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Review

Current scenario of marker-assisted selection in breeding of minor oilseed crops of India

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ABSTRACT

Sunflower, safflower, castor, sesame, linseed and niger are the minor oilseed crops having potential to contribute towards achieving self-sufficiency in vegetable oil production in India. Decades of breeding research have resulted in release of high yielding cultivars with resistance to biotic stresses. However, the productivity levels are stagnated; further improvement in genetic gain requires integration of molecular tools in breeding programmes. Molecular markers, genomics and marker-assisted selection technologies are widely exploited for improvement of crops. In this review, current status of development and application of molecular markers in the oilseed crops *viz.,* sunflower, castor, safflower, sesame, linseed and niger are presented.

Keywords: Genomics, GWAS, Marker assisted selection, Molecular markers, Oilseed crops, QTL

Oilseeds play a significant role in Indian agricultural economy next to cereals. India is one of the major growers and importers of edible oils. In India, nine annual oilseed crops (rapeseed and mustard, soybean, groundnut, sesame, sunflower, safflower and niger for edible oils; castor and linseed for industrial purposes) are grown in an area of about 26 million ha with an annual production of about 31 million tonnes of seeds. Of these, major portion of oilseed production [27.8 million tonnes (90.9%) from 22.3 million ha (86.7%)] is contributed by rapeseed & mustard, soybean and groundnut whereas the remaining 2.8 million tonnes is contributed by the minor oilseeds: sunflower, sesame, niger, safflower, castor and linseed from the area of 3.4 lakh ha (average of 2015-16 to 2019-20, Directorate of Economics and Statistics, Govt. of India). The oilseed crops are largely grown in marginal lands under rainfed farming conditions, signifying their role in livelihood security of resource poor farmers. Furthermore, demand for edible oils is ever increasing in India due to rise in population and standard of living but the domestic production is adequate to satisfy only about 40% of the requirement; thus, forcing the country to rely heavily on the imports. In 2019-20, net availability of edible oils from all domestic sources was 10.7 million tonnes and the import was 13.4 million tonnes (https://dfpd.gov.in/oil-division.htm). The situation underscores the need for concerted efforts to increase the oilseed production in the country. In this context, sunflower, castor, safflower, sesame, linseed and niger assume greater significance as they have the potential to contribute for enhancing oilseed production in the country through improvements in productivity, and area expansion. In addition, these crops have huge export potential. Export of oils and by-products including oil meals, castor oil, groundnut, sesame seeds, niger seeds etc., was INR 28000 crores (3728 million USD) in 2020-21 (https://commerce.gov.in/about-us/divisions/export-products-division/export-products- agriculture/).

Low productivity is a major concern in the research and development (R&D) of minor oilseed crops. Developing high yielding cultivars adapted to biotic and abiotic stresses has been a major breeding goal in these crops to achieve higher productivity. Classical plant breeding methods have tremendously contributed for developing cultivars with high yielding potential. However, further improvements in yield potential have stagnated, mainly due to slow response to selection in breeding programmes. Low genetic variation, genetic complexity, low heritability and long selection cycle are some of the important factors that contribute for slow plant breeding response. Traditionally, plant breeding is practiced by 'hit and miss' or 'trial and error' approaches due to lack of precise selection tools, and understanding of genetics of the traits. Molecular marker technology has provided improved and precise selection tools to plant breeders. Molecular plant breeding has been recognized as the foundation for crop improvement in the 21st century to increase crop production (Moose and Mumm, 2008). In this review, current status of development and application of molecular markers in the oilseed crops *viz.,* sunflower, castor, safflower, sesame, linseed and niger is presented.

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Overview of molecular markers, trait mapping and marker-assisted selection: A variety of DNA based marker systems (RAPD, AFLP, RFLP, DArT, SSR, SNP, SRAP, TRAP, SCoT etc.,) have been developed over the years since 1980 (Kadirvel *et al.*, 2015). Recently, next generation sequencing (NGS) technologies have emerged, which offer excellent opportunities to generate a large number of markers in any crop with less cost and time. Markers are used for characterizing genetic diversity in germplasm collections, mapping and identification of genes associated with important traits, mining of superior alleles and marker-assisted selection (MAS) of desirable genes/traits in breeding programmes. Integration of markers in mainstream breeding programmes improves breeding efficiency in terms of speed, cost and accuracy. Establishing a marker-assisted breeding programme in crop plants involves a series of steps: development of genetic resources (trait specific donor germplasm, mapping populations), development of genomic resources (reference genome sequences, marker discovery, designing of marker genotyping assays, genetic linkage maps), trait mapping and QTL discovery using various strategies *viz.,* linkage mapping and association mapping (genome wide association analysis-GWAS and candidate gene based allele mining), fine-mapping and candidate gene discovery, designing of MAS protocols and application in breeding programmes by adopting MAS strategies *viz*., marker-assisted pedigree selection (MAPS), marker-assisted backcrossing (MABC), marker-assisted recurrent selection (MARS) and genome-wide selection (GWS) depending upon the traits (simply inherited or complex) under consideration (Collard and Mackill, 2008). Scheme of molecular breeding process is depicted in Fig. 1.

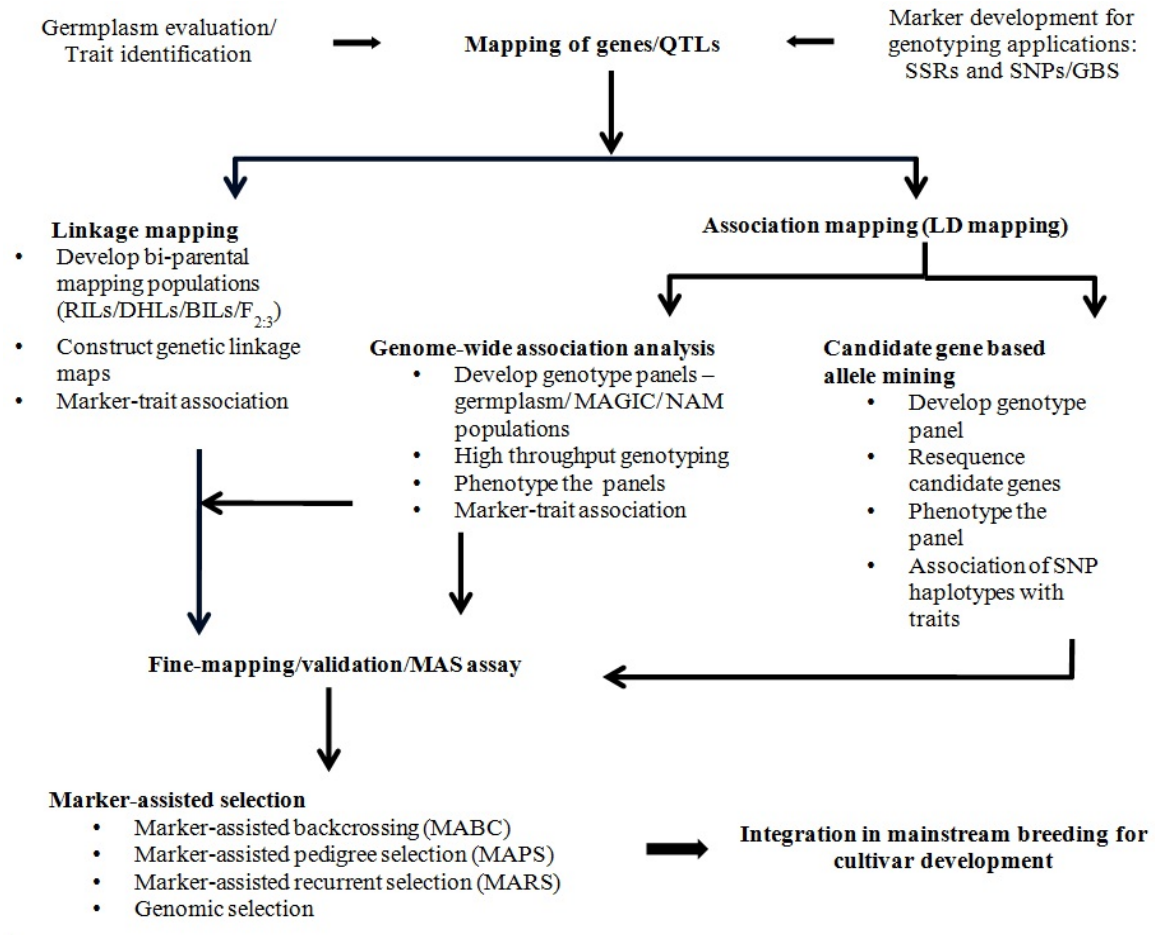

Fig. 1. Scheme of molecular breeding process in crops

Trait mapping is fundamental for establishing a molecular breeding programme in crops. Traditionally, linkage mapping [based on bi-parental mapping populations such as F_2, doubled haploid lines (DHL), recombinant inbred lines (RILs), backcross inbred lines (BILs)] has been performed to map QTLs. By this strategy, numerous QTLs have been detected for various traits in crops and several of them have been associated with candidate genes through positional cloning (Salvi and Tuberosa, 2007). Linkage mapping has been advantageous because QTLs could be roughly mapped using only a limited number of markers; subsequently, fine-mapping of the QTLs could be attempted by improving the resolution of the target QTL region. But it is restrictive with respect to capturing diversity of genes involved in complex traits because only two parents could be used at a time and a pedigree based population derived from those two parents is required. However, with the availability of genotyping by sequencing (GBS), high throughput SNP genotyping has become feasible, which has led to use of GWAS for QTL detection. GWAS can be performed directly in a diverse germplasm collection or multi-parent based populations [multi-parent advanced generation intercross (MAGIC)/nested association mapping (NAM) panel etc.,] using high density of markers (for desirable levels of linkage disequilibrium to achieve accuracy); thereby, diverse genes associated with various traits can be detected simultaneously, which would save time and resources. However, both the mapping strategies tend to throw spurious associations due to limitations in terms of phenotyping, population size, marker density, allele frequency, allelic effects etc. Therefore, the results need to be cautiously interpreted and the plausible QTLs need to be prioritized for validation and candidate gene analysis.

Sunflower: Sunflower (*Helianthus annuus* L.) is a diploid species with 2n=34 and genome size of about 3.5 Gb. The sunflower genome sequence has been published (Badouin *et al*., 2017). Being a globally important crop, substantial progress in molecular breeding has been achieved in sunflower. Genetic linkage maps using SSR and SNP markers have been developed (Tang *et al.*, 2002; Talukder *et al*., 2021). Several major genes conferring resistance to biotic stresses (downy mildew, rust and broomrape), fertility restoration, high oleic acid content, high tocopherol content and tolerance to herbicides have been identified in sunflower (Dimitrijevic and Horn, 2018). QTLs associated with several traits including domestication, self-incompatibility, flowering, male sterility, fertility restoration, seed dormancy, seed quality, oil content, high oleic acid content, tocopherol content, tolerance to drought, salinity or chilling stresses and resistance to downy mildew, rust, broomrape, chlorotic mottle virus and phomopsis stem canker have been mapped (Table 1). GWAS for flowering time, branching and *Sclerotinia* rot have been performed (Table 2). Molecular markers have been developed for the selection of fertility restoration, high oleic acid content, tocopherol content, resistance to downy mildew, rust, *Sclerotinia* white mold and broomrape and tolerance to herbicides in sunflower. Rouf *et al.* (2020) provides a detailed account of validated markers for MAS in sunflower.

In the Indian context, only a little information is available on the application of molecular markers in sunflower breeding. Nagarathna *et al.* (2011) reported validation of SSR marker associated with high oleic acid content in a collection of germplasm and parental lines being used in Indian breeding programmes. Kallamadi and Mulpuri (2020) reported three QTLs associated with resistance to powdery mildew, which require further validation. Efforts are needed to map the genes/QTLs governing resistance to necrosis, Alternaria leaf spot, downy mildew, *Macrophomina* root rot and other desirable agronomic traits to support Indian sunflower breeding programmes. Major genes associated with resistance to downy mildew, which have been reported in the exotic materials need to be validated in the Indian materials using molecular markers.

Castor: Castor (*Ricinus communis* L.) is a diploid species with 2n=20 and genome size of about 400 Mb. Draft genome sequence of castor has been published (Chan *et al.,* 2010). Senthilvel *et al.* (2019) published re-sequenced genomes of 14 diverse genotypes of castor. A chromosome scale assembly of wild castor accession has also been published (Lu *et al.,* 2021). Using the draft genome sequences, high throughput SSR and SNP markers have been developed in castor (Qiu *et al.,* 2010; Foster *et al.,* 2010; Sharma and Chauhan, 2011; Tan *et al.,* 2014; Senthilvel *et al.,* 2019; Dharajiya *et al.,* 2020). SSR based genetic linkage maps were developed by Liu *et al.* (2016) and Tomar *et al.* (2017) using F_2 populations. Senthilvel *et al.* (2019) developed high-density SNP maps using RIL populations of the crosses *viz.,* JC12 × 48-12 and DCS9 × RG1139 with more than 1000 SNP markers, which led to the development of a consensus map comprising of 1,978 SNP loci and spanning a total length of 995.8 cM with an average inter-marker distance of 0.55 cM. However, trait mapping efforts are very limited in castor. QTLs associated with resistance to Fusarium wilt (Tomar *et al.,* 2016; Shaw *et al.,* 2021) and charcoal rot (Tomar *et al.,* 2017), yield traits (Fan *et al.,* 2019), seed size and weight (Yu *et al.,* 2019) and agronomic traits (Xu *et al.,* 2021) have been reported. Candidate genes associated with cadmium tolerance (Yeboah *et al.,* 2021) and lupeol content (Li *et al.,* 2021) have been identified. A total of 69 SNPs associated with resistance to Fusarium wilt have also been identified in castor through GWAS (Shaw *et al.,* 2021). However, there are no reports published on MAS in castor till date. Details of QTL mapping and GWAS studies

performed for various traits in castor are presented in Table 1 and 2. At ICAR-IIOR, Hyderabad, important leads have been obtained in mapping resistance to Fusarium wilt in castor (Shaw *et al.,* 2021) and efforts are underway to design genotypic assays for selection of major genes//QTLs for wilt resistance (Senthilvel, unpublished). Trait mapping needs to be expedited for yield components, resistance to Botryotinia, *Macrophomina* root rot, sucking pests (leafhoppers, thrips, and whitefly) and tolerance to moisture stress, which are important for castor productivity in India.

Table 1 Reports of QTL mapping in minor oilseed crops of India

Mapping population	Marker type/Number	Traits mapped	No. of QTLs	QTL name	Linkage Group*	PVE (%)	Reference
		Sunflower					
Advanced backcross population (134 lines) derived from HA 89 (*H. argophyllus*) x Gray accession, PI 494573 cross	SNP (3110)	Basal stalk rot resistance	21	-	-	4.5-22.6	Talukder *et al.* (2021)
RILs of PS 2023 x TX16R cross	SSR (175)	Powdery mildew resistance	3	-	5, 10	-	Kallamadi and Mulpuri (2020)
F_6-RILs (164) of HA 89 x HA-R_3 cross	SNP (1,879)	Phomopsis stem canker resistance	15	-	-	5.24-17.39	Talukder *et al.* (2020)
F_2s (84) of '86-1' x 'L-1-OL-1' cross	SNP (6136)	Oleic acid content	3	OAC_1, OAC_2, OAC_3	-	5.18-12.05	Zhou *et a*l. (2018)
		Plant height	2	PH_1, PH_2		10.31-12.28	
		Head diameter	2	HD_1, HD_2	-	5.63-5.49	
		Stem diameter	1	SD_1	-	15.65	
F_4 lines of HA 300 × RHA 464 cross	SNP (2121)	Capitate glandular trichome	2	-	5, 6	11.61-14.06	Gao *et al*. (2018)
RILs (114) of PAC2 x RHA266 cross	SNP (384)	Sclerotinia head rot resistance	36	-	-	12.45-23.87	Zubrzycki *et al.* (2017)
F_2 (400) of ARG-1805 x ARG-1834 cross	SNP (530)	UV bullseye	1	-	2	20.1	Moyers *et al.* (2017)
		Flower head disc diameter	1	-	2	17.6	
		Ray ligule length	1	-	2	19.0	
		Total flower head diameter	1	-	2	21.2	
Two RIL populations derived from XRQ x PSC8 (117 F_8 RILs), and FU x PAZ2 (113 F_7 to F_{10} lines)	SSR (155), SNP (830), RGC (8)	Premature ripening	1	-	-	26.9-39.4	Bordat *et al.* (2017)
F_8 RILs (101) derived from HA89 and LR_1	SNP (951)	Resistance to broomrape (*Orobanche cumana* race F and G)	17	-	-	9.0-30.0	Louran *et al.* (2016)
F_7-RILs (106) of HA 441 x HA-439 cross	SNP (1053)	Basal stalk rot resistance	6	-	4, 9, 10, 11, 16, 17	6.4-28.9	Talukder *et al.* (2016)
BC_1 plants (975) derived from *H. debilis* ssp. *Cuccumerifolius* and *H. annuus* ssp. annuus	SNP (384)	Two fitness and 22 herbivore resistance, ecophysiological, phenological and architectural traits	110	-	-	-	Whitney *et al.* (2015)
RILs (148) derived from XRQ x PSC8 cross	SNP (2610)	Water use efficiency	9	-	-	5-7	Adiredjo *et al.* (2014)
		Carbon isotope discrimination	8	-	-	7.0	
F_8-RILs of INRA lines XRQ x PSC8 cross	SNP (235) + SSR (214)	Phytosterol traits	45	-	-	9.0-31.0	Merah *et al.* (2012)
RIL population derived from FU × PAZ2, and INEDI RIL population.	SNP SSR (451)	Downy mildew resistance	3	-	7, 8, 10	40.0-54.0	Vincourt *et al.* 2012
F_3 families (434) of CM625 x TUB-5-3234.	SSR (78)	Midstalk rot resistance	2	-	-	24.4-33.7	Micic *et al.* (2005a)

Table 1 (contd...)

