevity of flower was noted under the variety Nova Lux (10.07 days). The variations in quality parameters of gladiolus spikes due to different gladiolus varieties might be attributed due to the genetic differences of the varieties. Similar variations in spike quality parameters of gladiolus varieties were quoted by the workers *viz*. Rani *et al*. (2007) and Swaroop and Singh (2007) in gladiolus.

Corm yield and quality

The data presented in Table 2 indicated that, corms produced plant^{-1} of gladiolus the variety Psittacinus Hybrid (2.93) was found to be superior than other varieties and it was found at par with the varieties American Beauty (2.66), Phule Tejas (2.33) and Phule Neelrekha (2.20), whereas, minimum corms plant^{-1} were produced by the variety Pink Perfection (1.33). Superiority of some of the genotypes over the others in respect of corms plant^{-1} of gladiolus was also reported by Neeraj *et al*. (2000) and Kumar *et al.* (2009).

In respect of diameter of corm and weight of corms plant^{-1}, the gladiolus variety Nova Lux had recorded significantly maximum values (5.90 cm and 391.92 g,

Table 1. Effect of varieties on flowering, flower yield and quality of gladiolus.

Treatments	Days required for			Spikes plant^{-1}	Length of spike (cm)	Diameter of spike (cm) plant (days)	Length of rachis (cm)	Florets spike^{-1}	Longevity of flowers on
	First spike emergence	Opening of first pair of florets	50 % flowering						
T_1 - American Beauty	66.13	76.93	84.33	1.73	70.03	0.49	32.13	9.00	13.67
T_2 - Psittacinus Hybrid	81.40	90.20	90.00	2.73	66.45	0.54	31.75	8.33	12.07
T_3 - Nova Lux	72.73	84.47	88.67	1.27	80.25	1.11	37.63	10.00	10.07
T_4 - Monte Alto	76.53	86.93	86.33	1.13	80.76	0.77	43.43	13.60	14.37
T_5 - Pink Perfection	83.40	94.20	102.33	1.00	84.67	0.78	42.80	14.07	15.60
T_6 - Phule Ganesh	69.93	81.13	81.00	1.93	86.91	0.84	44.76	14.40	15.27
T_7 - Phule Tejas	59.70	71.60	76.00	2.10	57.10	0.59	30.62	8.87	12.80
T_8 - Phule Neelrekha	70.13	81.80	85.67	1.80	78.61	0.67	41.67	13.80	16.13
SE (m) ±	1.70	1.73	1.59	0.10	1.62	0.02	2.36	0.66	0.98
CD at 5%	4.95	5.03	4.62	0.29	4.72	0.06	6.80	1.91	2.84

Table 2. Effect of varieties on yield and quality of corms of gladiolus

Treatments	Corms plant^{-1}	Diameter of corm (cm)	Weight of corms plant^{-1} (g)
T_1 - American Beauty	2.66	4.01	199.51
T_2 - Psittacinus Hybrid	2.93	3.55	160.22
T_3 - Nova Lux	1.73	5.90	391.92
T_4 - Monte Alto	1.46	4.72	195.92
T_5 - Pink Perfection	1.33	4.61	202.80
T_6 - Phule Ganesh	1.73	4.78	229.02
T_7 - Phule Tejas	2.33	4.55	234.29
T_8 - Phule Neelrekha	2.20	4.45	263.18
SE (m) ±	0.25	0.26	28.57
CD at 5%	0.75	0.76	83.23

respectively), however, the minimum diameter and weight of corms plant^{-1} were observed with the variety Psittacinus Hybrid (3.55 cm and 160.22 g, respectively). The results of the present corm study confirms the findings of Neeraj *et al*. (2000), Rani *et al*. (2007) and Ranpise *et al*. (2007) in gladiolus.

From the results, it can be inferred that, the varieties Psittacinus Hybrid and Phule Tejas were found superior in respect of quantitative yield of spikes and corms, however, for quality production of spikes and corms, the varieties Phule Ganesh, Pink Perfection, Monte Alto and Phule Neelrekha were found better than the other varieties of gladiolus.

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Genetic Divergence in Land Races of Mustard

Indian mustard (*Brassica juncea* L.) is one of the most important oilseed crops in India. In recent years though there has been an increase in the area and production of rapeseed – mustard, the average productivity in India is quite low in comparison to that in some of the developed countries. In India, however production of edible oil is grossly short of the requirements. Consequently, large quantities have to be imported for making up the shortfall, which in turn is a heavy drain on foreign exchange resources. Vigorous efforts therefore are needed to increase the yield level and to achieve self sufficiency. Yield is one of the most important economic characters and is the product of multiplicative interaction of contributing characters. Hence, the important objective in mustard improvement is oriented to develop varieties which have high yielding potential (Dond, 2011). The assessment of genetic divergence and its components is the basic need for improvement of the crop to the desired level. The knowledge of nature and magnitude of genetic variation present in the population is desirable for deciding the parents to be used in any breeding programme. The local materials are supposed to be the store house of variability which can be exploited in a systematic manner if we know the extent of variation present among them. Availability of sufficient genetic diversity in the local collection is the basis for choice of suitable parents for hybridization programme. Genetic diversity play a huge role in survival and adaptability of a species. When a species environment changes slight genetic variation are necessary for it to adopt and survive. A species that has large degree of genetic diversity among its population will have more variation from which choosing the appropriate alleles become possible. Therefore, the first step to initiate a hybridization programme is to assess genetic diversity and thereby identify genetically diverse parents. Hence there is a need of genetic evaluation for genetic diversity in mustard local collections collected from different regions of Vidarbha. Keeping these views present investigation was executed.

The material used in this experiment consisted of 200 Individual plant selections (IPS) isolated from land races of mustard collected from different parts of Vidarbha region and ten promising varieties (Geeta, RH-819, Rohini, BioYSR, Kranti, PCR-10, BIO 902, Pusabold, Vardhan and ACN-9) of mustard. The experimental material were raised in randomized complete block design with two replications with a spacing of 45 x 15 cm^2 during *Rabi* 2012 in experimental farm of Botany Section, College of Agriculture, Nagpur (MS). Five plants were randomly selected and observations were recorded on seven characters *viz*., days to first flower, days to maturity, number of branches $plant^{-1}$, plant height (cm), number of siliquae $plant^{-1}$, 1000 seed weight (g), seed yield $plant^{-1}$ (g). The data were subjected to the D^2 analysis as per Mahalonobis (1936). Grouping of genotypes into clusters was performed as per by Rao (1952) and indentifying of superior genotypes was done as per the method described by Bhatt (1970),

The mean squares due to genotypes as observed from Table 1 were highly significant for all the seven characters studied indicating the presence of considerable genetic variation among the genotypes for the characters studied. The analysis of dispersion (Table 2) for the test of significance of differences in the mean values based on Wilk's criterion revealed highly significant differences among the genotypes for the aggregate of seven characters. ($\chi^2 = 5700.68$ at 1463 d.f.). Therefore the data were further evaluated for D^2, and cluster analysis. Sathi *et al.* (2012) and Pandey *et al.* (2013) also reported significant divergence among the genotypes for all the characters studied in mustard. The contribution of each character towards genetic divergence is presented in Table 3. Contribution of 1000 seed weight was maximum (63.91%) followed by number of siliquae $plant^{-1}$ (12.33%), seed yield $plant^{-1}$ (10.86%), plant height (6.32%), number of branches $plant^{-1}$ (2.87%), days to first flower (2.57%) and days to maturity (1.13%). This indicated that characters like 1000 seed weight, number of siliquae $plant^{-1}$ and seed yield $plant^{-1}$ were the important traits contributing towards genetic divergence. In agreement with the present result Pandey *et al*. (2013) also observed that maximum contributors towards genetic divergence in mustard was 1000 seed weight (46.87%), seed yield $plant^{-1}$ (20.91%) and number of siliquae on main raceme (8.38%). Hence, the traits like 1000 seed weight, number of siliquae $plant^{-1}$ and seed yield $plant^{-1}$ which contributed maximum towards the expression of genetic divergence could be used effectively in selecting promising genotypes.