Mapping population	Marker type/Number	Traits mapped	No. of QTLs	QTL name	Linkage Group*	PVE (%)	Reference
RILs (317) of NDBLOSsel x CM625 cross	SSR (41)	Midstalk rot resistance	2	-	8, 16	26.5	Micic *et al.* (2005b)
		Safflower					
F_9-RILs (98) of Mex.22-191 x Goldasht cross	AFLP (69)	Days to heading	1	qDTT_N-5-1	5	13.79	Poodineh *et al.* (2021)
		Days to heading (under stress)	1	qDTT_S-5-1	5	10.14	
		Grain yield (under stress)	1	qGY_S-4-1	4	18.18	
		Oil yield (under stress)	1	qOY_S-4-1	4	15.05	
		Harvest index	1	qHI_N-4-1	4	10.61	
		Number of branches/plant	1	qNB_N-11-1	11	13.86	
		Number of branches/plant (under stress)	2	qNB_S-7-1	7	6.73	
				qNB_S-9-1	9	6.73	
		Number of capitula/plant	2	qNC_N-3-1	3	5.87	
				qNC_N-5-1	5	19.34	
		Number of capitula/plant (under stress)	1	qNC_S-4-1	4	16.54	
		Plant dry weight	3	qDW_N-4-1	4	4.55	
				qDW_N-4-2	4	4.78	
				qDW_N-5-1	5	5.06	
		Thousand seed weight	1	qTSW_N-3-1	3	13.48	
		Days to flowering (under stress)	1	qDTF_S-2-1	2	14.08	
F_6-RILs (237) of CO-1 x EC-523368-2 cross	SSR (242)	Tolerance to aphid (days-to-wilt after aphid infestation)	2	qUc-Ct3.1	3	31.5	Jagadeeswaran *et al.* (2021)
				qUc-Ct5.1	5	9.1	
Segregating populations from Nira × *C. oxyacanthus*) and Nira × *C. palaestinus*) crosses	SSR	Resistance to Fusarium wilt	-	-	-	-	Anjani *et al*. (2018)
F_3 families (66) of Mex.22-191 × IL.111 cross	SSR and ISSR (119)	Plant height	2	qPh6_1	6	17.0	Mirzahashemi *et al.* (2015)
				qPh6_2	6	19.0	
		Branches/plant	3	qBpno4_1	4	48.0	
				qBpno 4_2	4		
				qBpno6	6		
		Capsules/plant	1	qCpno2	2	17.0	
		Dry weight/plant	3	qDw2	2	54.7	
				qDw4	4		
				qDw6	6		
		Seeds/plant	6	qSpno2	2	33.7	
				qSpno3	3		
				qSpno4	4		
				qSpno7	7		
				qSpno9	9		
				qSpno18	18		
		Seed yield/plant	2	qSyp2	2	37.0	
				qSyp9	9		

Table 1 (contd..)

Mapping population	Marker type/Number	Traits mapped	No. of QTLs	QTL name	Linkage Group*	PVE (%)	Reference
F_2 (276) of AC sunset x *C. palaestinus* cross	SNP (244)	Average leaf size	2	-	B, H	8.7-9.9	Pearl *et al.* (2014)
		Average leaf roundness	4	-	D, G, H, L	4.5-13.5	
		Spininess	3	-	E, H, L	4.5-32.7	
		Days to flower	3	-	D, H, I	5.6-11.9	
		Primary capitulum weight	7	-	A, D, H, I, L	4.5-9.9	
		Primary disc diameter	4	-	A, H, I, L	8.2-12.3	
		Number of heads	1	-	H	4.8	
		Flower colour	1	-	D	63.4	
		Stem height	3	-	E, H, I	6.3-7.8	
		Number of internodes	2	-	C, L	4.4-15.9	
		Internode length	4	-	A, E, L	4.2-7.6	
		Lowest branch height	1	-	G	5.9	
		Number of selfed seed	3	-	C, H, I	4.2-7.6	
		Achene weight	4	-	C, H, I, K	4.4-13.1	
		Achene length	4	-	C, D, I, K	5.2-12	
		Achene width	4	-	C, I, J, K	5.1-15.3	
		Seed dormancy	1	-	E, I, J, L	9.0	
		Palmitic acid	1	-	E	7.5	
		Oleic acid	3	-	C, G, H	6.3-11	
		Linoleic acid	2	-	G, H	8.6-8.7	
		Castor					
RILs (F_6) (185) of JC12 and 48-1 cross	SNP (1,090)	Resistance to Fusarium wilt based on days to wilt	1	-	7	44	Shaw *et al.* (2021)
RILs of Rc249 x Rc250 cross	SNP (2186)	Seed length	3	-	3, 5, 6	7.3-22.6	Xu *et al*. (2021)
		Seed thickness	4	-	3, 5, 6	4.5-15.9	
		Seed oil content	1	-	5	12.9	
		Single seed weight	4	-	3, 5, 6	3.7-19.8	
		Seed width	6	-	3, 4, 5, 6, 10	4.5-14.5	
F_4-RILs (200) of ZB306 x ZB107 cross	SNP (8896)	Seed length	4	qSL1	01	8.2	Yu *et al.* (2019)
				qSL3	03	7.7	
				qSL6-1	06	9.0	
				qSL6-2	06	5.1	
		Seed weight	4	qSW1	01	11.8	
				qSW3	03	6.5	
				qSW4	04	5.7	
				qSW6	06	9.1	
		Seed thickness	4	qST1	01	17.2	
				qST3	03	4.7	
				qST4	04	4.4	
				qST6	06	8.0	
		Single seed weight	4	qSSW1-1	01	6.2	
				qSSW1-2	01	4.6	
				qSSW3	03	10.9	
				qSSW6	06	20.7	

Table 1 (contd..)

Mapping population	Marker type/Number	Traits mapped	No. of QTLs	QTL name	Linkage Group*	PVE (%)	Reference
$F_{2:3}$ (190) of JI 357 x SKI 338 cross	SSR (300) + ISSR (100) + RAPD (520)	Charcoal rot resistance	3	-	2, 6, 9	11.3-71.2	Tomar *et al.* (2017)
		Sesame					
$F_{5:7}$ RILs (90) of Goenbaek x Osan cross	SNP (1657) + SSR (5)	Phytophthora blight resistance (Isolate: KACC48121)	1	qPhn-10_kacc48121	10	12.79	Asekova *et al.* (2021)
		Phytophthora blight resistance (Isolate: KACC48120)	1	qPhn-10_kacc48120	10	13.34	
		Phytophthora blight resistance (Isolate: No2526)	1	qPhn-10_no2526	10	13.34	
F_8 RILs (548) of Zhongzhi No. 13 x ZZM2748 cross	SSR (424)	Sesamin	1	qSmin_11.1	11	67.69	Xu *et al*. (2021)
		Sesamolin	1	qSmol_11.1	11	46.05	
RILs (488) of Zhongzhi No. 13 x ZZM2289 cross	SSR (81)	Leaf size	1	qLS15-1	15	5.81-27.5	Sheng *et al.* (2021)
BC_1 of Yuzhi 4 x BS cross	SLAF (3528)	Seed yield per plant	1	qSY_LG08-1	8	35-43	Mei *et al.* (2021)
		Number of capsules/plant	1	qCN_LG08	8	17.6-21.2	
		Number of seeds/capsule	2	qSN_LG04	4	12.35-15.23	
				qSN_LG08	8	14.6-16.3	
		Seed weight	1	qSW_LG04	4	9.26-13.59	
		Plant height	1	qPH_LG08	8	6.25-11.23	
		Height of the first capsule	2	qFCH_LG08-2	8	59.15-71.41	
				qFCH_LG08-1	8	23.83	
		Harvest index	1	qHI_LG05	5	6.49-10.69	
F_8 RILs (548) of Zhongzhi No. 13 x ZZM2748 cross	SSR (424)	Charcoal rot resistance	14	qCRR3.1	3	3.0-14.6	Wang *et al.* (2017)
				qCRR3.2	3		
				qCRR3.3	3		
				qCRR3.4	3		
				qCRR5.1	5		
				qCRR8.1	8		
				qCRR8.2	8		
				qCRR8.3	8		
				qCRR9.1	9		
				qCRR12.1	12		
				qCRR12.2	12		
				qCRR12.3	12		
				qCRR13.1	13		
				qCRR13.2	13		
BC_1 plants (150) of Yuzhi4 x Bengal cross	SLAF-Seq (9378)	Basal branching habit	1	qBH-LG5	5	78.64	Mei *et al*. (2017)
		Flowers/leaf axil	1	-	11	-	
$F_{8:9}$ RILs (224) of 'Miaoqianzhima' x 'Zhongzhi 14' cross	SNP SSR Indel (1230)	Plant height	2	Qph-6	6	6.0	Wu *et al*. (2014)
				Qph-12	12	5.6-9.1	
		First capsule height	3	Qfch-4	4	6.2	
				Qfch-11	11	8.2	
				Qfch-12	12	11.5	
		Capsule axis length	2	Qcal-5	5	8.1	
				Qcal-9	9	9.2	
		Capsule number/plant	1	Qcn-11	11	7.0	
		Thousand grain weight	1	Qtgw-11	11	7.7-12.3	
		Grain number/capsule	3	Qgn-1	1	6.8-11	
				Qgn-6	6	8-18.3	
				Qgn-12	12	7.9-13.6	
		Capsule length	4	Qcl-3	3	52.2-75-6	
				Qcl-4	4		
				Qcl-7	7		
				Qcl-8	8		
				Qcl-12	12		

Table 1 (contd...)

Mapping population	Marker type/Number	Traits mapped	No. of QTLs	QTL name	Linkage Group*	PVE (%)	Reference
F_3 lines (260) of COI1134 x RXBS cross	SSR (49) + AFLP (52) + RSAMPL (623)	Seed coat colour	4	QTL1-1	1	39.95	Zhang *et a*l. (2013)
				QTL11-1	11	20.61	
				QTL11-2	11	24.02	
				QTL13.1	13	30.56	
		Linseed					
F_2 (154) of JRF-4 x Chambal cross	SSR (193)	Capsules/plant	4	Qcp.nbri.2.1	2	8.2	Singh *et al*. (2021)
				Qcp.nbri.6.1	6	6.0	
				Qcp.nbri.7.1	7	8.6	
				Qcp.nbri.14.1	14	5.6	
		Capsule weight/plant	2	Qcwp.nbri.7.1	7	9.2	
				Qcwp.nbri.9.1	9	10.5	
		Seed weight/plant	2	Qsw.nbri.7.1	7	9.5	
				Qsw.nbri.9.1	9	1.0	
		Alternaria blight resistance	2	Qabr.nbri.14.1	14	9.2	
				Qabr.nbri.14.2	14	4.2	
F_2 (112) of DIANE x NY17 cross	SLAF (2339)	Plant height	1	-	1	18.77	Wu *et al*. (2018)
		Stem length	1	-	8	11.17	
		Seed yield	3	-	10, 12	10.11-19.33	
		Stem yield	3	-	5, 15	10.91-15.81	
		Fibre yield	2	-	1, 11	19.09-25.98	
		Fibre content	2	-	5, 11	13.27-15.14	
RILs (110) of Macbeth/Heiya No.14 (MH) cross; R_7 RILs (123) of P.I.249991/Heiya No.14 cross	SNP (4497)	Plant height	1	-	-	10.29-26.94	Zhang *et a*l. (2018)
		Technical length	1	-	-		
$F_{8:9}$ RILs of CDC Bethune x G1186/94 cross	SSR (91) CAPS (1)	Seed and flower colour	1	-	1	-	Sudarshan *et al.* (2017)
RILs (243) of CDC Bethune x Macbeth cross	SNP (329) SSR (362)	Palmitic acid	1	QPal.BM.crc-LG7	7	0.12	Kumar *et al*. (2015)
		Stearic acid	3	QSte.BM.crc-LG1	1	0.06	
		Oleic acid	3	QOle.BM.crc-LG3-1	3	0.13	
		Linoleic	2	QLio.BM.crc-LG3	3	0.08	
		Linolenic	1	QLin.BM.crc-LG5	5	0.10	
		Iodine value	2	QIod.BM.crc-LG5	5	0.08	
		Oil content	1	QOil.BM.crc-LG8	8	0.13	
		Seed protein	1	QPro.BM.crc-LG11	11	0.11	
		Cell wall	1	QCw.BM.crc-LG4	4	0.14	
		Straw weight	1	QSw.BM.crc-LG4	4	0.30	
		Thousand seed weight	1	QTsw.BM.crc-LG15	15	0.09	
		Seeds per boll	1	QSpb.BM.crc-LG4	4	0.20	
		Yield	1	QYld.BM.crc-LG4	4	0.08	
		Days to maturity	1	QDm.BM.crc-LG4	4	0.31	

*Linkage groups are indicated as defined by the authors and they are not comparable across studies.

Safflower: Safflower (*Carthamus tinctorius* L.) is a diploid species with 2n=24 and genome size of about 1.5 Gb. Very recently, chromosome scale reference genome of safflower has been published (Wu *et al.,* 2021). Substantial number of SSR markers have been developed in safflower through traditional EST mining, genomic library screening or NGS approaches (Chapman *et al.,* 2009; Mayerhofer *et al.,* 2010; Hamdan *et al.,* 2011; Yamini *et al.,* 2013; Lee *et al.,* 2014; Ambreen *et al.,* 2015; Usha Kiran *et al.,* 2019; Jegadeeswaran *et al.,* 2021). Only a few genetic linkage maps have been developed in safflower. Mayerhofer *et al.* (2010) first published a linkage map of safflower by using F_2 and BC_1 populations derived from interspecific crosses involving *C. tinctorius* and *C. oxyacanthus.* Subsequently, Garcia-Moreno *et al.* (2011) and Hamdan *et al.* (2012) published linkage maps of safflower involving SSR markers. Recently, Jegadeeswaran *et al.* (2021) published an SSR linkage map with 242 markers using a RIL population, which is relatively a dense SSR map of safflower to date. Bowers *et al.* (2016) published a high density linkage map with more

than two million SNPs by whole genome sequencing of a RIL population produced from the interspecific crosses involving *C. tinctorius* and *C. palaestinus.* At the moment, Bowers *et al.* (2016) map serves as a reference in safflower.

In safflower, trait mapping efforts were mainly focused on oil quality and other qualitative traits like flower colour and male sterility. Hamdan *et al.* (2008) reported that *Li* gene, controlling high linoleic acid content, was tightly linked to the nuclear male sterility gene, *Ms*, both flanked by SCAR markers. Mayerhofer *et al.* (2010) mapped a dominant gene *ctfc1* controlling yellow flower colour on to linkage group T9. Garcia-Moreno *et al.* (2011) mapped *Tph2* gene associated with high gamma-tocopherol content. Hamdan *et al.* (2012) mapped *Ol* gene associated with high oleic acid content. Anjani *et al.* (2018) reported the association of SSR markers with resistance to Fusarium wilt in interspecific crosses of Nira × *C. oxyacanthus* and Nira × *C. palaestinus.* To date, only a few reports are available on QTL mapping, which include domestication traits (Pearl *et al.,* 2014), tolerance to drought (Hussain *et al.,* 2016; Mirzahashemi *et al.,* 2015; Poodineh *et al.,* 2021) and aphids (Jegadeeswaran *et al.,* 2021). Preliminary studies on GWAS for drought tolerance (Ebrahimi *et al.,* 2008), yield, oil content and quality traits (Ambreen *et al.,* 2018), and 100-seed weight (Ali *et al.,* 2020) have been performed. Details of QTL mapping and GWAS studies performed for various traits in safflower are presented in Table 1 and 2.

To date, only one case of MAS has been reported in safflower. Liu *et al.* (2013) reported PCR based multiplex marker assay for selection of high oleic allele *'ol'* in safflower based on the mutation in the *CtFAD2-1* gene. Subsequently, Kadirvel *et al.* (2020) designed SNP genotyping assays such as Kompetitive Allele Specific PCR (KASP®) and the Amplifluor™ SNPs Genotyping System (Amplifluor®) for the prediction of *'ol'* allele. The assays were validated in segregating populations as well as in MABC scheme to introgress the *'ol'* allele in the background of popular cultivar. At ICAR-IIOR, Hyderabad, MAS for high oleic acid content trait is routinely implemented in safflower breeding programmes using these assays. Furthermore, efforts are underway to develop genetic and genomic resources and map QTLs associated with agronomic traits including yield components, oil content, resistance to Fusarium wilt and tolerance to aphids and moisture stress.

Sesame: Sesame (*Sesamum indicum* L.) is a diploid species with 2n=26 and genome size of about 950 Mb. Wang *et al.* (2014) published de novo genome sequence of sesame. SSR markers have been reported by various authors (Ke *et al.,* 2011; Wei *et al.,* 2011; Zhang *et al.,* 2012; Dossa *et al.,* 2017). SSR database namely SisatBase (Dossa *et al.,* 2017) and GinMicrosatDb (Purru *et al.,* 2018) have been developed. Kizil *et al.* (2020) reported genome-wide discovery of InDel markers using ddRADSeq. Yu *et al.* (2019) constructed pan-genome assembly based on genome assemblies of five sesame varieties including two landraces (*S. indicum* cv. Baizhima and Mishuozhima) and three modern cultivars (*S. indicum* var. Zhongzhi13, Yuzhi11 and Swetha), which serves as a rich resource for comparative genomic analyses and gene discovery in sesame research.

The first linkage map was constructed in 2009 using 220 EST-SSR, AFLP and RSAMPL (Random Selective Amplification of Microsatellite Polymorphic Loci) markers (Wei *et al.,* 2009). Zhang *et al.* (2013) developed high-density genetic linkage map in F_3 population using 724 polymorphic markers (653 SSR, AFLP and RSAMPL) corresponding to 14 linkage groups. Subsequently, RAD tag sequencing was applied on a sesame RIL population (Wu *et al.,* 2014). Uncu *et al.* (2016) identified 15,521 SNPs through genotyping by sequencing approach (GBS) and developed a linkage map with 432 markers (420 SNPs, 12 SSRs). Wang *et al.* (2017) constructed a genetic linkage map based on 424 novel polymorphic SSR markers using a RIL population.

Marker-trait associations have been reported in sesame for a few traits. Uzun *et al.* (2003) reported AFLP markers linked to closed capsule mutant. Uzun and Cagirgan (2009) identified ISSR markers linked to determinate growth habit in a segregating F_2 population of sesame derived from the cross between *dt-1* (mutant with determinate habit) and Muganli-57 (indeterminate wild type cultivar). The gene conferring recessive genic male sterility (RGMS) was mapped using AFLP markers (Zhao *et al.,* 2013). Liu *et al.* (2015) identified SSR markers associated with dominant genic male sterility (DGMS) in sesame. Liu *et al.* (2020) fine-mapped a novel locus in male-sterile mutant associated with wrinkled-leaf using bulk segregant analysis (BSA)-Seq and NGS.

QTLs associated with resistance to charcoal rot (Wang *et al.,* 2017), Phytophthora blight (Asekova *et al.,* 2021), seed oil and protein content (Li *et al.,* 2014), seed coat colour (Zhang *et al.,* 2013; Du *et al.,* 2019), yield related traits (Wu *et al.,* 2014; Du *et al.,* 2019; Mei *et al.,* 2021), leaf size (Sheng *et al.,* 2021), and sesamin and sesamolin variation (Xu *et al.,* 2021) have been reported. GWAS for seed related traits (Zhou *et al.,* 2018) and drought tolerance (Dossa *et al.,* 2019) have been performed and major effect QTLs have been detected. Details of QTL mapping and GWAS studies performed for various traits in sesame are presented in Table 1 and 2. In spite of the development of genomic resources, there is no example of MAS in sesame globally. Also, no trait mapping has been reported in sesame in India. Mapping of yield components, resistance to Phyllody, *Macrophomina* root rot and powdery mildew and tolerance to abiotic stresses including drought and flooding need to be expedited to assist plant breeding programmes in India.

Table 2 Reports of GWAS in minor oilseed crops of India

Population type/size	Marker type/number	Traits	No. of associated markers	PVE (%)	Reference
		Sunflower			
Germplasm	SNP	Rhizophagus intraradices colonization	3	-	Stahlhut *et al*. (2021)
Germplasm (601)	SNP (15483)	Docosanoic acid	53	35.4	Chernova *et al.* (2021)
		Fatty acids and oleic-linoleic acid ratio	140	-	
Germplasm (333)	SNP (8723)	Fertility restoration (*Rf7* gene)	24	-	Talukder *et al*. (2019)
		Safflower			
Germplasm (124)	SSR (93)	Oil content	5	9.7-23.4	Ambreen *et al.* (2018)
		Oleic acid	3	11.4-34.1	
		Linoleic acid	6	10.1-19.1	
		100 seed weight	2	8.9-24.52	
		Plant height	6	10-14.7	
		Number of capitula/plant	2	7.4-25.7	
		Number of primary branches	3	8.0-13.3	
		Days to 50% flowering	5	7.9-12.6	
Germplasm (100)	ALFP (341)	Seed yield (normal)	2	7.25-15.83	Ebrahimi *et al.* (2008)
		Seed yield (drought stress)	6	4.84-10.28	
		Oil yield (normal)	2	7.21-14.15	
		Oil yield (drought stress)	5	3.92-10.32	
		Oil content (normal)	3	5.75-12.12	
		Oil content (drought stress)	3	5.64-7.24	
		Number of capitula/plant (normal)	2	6.0-7.15	
		Number of capitula/plant (drought stress)	1	7.12	
		Number of seeds/capitulum (normal)	5	4.6-7.7	
		Number of seeds/capitulum (drought stress)	3	6.44-10.08	
		1000-seed weight (normal)	2	2.1-2.2	
		1000-seed weight (drought stress)	3	3.04-3.76	
		Number of branches/plant (normal)	2	8.0-9.6	
		Number of branches/plant (drought stress)	2	15.44-16.32	
		Plant height (normal)	1	2.2	
		Plant height (drought stress)	4	3.12-3.92	
		Castor			
Germplasm	SNP (3,465)	Resistance to Fusarium wilt based on days to wilt	69	0.063-0.215	Shaw *et al*. (2021)
Germplasm (175)	SSR (143)	Traits associated with cadmium tolerance - Plant height	3	7.3-15.91	Yeboah *et al.* (2021)
		Fresh weight shoot	3	10.18-13.0	
		Shoot length	5	5.63-19.43	
		Root length	1	15.11	
		Dry weight root	2	13.04	
		Fresh weight root	1	15.91	
		Dry weight shoot	2	13.26-19.43	
Germplasm (505)	SNP (23,14,859) by GBS	Plant height	2	-	Xu *et al*. (2021)
		Number of node	2		
		Diameter of main stem	9		
		Seed length	3		
		Seed width	2		
		Seed thickness	3		
		Seed area	4		
		Single seed weight	5		

Table 2 (contd..)

Population type/size	Marker type/number	Traits	No. of associated markers	PVE (%)	Reference
Germplasm (405)	SNP (1,487)	Capsule dehiscence	171	-	Fan *et al.* (2019)
		Endocarp thickness	48		
		Panicle height	24		
		Panicle length	3		
		Plant height	2		
		Ratio of male to female flowers	693		
		Seed length	37		
		Seed volume	145		
		Hundred grain weight	52		
		Sesame			
Germplasm (87)	SNP (8,883)	Phytophthora blight resistance	29	35.57-70.32	Asekova *et al.* (2021)
Germplasm (369)	SSR (112)	Oil content	8	4.0-29.0	Li *et al.* (2014)
		Protein content	9	3.0-29.0	
		Linseed			
Germplasm (200)	SNP (6,74,074)	Seed length, seed weight, 1000 seed weight	599 SNP (in 4 different environments)	-	Guo *et al.* (2020)
Germplasm (86)	SNP (10,057)	Days of 50% flowering	2		Singh *et al*. (2019)
		Seed weight/plant	2		
		Branches/plant	1	-	
		Oil content	1		
		Capsule weight/plant and seed weight	1		
Germplasm (370)	SNP (2,58, 873)	Pasmo resistance	692 unique QTNs associated with 500 putative QTLs	0.28-15.02	He *et al.* (2019)
Germplasm (200)	SNP (7,71,914)	Mucilage content	7	11.82-17.32	Soto-Cerda *et al.* (2018)
		Hull content	4	13.83-18.20	
Germplasm (224)	SNP (5,84,987)	Fruit number	1		Xie *et al.* (2018a)
		1000-grain weight	8		
		Palmitic acid content	1	-	
		Stearic acid	2		
		Linoleic acid	1		
		Linolenic acid	3		
Germplasm (224)	SNP (1,46,959)	Plant height, technical length, number of branches, number of fruits and 1000-grain weight	42	-	Xie *et al*. (2018b)
Germplasm (390)	SSR (464)	1000 seed weight	5	0.5-15.2	Soto-Cerdo *et al.* (2014)
		Start of flowering	1	7.1	
		End of flowering	1	7.6	
		Plant height	2	4.6-18.5	
		Plant branching	1	12.9	
		Lodging	2	7.1-8.9	

(QTNs: Quantitative trait nucleotides)

Linseed: Linseed (*Linum usitatissimum* L.) is a diploid species with 2n=30 and genome size of about 686 Mb. Genome sequence of fibre flax cultivar has been reported (Wang *et al.,* 2012; Dmitriev *et al.,* 2021). SSR (Ragupathy *et al.,* 2011; Soto-Cerda *et al.,* 2011; Kale *et al.,* 2012; Wu *et al.,* 2017) and SNP markers (Yi *et al.,* 2017) have been developed using NGS. QTLs associated with fatty acid composition and yield (Cloutier *et al.,* 2011; Kumar *et al.,* 2015), oil content and yield-related traits (Chandrawati and Yadav, 2017), plant height (Zhang *et al.,* 2018), fibre related traits (Wu *et al.,* 2018), seed and flower colour (Sudharsan *et al.,* 2017) and resistance to powdery mildew (Asgarinia *et al.,* 2013) have been reported. GWAS for agronomic traits

(Soto-Cerda *et al.,* 2014) and seed quality traits (Soto-Cerda *et al.,* 2014) have been performed. You and Cloutier (2020) reviewed extensively about linkage maps, trait mapping, and linked markers in flax. Till date, there is no example of MAS in linseed globally. Details of QTL mapping and GWAS studies performed for various traits in linseed are presented in Table 1 and 2. In India, work on trait mapping in linseed is very limited.

Niger: Niger [*Guizotia abyssinica* (L. f.) Cass.] is a diploid species with 2n=30 and genome size of about 7 Gb. To date, only two reports are found on the development of SSR and SNP markers. Dembewolf *et al.* (2010) developed 43 SSR markers using an EST library. These authors also sequenced the chloroplast genome of niger. Tsehay *et al.* (2020) identified SNP markers through transcriptome sequencing of two genotypes and designed KASP assays for 554 SNPs for genotyping applications in niger. There are no reports of trait mapping and MAS in niger globally.

Future prospects: Progress in development and application of molecular markers in breeding of minor oilseed crops of India (except sunflower) are very limited compared to the major oilseed crops such as rapeseed (Hu *et al.,* 2021), soybean and groundnut (Desmae *et al.,* 2019). Practical applications of MAS are not yet available in castor, sesame, linseed and niger. In safflower, MAS protocol is available only for high oleic acid content trait. Molecular breeding research in these crops must focus on the following areas: (1) developing genetic and genomic resources such as mapping populations, re-sequenced genomes, high throughput marker assays, etc. to facilitate discovery of genes/QTLs associated with agronomically and economically important traits, (2) prioritizing genes/QTLs for validation across populations and environments, (3) designing MAS protocols for routine use in breeding programmes.

In India, progress in molecular breeding in minor oilseed crops has been very slow due to the lack of adequate funding support and critical manpower. In order to bridge this gap, a new impetus has been given in R&D of sesame, linseed, safflower and niger under a mission mode programme on "Minor Oilseeds of Indian Origin" to harness the benefits of rich genetic resources through cutting-edge genomic technologies with the financial support from Department of Biotechnology, Govt. of India (ICAR-IIOR, 2020). It is expected that such initiatives would help advancing research and enhance critical manpower in the areas of genomics and marker-assisted breeding in the minor oilseed crops of India, which have been late entrants into the genomics era and have the benefit of knowledge accrued from the genomics of major crops (Siddiq and Vamireddy, 2021); therefore, rapid progress in molecular breeding of these crops is expected in the near future.

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Hayman's diallel analysis of elite x elite crosses in sesame (*Sesamum indicum* L.)

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ABSTRACT

The present investigation was carried out to study the genetic components of yield and its ancillary characters in a 8 x 8 full-diallel cross between elite sesame cultivars grown in different geographical regions of India. Hayman's analysis of variance indicated the presence of both additive and dominance genetic variance for all six characters studied. Ambidirectional dominance was indicated for all the characters with asymmetrical gene distribution except for seed yield and number of capsules/plant and residual dominance effects for all the characters studied. Branches/plant and test weight indicated epistasis. Seed yield, plant height and oil content showed over dominance while capsules/plant were under partial dominance. Parents *viz*., HT-1, VRI-3 and TKG-22 had dominant genes with positive effects for seed yield; Phule til, Swetha til and RT-351 for capsule number/plant and crosses between HT-1, TKG-22 and E-8 results in segregants with high oil content. Estimates of components of variance demonstrated the involvement of additive gene effects for seed yield and capsule number, additive and dominant effects for plant height and oil content. Influence of the environment was strong on these characters, which followed simple additive-dominance inheritance.

Keywords: Additive, Diallel, Dominance, Gene action, Hayman, Sesame

Sesame (*Sesamum indicum* L.) is considered as 'Queen of Oilseeds' for its high oil content and better quality and is grown widely in tropical and subtropical conditions. The quality edible oil and seeds produced from this crop are widely used since time immemorial. Globally, sesame is cultivated in 12.05 m ha distributed across 79 countries, accounting for the production of 6.4 million tonnes and the productivity is 535 kg/ha. Sudan, India, Myanmar and United Republic of Tanzania are the top four sesame producing countries (FAOSTAT, 2020). India is the second largest producer of sesame, cultivated in 1.56 million hectares to produce 0.784 m tonnes, with average productivity of 502 kg/ha (Anonymous, 2018). Sesame is cultivated in 21 states of the country in a considerable area across different agro-climatic regions, under both rainfed and irrigated conditions. The top 4 states with the maximum area under sesame are Madhya Pradesh, Uttar Pradesh, West Bengal, and Rajasthan. The majority of the area under sesame is during kharif in northern and western parts of India. In eastern and southern parts of India, sesame is a summer crop.

The average yield potential of the released varieties is 700-800 kg/ha (Ranganatha, 2014). The genetic gain for yield in sesame is considerably low among other oilseed crops. Genetic improvement through mass selection from a locally adaptive population was followed to develop improved cultivars. Currently, hybridization between two purelines followed by pedigree or bulk selection is the most popular method. However, the current data on productivity clearly indicates, very poor improvement in seed yield. Yield being a complicated quantitative trait needs to be addressed by operating different improved technologies for selection. Operating appropriate selection in a population is possible by understanding the inheritance pattern of the trait. The insight into the inheritance of characters is useful to plant breeders for, 1) selection of parents for hybridization, 2) choosing appropriate breeding and selection procedures for the genetic improvement of various quantitative traits, and 3) estimating the other genetic parameters.

Comprehensive studies on the inheritance pattern of yield and its attributes are limited in sesame and more information is required on these aspects. Diallel analysis of crosses is one most informative technique to understand the gene action of the traits. The pattern of inheritance for yield and its attributing characters along with phenological characters were studied through combining ability studies by Griffing's method of diallel analysis (Ravindran and Raghinam, 1996; Saravanan and Nadarajan, 2003; Banerjee and Kole, 2009; Pandey *et al.,* 2018). The above studies reported additive or non-additive gene action and identified crosses with high GCA and SCA, but further elucidating the other parameters of additive and dominance effects was lacking. Hayman's diallel analysis is robust in providing information on additive and dominance effects of genes, the proportion of dominance, the average degree of dominance, the direction of dominance, genes distribution among parents, maternal and reciprocal effects, the ratio of dominant to recessive

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alleles in all the parents, and broad sense (H^2) and narrow sense (h^2) heritability (Makumbi *et al.,* 2018). The use of this technique in sesame research is very limited (Vekaria *et al.,* 2015; Tripathy *et al.,* 2016; Suganthi, 2018; Dash *et al.,* 2020) and is gaining importance in present days. Sedack *et al.* (2013) used half diallel cross of 8 parents under Egyptian conditions to study the gene action for yield and its related characters. This study reported that both additive and dominance effects were significant for yield and yield contributing traits, where the magnitude of the dominant component was higher along with the predominant number of dominant alleles. The gene action depends on the distribution and expression of the genes present in the parents involved in developing diallel crosses. Parents may harbor favorable alleles at different loci, which need to be combined through crossing to develop an array of segregants with favorable genetic combinations expressing economically exploitable traits. Information on genetic systems governing the inheritance of characters by analyzing parents and cross combinations is necessary. Therefore, gene actions are particular to the parents and crosses studied. Knowledge of the genetic effects of the character in the crosses handled by the breeder helps in operating the right selection and generation advancement strategies of the segregating progenies. In the present study, an 8x8 full diallel cross was subjected to Hayman's method of diallel analysis (Hayman, 1954 a&b) to elucidate the genetic inheritance pattern and identify elite parents with dominant or recessive genes with positive and negative effects for yield and its attributing traits.

MATERIALS AND METHODS

Experimental site and plant material: The experiment was conducted at the experimental farm of ICAR-Indian Institute of Oilseeds Research, Hyderabad characterized with red sandy loam type of soil (17°15' N latitude and 78°18' E longitude at an altitude of 542m above mean sea level). Eight elite varieties *viz.,* E-8 grown in Karnataka (*kharif*), GT-2 in Gujarat (*kharif*), HT-1 in Haryana (*kharif*), Phule til in Maharashtra (*kharif*)), RT-351 in Rajasthan (*kharif*)), Swetha til in Telangana (summer), TKG-22 in Madhya Pradesh (*kharif*) and VRI-3 in Tamil Nadu (summer) were selected as parents. Eight parents were crossed in full diallel mating design (Hayman, 1954a) during summer 2018. All the 56 F_1's including reciprocals and the parents comprising of 64 entries were raised in the plot size of 4.05 sq m to evaluate for yield and its attributes during *kharif* 2018. The experimental design adopted was a balanced block design with 2 replications. The standard recommended practices for sesame under the Telangana region were followed to raise a healthy crop.

Data recording: Data on number of capsules (NC); plant height (PH in cm); number of primary branches (PB) were collected from 5 randomly sampled plants in each replication. Seed yield (Sy in g) obtained from 4.05 sq m plot was quantified and the quantity obtained was divided by the number of plants/plot to obtain seed yield/plant (in g). 1000 seed weight (TW) was measured to obtain test weight (in grams) and oil content (OC in percentage) were estimated after harvesting using the Nuclear Magnetic Resonance (NMR) method.