The entire 210 genotypes on the basis of D^2 statistics were grouped into 16 cluster as reported in

Table 4. The cluster I was largest comprising of 110 genotypes followed by cluster II (44 genotypes), cluster III (30 genotypes), cluster IV (9 genotypes), cluster VII (6 genotypes). Clusters V, VI, VIII, IX, X, XI, XII, XIII, XI V, XV and XVI were the smallest comprising of single genotype in each cluster.The promising varieties like ACN-9, Vardhan, PCR-10, Pusa bold, Rohini, Kranti and Bio-902 were grouped in cluster II along with 37 local lines of mustard. The drought resistant genotypes RH-819 and Geeta were grouped in cluster VII along with four local lines. Eleven cluster were having only one local line in each of the cluster. This indicates that there are many local lines which were highly diverse from the check and hence offers good scope for improvement. Similar result were also reported by Malik *et al.* (2006) grouped 30 lines into 6 clusters, Budhanwar *et al.* (2010) grouped 270 recombinant lines into 17 clusters and Sathi *et al.* (2012) grouped 25 genotypes into 6 clusters in mustard. The number of clusters into which genotypes were grouped is often noticed to vary with set of genotypes used for cluster analysis depending on the extent of distance from one another.

The comparison of cluster means (Table 5) for seven characters under study marked considerable genetic difference between groups. Overall study for cluster means considering all the seven characters indicated that cluster X possessed the highest cluster mean for days to first flower and days to maturity. Cluster XVI showed maximum cluster mean for number of branches plant^{-1}, number of siliquae plant^{-1} and seed yield plant^{-1}. Cluster XI showed maximum mean for plant height. The variance of cluster means for all the characters indicated

Table 1. Analysis of variance for seven characters in Indian mustard.

Sources of variation	df	Mean sum of squares						
		Days to first flower	Days to maturity	Plant height	No. of branches plant^{-1}	No. of siliquae plant^{-1}	1000 seed weight	Seed yield plant^{-1}
Replications	1	46.46	1480.31	1.43	0.31	14417.94	0.030	47.46
Genotypes	209	16.78**	49.94*	785.32**	2.01**	12577.29*	0.664**	12.31**
Error	209	5.69	29.95	125.63	0.55	1139.74	0.006	1.29

* Significant at 5% level ** Significant at 1 % level

Table 2. Analysis of dispersion.

Sources of variations	df	Sum of squares	Mean sum of squares
Genotypes	209	7.9235E12	3.7912E10**
Error	208	7.4768E04	3.5946E02
Total	417	7.9235E12	1.9001E10

Table 3. Contribution of different characters towards genetic divergence.

S.N.	Characters	Times ranked 1st	Per cent contribution
1	Days to first flower	565	2.57
2	Days to maturity	249	1.13
3	Plant height	1386	6.32
4	Number of branches plant^{-1}	630	2.87
5	Number of siliquae plant^{-1}	2705	12.33
6	1000 seed weight	14026	63.91
7	Seed yield plant^{-1}	2384	10.86
	Total	**21945**	**99.99 (@ 100)**

that the maximum variation was accounted by number of siliquae plant^{-1} (21968.75) followed by plant height (3779.03), days to maturity (709.67), seed yield plant^{-1} (24.08), days to first flower (6.51) and number of siliquae plant^{-1} (5.43). In the present study the results on variance of cluster mean indicated that number of siliquae plant^{-1}, plant height, days to maturity and seed yield plant^{-1} were important source of variation which suggest that these characters were highly responsible for genetic divergence in the present material.

Average intra and inter cluster distance among seven characters were worked out by Tocher's method and are presented in Table 6. The inter cluster distance in most of the cases were higher than the intra cluster distance. The intra cluster distance ranged from 0.00 to 43.47. Cluster VII possessed highest intra cluster distance (D^2= 43.47) followed by cluster II (D^2= 34.30), cluster III (D^2= 28.60) and cluster I (D^2= 26.51). The average inter cluster distance was maximum between cluster VII and cluster XIII (D^2= 1015.48) followed by cluster VII and

Table 4. Distribution of 210 genotypes of mustard in different clusters.

Cluster	Total no. of genotypes	Name of genotypes
I	110	L42,L179,L81,L78,L177,L121,L94,L178,L79,L166,L86,L135, L74,L140,L73,L137,L144,L77,L175,L171,L187,L115,L31,L145, L138,L40,L132,L76,L56,L150,L107,L58,L122,L163,L148,L123, L126,L130,L134,L133,L111,L120,L174,L136,L147,L33,L36,L99, L18, L59,L118,L176,L54,L97,L113,L100,L34,L143,L142,L141, L114,L149,L39,L125,L84,L88,L53,L71,L129,L63,L116,L95, L127,L68,L69,L128,L173,L87,L29,L38,L62,L55,L14,L117,L193, L83,L9,L13,L16,L15,L52,L124,L139,L190,L85,L164,L180,L198, L64,L189,L195,L11,L17,L96,L72,L32,L194,L57,L10,L191.
II	44	L6,L197,L 7,L104, L185,L162, L196,L3, L1,L21, L181,L49, L41, L200,L45, L25,L43,L4,L22,L48,L146,L80, L44,L28, L169,L47, L51,L46, L50,L105, L89,L109, L165,ACN-9, Vardhan, PCR-10, Pusa bold, Rohini,L101, L112, Kranti ,L30, L108,BIO-902,
III	30	L183,L186,L167, L168,L103, L12,L106, L192,L184, L60,L2, L75,L93, L35,L5, BioYSR, L91, L110,L27,L8, L23,L170,L199, L82,L90, L24,L 61,L20, L188,L67
IV	9	L151,L156, L154,L159, L155, L153,L158,L152,L 160
V	1	L98
VI	1	L66
VII	6	L182,RH-819, Geeta, L26, L92, L161
VIII	1	L19
IX	1	L131
X	1	L172
XI	1	L119
XII	1	L102
XIII	1	L70
XIV	1	L157
XV	1	L37
XVI	1	L65

cluster XII (D^2= 1010.69), cluster VII and cluster XIV (D^2= 990.01) and cluster VII and cluster IX (D^2= 925.36) suggesting more variability in genetic make- up of genotypes included in these clusters. Widely diverged clusters remains distinct in different environment. Therefore the genotypes belonging to the distant clusters may be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. These findings are in conformity with the findings of Thul *et al.* (2003), Vaishnava *et al*. (2006), Sathi *et al*. (2012) and Pandey *et al*. (2013).

Inter crossing best divergent parents are expected to produce high heterotic hybrids and generate a broad spectrum of variability in segregating generation leading to development of useful genetic stock and varieties. According to Bhatt (1970) the mean inter cluster distance ($\bar{D}$ = 198.36) formed from different clusters were arranged in descending order of magnitude of genetic distance and promising 42 cluster combination were considered arbitrarily as a guideline and crosses between parents belonging to different clusters having same or higher inter cluster distance than the mean statistical distance may be attempted. The crosses were chosen from widely separated clusters. But, as it was observed in the present study, several genotypes were included in widely separated clusters, then the question arises which of the genotypes from these more diverse clusters may be used for crossing. In that case, genotypes which perform better for the characters (number of siliquae plant^{-1} and seed yield plant^{-1}) which contributed much towards genetic divergence were given preference. Based on this present investigation revealed importance of crossing L92, L161 and RH-819 with L70, L98, L66, L37, L18, L128, L82, L55, L32, L72, L52, L96, L19, L101, L112, L12, L110 and L20. Similarly L101 and L112 can be crossed with L65, L66, L119, L98, L37, L18, L128, L62, L55, L52, L96, L72, L32, L19 and L70. These two sets of crossing programme may be considered suggested to get potential segregant with high number of siliquae plant^{-1} and seed yield plant^{-1}.