Statistical analysis: The quantitative data recorded were analyzed for analysis of variance (ANOVA), where the total sum of squares is partitioned into different variance components *viz*., a (additive), b (non-additive, which is further subdivided into b_1, b_2, and b_3), c (maternal) d (reciprocal differences other than maternal). The Vr-Wr graph was plotted following Hayman (1954 a&b). An approach of Jinks and Hayman (1953) based on Mather's notation (Mather and Jinks, 1982) was used to estimate components of genetic parameters. The analysis was done using SAS software version 9.4 (SAS Institute Inc., Cary, NC, USA) as per the programme code SASHAYDIALL (Makumbi *et al*., 2018).

RESULTS AND DISCUSSION

Analysis of variance of 8x8 Diallel: The parents used in the study for diallel analysis were elite lines cultivated in different sesame regions of the country. The matrix mean of the characters studied for parents and F_1 is given in Table 1. Hayman's (1954a) analysis of variance for 8 x 8 diallel presented in table 2 indicates significant differences ($P<0.0001$) among the genotypes for all the traits studied. Significant additive and non-additive effect were observed for all the characters studied. Dash *et al.* (2020) reported a non-additive effect for yield contributing traits in half diallel analysis. The magnitude of additive effects was high for all the characters except for number of primary branches/plant (PB). The mean deviation of F_1 from the mid parental value (b_1) was non-significant indicating ambidirectional dominance and therefore F_1 was intermediate between respective parents and hence, no heterosis effect for the characters studied. Ambidirectional dominance was indicated when the crosses specify dominance in the direction of high yield, but few crosses specified dominance in the opposite direction. In contrast, Aladji (2014) reported unidirectional dominance for capsule number in diallel analysis from the cross between local cultivars from Cameroon.

Stabilized selection for the characters among the parents would consequently result in either an absence of dominance or ambidirectional. Whereas, in the directional selection of genes, a dominant allele responsible for high yield could be favoured and thus gets fixed leading to unidirectional dominance (Crusio, 2007). Asymmetric gene distribution was

observed for significant values of b_2 for number of primary branches, test weight and oil content, reflecting that some parents harbored a considerable amount of dominant genes over other parents. For example, the array of F_1 developed with HT-1 as a parent resulted in significantly higher oil content than other arrays. Residual dominance which is unique to each F_1 (b_3) was significant for the characters studied, which indicated that some effect of unexplained dominant effect existed for all the characters. Diallel crosses of elite x elite crosses show the significant maternal effects and reciprocal differences other than maternal effects which are indicated by significant estimates of c and d, respectively (Table 2). Phule til, RT-351 and Swetha til can be used as female parents for improving capsule numbers, whereas HT-1 and Phule til are for oil content improvement. The block effect was non-significant, indicating homogeneity; therefore, all other components interacting with blocks are also non-significant. The diallel analysis for elite x elite crosses indicated that the capsule number/plant, number of primary and secondary branches/plant, plant height, seed yield, test weight and oil content are under the influence of both additive and non-additive effects in addition to maternal effects. Since the dominance effects were significant, further analysis to derive variance and covariance components was carried out.

Testing validity of the hypothesis: A test for the adequacy of the additive-dominance model was carried out using the 't^2' test (Table 3). The non-significant values in all the characters indicated that Vr-Wr could be regarded as consistent over arrays, which implied that the additive-dominance model was satisfactory. Supplementing to the model, the regression coefficient with a unit slope in the absence of non-allelic interaction was observed for NC, PH, SY and OC. The slope was negative and the test value was significant, therefore the null hypothesis (b=1) was rejected for primary branches and test weight (Singh and Chaudary, 1985) reflecting the presence of non-allelic interactions for PB and TW. Kamala (1999) and Abd El-Kader *et al.* (2017) also reported non-allelic interactions for branches/plant, test weight and seed yield. Dominance being predominant, TW is under the influence of additive x dominance and dominance x dominance gene interaction (Sharmila *et al.,* 2007). Selection for these two traits should be postponed to advance generations. Therefore, the Vr-Wr graph and numerical approach (Hayman, 1954b) were carried out for seed yield/plant, capsule number/plant, plant height, and oil content.

Vr-Wr graph: The regression line for the array of parent-offspring covariance (Wr) on the array variance (Vr) with the unit slope crosses the Wr axis was above the origin (intercept =96.7) for NC indicating that this trait was under the influence of incomplete dominance. It was below the origin for PH (intercept=-27.86), SY (intercept = -0.604) and OC (intercept= -0.436), indicating PH, SY and OC being under the influence of overdominance (Fig. 1). The reports are in agreement with Aladji *et al.* (2014), Mothilal *et al.* (2005) and Suganthi (2018). The regression coefficient (Wr on Vr) for NC and OC was low at 0.216 and 0.649 respectively, while for SY and OC it was high at 0.824 and 0.846 respectively (Fig. 1). The parents E-3, Swetha til, and TKG-22 possessed alleles dominant at most loci for NC; for PH parents RT-351 and E-8; for SY parents HT-1 and RT-351; and for OC parents HT-1, TKG-22 and Phule til harbored dominant alleles as indicated by position on the graph (Fig. 1) at near the origin. Plotting standardized values of parental means and (Wr+Vr) values for 8 arrays represented dominant and recessive alleles with positive and negative effects (Fig. 2) (Dabholkar, 1999). For NC, parents Phule til, Swetha til and RT-351 possessed most of the dominant genes with positive effects, while TKG-22 and E-8 possessed dominant genes with negative effects, VRI-3 possessed recessive genes with negative effects and GT-2 and HT-1 were neutral since they were at borderline (Figure 2a). For PH, dominant genes with positive effects were harbored in RT-351, negative effects in Swetha til and E-8, recessive positive effects in TKG-22, VR-3, Phule til and HT-1, recessive negative effect in GT-1 (Fig. 2b). Parental lines HT-1, Swetha til and VRI-3 possessed dominant genes with positive effects, while RT-351 possessed negative effects for seed yield, recessive genes with positive effects were observed in TKG-22 and negative effects in E-8, GT-1 and Phule til (Fig. 2c). Dominant genes with positive effects on oil content were found in HT-1, TKG-22 and recessive genes with positive effects in E-8 and negative effects in RT-351, while parental lines Swetha til, VRI-3, GT-2 and Phule til could possess an equal proportion of dominant and recessive genes (Fig. 2d). High frequency for segregants for increased capsule number could be expected in crosses between Phule til, RT-351 and Swetha til; for plant height from crosses between, HT-1, Phule til, RT-351 and VRI-3; for seed yield from crosses between HT-1, VRI-3 and TKG-22; for oil content, crosses between HT-1, TKG-22 and E-8. Riggs and Hayter (1973) identified parents with dominant and positive effects for increased grain number in spring barley. Sesame being a short-day plant (Weiss, 1983) and sensitive to photoperiod, localized varieties are grown in the major crop area. The varieties grown in one region do not perform to their potential in another region due to photo and thermo-sensitivity. The varieties are released specifically for *kharif* and summer and are also specific to the particular region. The local adaption of the crop to season and location has gradually led to genetic variation among cultivated varieties. The diversity analysis using RAPD (Sharma et al. 2014) and microsatellites (Ramprasad *et al.*, 2017; Iqbal *et al.*, 2018) grouped the varieties into different clusters.

Table 1 The matrix of mean values of six characters studied in 8 x 8 diallel cross along with parents (Parent values are in bold)

Parents	E-8	GT-2	HT-1	Phule til	RT-531	Swetha til	TKG-22	VRI-3
				Number of capsules/plant				
E-8	**68.5**	69.3	73.3	84.0	78.5	84.0	61.0	67.5
GT-2	69.3	**81.0**	85.0	92.5	88.0	93.3	70.0	70.0
HT-1	73.3	85.0	**85.0**	114.0	90.3	77.5	74.0	92.0
Phule til	84.0	92.5	114.0	**103.0**	70.0	89.5	74.8	92.3
RT-531	78.5	88.0	90.3	70.0	**110.0**	92.5	84.5	116.5
Swetha til	84.0	93.3	77.5	89.5	92.5	**106.0**	83.5	88.3
TKG-22	61.0	70.0	74.0	74.8	84.5	83.5	**61.5**	65.3
VRI-3	67.5	70.0	92.0	92.3	116.5	88.3	65.3	**63.5**
				Primary branches/plant (No.)				
E-8	**6.0**	4.5	6.0	6.0	4.5	5.0	4.5	4.5
GT-2	4.5	**6.0**	6.0	5.0	6.0	5.0	5.0	5.0
HT-1	6.0	6.0	**5.0**	4.5	6.0	6.0	6.0	5.0
Phule til	6.0	5.0	4.5	**4.0**	4.0	5.0	5.5	6.0
RT-531	4.5	6.0	6.0	4.0	**6.0**	5.0	6.0	6.0
Swetha til	5.0	5.0	6.0	5.0	5.0	**4.0**	5.0	5.0
TKG-22	4.5	5.0	6.0	5.5	6.0	5.0	**6.0**	4.5
VRI-3	4.5	5.0	5.0	6.0	6.0	5.0	4.5	**4.0**
				Plant height (cm)				
E-8	**124.5**	124.8	138.0	138.5	140.0	143.8	122.5	133.8
GT-2	124.8	**133.0**	141.3	142.3	136.8	110.5	128.0	132.0
HT-1	138.0	141.3	**154.5**	153.0	134.5	130.8	149.5	152.5
Phule til	138.5	142.3	153.0	**152.5**	134.0	122.8	127.3	139.3
RT-531	140.0	136.8	134.5	134.0	**149.0**	135.3	143.0	126.8
Swetha til	143.8	110.5	130.8	122.8	135.3	**123.5**	137.0	126.3
TKG-22	122.5	128.0	149.5	127.3	143.0	137.0	**143.0**	120.8
VRI-3	133.8	132.0	152.5	139.3	126.8	126.3	120.8	**148.0**
				Seed yield/plant (g)				
E-8	**10.5**	9.3	12.9	9.9	11.2	12.9	11.6	13.2
GT-2	9.3	**10.2**	12.7	10.7	11.0	10.8	11.2	14.1
HT-1	12.9	12.7	**12.2**	12.0	11.2	11.7	10.4	11.2
Phule til	9.9	10.7	12.0	**11.3**	12.2	14.8	13.4	11.8
RT-531	11.2	11.0	11.2	12.2	**9.8**	12.7	10.5	12.1
Swetha til	12.9	10.8	11.7	14.8	12.7	**14.3**	12.4	13.6
TKG-22	11.6	11.2	10.4	13.4	10.5	12.4	**12.8**	14.9
VRI-3	13.2	14.1	11.2	11.8	12.1	13.6	14.9	**12.5**
				Test weight (g/1000 seeds)				
E-8	**3.3**	3.3	3.2	3.2	3.3	3.3	3.6	2.9
GT-2	3.3	**3.0**	3.6	2.9	3.1	3.3	3.2	3.0
HT-1	3.2	3.6	**3.2**	3.0	3.4	3.3	3.4	2.6
Phule til	3.2	2.9	3.0	**2.8**	3.0	3.3	3.2	2.9
RT-531	3.3	3.1	3.4	3.0	**3.1**	3.2	2.9	3.3
Swetha til	3.3	3.3	3.3	3.3	3.2	**3.2**	3.1	3.4
TKG-22	3.6	3.2	3.4	3.2	2.9	3.1	**2.8**	2.8
VRI-3	2.9	3.0	2.6	2.9	3.3	3.4	2.8	**3.3**
				Oil content (%)				
E-8	**46.2**	45.6	45.4	47.0	42.6	45.0	45.4	45.4
GT-2	45.6	**45.6**	45.8	45.6	45.4	44.2	44.1	42.5
HT-1	45.4	45.8	**47.8**	47.8	47.7	47.0	46.9	46.5
Phule til	47.0	45.6	47.8	**45.5**	46.2	47.6	45.6	45.4
RT-531	42.6	45.4	47.7	46.2	**41.8**	45.4	45.8	45.5
Swetha til	45.0	44.2	47.0	47.6	45.4	**45.3**	43.8	42.9
TKG-22	45.4	44.1	46.9	45.6	45.8	43.8	**45.6**	45.3
VRI-3	45.4	42.5	46.5	45.4	45.5	42.9	45.3	**45.3**

Table 2 Analysis of variance of a 8 x 8 diallel table for number of capsules (NC), primary branches (PB), secondary branches (SB), plant height (PH), seed yield (SY), test weight (TW) and oil content (OC) in sesame

Components	Df	NC	PB	PH	SY	TW	OC
Rep	1	122.07*	0.125	21.13NS	0.23	0.024	1.54*
Entry	63	722.78**	1.681**	400.30**	9.71**	0.210**	5.67**
total	63	722.78**	1.681**	400.30**	9.71**	0.210**	5.67**
a	7	1799.36**	1.536*	748.76**	13.85*	0.298**	17.56**
b	28	418.74**	1.719**	287.26**	5.25**	0.166**	4.73**
b_1	1	51.59	0.161	601.29	1.61	0.151	0.16
b_2	7	222.69	1.655**	118.63**	1.43	0.124**	5.97**
b_3	20	505.71*	1.819**	330.57**	6.77**	0.181**	4.53**
c	7	1925.60**	1.786*	1299.82**	26.41**	0.199**	5.75**
d	21	368.37**	1.643**	135.04**	8.71**	0.242**	2.91**
total x Block	63	32.72	0.252	18.62	1.73	0.012	0.33
a x Block	7	8.61	0.393	26.84	2.71	0.011	0.11
b x Block	28	26.93	0.219	15.16	1.57	0.010	0.36
b_1 x Block	1	5.31	0.446	27.16	1.87	0.007	0.62
b_2 x Block	7	63.66	0.131	5.61	1.49	0.014	0.28
b_3 x Block	20	15.16	0.238	17.90	1.59	0.009	0.38
c x Block	7	87.94*	0.357	47.89	2.14	0.013	0.07
d x Block	21	30.07	0.214	10.73	1.49	0.014	0.45
Residuals	63	32.72	0.252	18.62	1.73	0.012	0.33

*, ** - Significant at 0.01 and 0.05 probability levels respectively; Df - Degrees of freedom; a - additive effect; b - dominance effect; b_1 - measures of directional dominance; b_2- measure of ambidirectional dominance; b_3- residual dominance, c-average maternal effect of each parent; d- residual reciprocal variation

Estimation of components of variation: Estimates of genetic components were computed for the characters studied (Table 3). A significant estimate of additive variance indicated that the capsule number in the plant was controlled by additive effects of genes. The parents under study carried different proportions of dominant and recessive genes with uneven allelic frequencies. The correlation between mid parents and F_1 hybrids was negative, low and non-significant, thus parents contained the most dominant genes with both increasing and decreasing effects. Positive correlation indicated that recessive genes were in favor of capsule number/plant (Nassar, 1965; El-Bramawy and Shaban, 2008). Parents could not be classified as dominant or recessive since the measure of proportion of the dominant to recessive genes was not less than unity. The narrow-sense heritability was high at 47.2% (Robinson, 1966), therefore, the response to selection could be high for the trait. Crosses made between Swetha til, Phule til and RT-351 can produce an array of segregants with high NC. Selection can be made in early segregating generations and the trait can be fixed by further re-selection in every generation for characters with additive effects with moderate heritability (Tanaka and Niikura, 2006).

The dominance variation component, indicating asymmetry of positive and negative effects of genes (H_2) was significant for seed yield, indicating that the character was under the influence of additive effects of genes. The mean degree of dominance (1.34), >1 indicated over dominance supporting the graphical analysis. The proportion of dominant and recessive genes in parents was equal to unity, indicating symmetry in the distribution of increasing and decreasing alleles in the parents. A negative and non-significant correlation coefficients for seed yield (-0.197) indicated both increasing and decreasing effects of dominant genes among parents. The parents in the study are elite lines that were historically selected for their higher yield possessing alleles with increasing effects, due to the symmetry in the distribution of genes that was observed in the study. Narrow sense heritability for seed yield was medium (Robinson, 1966). Seed yield is a complex character, and non-allelic interactions have been reported with additive-dominance gene effects (Kumar and Sivasmy, 1996; Kamala, 1999; Solanki and Gupta, 2003; Swain *et al.,* 2001; Abd El-Kader *et al.,* 2017).

Table 3 Genetic component estimates for number of capsules/plant (NC), primary branches/plant (PB), plant height (PH), seed yield/plant (SY), test weight (TW) and oil content (OC) in sesame

Parameter	NC	PB	PH	SY	TW	OC
	Estimate±SE	Estimate±SE	Estimate±SE	Estimate±SE	Estimate±SE	Estimate±SE
Additive variation (D)	351.92±95.53*	0.73±0.19*	134.81±26.50*	0.56±0.35*	0.03±0.03	2.46±0.5*
Dominance variation (H1)	412.26±219.60	1.65±0.43*	280.55±60.91*	1.017±0.81	0.18±0.07*	6.07±1.15*
Dominance variation component indicating asymmetry of positive and negative effects of genes (H2)	353.23±191.05	1.22±0.37*	250.02±53.00*	1.78±0.71*	0.14±0.06*	4.08±1.0*
Overall mean dominance effect of heterozygous loci (h2)	0.000±128.13	0.000±0.25	123.39±35.54*	0.000±0.45	0.03±0.04	0.000±0.67
Relative frequency of dominant and recessive alleles in the parents (F)	194.14±225.72	1.03±0.44*	76.4±62.61	0.000±0.84	0.03±0.07	2.34±1.18*
Environmental variation (E)	32.72±31.84	0.25±0.06*	18.62±8.83*	1.73±0.12*	0.01±0.10	0.33±0.17*
Mean Degree of Dominance	1.08	1.50	1.44	1.35	2.48	1.57
Proportion of dominance	0.21	0.18	0.22	0.44	0.2	0.17
Proportion of dominant and recessive genes in parents	1.68	2.78	1.49	1.000	1.57	1.87
Correlation between Wr+Vr and Yr	-0.53	0.16	0.26	-0.2	-0.404	-0.87*
Prediction for measurement of completely dominant and recessive parents	0.28	0.03	0.07	0.04	0.16	0.76
Heritability in narrow sense	0.47	0.10	0.35	0.00	0.26	0.44
Broad-sense Heritability	0.86	0.59	0.85	0.17	0.82	0.86
Intercept of regression line (b Vr, Wr)	96.71	-	-27.86	-0.60	-	-0.43
t^2	0.02	0.37s	1.61	0.14	1.05	0.26
H0 :b=1	1.85	2.53*	0.33	0.53	4.05 *	1.48

Wr, covariance between families within the i^{th} array and their nonrecurrent parent; Vr, the variance among family (F_1+reciprocal) means within an array; Yr, mean parental value; ** significant at $p<0.05$

The significant estimates of additive and dominance variance for PH and OC indicated the additive and dominance components of genotypic variance, and also the influence by the environment in the variation observed. Variation due to dominance component indicating asymmetry of positive and negative effects of genes was significant, indicating both high and low values for PH and OC that were controlled by dominance effects of the genes at different loci. Hence, the dominant genes were preponderant exhibiting the dominance effect of genes of OC. The mean degree of dominance ratio was more than 1 indicating over dominance of alleles in a heterozygous state (Comstock and Robinson, 1952). The ratio, dominant and recessive genes in parents was >1 and dominant genes were preponderant

resulting in an asymmetrical distribution of dominant and recessive genes among the parental genotypes. Provided that the dominant genes were preponderant, the proportion of alleles with increasing and decreasing effects was also asymmetrically distributed and skewed towards increasing effects since the ratio was less than 0.25. The correlation between the degree of dominance of parents and the mean of a common parent was negative, high and significant for OC (-0.873). The prediction for measurement was not less than unity, so completely dominant or recessive parents were not identified. Over dominance was involved in PH and OC as indicated by the mean degree of dominance and the Vr-Wr graph (Fig. 1 b&d). When over dominance is involved, gene action can be best exploited by biparental mating with pedigree selection in every segregating generation in the direction of high oil content, which is likely to lead to substantial improvement in the character. Population improvement through simple recurrent selection is also a better approach for improving the traits under the influence of over dominance gene action in self-pollinated crops since the exploitation of heterosis is laborious. The selection favoring heterozygotes over both homozygotes facilitate equilibrium in allele frequencies. The heritable variation is high at 86.3%, consequently, recurrent selection for high oil content from early generation (F_2) and a subsequent generation may be carried out to fix the dominant genes. Tripathy *et al.* (2016) reported dominant gene action with an increasing effect at one locus for high oil content.

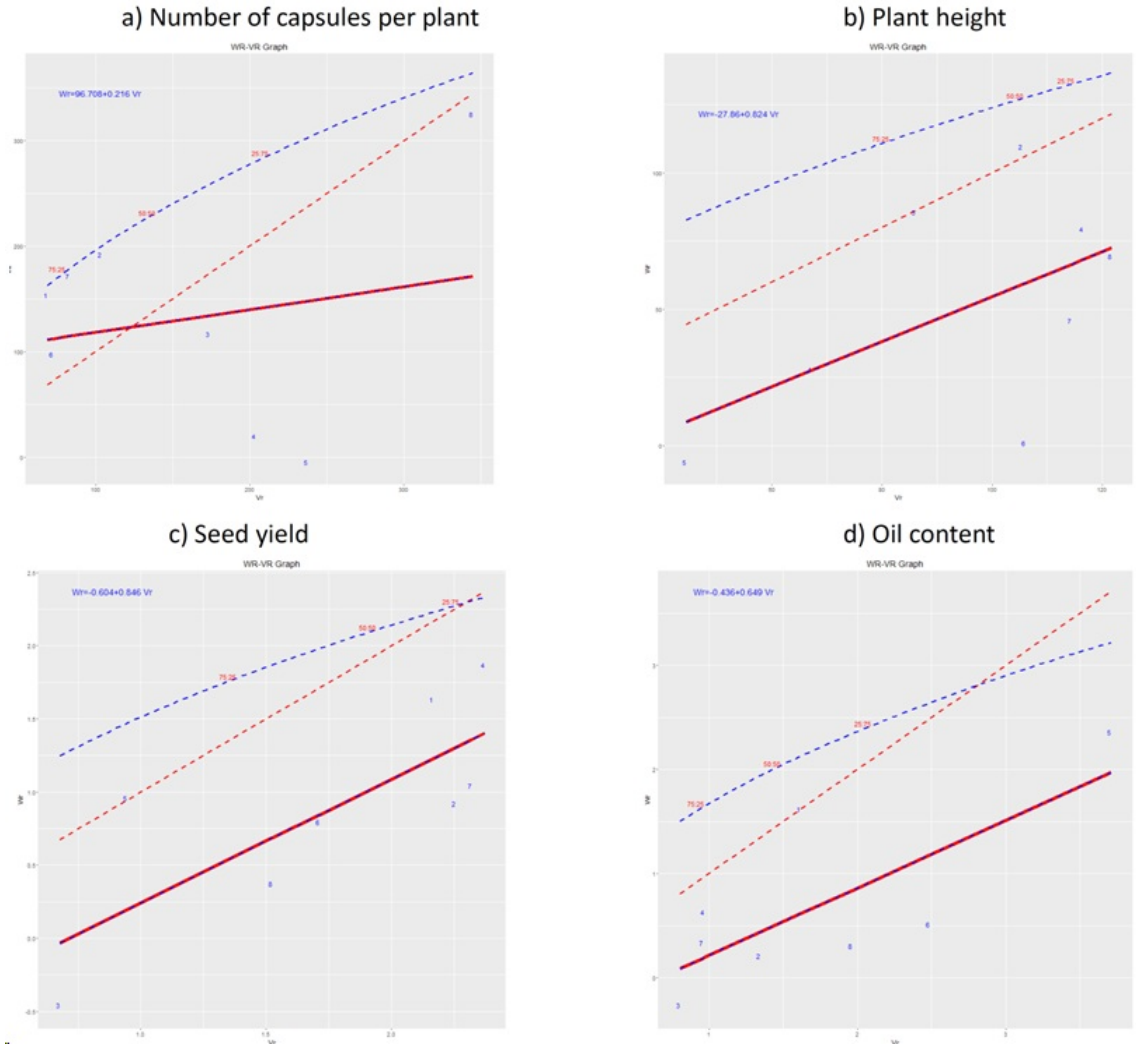

Fig. 1. (Vr,Wr) graph of (a) number of capsules/plant Wr=96.708+0.216Vr, (b) Plant height, Wr=-27.86+0.824Vr, (c) Seed yield/plant, Wr=-0.604+0.846Vr and (d) Oil content, Wr=-0.436+0.649Vr. Solid line represents the best fitting regression of Wr on Vr and dotted line represents the regression with the theoritical slope of 1 expected in the adsence of non-allelic interaction

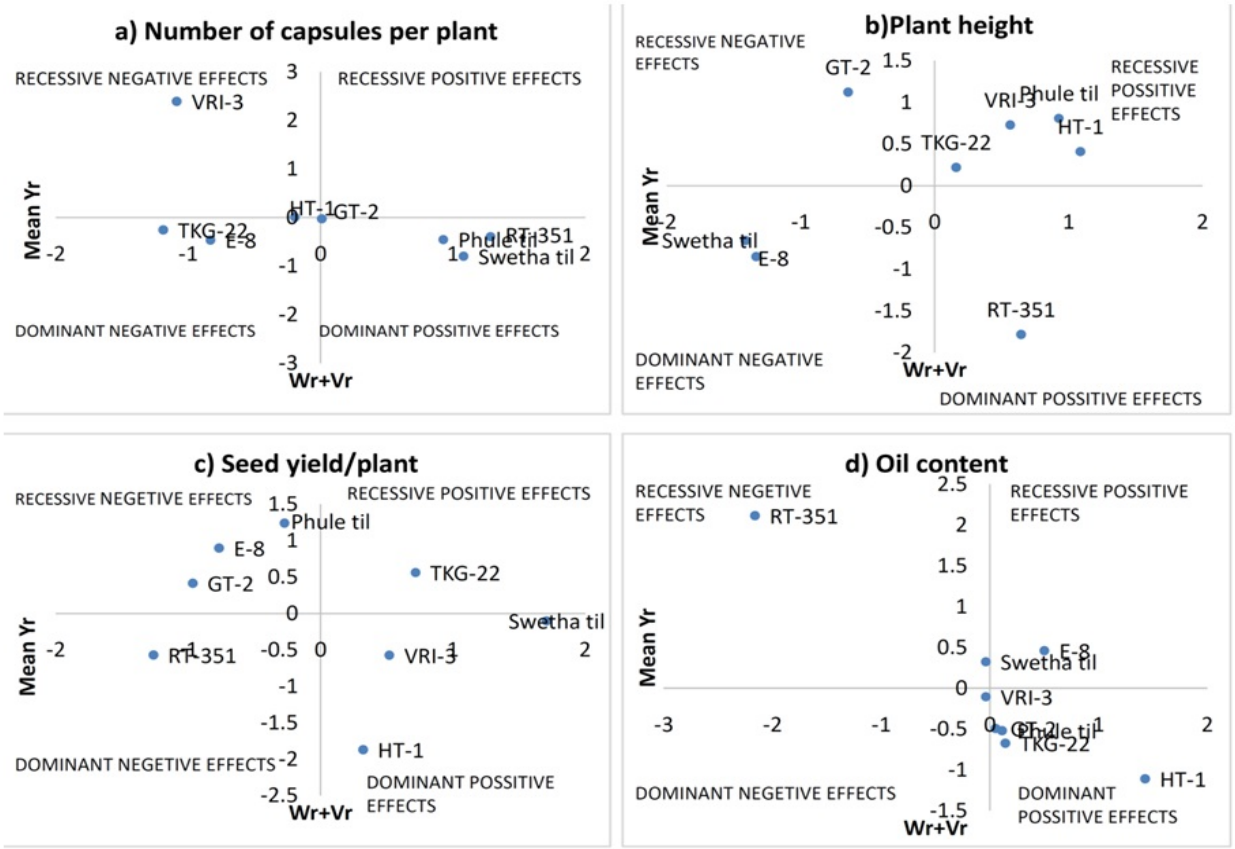

Fig. 2. Standardised deviation of mean Yr and Wr+Vr of (a) capsules number/plant, (b) plant height, (c) seed yield/plant and (d) oil content

The present study helps in understanding the gene action of sesame elite x elite combinations and deciding the selection procedure for the improvement of yield. The results showed that both additive and dominance gene actions influenced the yield and its attributing characters in sesame. The gene action for seed yield and its major attributing character, capsules number/plant was under additive effects of genes and under the absence of gene interactions, thus selection made for higher number of capsules/plant and high seed yield can be fixed. Selections for capsules number/plant can be accurate since it can be done by visual counting, consequently, seed yield will improve. Biparental mating and recurrent selection in segregating material is the best way to improve capsule number/plant and oil content by forwarding the F_1's of crosses from Phule til and RT-351. The single seed descent method is appropriate for forwarding the generation in place of the bulk method.

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Genetic analysis and diversity studies in sesame (*Sesamum indicum* L.)

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ABSTRACT

Genetic variability, path coefficient and diversity were studied using 56 genotypes of sesame [*Sesamum indicum* (L.)] in RBD with three replications at Agricultural Research Station, Mandor, Jodhpur during *kharif* 2019. The mean squares for all the characters were significant indicating the presence of wide genetic variability. The high magnitudes of PCV and GCV for seed yield and moderate values for primary branches/plant depicted the presence of high amount of variation. High heritability coupled with high genetic advance for seed yield suggesting that it could be improved through direct selection due to predominant additive variation. High heritability with moderate genetic advance as 5% of mean were observed for plant height and 1000 seed weight indicating the influence of non-additive gene action in the expression of these traits. Correlation coefficient analysis showed that seed yield had significant positive association with number of capsules/plant followed by 1000 seed weight and oil content at both genotypic and phenotypic level. Path coefficient analysis revealed that number of capsules/plant possess the highest positive direct effect (0.473) followed by 1000 seed weight (0.432) and plant height (0.313) on seed yield, which suggested that during selection more emphasis should be given to these characters to develop a desirable plant type. In the diversity study, the maximum intra-cluster distance was estimated in cluster-VIII (11.77) followed by cluster-VI (10.74), cluster-I (8.94), cluster-II (8.76), cluster-III (7.11) and cluster-IV (5.12) indicating wide genetic variability within the genotypes of these six clusters. The maximum inter-cluster distance was estimated between cluster-III and VIII (69.10) followed by cluster-III and IV (62.33) and cluster-III and VI (62.24), suggesting wide diversity between genotypes of these clusters.

Keywords: Correlation coefficient, Genetic variability, Genetic diversity, Path coefficient, Sesame

Sesame (*Sesamum indicum* L.) is one of the most commonly referred to as the "Queen of Oilseeds" crops and its seeds contain 45-60% oil and 18-25% protein. It is one of the most important edible oilseed crops, grown in warm temperate to tropical areas from about 40° N latitude to 40° S latitude. Sesame is adaptable to a range of soil types, although it performs well in well-drained fertile soil of medium texture (typically sandy loam soil) at neutral pH depending upon light intensity and day length in various regions with different photoperiod requirements. India is the largest grower, producer, consumer and exporter of sesame in the World. Apart from India, China, North Africa, Syria, Egypt, Iran and Turkey also cultivate this crop. In India, sesame growing states are Uttar Pradesh, Gujarat, Rajasthan, Andhra Pradesh, Tamil Nadu, Madhya Pradesh, Maharashtra, Karnataka, West Bengal, Odisha and Assam. In Rajasthan, it is being grown in 2.79 lakh hectare area with a production of 0.92 lakh tons and productivity of 327 kg/ha (Anonymous 2020). Like flax, sesame is a valuable oil crop with immense therapeutic uses and its oil has the highest antioxidant content and contains several fatty acids like oleic acid (43%), linoleic acid (35%), palmitic acid (11%) and out of which 35% monounsaturated fatty acids (MUFA) and 44% polyunsaturated fatty acids (PUFA) in general (Hansen, 2011). Sesame oil has significant resistance against oxidation as it contains endogenous antioxidants including tocopherols and lignans (Elleuch *et al.,* 2007; Lee *et al.,* 2008).

Sesame is generally self-pollinated crop but cross-pollination may occur and range from 5 to over 50% (Pathirana, 1994). This is cultivated in *kharif* and summer season both. Seed yield is a complex quantitative character and it depends on a number of component traits, hence selection of seed yield becomes difficult unless the association among the yield contributing characters is known. It is important to examine the contribution of each of the traits in order to give more attention to those having the greatest influence on seed yield. Therefore, determination of correlation coefficient between yield and different yield contributing traits helps to identify the relative contribution of these component characters towards seed yield. The path co-efficient analysis provides the direct and indirect effects of each component trait upon seed yield. Path analysis specifies the cause and effect relationship and measures the relative importance of each variable (Wright, 1959). Correlation and path coefficient analysis together can act as an important tool to quantify the direct and indirect influence of one character on another (Dewey and Lu, 1959). Therefore, the present study was conducted for the

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estimation of correlation among yield and yield contributing traits and path coefficient analysis for selection of desirable genotypes suitable for different breeding objectives. The phenotypic as well as genotypic coefficient of variation along with heritability provides the information regarding presence of variability and amount of characters transferred to the next generation. Genetic diversity studies are helpful tool in identification of traits for crop improvement and association between them helps a breeder to improve seed yield through directional breeding approaches. Keeping the above facts in view, the present study was conducted for character association and genetic diversity studies in sesame with the germplasm available at ARS, Mandor, Jodhpur, Rajasthan.

MATERIALS AND METHODS

The materials for present investigation comprised of 56 genotypes of sesame procured and developed at Agricultural Research Station, Mandor, Jodhpur and the same were grown in Randomized Block Design with three replications during *kharif* 2019. Each genotype was sown in two rows of 4 m length with row to row spacing of 30 cm in each replication. Recommended agronomic and cultural practices were applied to the experiment throughout the growing season. From each plot a sample of five competitive plants were randomly selected and data were recorded for the characters *viz*., plant height (cm), No. of primary branches/plant and No. of capsules/plant, and for days to 50% flowering, maturity, 1000 seed weight (g), oil content (%), seed yield/plot (g) was recorded for whole plot in each replication and seed yield was converted into seed yield kg/ha for each of the genotypes. The data were subjected to analysis of variance as suggested by Panse and Sukhatme, 1978. Genotypic and phenotypic coefficients of variation were calculated using the formula given by Singh and Chaudhary, 1985, broad sense heritability and genetic advance (GA) as percent of mean at 5% selection intensity were estimated as per Johnson *et al.* (1955) and path coefficient analysis was carried out by following the method given by Dewey and Lu (1959). Clustering was performed by procedure of Ward's minimum variance method (Ward, 1963).