Table 5. Cluster means for seven quantitative characters

Clusters	Days to first flower	Days to maturity	Plant height (cm)	No. of branches plant^{-1}	No. of siliquae plant^{-1}	1000 seed wt. (g)	Seed yield plant^{-1} (g)
I	47.34	109.25	174.45	5.28	229.39	1.79	6.62
II	43.98	110.53	171.54	4.38	182.03	2.98	6.97
III	45.52	110.19	172.12	4.68	194.61	2.31	7.18
IV	44.19	98.31	96.68	3.66	48.72	2.13	1.78
V	47.60	109.40	180.30	5.40	358.70	1.50	6.80
VI	50.20	111.80	177.00	6.80	409.40	1.70	11.82
VII	44.40	110.37	166.42	4.50	202.38	3.72	7.82
VIII	48.50	111.50	177.30	5.30	406.00	2.05	8.49
IX	44.60	109.80	144.90	4.50	131.00	1.40	4.01
X	53.10	113.80	172.90	3.40	93.90	1.50	2.63
XI	47.80	99.10	196.20	5.40	202.90	1.70	11.42
XII	44.90	102.80	181.50	4.50	187.50	1.30	6.97
XIII	47.90	112.00	180.80	7.30	310.10	1.30	7.90
XIV	45.05	99.70	82.51	2.00	23.90	1.40	0.80
XV	48.30	105.50	98.60	5.80	323.40	1.70	7.52
XVI	49.10	112.50	187.90	8.00	425.70	1.70	18.51
S.D.	2.5	26.64	61.47	2.33	148.22	1.00	4.91
Variance	6.51	709.67	3779.03	5.43	21968.75	1.00	24.08
C.V.(%)	5.16	5.01	6.62	15.21	16.25	3.59	17.09

Table 6. Average intra and inter cluster distance D^2 values.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	**26.51**	269.47	74.87	128.12	45.06	52.91	657.72	54.67	55.90	54.16	51.55	61.96	62.98	151.28	74.88	134.45
II		**34.30**	105.04	201.37	417.54	347.25	128.63	211.97	438.81	396.11	326.21	495.38	508.98	511.54	347.72	429.42
III			**28.60**	99.69	154.61	125.92	364.92	69.92	163.89	145.71	108.36	191.18	203.01	247.77	139.01	201.58
IV				**20.93**	217.63	238.24	495.97	171.18	134.99	144.56	211.62	225.36	263.55	107.72	117.73	375.97
V					**0.00**	28.21	875.73	54.18	56.11	69.13	78.52	41.71	20.12	167.47	63.16	121.72
VI						**0.00**	748.31	33.48	111.84	125.05	55.48	84.00	45.62	250.23	66.53	42.46
VII							**43.47**	529.97	925.36	855.25	737.29	1010..69	1015.48	990.01	738.85	831.41
VIII								**0.00**	145.10	138.76	102.07	146.40	114.21	255.82	68.83	121.19
IX									**0.00**	26.20	92.31	24.89	48.44	50.57	79.52	215.10
X										**0.00**	93.13	46.80	72.01	89.19	121.03	244.80
XI											**0.00**	49.64	71.57	224.43	139.70	66.82
XII												**0.00**	26.29	123.87	120.48	147.51
XIII													**0.00**	180.04	95.94	112.24
XIV														**0.00**	110.72	399.54
XV															**0.00**	169.66
XVI																**0.00**

$\bar{D}$ = 198.36 Bold figures are average intra cluster distance.

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Direct in Vitro Propagation Using Auxillary Buds in White Marigold

Marigold (*Tagetes erecta* L.) is an Asteraceous plant of industrial and medicinal importance. This herbaceous plant is native to Mexico, where it is used in traditional medicine and for ornamental purposes. This plant contains bioactive compounds that exhibit nematicidal, fungicidal and insecticidal activity (Vasudevan *et al.*, 1977). The flowers are utilized as a source of pigments for food coloring in industry as a source of pigments for food coloring in industry, mainly of poultry skin and eggs (Delgado-Vargas *et al.* 2000). Lutein is the main pigment in marigold flowers. It is synthesized through the isoprenoid pathway, which could be modified to produce new high-value-added carotenoids or to increase production for pigmentation purposes and phytochemical functionality. The wide range of uses of this plant underlines the importance of establishing a reliable plant regeneration system for further genetic manipulation.

There are few reports on marigold tissue culture. These reports use a wide range of explants sources, different types and combinations of plant growth regulators and results in organ or embryo formation (Kothari and Chandra, 1984; Belarmino *et al.,* 1992; Bespalhok and Hattori, 1998; Misra and Datta, 1999). However, the reproducibility of the results was poor. Hence, in this study an attempt was made to develop a protocol for direct differentiation of shoots from axillary buds of white marigold without any intervening callus. This protocol will be useful for large-scale clonal multiplication as well as for future transformation studies.

The explants axillary buds collected from the white marigold at the active stage of growth before flowering were used as source material. The plant source for collecting the explants were available at Botanical Garden, College of Agriculture, Nagpur. The explants were surface sterilized with 0.1per cent $HgCl_2$ for 5 minutes followed by 4-5 washings with distilled water and sterile water. After surface sterilization the explants of 1-1.5 cm were cut and inoculated on MS basal media fortified with different concentrations of BAP, IAA and GA_3 alone or in combinations. The media was solidified with 0.8per cent agar and the pH was adjusted to 5.8. For observing morphogenic response of explants, culture were maintained at 25 ± 2^0 C with a photoperiod of 16 hrs. light and 8 hrs. dark. The multiple shoots were transferred to MS media with different concentrations of IAA, IBA, NAA any one for rooting. Observations were recorded periodically after inoculation on response to shoot initiation (per cent), days for shoot initiation, number of shoots culture^{-1}, number of shoots elongated culture^{-1}, response on root initiation(per cent) and days for root initiation. The experiment was conducted in CRD and 10 aliquots having one explants of each were used for recording observations for the analysis of variance, the mean values of 5 aliquots were used in duplex for statistical analysis.

The results on shoot initiation, days to shoot initiation and no. of shoots culture^{-1} and no. of shoot elongated culture^{-1} are presented in Table 1. It was observed from the data that explants established in all the treatments (Plate 1). The overall mean response of shoot initiation to culture media was observed to be 74 per cent. This indicates that the explants axillary bud had high potential to induce shoot buds which may be due to the fact that the axillary bud tissue culture system stimulate the genesis of shoots from newly formed and pre-existing meristematic regions of nodal tissue. Misra and Datta (2001) and Vanagas *et al.*(2002) also reported the superior efficiency of axillary bud in marigold. The response of shoot initiation expressed in per cent ranged from 60 per cent (T8- MS + BAP 8.88µm + IAA 1.42 µm + GA_3 14.43 µm, T9- MS + BAP 8.88µm + IAA 2.84 µm + GA_3 14.43 µm, & T3- MS + BAP 8.88µm + GA_3 14.43 µm) to 96 per cent (T7- MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm). The treatment T7 (MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm) showed 96per cent response followed by T2- MS + BAP 4.44µm + GA_3 14.43 µm (92per cent), and T1 & T5 (80per cent). The treatments T7 (MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm) and T2- MS + BAP 4.44µm + GA_3 14.43 µm were observed as most effective treatment exhibiting maximum percentage response of shoot initiation.

The axillary bud produced shoot bud by the sprouting of axillary bud by the formation of adventious bud as observed from Plate 2. The data on days to shoot initiation indicated significant variation for this trait among the treatments. On an average shoot initiation in white marigold started 8.78 (@9days) days after inoculation in the present study. However minimum number of days required for shoot initiation was observed in the treatment T6- MS + BAP 4.44µm + IAA 1.42 µm + GA_3 14.43 µm (7.57

Table 1. Effect of different treatments of culture media on four different traits of shoot differentiation

STreatment (mg l^{-1})		Response of shoot initiation (%)	Days to shoot initiation	No. of shoots $culture^{-1}$	No. of shoots elongated $culture^{-1}$
T_1	MS + BAP 2.22µM + GA_3 14.43 µM	80	9.13	4.50	3.00
T_2	MS + BAP 4.44µM + GA_3 14.43 µM	92	8.17	6.67	4.83
T_3	MS + BAP 8.88µM + GA_3 14.43 µM	60	8.00	6.13	4.13
T_4	MS +BAP 2.22µM+IAA 1.42 µ +$GA_3$14.43 µM	70	9.57	5.29	3.57
T_5	MS+ BAP 2.22µM + IAA 2.84 µM+$GA_3$14.43 µM	80	11.75	3.75	2.38
T_6	MS+BAP 4.44µM + IAA 1.42 µM+$GA_3$14.43 µM	70	7.57	6.00	4.00
T_7	MS+BAP 4.44µM+IAA 2.84 µM+$GA_3$14.43 µM	96	8.13	7.59	4.88
T_8	MS+BAP 8.88µM + IAA 1.42 µM + $GA_3$14.43 µM	60	8.00	5.67	3.83
T_9	MS + BAP 8.88µM + IAA 2.84 µM+$GA_3$14.43 µM	60	9.67	5.00	3.50
	Mean	74	8.78	5.55	3.79
	SE (m) ±	4.56	0.35	0.35	0.27
	CD (5%)	31.01	3.52	3.46	2.69

Table 2. Effect of different treatments of culture media on different traits of root differentiation

Treatment (mg l^{-1})		Response of root initiation (%)	Days to root initiation
T_1	MS + IAA 0.27 µM	48	4.33
T_2	MS + IAA 0.54 µM	43	4.83
T_3	MS + IBA 0.27 µM	45	6.17
T_4	MS + IBA 0.54 µM	50	4.67
T_5	MS + NAA 0.27 µM	83	4.50
T_6	MS + NAA 0.54 µM	67	5.83
	Mean	56.00	5.06
	SE (m) ±	6.46	0.31
	CD(%)	52.90	2.53

days) followed by T3- MS + BAP 8.88µm + GA_3 14.43 µm & T8 - MS + BAP 8.88µm + IAA 1.42 µm + GA_3 14.43 µm (8.00 days), and T7 - MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm (8.13 days). In contrary to this Mishra and Datta (2001) obtained shoot buds from the explants after 2 weeks of inoculation in marigold. The overall mean number of shoot buds obtained was 5.55 $culture^{-1}$. The maximum number of 7.59 shoot buds were obtained from axillary bud explants in treatment T7 (MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm) followed by T2- MS + BAP 4.44µm + GA_3 14.43 µm (6.67), T3- MS+ BAP 8.88µm + GA_3 14.43 µm (6.13) and T6- MS + BAP 4.44µm + IAA 1.42 µm + $GA_3$14.43 µm (6.00). The shoot buds when allowed to elongate and develop into shoots on the same shoot differentiation media it was observed that all buds did not develop into an elongated shoot. The average number of shoot elongated was observed to be 3.79 $shoots\ culture^{-1}$. The maximum number of shoots elongated was observed to be 4.88 shoot in T7 (MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm) followed by 4.83 in T2 (MS + BAP 4.44µm + GA_3 14.43 µm) and 4.00 in T6 (MS + BAP 4.44µm + IAA 1.42 µm + GA_3 14.43 µm). Differentiation of shoots of white marigold was achieved in a combination T7 (MS + BAP 4.44µm + IAA 2.84µm + GA_3 14.43µm). When the concentration of BA was increased upto to 8.88 µm, it became supraoptimal for the explants to differentiate, as they showed hyperhydricity without any further increase in the number of shoots. This problem was also reported by Mishra and Datta (2001). GA_3 played a very significant role for the induction of shoot buds. The differentiation

Plate 1

Plate 2

Plate 3

Plate 4

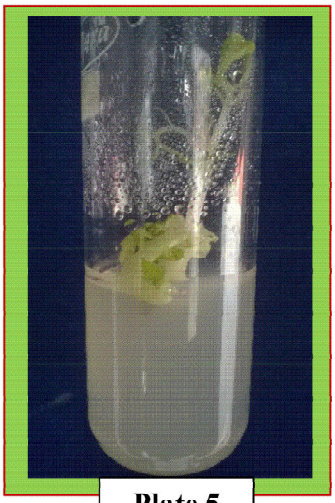

Plate 5

1. Axillary bud inoculated
2. & 3. Shoot buds sprouted
4. & 5. Elongated shoots
6. Rooting associated with callusing and vitrification
7. Formation of root
8. Plants kept for hardening

Plate 6

Plate 7

Plate 8


Plate 1


Plate 2

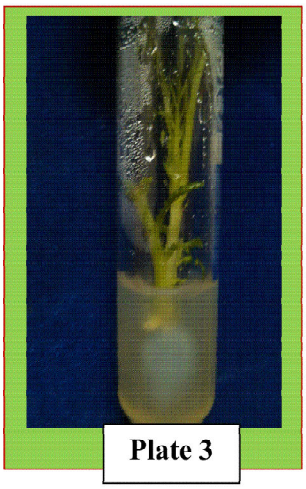
Plate 3


Plate 4


Plate 5


Plate 6

1. Axillary bud inoculated 2. Shoot buds sprouted 3. Elongated shoots
4. Rooting associated with callusing and vitrification 5. Formation of root
6. Plants kept for hardening

of shoot buds was direct without any associated callus. When the differentiated shoots were kept in the same regeneration medium, there was no further proliferation of shoots. Therefore the shoots were subcultured twice in MS media with low concentration of BA (1.1 µm) along with GA_3 (14.43 µm) to get elongated shoots for transferring for rooting.

The roots formed occasionally on proliferated shoots did not help in establishment of the plants in soil. Therefore, isolated shoots (Plate 3) were excised and rooted using MS media containing different concentrations of IAA, IBA and NAA with MS media. Average response of root initiation over the treatments was observed to be 56 per cent. (Table 2). The highest response for root initiation was observed in treatment T5 (MS + NAA 0.27µm) with 83per cent followed by T6 (MS+ NAA 0. 54µm) with 67 per cent. When NAA was used for root induction 67 to 83 per cent rooting was achieved (Plate 5), whereas using IAA and IBA the rooting was 43 to 50per cent but associated with callusing and vitrification of shoot (Plate 4). Average number of days required for

root initiation was 5.06 days which indicates that in marigold root initiation can start 5 days after transferring shoots for rooting. In contrary to this Mishra and Dutta (2001) reported 100per cent rooting when NAA was used and when IAA and IBA were used the rooting they obtained were 100per cent but associated with some callusing and vitrification of shoots. The rooted plants were transferred to cups containing sterilized potting mixture for hardening (Plate 6). The percentage survival of the plantlets was observed to be only 40per cent when estimated over the rooted plantlets obtained from all the treatments used for root initiation.

It can be inferred from this study that, the axillary bud explants responded well for all the traits studied. The treatment T7 (MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm) and T2 (MS + BAP 4.44µm + GA_3 14.43 µm) was found to be exhibit good performance for response to shoot initiation (per cent), days to shoot initiation, number of shoots culture^{-1} and number of shoots elongated culture^{-1}. Hence, these two treatments can be considered as the optimum media for *in vitro* shoot propagation of white marigold. The shoot propagated from axillary bud were found to root well in treatment T5 (MS+ NAA 0.27µm) and T6 (MS + NAA 0. 54µm). Thus, *in vitro* propagation of white marigold can be done successfully by inoculating axillary bud explants in T7 (MS + BAP 4.44µm + IAA 2.84 µm + GA_3 14.43 µm) and T2 (MS + BAP 4.44µm + GA_3 14.43 µm) for shoot induction and proliferation followed by transferring the shoots to T5 (MS+ NAA 0.27µm) for rooting. The repeatability of the results are to be confirmed by repeating this experiment once or twice before using for large scale propagation.