RESULTS AND DISCUSSION

Crop improvement programme depends upon the availability of the variability at phenotypic as well as genotypic level. Seed yield, being a complex character, is influenced by several quantitative traits and some of these are highly associated. Understanding the relationship among these traits and their association with seed yield is very much essential to establish selection criteria to develop a high yielding variety. Therefore, the present study was aimed at estimating variability, correlation coefficient, path coefficient and diversity among the available genotypes. The analysis of variance revealed highly significant mean squares indicating sufficient variability present in study material (data not presented). The data given Table 1 and 2 showed that the range of seed yield was from 267 kg/ha (RMT 563) to 994 kg/ha (RMT 573) with a general mean of 599 kg/ha. The variety RT 54 was found to be the earliest in days to 50% flowering (38 days) and maturity (82 days). Plant height ranged from 98.8 cm (RMT 562) to 175.1 cm (RMT 546). Sesame variety GT 10 recorded maximum number (3.8) of primary branches/plant and RMT 563 and RMT 564 the least (2.0). The number of capsules/plant was maximum in RMT 505 (59.4) and lowest in RMT 583 (39.4). Oil content varied from 34.4% (RT 54) to 46.8% (RMT 546) and 1000 seed weight ranged from 2.45 g (RMT 563) to 3.66 g (RMT 541). In the study, phenotypic coefficients of variability values were slightly higher than that of genotypic coefficient of variability, indicating the influence of environment on the traits. But, smaller differences between PCV and GCV values were observed for all the characters, which indicated less influence of the environment and thus pointed to the reliability of selection based on these traits. The high magnitudes of phenotypic as well as genotypic coefficient of variation was found only for seed yield which indicated that a greater amount of genetic variability present which provided greater scope for selection for improvement in seed yield while for other characters it was moderate to low. The heritability values estimated were at moderate levels for plant height (65.2%), seed yield (68.8%), days to maturity (75.2%) and 1000 seed weight (75.4%) and thus showed considerable effect of environment and similar results were also reported by Abhijatha *et al.* (2017), Patil and Lokesha (2018), Patil *et al.* (2018), Singh *et al.* (2018) and Rhaman *et al.* (2019). The moderate heritability combined with moderate genetic advance as 5% of mean for seed yield (43.9), number of primary branches/plant (16.6), number of capsules/plant (14.8), plant height (13.6%) and 1000 seed weight (13.2) revealed that these characters were controlled by additive genes and also additive x dominance gene action and there was role of environment to some extent but selection for these traits might be effective for improvement of the crop (Table 1). These results were in agreement with those reported by earlier workers (Teklu *et al.,* 2017; Patil *et al.,* 2018; Ismail *et al.,* 2018; Singh *et al.,* 2018).

It is evident from the results that the genotypic correlation coefficient were higher than the corresponding phenotypic correlation coefficient (Table 3), which indicated a strong inherent association between the characters studied and suppressive effect of the environment modifying the phenotypic expression of these traits by reducing phenotypic correlation values. Positive significant correlations with seed yield were showed by number of capsules/plant (G=0.562, P=0.403), 1000 seed weight (G=0.539, P=0.489), oil content (G=0.430, P=0.394) and plant height (G=0.428, P=0.351). Similar results were also observed by Daniya *et al.* (2013),

Aristya *et al.* (2017), Lalpantluangi and Shah (2018) and Rhaman *et al.* (2019). However, maximum positive significant correlation value was estimated for days to maturity with days to 50% flowering (G=0.831, P=0.626). Oil content had positive association with 1000 seed height (G=0.509, P=0.361), plant height (G=0.476, P=0.410) and with number of capsules/plant (G=0.199, P=0.177). Similarly, number of capsules/plant had significant positive correlation with plant height (G=0.272, P=0.249) and number of primary branches/plant (G=0.239, P=0.238). Seed yield showed negative significant correlation with days to 50% flowering (G=-0.248, P=-0.214) and days to maturity (G=-0.249, P=-0.199). Characters, days to 50% flowering and days to maturity exhibited significant negative correlation with number of capsules/plant and 1000 seed weight. Similar results were also observed by Abdou *et al.* (2015), Aristya *et al.* (2017) and Patil and Lokesha (2018). Path analysis: Correlation analysis may not provide a complete understanding of the character that depends on the other characters, therefore, the direct and indirect influence of each of the component characters on seed yield provides a clear picture of the inter-relationship between seed yield/plant and other yield attributes. Path coefficient analysis allows partitioning of correlation coefficients into direct and indirect effects via unidirectional and alternate pathways. Seed yield was considered as a resultant (dependent) variable and plant height, number of primary branches/plant, number of capsules/plant, oil content, 1000 seed weight (g), days to 50% flowering and maturity were causal (independent) variables. The results of path coefficient analysis revealed that genotypic correlations were higher over their corresponding phenotypic values (Table 4). Number of capsules/plant showed the highest positive direct effect (0.473) on seed yield followed by 1000 seed weight (0.432), and plant height (0.313) while days to maturity had the highest negative direct effect (-0.355) on the seed yield which suggested that during selection more emphasis should be given to number of capsules/plant, 1000 seed weight and plant height to develop desirable plant type having high seed yield. These results showed similarity with earlier findings of Kumhar *et al.* (2013), Abate *et al.* (2015), Saxena and Bisen (2016) and Abhijatha *et al.* (2017). Days to 50% flowering showed the high positive indirect effect on seed yield through days to maturity (-0.296) and 1000 seed weight, moderate indirect effect was through days to 50% flowering (-0.141) while rest of the characters showed low to negligible indirect effect. These similar results were also showed by earlier findings of Sumathi *et al.* (2007), Ibrahim and Khidir (2012) and Abhijatha *et al.* (2017).

Table 1 Estimates of genetic parameters of seed yield and its component traits in sesame

Character	Mean	Range		Coefficient of variation (%)		Heritability (%)	Genetic advance as 5% of mean
		Min.	Max.	GCV	PCV		
Seed yield (kg/ha)	599	267	994	25.7	30.9	68.8	43.9
Days to 50% flowering	45	38	49	3.9	4.5	77.1	7.1
Days to maturity	86	82	90	1.9	2.2	75.2	3.4
Plant height (cm)	145.6	98.8	175.1	8.2	10.1	65.2	13.6
No. of Primary branches/ plant	2.6	2.0	3.8	11.9	17.6	45.9	16.6
No. of capsules/ plant	49.4	39.4	59.4	9.8	13.4	53.5	14.8
1000 seed weight (g)	3.13	2.45	3.66	7.4	8.5	75.4	13.2
Oil content (%)	42.1	34.4	46.8	5.1	6.9	54.0	7.7

Genetic diversity: A hierarchical cluster analysis of Ward's minimum variance method produced a dendrogram showing successive fusion of individuals which clearly partitioned the genotypes into eight clusters (Fig. 1). The cluster-VII contained maximum (12) genotypes, while cluster-I and IV had 11, cluster-II and V had 8 each, cluster-VIII included 3, cluster-VI had 2 and cluster-III was mono-genotypic (Table 5). The genotypes within each cluster were closer to each other than the genotypes grouped into different clusters.

Average intra and inter-cluster Euclidean2 distances are presented in Table 6. The maximum intra-cluster distance was observed in cluster-VIII (11.77) followed by cluster-VI (10.74), cluster-I (8.94), cluster-II (8.76), cluster-III (7.11) and cluster-IV (5.12) indicating wide genetic variability within the genotypes of these six clusters. The highest inter-cluster distance was observed between cluster-III and VIII (69.10) followed by cluster-III and IV (62.33) and cluster-III and VI (62.24), suggesting wide diversity between genotypes of these clusters. Therefore, genotype belonging to these clusters may be used in hybridization programme for improvement as they might yield better segregants. The least inter-cluster distance was observed between cluster-IV and V (7.47) indicating close relationship between the genotypes of these two clusters.

Table 2 Mean performance of genotypes for seed yield and ancillary traits in sesame

Genotype	Seed yield (kg/ha)	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of capsules/plant	1000 seed weight (g)	Oil content (%)
RMT 441	810	45	86	145.3	2.5	58	3.46	43.3
RMT 504	576	45	87	140.3	2.7	50	3.45	44.0
RMT 505	753	46	88	131.3	2.1	59	3.56	43.5
RMT 506	633	46	86	159.7	2.3	59	3.32	44.3
RMT 510	408	47	86	142.7	2.5	46	3.13	42.7
RMT 523	654	48	90	166.3	2.8	51	3.20	43.6
RMT 525	514	45	86	144.3	2.9	48	3.12	43.3
RMT 531	558	47	88	151.6	2.4	44	3.03	44.0
RMT 533	573	45	88	157.0	3.3	46	3.14	44.1
RMT 540	658	46	86	153.7	2.9	48	3.25	43.7
RMT 541	729	44	84	126.7	2.9	42	3.66	43.5
RMT 544	815	47	89	154.5	2.8	54	3.13	44.7
RMT 546	910	47	85	175.1	3.3	56	3.29	46.8
RMT 548	593	47	87	138.8	2.9	47	3.04	43.9
RMT 552	650	48	89	157.0	3.3	50	3.22	40.9
RMT 555	802	44	85	148.0	2.9	57	3.35	43.3
RMT 496	350	46	85	149.9	2.7	48	2.97	44.5
RMT 503	775	45	86	148.3	2.7	50	3.28	43.2
RMT 512	600	40	84	143.5	3.0	52	3.37	43.0
RMT 515	794	46	86	153.0	2.9	59	3.22	43.8
RMT 537	569	47	89	132.3	2.8	51	3.44	39.2
RMT 539	600	47	86	134.1	2.1	47	2.88	42.0
RMT 542	839	46	85	153.7	2.7	57	3.18	42.9
RMT 550	672	43	84	138.7	2.7	51	3.13	41.9
RMT 551	500	45	86	140.1	3.1	48	3.02	39.4
RMT 562	311	46	87	98.8	2.1	42	2.84	39.0
RMT 563	267	49	88	126.3	2.0	46	2.45	37.8
RMT 564	844	43	84	143.1	2.0	50	3.19	43.3
RMT 565	606	48	87	137.1	2.7	49	3.01	41.6
RMT 566	694	45	85	139.2	2.6	49	2.91	41.7
RMT 567	672	46	86	142.8	2.7	52	2.67	37.9
RMT 568	400	48	89	158.8	2.5	52	2.78	41.2
RMT 569	411	45	86	151.3	2.9	59	2.96	40.6
RMT 570	617	46	86	157.3	2.7	52	3.14	43.2
RMT 571	322	46	88	152.2	2.7	48	3.17	40.9
RMT 572	450	48	90	149.7	2.6	47	2.91	37.1
RMT 573	994	43	85	164.2	2.3	59	3.32	44.6
RMT 574	583	46	87	147.7	2.1	46	3.15	42.4
RMT 575	922	44	85	158.5	2.4	57	3.27	42.3
RMT 576	483	45	86	151.4	2.5	41	2.98	38.2
RMT 577	656	46	88	151.5	2.7	44	2.99	40.0
RMT 578	686	46	86	155.5	2.9	52	3.16	40.2
RMT 579	614	46	85	149.4	2.5	42	2.98	41.5
RMT 580	506	45	86	154.6	2.3	44	2.82	46.5
RMT 581	606	44	84	146.9	2.6	47	2.89	40.5
RMT 582	478	46	87	149.3	2.7	44	3.18	41.2
RMT 583	450	45	84	130.9	2.3	39	3.30	42.5
RMT 584	278	49	86	147.6	2.5	44	2.90	42.9
RMT 585	644	45	86	160.3	2.5	45	3.56	42.1
RMT 586	506	43	84	138.5	2.3	46	3.46	45.2
RMT 587	517	45	86	144.2	2.5	41	3.11	38.7
RMT 588	683	44	85	129.9	2.3	40	3.56	40.8
RT 351(C)	617	46	89	139.9	2.2	54	3.20	46.0
RT 54 (C)	396	38	82	109.0	3.5	58	2.84	34.4
Pragati(ZC)	495	45	89	140.5	2.9	47	3.16	42.9
GT 10(NC)	481	48	90	141.0	3.8	53	2.74	41.9
Mean	599	46	86	145.6	2.6	49.4	3.13	42.1
SEm (±)	59.82	0.566	0.541	5.022	0.198	2.613	0.076	1.138
CD(P=0.05)	167.65	1.59	1.52	14.07	0.55	7.32	0.21	3.19
CV (%)	17.31	2.15	1.08	5.97	12.93	9.16	4.2	4.68

Table 3 Correlation coefficients between seed yield and its component characters in sesame

Characters	Level	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of capsules/ plant	1000 seed weight (g)	Oil content (%)	Seed yield kg/ ha
Days to 50% flowering	G	1.000	0.831**	0.285**	-0.113	-0.205**	-0.326**	0.099	-0.248**
	P	1.000	0.626**	0.197*	-0.047	-0.172*	-0.279**	0.013	-0.214**
Days to maturity	G		1.000	0.211**	0.083	-0.032	-0.217**	0.004	-0.249**
	P		1.000	0.132	0.037	-0.019	-0.169*	-0.016	-0.199**
Plant height (cm)	G			1.000	0.203**	0.272**	0.136	0.476**	0.428**
	P			1.000	0.094	0.249**	0.140	0.410**	0.351**
No. of primary branches/ plant	G				1.000	0.239**	-0.056	-0.118	0.002
	P				1.000	0.238**	-0.027	-0.098	0.003
No. of capsules/ plant	G					1.000	0.160*	0.199**	0.562**
	P					1.000	0.136	0.177*	0.403**
1000 seed weight (g)	G						1.000	0.509**	0.539**
	P						1.000	0.361**	0.489**
Oil content (%)	G							1.000	0.430**
	P							1.000	0.394**
Seed yield kg/ha	G								1.000
	P								1.000

Residual effect Genotypic = 0.594 and Phenotypic = 0.748, *and ** significant at 5% and 1% level, respectively.

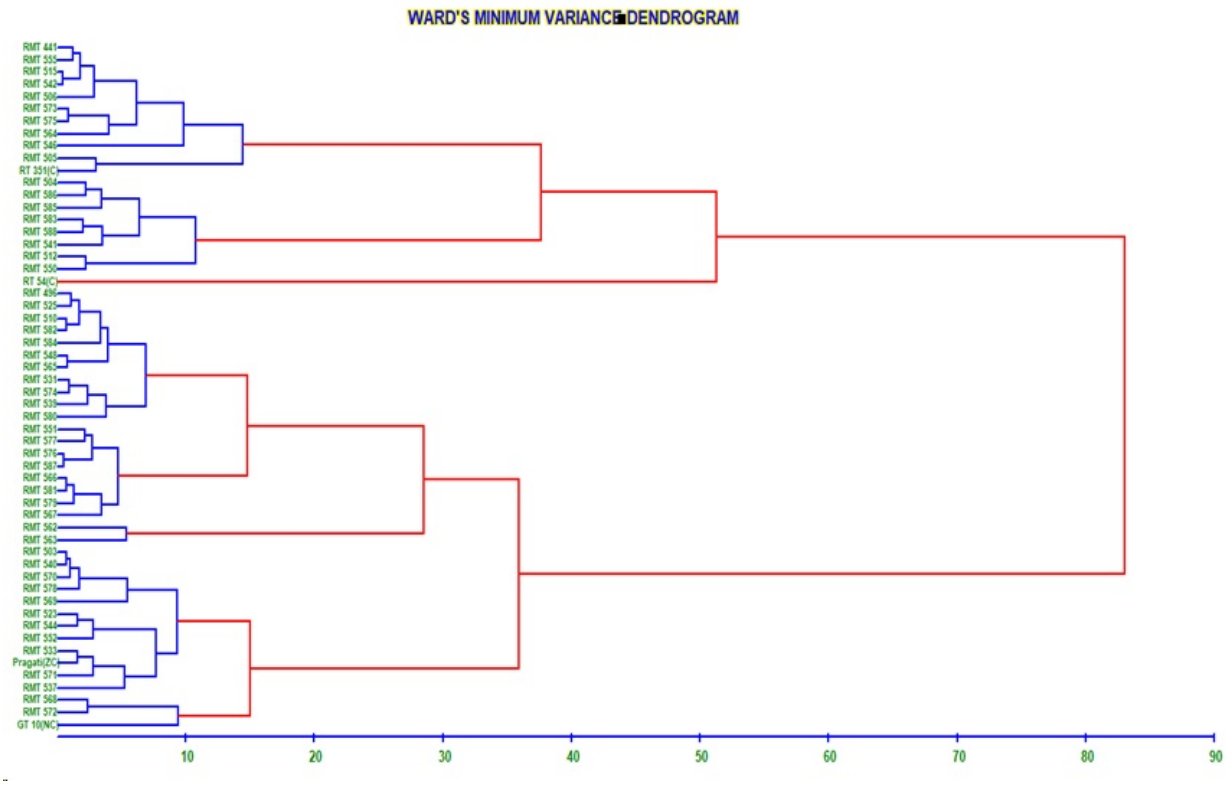

Fig. 1. Dendrogram showing clustering pattern of sesame genotypes

Table 4 Path coefficient analysis showing direct (bold) and indirect effects of different characters on seed yield in sesame

Characters	Level	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of capsules/ plant	1000 seed weight (g)	Oil content (%)	Correlation with Seed yield kg/ha
Days to 50% flowering	G	**0.081**	-0.295	0.089	0.121	-0.097	-0.141	-0.006	-0.248**
	P	**-0.024**	-0.090	0.041	0.003	-0.050	-0.096	0.002	-0.214**
Days to maturity	G	0.157	**-0.355**	0.066	-0.009	-0.015	-0.093	-0.003	-0.249**
	P	-0.015	**-0.144**	0.028	-0.002	-0.005	-0.058	-0.002	-0.199**
Plant height (cm)	G	0.054	-0.075	**0.313**	-0.022	0.129	0.059	-0.030	0.428**
	P	-0.005	-0.019	**0.209**	-0.006	0.072	0.048	0.051	0.351**
No. of primary branches/ plant	G	-0.022	-0.029	0.064	**-0.107**	0.113	-0.024	0.007	0.002
	P	0.001	-0.005	0.019	**-0.060**	0.069	-0.009	-0.012	0.003
No. of capsules/ plant	G	-0.039	0.012	0.085	-0.025	**0.473**	0.069	-0.013	0.562**
	P	0.004	0.003	0.052	-0.014	**0.289**	0.047	0.022	0.403**
1000 seed weight (g)	G	-0.062	0.077	0.042	0.006	0.076	**0.432**	-0.032	0.539**
	P	0.007	0.024	0.029	0.002	0.039	**0.343**	0.045	0.489**
Oil content (%)	G	0.019	-0.002	0.149	0.013	0.094	0.220	**-0.063**	0.430**
	P	-0.001	0.002	0.086	0.006	0.051	0.125	**0.125**	0.394**

Residual effect Genotypic = 0.594 and Phenotypic = 0.748, *and ** significant at 5% and 1% level, respectively.