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Effect of Abiotic Factors on the Population Density of Predator Syrphid Fly, and its Feeding Potential on Aphids

Cotton crop as commercial commodity plays an important role in the agrarian and industrial activities of the nation and has a unique place in Indian economy and social affairs. (Mayee and Rao, 2002). Amongst various reason of low productivity of *Bt* cotton, the sucking pests gain much importance due to havoc created by most of the sucking pest in the recent years. The important sucking pests attacking on cotton crops are, Aphids (*Aphis gossypii* Glover), Jassids (*Amrasca biguttula biguttula* Ishida), Thrips (*Thrips tabaci* Linderman) and White fly (*Bemisiatabaci* Gennadius).

To tackle this sucking pest menace, a number of chemical insecticides are liberally sprayed on this cotton crop which led to several problems like toxic residues, elimination of natural enemies, environmental disharmony and development of resistance. Due to presence of pesticidal residues in the final commodity, there is a risk of rejection of whole consignments during export.

Several species of syrphidfly (Diptera: Syrphidae) have been recorded as predators of aphids attacking cruciferous crops (Chitra Devi *et al.*, 2002). Amongst them, *Ischiodonscutelaris* (F.) has been reported as an important predator of aphids (Hemiptera: Aphididae) in vidarbha region of India. The larvae are voracious predators of small insects, especially aphids and all aphid-feeding (aphidophagous) species are in the subfamily Syrphindae. As noted, the larvae of syrphid flies feed primarily on aphids. However, they will also feed on thrips, whiteflies, small caterpillars and other small insects (Stewart and Layton, 2009). The potential of this predator is evident from its role in regulating *L. erysimi* in *toria* fields during 2006-07 and 2007-08 *rabi*seasons as it constituted 20-24 per cent of the total natural enemy population (Roshmi Borah and Dutta, 2010). The efficiency of a predator in the control of aphids depends upon anumber of factors including predatory potential, fecundity, and its relative abundance. Chitra Devi *et al*. (1996) reported that *E. balteatus* consumed 392 individuals of *L. erysimi*, while *E. viridaureus* (Wiedemann) consumed 464 *Brevicoryne brassicae* during its larval period (Kotwal *et al*., 1989). No information is available on the effect of abiotic factors on the population density of Syrphidfly, *Ischiodon scutelaris* and its predatory potential on cotton aphids (*Aphis gossypii,* Glover) from Maharashtra. Keeping in view its abundance and future prospect of utilization in biocontrol programmes, attempts were made to study the effects of abiotic factors and predatory potential of syrphid utilising *Aphis gosypii*as host.

Seasonal variation of syrphid and aphid, and their correlation with weather parameter

Seasonal occurrence of syrphid fly and incidence of its prey aphid and their correlation with weather parameters was assessed on cotton crop in the field of Department of Agril. Entomology of this University during the year 2013-14.

A plot size of 10 x 10 m was kept free from insecticides treatment and all the recommended agronomic practices were followed. The observations on syrphid and aphid were recorded at 3 days interval on 20 randomly selected plants. Density of both predators and aphids was counted from the selected plants. During the study period, the meteorological parameters were recorded from Meteorology, Dept. of Agronomy. Observations started from last week of July, 2013 to last week of December, 2013. Observations of aphid were recorded on 3 leaves from top, middle and bottom of the plant and worked out as a number of aphids leaf^{-1}. The observations on syrphids were recorded on whole plant which was selected for the observation of aphid and averaged out as a syrphids plant. The data thus collected were subjected to statistical analysis in simple linear correlation coefficient to find out the relationship with weather factors and population density of the aphids and syrphids.

Studies on life stages of syrphid on cotton aphids

Larvae of syrphids were collected from the field of Department of Agricultural Entomology, Post Graduate Institute, Dr. PDKV, Akola. About 15-20 sites selected, where large number of aphids were observed. These sites were visited daily for 3-4 days. For the study of incubation period a pair of mated adults of syrphid was released in a rearing chamber with having cotton plant and aphid incidence. Eggs laid by syrphid were collected and kept in glass vials and incubation period of eggs was observed. For larval instar duration study, the freshly laid eggs of syrphid were collected from the field and brought to the

laboratory. After hatching in the laboratory, the freshly hatched ten larvae of syrphid were kept separately in glass vials and mouth of the vials closed with cotton plug. The individual larva was provided with fresh aphids daily and the number was increased as the growth of larvae advances. The date of each moult was recorded to determine the duration of each larval instar and larval period was recorded.

Study of pupal duration of syrphid was carried out by taking ten 3rd instar mature larvae (Whose feeding was stoped) were kept in a plastic vial. When these larvale enter into prepupal stage, observations regarding prepupale stage were noted. When these ten prepupal enter the pupal stage, they were kept in a rearing cage covered with cotton leaf and observed till the adult emergence and thus pupal period was recorded.

Freshly emerged adult male and female syrphids were kept in rearing cage for adult longevity study. Cotton swab dipped in honey solution was tied in cage as a supplementary food. Adult longevity period was recorded till death of the adults .

Feeding potential of syrphid on cotton aphids

The 1st instar larva of syrphid was kept in petridish individually and it was provided with known number of aphids as prey, sufficient enough for the next 24 hrs. Such 10 petridishes each containing larvae of syrphid were maintained. On the next day, live aphids in each petridish were counted and aphids consumed by each larva were recorded. The no. of aphids consumed by the larvae in each instar and also total number of aphids consumed during the larval period were calculated. The data thus collected was subjected to statistical analysis.

Seasonal activities of syrphid fly in cotton

Syrphid population was noticed from 31th MW to 51st MW. The peak population of syrphid larvae was observed two time, i.e. 33rd MW (0.65 larva plant^{-1}) and later on in 45th MW (0.33 larva plant^{-1}). In remaining MWs, the syrphid population was in the range of 0 to 0.65 larva/ plant. More or less similar trend of syrphid population was observed as that of cotton aphid population (Table 1).Similar observations were also recorded by earlier worker *viz*. Chouhan *et. al.* (2011) in their study on the activity of aphids and syrphid fly on cotton, cabbage and mustard crop they found that larval population of syrphid followed same trend at its host aphids. Simillarly, Mandal and Patnaik (2008) conducted study on the three species of aphids that damaged the cabbage crop and the two species of syrphid predators,*Ischiodon scutellaris* (Fab.) and *Eumerfu salbifrons,* they found that *I. scutellaris* appeared during early November, *E. albifrons* appeared during early December. Thus confirms the present findings i.e. maximum population of syrphid, *Ischiodon scutellaris*in the month of November.

Table 1. Seasonal incidence syrphid fly and its host aphid in cotton ecosystem

Meteorological week	Aphid incidence (No. of aphid leaf^{-1})	Syrphid population (Larvae plant^{-1})
30	6.00	0.00
31	12.17	0.15
32	39.56	0.35
33	29.56	0.65
34	11.98	0.30
35	7.65	0.10
36	3.66	00
37	2.18	0.1
38	1.66	00
39	0.35	00
40	0.55	00
41	0.51	00
42	0.40	00
43	0.46	00
44	2.00	0.25
45	3.33	0.33
46	6.80	0.25
47	12.66	0.25
48	8.80	00
49	5.35	00
50	1.85	00
51	1.18	0.10
52	1.00	0

Seasonal incidence aphid in cotton

Incidence of cotton aphids was noticed from 30th Meteorological week (MW) on cotton crop and it was observed up to 52nd MW. Two peaks of incidence of aphids on cotton was observed i.e. first at 32nd MW and later on in 47th MW. Aphid population on cotton was above ETL from 31st (12.17 Aphid leaf^{-1}) to 34th MW(11.98 Aphids leaf^{-1}) and in 47th MW (12.66 Aphids leaf^{-1}). (Table 1).

These results are on the same line as Bhavya Rani (2006) who noticed the incidence of aphid from 15

DAS (Days After Sowing); the population of aphids gradually increased and significantly higher at 30 and 60 DAS. The pest population was again increased at late stage of the crop growth at 120 DAS and 135 DAS. Similar results were also reported by the earlier researchers, in which maximum incidence of aphids (25.90 plant^{-1} on 3 leaves) was recorded in 33th MW (12-18 Aug 2013) (Anonymous, 2014) as well as maximum incidence of aphids (17.60 plant^{-1} on 3 leaves) was recorded in 34th MW (20-26 Aug 2012) (Anonymous, 2013).

Correlation of syrphid population with weather parameter

Data given in the Table 2 revealed that the weather parameter maximum temperature, minimum temperature, morning relative humidity, evening relative humidity, bright sunshine hour, wind velocity, evaporation rate and rainfall had shown non significant correlation with the syrphid population. Whereas, syrphid population had shown highly significant correlation with the aphid population at 1per cent and 5 per cent level.

Table 2. Correlation of syrphid population with weather parameter

S.N.	Weather parameter	'r' value of Syrphid population
1	T max (^{0}C)	-0.196
2	T min (^{0}C)	0.168
3	BSH (hrs)	-0.186
4	Ws (km hr^{-1})	0.017
5	RHI (per cent)	0.224
6	RHII (per cent)	0.289
7	Evap (mm)	-0.096
8	RF (mm)	0.169
9	Aphid	0.684*,**

No. of Observations =35 r value =0.325* at 5per cent . r value of = 0.418** at 1per cent

The present finding are in the line with Romabai Devi et al. (2012) who studied the role of the predatory syrphid, *Episyrphus balteatus* in regulating the field population of the mustard aphid, *Lipaphis erysimi*(Kalt.) for two subsequent crop-seasons during 2008 to 2010 on cabbage. The numerical density of the predator was recorded to increase in response to density of the aphid prey in the field. The correlation analysis showed significant positive correlation between the predator and prey species.

Correlation of aphid population with weather parameter

Data given in the Table 3, revealed that aphid population had negative significant correlation with the maximum temperature. However, the relative humidity of evening and rainfall had positive significant correlation with aphid population. The other weather parameters viz., minimum temperature, morning relative humidity, bright sunshine hour, wind velocity and evaporation rate did not show significant correlation with the aphid population.

Table 3: Correlation of aphid population with weather parameter

S. N.	Weather parameter	r value of aphid population
1	T max (^{0}C)	-0.342*
2	T min (^{0}C)	0.163
3	BSH (hrs)	-0.287
4	Ws (km hr^{-1})	0.074
5	RHI (per cent)	0.244
6	RHII (per cent)	0.372*
7	Evap (mm)	-0.029
8	RF (mm)	0.370*

No. of Observations =35 r value =0.325 at 5per cent

The findings of current study are in corroboration with Tomer and Singh (2010) who conducted a field experiment during 2004-05 and 2005-06 to study the effect of weather factors on aphid population in cotton. Aphid population was recorded for the first time in 28th standard week, which remained active up to 1st standard week having its peak density (18.15 leaf^{-1}) in 37th standard week. Weather parameters lake, minimum temperature and relative humidity showed positive correlation with aphid population. Similar results are also recorded in earlier work wherein correlation studies of sucking pests and weather parameters revealed highly significant negative correlation between aphid population and maximum temperature and highly significant positive correlation with relative humidity at evening. Further it was also reported that maximum temperature showed significant negative correlation with aphid population (Anonymous, 2014).

Duration of life stages of syrphid fly in cotton

Studies carried out on the life stages of syrphid on cotton aphid revealed that(Table 4) duration of egg period was of 4.05 ± 0.52 (3-5) days. The three successive larval instars occupied 2.35 ± 0.641 (2- 3), 3.55 ± 0.787 (3-4) and 2.6 ± 0.197 (2-3) days, respectively with a total larval

period of 8.65 ± 0.91 (7-10) days. The pupal period lasted for 6.55 ± 0.668(6-7) days and the longevity of adult male and female was recorded at 14.65 ± 0.653 (14-15) days, 17.6 ± 1.52 (16-18) days, respectively.

Table 4. Duration of life stages of syrphid fly on cotton aphid

Stages	Duration (days)	
	Range	Mean ±SD
Egg	3-5	4.05 ± 0.523
1st Instar	2-3	2.35 ± 0.641
2nd Instar	3-4	3.55 ± 0.787
3rd Instar	2-3	2.6 ± 0.197
Total larval period	7-10	8.65± 0.91
Pre pupa	0.5-1	0.75 ± 0.74
Pupa	6-7	6.55 ± 0.668
Adult Male	14-15	14.65 ± 0.653
Adult female	16-18	17.6. ±1.52

The results on biological parameters are in conformity with the earlier work wherein, the life cycle of syrphid studied in the laboratory and in field conditions at Dharwad University revealed that the predator completed three larval instars with a total larval period of 12.12+0.31 (10-14) days. Pupal period ranged from 7 to 9 days with a mean of 8.30+0.26 days. The longevity of male and female was recorded at 13.27+0.89 (10-20) days and 17.6+1.52 (10-22) days, respectively(Anonymous, 2006).

Feeding potential of Syrphid fly

The total number of cotton aphids consumed during the entire larval period of syrphid larvae was as high as 390.6 in 7 to 10 days (Table 5).

Table 5. Feeding potential of syrphid fly larvae on cotton aphid

Larval stages	No. of aphids consumed/day		Total number of Aphids consumed/ instar Mean
	Range	Mean± SD	
1st Instar	17 – 23	24.1 ± 1.02	48.2
2nd Instar	47 – 55	42.5 ± 2.42	170.0
3rd Instar	52- 75	57.46± 3.79	172.4
Total	-	-	390.6
Average	-	-	45.15

Larva of syrphid consumed an average of 48.2, 170 and 172.4 cotton aphid during the first, second and third instar, respectively. Syrphid larva are 390.6 cotton aphids at the rate of 45.15 aphids day^{-1}.

According to earlier study a single larva of *E. confracter* consumed 442.74 sugarcane woolly aphids in its total larval period at a rate of 36.53 aphids/ individual/ day. The instar-wise consumption was 45.83, 133.52 and 263.39 aphids during first, second and third instar, respectively(Anonymous, 2006).

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Nutrition Security Through Kitchen Garden

In rural areas peoples were not aware about balanced diet so generally deficiency of micronutrient is found. The green leafy vegetables and tubers are rich sources of carotene, iron, calcium, ascorbic acid, riboflavin, folic acid and other minerals.(Devdas and Saroja 1980). The consumption of leafy vegetables for adult is 100 g as recommended by Indian Council of Medical Research but the actual consumption was found to be 10-20 g which is only 20 per sent of the recommended requirement (Gopalan *et al* 1989). Low consumption of green leafy vegetables leads lower intake of vitamins and minerals. As a result majority of population in rural areas suffer from iron and vitamin A deficiency. Malnutrition is a serious public health problem. It retards child growth, increases the risk and duration of illness, reduces work efficiency and slows social and mental development. Malnutrition among women of reproductive age increases the risk of mortality during labour and delivery and puts their newborn children at risk of long-term deficiencies. Improving nutritional status, including micronutrient status, can lead to increased productivity, increased child survival and growth and reduced maternal morbidity and mortality.

Various types of green leafy vegetables are consumed all over the country. However green leafy vegetables are seasonal and available only in particular season. The rural peoples will get GLV and Tubers in sufficient quantity in their daily diet. It will prevent malnutrition, anaemia, night blindness which is serious problem in many rural areas (WHO, 2001 and WHO 2004). A kitchen garden is an integrated system which comprises the family house, a recreational area and garden producing a variety of foods including vegetables, fruits and medicinal plants for home consumption or sale.