Table 5 Clustering pattern of 56 sesame genotypes

Cluster	No. of genotypes	Varieties/ genotypes
Cluster-I	11	RMT 441, RMT 555, RMT 515, RMT 542, RMT 506, RMT 573, RMT 575, RMT 564, RMT 546, RMT 505, RT 351
Cluster-II	8	RMT 504, RMT 586, RMT 585, RMT 583, RMT 588, RMT 541, RMT 512, RMT 550
Cluster-III	1	RT 54
Cluster-IV	11	RMT 496, RMT 525, RMT 510, RMT 582, RMT 584, RMT 548, RMT 565, RMT 531, RMT 574, RMT 539, RMT 580
Cluster-V	8	RMT 551, RMT 577, RMT 576, RMT 587, RMT 566, RMT 581, RMT 579, RMT 567
Cluster-VI	2	RMT 562, RMT 563
Cluster-VII	12	RMT 503, RMT 540, RMT 570, RMT 578, RMT 569, RMT 523, RMT 544, RMT 552, RMT 533, Pragati, RMT 571, RMT 537
Cluster-VIII	3	RMT 568, RMT 572, GT 10

The cluster means generally indicate the characteristic features of the clusters and help in identifying potential clusters for different characters based on the mean values. The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 7). The maximum/desirable cluster means were revealed by cluster-III for number of primary branches/plant, number of capsules/plant, days to flowering and days to maturity while cluster-I for seed yield and oil content, cluster-II for 1000 seed weight and cluster-VII for plant height and the remaining clusters were having lower mean values for one or the other characters. These results showed that genotypes of different clusters were superior for different characters and genotypes having these characters would offer a good scope of improvement of sesame through selection. Amongst the characters 1000 seed weight contributed maximum towards genetic divergence (21.75%) followed by days to maturity (20.52%), seed yield (17.47%) and days to 50% flowering (15.39%) while the remaining characters contributed low to genetic divergence (Table 7). These results are in conformity with those reported by Anuradha and Reddy (2005), Kumhar *et al.* (2013),

Narayanan and Murugan (2013), Tripathi *et al.* (2014) and Patil *et al.* (2018).

Since varieties with narrow genetic base are more vulnerable to diseases and adverse climatic conditions, therefore, the availability of the genetically diverse genotypes for hybridization programme and selection becomes more important. Since quantitative characters viz, seed yield, 1000 seed weight and days to maturity contributed maximum towards the divergence, direct selection of these traits helps in crop improvement. Conclusively, development of varieties with high yield potential is the ultimate goal of a plant breeder in any crop improvement programme and seed yield with earliness, bold seed size and higher number of capsules/plant are the most important traits in sesame. From this point of view, the genotypes of cluster III and cluster-I were high yielding, having higher number of capsules and early maturing type (RMT 441, RMT 515, RMT 506, RMT 573, RMT 575, RMT 546, RMT 505, RT 351) whereas, genotypes of cluster-IV and II were having the characters like tallness and bold seed size (RMT 503, RMT 540, RMT 496, RMT 525, RMT 510). Therefore, selected genotypes of these clusters may be crossed among each other for recombination breeding and further improvement of sesame.

Table 6 Intra (diagonal) and inter Euclidean²cluster distance among eight clusters in sesame

Cluster	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII	Cluster-VIII
I	**8.94**	16.02	66.24	16.46	17.84	48.351	13.83	29.91
II		**8.76**	51.32	13.09	13.01	36.85	15.65	32.26
III			**0.00**	62.33	45.92	62.24	61.87	69.10
IV				**5.12**	7.47	21.53	9.34	14.86
V					**4.46**	21.22	10.38	15.32
VI						**10.74**	33.51	25.52
VII							**7.28**	13.53
VIII								**11.77**

Table 7 Cluster means for eight clusters and percent contribution of different characters in sesame

Cluster	Seed yield (kg/ha)	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of capsules/plant	1000 seed weight (g)	Oil content (%)
Cluster-I	811	45.0	85.8	151.9	2.5	56.9	3.31	44.0
Cluster-II	608	43.7	84.7	138.5	2.6	45.7	3.44	42.9
Cluster-III	396	38.3	82.0	109.0	3.5	57.9	2.84	34.4
Cluster-IV	498	46.6	86.4	145.2	2.5	46.0	3.02	43.2
Cluster-V	593	45.3	85.8	145.7	2.6	45.5	2.94	39.7
Cluster-VI	289	47.5	87.5	112.6	2.1	44.0	2.64	38.4
Cluster-VII	602	46.2	87.7	152.2	2.9	50.6	3.19	42.3
Cluster-VIII	444	48.1	89.4	149.8	3.0	50.5	2.81	40.1
Mean	599	45.6	86.4	145.6	2.6	49.4	3.13	42.1
Contribution to Diversity (%)	17.47	15.39	20.52	6.75	3.90	6.95	21.75	7.27

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Combining ability analysis of newly developed male lines of castor (*Ricinus communis* L.) in Rajasthan

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ABSTRACT

Genetic parameters of 50 castor hybrids developed using 10 newly developed male inbred lines and 5 stable pistillate lines were estimated in a line x tester design. Analysis of combining ability depicted significant mean sum of squares for both general combining ability (GCA) and specific combining ability (SCA) for all the characters which indicated the presence of both additive and non-additive gene actions. The high amount of σ^2 SCA and ratio of GCA to SCA variances near to zero indicated that the dominance gene effect was predominant in newly developed lines for all the characters under study. The highest positive gca effect was exhibited by MCP-1-1, for seed yield and number of capsules on primary raceme, effective length of primary raceme and height up to primary raceme. SKP-84 was also good general combiner for traits such as 100-seed weight, number of capsule on primary raceme, nodes to primary raceme and height up to primary raceme. Among the male parents, MP-11-17 was found the best general combiner for cumulative seed yield, raceme length and number of capsule. Cross M-574 x MP-17-17 was identified as the best cross for cumulative seed yield followed by MCP-3 x MP-7-17 and SKP-84 x MP-11-17. These combinations of crosses would be useful in breeding programme for improvement in cumulative seed yield of castor.

Keywords: Castor, Combining ability, Gene action, Line x tester

Castor (*Ricinus communis* L., 2n = 2x = 20, Family: Euphorbiaceae) is an industrially important non-edible oilseed crop widely cultivated in the arid and semi-arid regions of the world. The genus *Ricinus* is monotypic and R. communis is the only species with the most polymorphic forms known (Weiss, 2000). It is cultivated in about 30 countries on commercial scale, while India, Brazil, China, Russia, Thailand and Philippines are the principal castor growing countries. Being the largest producer, India is also the largest exporter of castor seed oil. Total area and production of castor crop in India for the year 2019-20 was 9.38 lakh hectares and 17.37 lakh tonnes which was 7.07% and 42.96 % higher respectively than the previous year. Average yield for the year 2019-20 was 1852 kg/ha as against 1387 kg/ha during the year 2018-19 (Anonymous, 2019). In Rajasthan, a total area sown during 2019-20 was 2.04 lakh hectares with total production of 3.26 lakh tonnes with 1598 kg/ha productivity.

Castor is usually cultivated as a hybrid in India, as hybrids give significantly higher yields than pure lines or open pollinated varieties (Gopani *et al.,* 1968; Punewar *et al.,* 2017). Even though, many mating designs are being used by various research workers, line x tester mating design is widely used in cross pollinated crops to estimate general and specific combining ability effects and it also provides information on fixable genetic variance. At the same time, it provides the nature and magnitude of components of genetic variance on which success of plant breeding programme rests. Line x tester analysis technique becomes more manageable with large number of parents besides being more comprehensive for understanding the genetic basis at population level (Kempthorne, 1957). Keeping these in view, combining ability analysis in castor was carried out to estimate gca and sca effects of newly developed male lines.

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MATERIALS AND METHODS

The material for present investigation was generated by crossing 10 newly developed pollen parents (testers) *viz*., MP-1-17, MP-4-17, MP-7-17, MP-9-17, MP-10-17, MP-11-17, MP-14-17, MP-17-17, MP-18-17 and MP-20-17 (Pedigree in table 1) with 5 already stabilised pistillate parents (lines) *viz.,* MCP 1-1, VP-1, MCP-3, M-574 and SKP-84 during *kharif*, 2017-18. A total of 50 F_1 were grown during *kharif*, 2018-19 at Agriculture Research Station, Mandor (Agriculture University, Jodhpur) in three replications in a randomized block design. Each genotype was grown at 120 x 90 cm^2 spacing, in two rows of 9 m length. Recommended agronomic practices with drip irrigation were followed for growing a healthy crop. Observations were recorded on cumulative seed yield (q/ha) at 120, 150, 180 and 210 DAS, days to 50% flowering of primary, nodes up to primary raceme, height up to primary raceme (cm), effective length of primary raceme (cm), number of capsules on primary raceme, number of effective spikes, 100 seed weight (g), volume weight ratio (g/100ml) and oil content (%). The data recorded on the material as per

line x tester model of Kempthorne (1957) were subjected to analysis of variance as per the line x tester model given by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

The results of the analysis of variance for the newly developed castor hybrids are presented in Table 1. All the hybrids, testers and lines depicted significant difference with respect to the traits under consideration indicating significant variation among lines, testers and hybrids, therefore, it is possible to compute the general and specific combining abilities. Likewise, interactions between lines and testers also significantly varied for all the characters giving sufficient evidence for availability of variability and diversity among new male lines developed at ARS, Mandor.

Table 1 Pedigree of various male inbred lines

Name of inbred line	Pedigree
MP-1-17	SVT-10-05 x [(48-1 x RG-10) x DCS-9]
MP-4-17	[(48-1 x RG-10) x DCS-9] x MCI-3
MP-7-17	RG-125 x MCI-4
MP-9-17	JI-368 x MCI-12
MP-10-17	DCS-107 x MP-1-05
MP-11-17	MCI-3 x MP-36-05
MP-14-17	48-1 x MP-1-05
MP-17-17	[(48-1 x RG-10) x DCS-9] x MCI-3
MP-18-17	[(48-1 x RG-10) x DCS-9] x MCI-3
MP-20-17	[(48-1 x RG-10) x DCS-9] x MCI-3

Table 2 Analysis of variances for various characters in castor

Source	DF	Cumulative seed yield at (q/ha)				Days to 50% flowering	Nodes up to primary raceme	Plant height up to primary raceme (cm)	Effective length of primary raceme (cm)	Number of capsules on primary raceme	Number of effective spikes/ plant	100-seed weight (g)	Volume weight ratio (g/100ml)	Oil (%)
		120 DAS	150 DAS	180 DAS	210 DAS									
Replication	2	0.18	58.23	50.83	62.41	5.95	0.55	41.61	34.16	804.08	5.45	2.24	19.83	0.27
Treatment	49	36**	243.39**	261.67**	370.58**	53.39**	7.56**	579.15**	332.47**	4171.01**	57.79**	24.48**	35.04**	6.31**
Lines	4	61.81**	471.73**	761.03**	1151.22**	169.38**	39.78**	2112.19**	771.93**	13441.6**	71.29**	92.27**	55.83**	2.37*
Tester	9	99.28**	761.02**	571.22**	620.53**	102.15**	13.32**	1049.62**	632.13**	10294.32**	55.37**	57.3**	65.97**	12.94**
L x T	36	17.31**	88.61**	128.8**	221.35**	28.32**	2.54**	291.20**	208.73**	1610.12**	56.89**	8.75**	24.99**	5.09**
Error	98	1.73	2.13	12.37	17.94	3.71	0.85	31.24	20.17	104.78	10.67	1.92	4.32	0.77
σ^2 GCA	-	0.28	2.29	1.96	2.21	0.37	0.07	4.26	1.83	37.85	0.01	0.23	0.15	0.02
σ^2 SCA	-	5.19	28.83	38.81	67.80	8.20	0.56	86.65	62.85	501.78	15.41	2.28	6.89	1.44
σ^2 GCA/ σ^2 SCA		0.053	0.079	0.051	0.033	0.045	0.131	0.049	0.029	0.075	0.001	0.102	0.022	0.013
σ^2 D	-	0.55	4.58	3.93	4.41	0.74	0.15	8.51	3.66	75.71	0.03	0.47	0.30	0.04
σ^2 H	-	5.19	28.83	38.81	67.80	8.20	0.56	86.65	62.85	501.78	15.41	2.28	6.89	1.44
Degree of Dominance	-	0.33	0.40	0.32	0.26	0.30	0.51	0.31	0.24	0.39	0.04	0.45	0.21	0.16
G. Mean	-	10.3	20.0	33.3	40.6	46.4	13.3	70.7	55.5	113.3	33.8	27.7	62.6	45.5
SEm ±	-	0.8	0.8	2.0	2.4	1.1	0.5	3.2	2.6	5.9	1.9	0.8	1.2	0.5
C.D.(P=0.05)	-	2.1	2.4	5.7	6.9	3.1	1.5	9.1	7.3	16.6	5.3	2.2	3.4	1.4
C.V. %	-	12.8	7.3	10.6	10.4	4.2	6.9	7.9	8.1	9.0	9.7	5.0	3.3	1.9

*, ** Significant at 5% & 1%, respectively

The variance due to general combining ability (σ^2 GCA) and specific combining ability (σ^2 SCA), ratio of GCA to SCA variances, additive variance (σ^2D), non-additive variance (σ^2 H) and degree of dominance $[\sigma^2 D / \sigma^2 H]^{1/2}$ for the traits under study for castor genotypes are presented in Table 1. SCA variance was greater than GCA variance for all the characters under study which revealed that non-additive gene effects were dominant and controlled the characters genetically. The high amount of σ^2 SCA and ratio of GCA to SCA variances near to zero indicated that the dominance

gene effect was predominant in newly developed lines for all the characters under study. The proportion of additive effect was very low among all the character in gene action. It indicated the predominance of non-additive gene action for all the characters, thus, exploitation of hybrid vigour could be the best method for improvement of all the characters. Similar observations also were made by Patel *et al*. (2015); Punewar *et al*. (2017) and Bindu Priya *et al*. (2018) with minor deviations. Among the female parents, the highest positive gca effect was exhibited by MCP-1-1, for seed yield and number of capsules on primary raceme, effective length of primary raceme and height up to primary raceme. SKP-84 was also good general combiner for traits such as 100 seed weight, number of capsule on primary raceme, nodes to primary raceme and height up to primary raceme (Table 2).

Among the male parents, MP-11-17 was the best general combiner for cumulative seed yield, raceme length and number of capsules. For cumulative seed yield, MP-11-17 followed by MP-17-17, MP-18-17 and MP-9-17 were good general combiners. The parent MP-4-17 was good combiner for traits such as, plant height up to primary raceme, effective length of primary raceme, number of capsules on primary raceme, number of effective spikes/plant, volume weight ration and oil per cent and also an average combiner for seed yield can be exploited for development of new hybrids and as a good source for new combiner development. The MP-9-17 was the best combiner for earliness in flowering and good combiner for volume weight ratio and oil content. MP-17-17 was also good combiner for days to flowering, 100 seed weight and nodes to primary raceme. These parents can be effusively used in breeding programmes in various cross combinations for improvement in seed yield and other agronomic characters because of their ability to transmit characters to off springs.

The *sca* effects of all 50 crosses presented in Table 3. Cross M-574 x MP-17-17 found the best cross among all the crosses for cumulative seed yield followed by MCP-3 x MP-7-17 and SKP-84 x MP-11-17. The cross VP-1 x MP-20-17 had significant and positive highest *sca* effect for 100 seed weight, M-574 x MP-20-17 for volume weight ratio and M-574 x MP-18-17 for oil content. Similar reports were also made earlier by Lavanya and Chandramohan (2003); Solanki *et al.* (2004); Patel *et al.* (2015) and Bindu Priya *et al.* (2018).

Based on combining ability, good general combiner parents were involved in generation of good SCA hybrids, although, some of the hybrids deviated. There for, improvement of such character can be done through recurrent selection of population or bi-parental matting.