The kitchen home^{-1} gardens have been found to play an important role in improving food security for the resource poor rural households in developing country (Asaduzzaman, 2011) and can do the same in India. The advantages of Nutrition Kitchen Garden is to supply of fresh fruits and vegetables in high nutritive value and free from toxic chemicals. It helps to save expenditure on purchase of vegetables and economize therapy. Vegetables harvested from kitchen garden taste better than those purchased from market. It will prevent malnutrition, Anaemia, night blindness which is serious problem in many rural areas (Bloem *et al*., 1998). Therefore, the present study was carried out with an objective to train the housewives for nutrition kitchen garden and to investigate the role of kitchen gardens in addressing food and nutritional security.

The study was conducted by Suvide Foundation's Krishi Vigyan Kendra, Karda Washim (M.S.). The total number of 60 household covered in the rural areas during 2013 and 2014 and was selected randomly. The housewives of selected household were personally interviewed to elect the information regarding consumption practices of green leafy and other vegetables and expenditure on it. A questionnaires was formed covering socio-economic status and different aspect of consumption and expenditure on vegetables, awareness of nutrient contents, in addition to this educational status, food habits of selected subject were also include in the questionnaires.

The study population is about 60 households who live in the village. According to Small sample technique (Morgan, 1970) a sample would be most ideal at 95 level of confidence. However this puts a very big impact on the cost of the study as to administer the questionnaire alone will require in excess of 4 months having in mind that the workers may only be available for not more than a three hour window when workers are in their houses after work. 60 households were sampled for this study.

Table 1. Socioeconomic background of selected household (n=60)

S.N.	Particulars	Number	Percentage
1	Age Group		
	20-30	00	00
	31-40	24	40
	41-50	22	36
	51-60	8	13
2	Literacy level (Male)		
	Primary education	24	40
	Secondary	20	33
	Higher secondary	12	20
	Graduated	4	6.66
3	Yearly Income		
	Rs. 20000-40000	18	30
	Rs 41000-60000	24	40
	Rs 61000-80000	6	10
	Rs 81000-100000	12	20
4	Food Habits		
	Vegetarian	42	70
	Non Vegetarian	18	30

To avoid biasness a stratified random sample was used. This was done to help cover the stratified nature of the workers and in turn help to capture all the possible perceptions across the groups. Various income groups have different perceptions about food and this can only be captured by a random stratified sample.

Trainings on kitchen garden were organized for the housewives and also kitchen garden kit was supplied to 60 households. Various types of vegetable seeds such as spinach, fenugreek, shepu, okra, brijal, curry leaves, sponge guard, ridge guard, cluster bean, chilli, tomato and beet was provided to the trainees as kitchen garden kit for nutritional kitchen garden (Marsh, 1996)

The general information regarding the socio-economic status of selected household is given in Table 1

The maximum percentage (40per cent) of selected housewives was found in the age group of 31 to 40 years and minimum percentage (0per cent) was found in the age group of 20 to 30 years (Fig. 1).

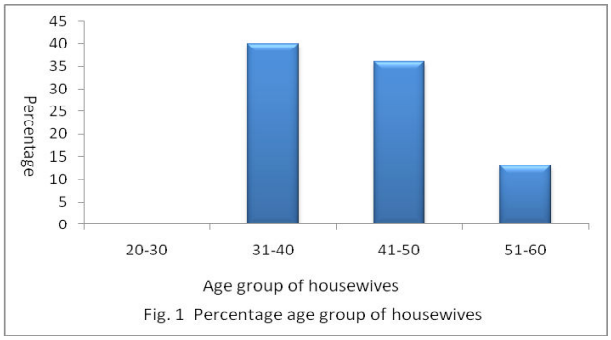

Fig. 1 Percentage age group of housewives

From Fig. 2 It shows that the educational status of literate housewives varied from primary education (40%), Secondary education (33%), higher secondary education (20%) and Graduate are only (6.66 %).

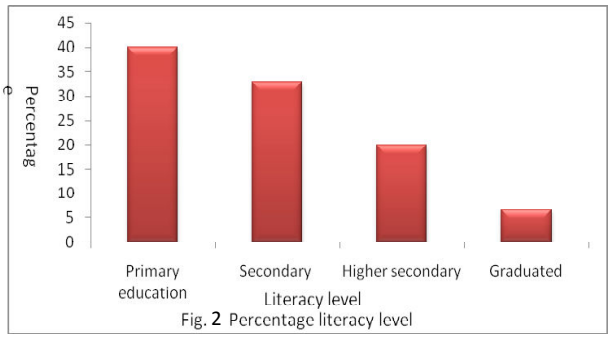

Fig. 2 Percentage literacy level

The majority of the household (40 %) were having yearly income between Rs. 41000-60000, 10 per cent had income between Rs. 61000-80000 /year and 30 per cent families were having yearly income less than 20000-40000and only 6 per cent families earned more than 80000 rupees per year. Majority of the household (70 %) were non-vegetarian and (30 %) families found to be Vegetarian (Table 1).

Above result indicate that majority of the surveyed housewives were middle aged. The literacy level of house wives as well as heads of families was good. Most of them were primary educated and middle income group.

Table 2 Expenditure on GLV and other vegetables by selected areas (n=60)

Particulars	Before giving training and kitchen garden kit training		After giving and kitchen garden kit	
Spend money	**Number**	**Percentage**	**Number**	**Percentage**
monthly on vegetable purchasing				
100-200	10	16.66	30	50
201-300	30	50	16	26.66
301-400	14	23.33	12	20
401-500	6	10	1	3.33

Before intervention majority of the household (50per cent) were spend money on purchasing vegetables between Rs. 201-300 month^{-1} and only 10per cent household were spend money on purchasing vegetables between Rs. 401-500 month^{-1}. 23 per cent household were spend money on purchasing vegetables between Rs. 301-400 month^{-1} and 16.66per cent household were spend money on purchasing vegetables between Rs. 100-200 month^{-1} (Table 2).

After participation in the training and supply of vegetable kit of kitchen garden, 50 per cent household were spend their money for purchasing vegetables between Rs. 100-200 per month and only 3.33 per cent families were spend money on purchasing vegetables between Rs. 401-500 month^{-1}.

Table 3. Daily consumption of vegetables and tubers by selected area

Particulars	Before giving training and kitchen garden kit training		After giving and kitchen garden kit	
Daily Consumption of vegetable	Number	Percentage	Number	Percentage
125-250gm day^{-1}	14	23	5	8.33
250-375gm day^{-1}	25	41.66	10	16.66
375-500gm day^{-1}	12	20	15	25
Above 500gm day^{-1}	9	15	30	50

From results it is clear that the beneficiaries who got the training and support on kitchen garden, they grows fresh vegetables in their household only and save near about 200 to 300 Rs per month. Only 3.33 percent people invest their money on purchasing of vegetables.

Before training on kitchen garden 23per cent families consumed vegetables and tubers between 125-250 g/day and only 15per cent families were consumed vegetables and tubers above 500 g per day. After training and getting knowledge about healthy food 50per cent families were consumed vegetables and tubers above 500 g/day and only 8per cent families were consumed vegetables and tubers between 125-250 g per day.

This result indicates that after getting training and kitchen kit the consumption vegetables and tubers increased by 27per cent.

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Screening of Arjuna Germplasm for Morphological and Chemical Variability

Arjuna is large size deciduous tree; plant height will be up to 20-22 m. It is evergreen tree with yellow flowers and conical leaves. It has a smooth gray bark contains Triterpene glycosides, arjunetin, arjunetoside, arjunaphthanoloside, together with oleanolic and arjunic acids, terminic acid, a cardenolide. One of the most promising constituents of the Arjun bark is arjunic acid, belonging to triterpenoid saponins. Arjuna helps in maintaining the cholesterol level as it contains the antioxidant properties similar to the Vitamin E. It strengths the heart muscles and maintains the heart functioning properly. It also improves functioning of cardiac muscle. Arjuna is used for the treatment of coronary artery disease, heart failure, edema, angina and hypercholesterolemia.

Conventionally Arjuna tree (*Terminalia arjuna*) are multiplied through seeds collected from the forest. Because of this, the Arjuna plants are not true-to-type and show significant variation in yield and tannin content**.** In all 209 plants of Arjuna planted during 1998-99 were undertaken for the screening in respect of plant height (m), stem girth (cm), bark thickness (mm) and tannin content during 2013-14. The bark from (10 x 15 cm) unit area was removed from all the plants and fresh and dry weight of bark was recorded. The tannin content in the bark was estimated by Folin-Denis method (Sadasivam and Manickam, 2010)

The data presented in Table-1 revealed that for plant height of tree the genotype AKAr 3-12, AKAr 4-4, AKAr 10-11, AKAr 1-5, AKAr 1-9 and AKAr 11-15 recorded significantly superior plant height i.e. mean + double standard deviation. Similarly seven different plants out of 209 plants recorded significance in respect of stem girth AKAr 1-11, AKAr 13-11, AKAr 7-1, AKAr 6-1, AKAr 10-11, AKAr 6-11, AKAr 9-15, bark thickness AKAr 9.15, AKAr 11-13, AKAr 1-9, AKAr 1-11, AKAr 7-1, AKAr 11-8, AKAr 11-15, fresh bark weight AKAr 12-14, AKAr 14-8,

Table: Morphological and chemical characters of Promising genotypes (*Terminalia arjuna*)

SN	Height (m)	Stem Girth (cm)	Bark Thickness (mm)	Freh Bark weight (g)	Dry Bark weight (g)	Tanin (%)
1	AKAr 3-12	AKAr 1-11	AKAr 9-15	AKAr 12-14	AKAr 12-14	AKAr 3-11
	(12.00)	(106.00)	(39)	(332)	(156)	(17.18)
2	AKAr 4 -4	AKAr 13-11	AKAr 5-8	AKAr 14-8	AKAr 14-8	AKAr 1-9
	(12.00)	(106.00)	(36)	(301)	(133)	(16.89)
3	AKAr 10-11	AKAr 7-1	AKAr 11-13	AKAr 11-13	AKAr 9-16	AKAr 4-12
	(12.00)	(105.00)	(36)	(290)	(122)	(16.71)
4	AKAr 1-5	AKAr 2-6	AKAr 1-9	AKAr 1-5	AKAr 11-13	AKAr 7-4
	(11.95)	(103.00)	(35)	(288)	(121)	(16.71)
5	AKAr 1-9	AKAr 1-2	AKAr 1-11	AKAr 8-6	AKAr 10-16	AKAr 11-7
	(11.50)	(100.00)	(35)	(284)	(120)	(16.63)
6	AKAr 11-15	AKAr 6-1	AKAr 7-1	AKAr 9-16	AKAr 13-11	AKAr 1-10
	(11.50)	(100.00)	(35)	(277)	(118)	(16.43)
7	AKAr 4-7	AKAr 10-11	AKAr 11-8	AKAr 3-8	AKAr 11-15	AKAr 1-13
	(11.10)	(99.00)	(35)	(271)	(116)	(16.39)
Lowest	AKAr 14-9	AKAr 2-13	AKAr 11-14	AKAr 11-6	AKA 11-6	AKAr 6-18
	(4.00)	(16.40)	(21.00)	(55)	(23)	(10.54)
Mean	**8.06**	**64.36**	**28.07**	**178.09**	**68.02**	**13.61**
SD ±	**1.65**	**16.57**	**3.21**	**46.16**	**22.04**	**1.25**
CV %	**20.46**	**25.74**	**11.43**	**25.92**	**32.40**	**9.15**

AKAr 11-3, AKAr 1-5, AKAr 8-6, AKAr 9-16, AKAr 3-8 and dry bark weight AKAr 12-14, AKAr 14-8, AKAr 9-6, AKAr 11-13, AKAr 10-6, AKAr 13-11, AKAr 11-15. However, the tannin content was also recorded significantly higher in seven different plants viz, AKAr 3-11, AKAr 1-9, AKAr 4-12, AKAr 7-4, AKAr 6-9, AKAr 3-9 and AKAr 5-9.

CONCLUSION

Significantly superior fresh bark weight recorded in genotype AKAr 12-14, AKAr 14-8, AKAr 11-3, AKAr 1-5, AKAr 8-6, AKAr 9-16, AKAr 3-8. However, the tannin content was also recorded significantly higher in seven different plants viz, AKAr 3-11, AKAr 1-9, AKAr 4-12, AKAr 7-4, AKAr 6-9, AKAr 3-9 and AKAr 5-9.

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Incidence of Mermis on Natural Population of Hieroglyphus spp (orthoptera) in Akola District of Vidarbha

Mass rearing of Hieroglyphus spp. was undertaken in ambient temperature and humidity in the laboratory. For this purpose field population of Hieroglyphus spp. (adults and nymphs) were collected from the infested fields of sorghum, maize, sweet sorghum which were without any insecticide application. The populations were also collected from the open grass lands and under the street lights (Table 1). They were released in separate wooden rearing cages and fed with fresh sorghum leaves. A continuous supply of fresh food was maintained throughout the experimental period. Moist sandy soil was kept at the bottom of the rearing cage for egg laying. The activity of the individuals was monitored periodically for knowing the death rate and to identify key factor, if any, responsible for mass killing of Hieroglyphus population in field.

The observations (Table 1) revealed that a nematode Mermis spp. (Order Mermithids ; Family – Mermithidae) was the key of infection causing the death in Hieroglyphus populations collected from various sources. Emergence of nematode Mermis was observed from the body of live grasshopper, when they were quite active and moving. Cessation of feeding was the early symptom observed in the infested individuals. The infected individuals were found quite active and mobile for 48 hours even after emergence of nematode from their body. The highest i.e. upto 8 per cent grasshoppers collected from sweet sorghum found harbouring Mermis, which later on left the body of grasshoppers during these period the grasshopper were alive and active.

Emergence of Mermis from the body of grasshopper took place from the intersegment septum of dorsum, ventron, pleuron and anal. After the emergence of nematodes from the body the individuals were found quite active and mobile upto 48 hr, which later on climbed up and holding the substratum firmly and died at the same place. 96 per cent of grasshoppers collected from under street, light showed this typical symptom. None of the grasshoppers collected from grassland and under street light, survived, indicating the infected left out populations from the major food source. The rate of survival of grasshoppers collected from other sources (Sweet Sorghum, Maize and sorghum) was also low (6 to 10 per cent) indicating epidemic situation. None of the grasshopper female was found laying eggs.

The emerged Mermis were tinch orange – reddish in colour. There length vary, the highest length of Mermis was 120 cm in sorghum grasshopper, followed by sweet sorghum 118 cm. The lowest length of Mermis was observed from street light collected grasshoppers. It was also observed when the Mermis leave the body of

Table 1. Hieroglypus collected from different host along with percentage of Mermis emerged, grasshopper died and average length of Mermis

S.N.	Host on which collected	No of grass hopperd collecte	Per cent of grass hopper with Mermis	Per cent of grass hopper died showing peculiar symptoms	Per cent of grass hopper did not die	Average length of Mermis
1	Sweet Sorghum	50	8	82	10	118 cm
2	Maize	50	2	86	6	95 cm
3	Sorghum	50	4	88	8	120 cm
4	Grass land	50	6	94	0	85 cm
5	Under Street light	50	4	96	0	108 cm

grasshopper fall on the ground and immediately enter inside the moist soil kept in the rearing cages and if the emerging nematode falls on hard and dry surface after losing the mobility forms a white clump.

Christhe (1937) reported the occurrence of Mermis from North and South America, Europe, and Asia on grasshoppers and many other insect species. Capinera (1987), observed that the female Mermis deposit eggs under ample moisture conditions on vegetation, particularly seen in grasslands, meadows and other vegetations, but not on the tree covered habitats. The adult Mermis live buried in the soil while larvae live as parasite inside the host. Authors fill that this may be one of the main reasons to get maximum mortality from grass land and street light collected grasshoppers. That is turbulence motivated for migration of grasshopper.

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