Table 3 General combining ability of various pistillate and pollen parents

Source	Cumulative seed yield (q/ha)				Days to 50% flowering	Nodes up to primary raceme	Height up to primary raceme (cm)	Effective length of primary raceme (cm)	Number of capsules on primary raceme	Number of effective spikes	100 seed weight (g)	Volume weight ratio (g/100ml)	Oil (%)
	120 DAS	150 DAS	180 DAS	210 DAS									
MCP-1-1	1.44**	6.28**	7.37**	9.00**	0.11	0.14	7.39**	8.21**	28.02**	-0.69	0.19	-0.49	0.1
VP-1	1.01**	-0.30	1.03	1.00	-1.95**	-1.24**	-9.48**	-5.30**	-8.25**	1.09	-1.46**	1.30**	0.02
MCP-3	-0.19	-2.38**	-2.89**	-3.32**	-2.65**	-1.00**	-8.80**	-2.71**	-29.14**	0.61	0.29	1.39**	0.41*
M-574	-2.26**	-4.17**	-6.11**	-7.71**	3.15**	0.52**	5.93**	-0.24	-0.09	1.37*	-1.70**	-0.34	-0.27
SKP-84	0.01	0.57*	0.60	1.02	1.35**	1.58**	4.96**	0.04	9.46**	-2.37**	2.68**	-1.86**	-0.26
MP-1-17	-2.84**	-7.32**	-6.51**	-6.36**	-0.05	1.29**	-2.43	-1.08	-3.10	0.59	0.46	-1.41*	0.26
MP-4-17	-1.45**	-3.08**	-0.88	0.66	2.88**	1.22**	14.63**	10.59**	40.66**	2.12*	-0.86*	1.97**	0.46*
MP-7-17	-3.27**	-8.07**	-7.69**	-7.97**	1.88**	-0.14	-10.06**	-2.26	-18.21**	-0.48	3.52**	-0.17	-0.38
MP-9-17	0.06	-3.42**	0.29	3.33**	-4.85**	-0.47	-4.66**	2.97*	3.50	0.88	-2.6**	3.05**	1.1**
MP-10-17	-3.39**	-7.23**	-6.96**	-7.36**	1.75**	0.93**	9.72**	-5.83**	-18.56**	1.85*	1.93**	1.45**	0.46*
MP-11-17	2.1**	14.04**	12.33**	13.05**	3.48**	0.42	2.34	8.86**	47.08**	-1.92*	-2.96**	-1.27*	0.16
MP-14-17	1.88**	1.57**	-0.16	-1.95	-1.79**	-1.27**	-7.68**	0.10	-6.88*	-1.44	-0.41	1.38*	0.82**
MP-17-17	3.27**	5.24**	4.16**	3.44**	-2.45**	-1.11**	0.41	-6.23**	-33.56**	-3.88**	1.24**	0.88	0.25
MP-18-17	2.82**	5.35**	4.69**	4.00**	-1.19*	-0.02	6.77**	-9.70**	-19.16**	0.63	-0.24	-2.37**	-1.25**
MP-20-17	0.82*	2.92**	0.72	-0.84	0.35	-0.85**	-9.06**	2.59*	8.24**	1.65	-0.08	-3.51**	-1.89**

*, ** Significant at 5% & 1%, respectively

Table 4 Specific combining ability of various hybrids for seed yield and related traits

Source	Cumulative seed yield (q/ha)				100 Seed Weight (g)	Volume Weight Ratio (g/100ml)
	120 DAS	150 DAS	180 DAS	210 DAS		
MCP-1-1 x MP-1-17	-0.20	-2.92**	-2.77	-3.16	0.18	-1.80
MCP-1-1 x MP-4-17	1.82*	1.24	3.41	5.04*	0.56	-0.18
MCP-1-1 x MP-7-17	1.84*	0.58	2.77	4.42	-0.09	1.03
MCP-1-1 x MP-9-17	-0.44	-4.01**	-4.10*	-4.73	0.76	-0.59
MCP-1-1 x MP-10-17	2.06**	0.81	3.23	5.10*	0.37	1.01
MCP-1-1 x MP-11-17	-0.86	2.29**	1.12	1.29	-1.43	-0.39
MCP-1-1 x MP-14-17	1.75*	3.45**	4.88*	7.66**	-0.64	-2.84*
MCP-1-1 x MP-17-17	-5.17**	-7.16**	-12.65**	-16.8**	0.14	0.74
MCP-1-1 x MP-18-17	1.20	2.46**	3.34	5.58*	0.71	-0.35
MCP-1-1 x MP-20-17	-1.79*	-1.47	-3.58	-4.34	-1.03	2.82*
VP-1 x MP-1-17	0.22	0.8	1.33	1.78	-0.86	-0.58
VP-1 x MP-4-17	-3.10**	-5.24**	-8.03**	-10.9**	-0.12	-1.69
VP-1 x MP-7-17	0.12	1.77*	2.21	2.56	1.47	-3.15*
VP-1 x MP-9-17	-1.66*	-2.45**	-3.79	-5.22*	0.12	-0.34
VP-1 x MP-10-17	-5.04**	-5.4**	-10.12**	-14.93**	-4.26**	-2.14
VP-1 x MP-11-17	0.73	1.15	1.56	1.62	2.58**	1.88
VP-1 x MP-14-17	-1.65*	2.62**	0.65	-1.67	-0.39	1.24
VP-1 x MP-17-17	-0.68	1.37	0.37	-0.97	0.66	1.08
VP-1 x MP-18-17	2.69**	4.76**	7.13**	9.16**	-1.14	-0.84
VP-1 x MP-20-17	3.27**	4.65**	7.59**	10.19**	3.86**	0.26
MCP-3 x MP-1-17	0.11	-1.32	-1.23	-1.53	-0.47	0.87
MCP-3 x MP-4-17	1.19	-2.08*	-0.91	-0.13	0.58	3.46**
MCP-3 x MP-7-17	3.89**	3.43**	7.30**	10.78**	-2.18**	0.30
MCP-3 x MP-9-17	-1.80*	-0.77	-2.59	-4.79	-0.46	2.11
MCP-3 x MP-10-17	1.49	1.41	2.88	3.97	1.05	-1.95
MCP-3 x MP-11-17	-2.71**	0.90	-0.67	-1.34	-0.02	4.90**
MCP-3 x MP-14-17	0.03	2.69**	0.34	1.41	0.77	0.18
MCP-3 x MP-17-17	-1.25	0.29	-2.62	-4.87*	-0.11	-0.38
MCP-3 x MP-18-17	-0.50	0.77	1.08	-1.06	0.60	0.23
MCP-3 x MP-20-17	-0.66	-0.35	-0.67	-0.82	-3.03**	-4.42**
M-574 x MP-1-17	1.72*	-8.61**	-6.41**	-8.11**	0.00	1.94
M-574 x MP-4-17	-0.21	4.05**	4.12*	4.97*	-1.08	-0.91
M-574 x MP-7-17	2.27**	-2.05*	1.23	0.40	0.30	0.02
M-574 x MP-9-17	1.01	0.67	1.83	1.69	1.22	3.40**
M-574 x MP-10-17	0.08	6.36**	6.12**	7.66**	1.82*	-4.45**
M-574 x MP-11-17	1.54*	-8.58**	-5.92**	-7.73**	0.32	0.76
M-574 x MP-14-17	5.13**	3.19**	9.57**	10.08**	-0.60	-0.66
M-574 x MP-17-17	2.54**	10.20**	11.05**	16.50**	-0.68	-1.20
M-574 x MP-18-17	0.52	-0.12	-2.16	0.71	1.80*	3.18**
M-574 x MP-20-17	-0.26	5.83**	5.87**	7.16**	2.80**	5.80**
SKP-84 x MP-1-17	-0.80	5.08**	4.76*	7.08**	0.48	-2.58*
SKP-84 x MP-4-17	-2.35**	-4.06**	-6.13**	-6.71**	-0.94	4.23**
SKP-84 x MP-7-17	-1.10	-5.58**	-5.67**	-6.78**	-1.55	0.86
SKP-84 x MP-9-17	-1.58*	-8.02**	-9.46**	-11.18**	-2.40**	-5.29**
SKP-84 x MP-10-17	1.47	-1.96*	-0.82	-0.76	-1.17	-0.84
SKP-84 x MP-11-17	0.25	11.21**	8.24**	10.10**	-0.77	-5.03**
SKP-84 x MP-14-17	-2.61**	-5.87**	-7.90**	-9.75**	1.85*	-2.85*
SKP-84 x MP-17-17	-2.45**	-2.86**	-3.99	-5.24*	2.04*	0.69
SKP-84 x MP-18-17	0.55	6.71**	8.70**	9.84**	-1.22	-1.53
SKP-84 x MP-20-17	-0.62	-9.87**	-10.51**	-13.24**	-0.42	3.91**

Table 4 (contd...)

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Source	Days to 50% flowering	Nodes up to primary raceme	Height up to primary raceme (cm)	Effective length of primary raceme (cm)	Number of capsules on primary raceme	Number of Effective Spikes	Oil (%)
MCP-1-1 x MP-1-17	-1.45	0.95	10.79**	-1.06	12.93*	-1.51	0.59
MCP-1-1 x MP-4-17	1.29	0.01	9.50**	4.61	-10.38	1.74	-0.92
MCP-1-1 x MP-7-17	-3.71**	-0.08	1.19	-2.43	1.38	1.00	-0.53
MCP-1-1 x MP-9-17	0.02	-0.41	3.79	-5.77*	-1.22	-1.46	0.03
MCP-1-1 x MP-10-17	-3.91**	0.52	-6.70*	6.70*	-3.60	2.00	0.52
MCP-1-1 x MP-11-17	0.95	-0.23	-7.79*	0.68	-19.68**	-1.84	-0.43
MCP-1-1 x MP-14-17	-1.65	-1.28*	-17.08**	0.68	3.45	-1.15	-0.85
MCP-1-1 x MP-17-17	8.35**	-0.48	-5.39	8.97**	1.76	-1.78	-0.26
MCP-1-1 x MP-18-17	-4.58**	-1.03	-4.90	8.41**	3.05	7.65**	-0.39
MCP-1-1 x MP-20-17	-1.85	-0.43	1.83	-11.12**	2.01	11.22**	0.62
VP-1 x MP-1-17	0.32	-1.02	0.53	-0.80	-1.57	8.19**	0.20
VP-1 x MP-4-17	-1.61	0.27	-1.20	2.42	14.45*	-2.45	-0.20
VP-1 x MP-7-17	-1.95	0.29	4.49	-6.29*	-5.79	0.26	-0.60
VP-1 x MP-9-17	3.12**	1.18*	5.42	2.60	14.61*	-3.21	-0.03
VP-1 x MP-10-17	-1.15	-1.66**	-10.29**	-6.82**	-39.77**	-7.96**	-1.47**
VP-1 x MP-11-17	-0.15	-0.88	-7.42*	-1.93	-1.74	-2.79	-0.45
VP-1 x MP-14-17	1.59	0.52	3.73	-3.04	22.62**	3.35	-0.17
VP-1 x MP-17-17	1.92	0.10	-2.58	1.24	7.60	1.72	1.96**
VP-1 x MP-18-17	-0.68	-0.34	-9.31**	-1.20	-4.56	1.92	-0.67
VP-1 x MP-20-17	3.39**	0.48	3.09	0.49	9.51	-1.61	0.26
MCP-3 x MP-1-17	0.32	1.18*	3.89	3.11	10.05	-2.05	0.09
MCP-3 x MP-4-17	0.39	0.47	5.04	-4.67	-30.15**	-1.48	2.13**
MCP-3 x MP-7-17	-4.61**	0.16	2.29	-1.49	-4.95	-1.21	-0.56
MCP-3 x MP-9-17	2.12	0.60	5.00	-4.04	-11.88*	-4.90*	1.06*
MCP-3 x MP-10-17	3.52**	1.09*	12.07**	10.76**	31.85**	-3.65	0.08
MCP-3 x MP-11-17	1.02	0.48	2.46	7.01**	48.64**	5.67**	0.41
MCP-3 x MP-14-17	-1.05	-0.50	-6.30	-1.01	3.04	-1.15	-0.74
MCP-3 x MP-17-17	0.62	-0.43	6.94*	-1.01	-15.71**	-6.15**	0.63
MCP-3 x MP-18-17	2.35*	-0.19	-12.74**	2.90	-20.78**	0.78	0.68
MCP-3 x MP-20-17	4.82**	-0.36	-8.92**	-9.94**	-14.29*	-0.91	-0.65
M-574 x MP-1-17	-2.58*	-0.70	-1.57	7.52**	-2.3	-4.89*	-0.2
M-574 x MP-4-17	3.02**	1.55**	15.9**	2.83	15.21*	-3.38	0.13
M-574 x MP-7-17	-1.65	-0.16	-15.08**	-3.17	6.23	-1.04	0.88
M-574 x MP-9-17	-1.25	1.30*	25.9**	-11.03**	-13.95*	-3.78*	1.49**
M-574 x MP-10-17	1.22	1.46**	8.17*	-3.77	4.21	-1.02	-1.00
M-574 x MP-11-17	-3.55**	0.29	-6.80*	-16.07**	-21.08**	-1.30	-1.66**
M-574 x MP-14-17	0.05	0.87	5.78	-5.87*	-22.12**	-1.79	-0.41
M-574 x MP-17-17	3.05**	-0.18	4.58	-0.76	11.45	0.88	-0.63
M-574 x MP-18-17	0.79	-0.49	-7.44*	3.82	23.28**	5.92**	2.49**
M-574 x MP-20-17	0.92	0.45	4.93	27.76**	26.54**	1.46	2.31**
SKP-84 x MP-1-17	-0.01	-0.45	2.69	-6.87**	-63.58**	-1.83	1.67**
SKP-84 x MP-4-17	-1.08	-0.54	-0.07	2.00	1.93	1.90	0.67
SKP-84 x MP-7-17	-1.75	1.19*	11.4**	10.67**	-7.05	1.12	0.97
SKP-84 x MP-9-17	-0.35	-0.23	2.60	3.36	34.89**	-4.93*	-2.33**
SKP-84 x MP-10-17	-2.88*	0.15	-4.13	-4.71	0.38	1.15	-1.90**
SKP-84 x MP-11-17	5.12**	0.38	3.22	8.40**	38.32**	2.35	-0.23
SKP-84 x MP-14-17	-0.95	-1.38*	-15.31**	2.04	1.94	4.41*	0.35
SKP-84 x MP-17-17	-0.28	-0.42	-7.84*	-5.73*	5.08	5.19**	-1.85**
SKP-84 x MP-18-17	-1.55	-0.40	-8.31*	0.96	-23.44**	2.01	-2.32**
SKP-84 x MP-20-17	-4.08**	-1.69**	-0.04	-9.33**	-16.84**	-0.68	1.25*

*, ** Significant at 5% & 1%, respectively

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A new high yielding and high oil content Indian mustard variety 'GM 6' (Banas Sona) recommended for Gujarat state

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ABSTRACT

A high yielding genotype of Indian mustard SKM 1328 was evolved from cross between IC 385682 and SKM 0820 at Castor-Mustard Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar and identified for release as Gujarat Mustard 6 (Banas Sona) for Gujarat state. The genotype SKM 1328 was identified owing to its superior performance in preliminary yield trial conducted at Sardarkrushinagar during 2013-14. It was evaluated in multi location trials from 2014-15 to 2018-19, simultaneously it was screened against aphid and powdery mildew under late sown epiphytotic conditions at Sardarkrushinagar. Under AICRP trial, it was tested under Initial Varietal Trial (Timely sown, irrigated) at four different centres of zone IV in the year 2017-18. The mean seed yield of GM 6 (Banas Sona) variety under timely sown irrigated condition in Gujarat state was 2541 kg/ha with an increase of 14.20, 13.98 and 11.94 per cent over the check varieties Kranti, GM 3 and GDM 4, respectively. Under limited irrigation conditions, GM 6 recorded 1758 kg/ha of seed yield which was 8.85, 27.21, 9.85 and 17.75 per cent higher over the check varieties Kranti, GM 1, GM 3 and GDM 4, respectively. It was also found superior in quality traits. It recorded high oil content (38.89 %) with oil yield of 988 kg/ha which was 20.34, 24.75 and 15.02 per cent higher as compared to the check varieties Kranti, GM 3 and GDM 4, correspondingly. Besides, it also possessed comparatively high oleic acid (12.51%) than the check varieties. It has higher 1000 seed weight (5.66 g) as compared to all three checks except GM 3 which recorded 5.72 g 1000 seed weight. Considering the average seed yield in irrigated as well as limited irrigated condition and quality of the genotype SKM 1328, it was proposed and identified for release as Gujarat Mustard 6 (Banas Sona) for general cultivation by mustard growing farmers of Gujarat state.

Keywords: GM 6, Oil content, Seed yield, Indian mustard

Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is an important edible oilseed crop after groundnut. Indian mustard belongs to family *Brassicacae* and genus *Brassica*. It is a natural amphidiploid (2n=36) of *Brassica campestris* (2n=20) and *Brassica nigra* (2n=16) (Nagaheru, 1935). Mustard is largely self-pollinated but certain amount (5-18%) of cross pollination may also take place (Labana and Banga, 1984). In India, there was remarkable increase in the production of mustard during last 33 years. The production was around 2.68 million tonnes with productivity of 674 kg/ha until 1985-86 which is increased to 9.34 million tonnes with productivity of 1499 kg/ha in 2018-19 (Anonymous, 2018). On the other hand, the demand of edible oils is increasing very rapidly with increasing population and has been estimated to be 28.40 million tonnes by 2030 and 41.6 million tonnes by 2050 (Kumar, 2017).

In Gujarat, mustard was cultivated in 1.95 lakh hectares area with the production of 3.48 lakh tonnes and productivity of 1745 kg/ha (Anonymous, 2018). The average productivity of Gujarat is higher than the national average productivity and ranks second after Haryana. Mustard is one of the most important *rabi* oilseeds crops in Gujarat. Wherein, North Gujarat region is ideally suited for the cultivation of mustard which includes Banaskantha, Mehsana, Patan, Gandhinagar, Sabarkantha, Arvalli and Kutch districts which cover more than 95% of total cultivated area under mustard in Gujarat. Winter is short in this region as temperature rise early at the end of season, hence, short duration and high yielding varieties are the most suitable ones. Early efforts made in this direction resulted in the release of two mustard varieties, Gujarat Mustard 2 (in 1995) and Gujarat Mustard 3 (in 2005) (Thakkar *et al.,* 2010). Breeding efforts have been continued and the last variety was released as GDM 4 (Gujarat Dantiwada Mustard 4) in 2011 (Prajapati *et al.,* 2017), which is a predominant variety having good yield potential at farmer's fields. However, to enhance the production of mustard in order to fulfill the requirement of edible oil production, there is an urgent need to develop a variety with high yield potential, adaptable to varying climatic conditions and better seed quality. Keeping this objective in view, breeding efforts were initiated to evolve new high yielding variety suitable for different agro-climatic conditions.

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MATERIALS AND METHODS

In order to improve mustard yield potential, hybridization programme was initiated in 2008-09 at Castor-Mustard Research Station, Saradarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The genotype SKM 1328 was evolved from the cross between IC 385682 and SKM 0820. The elite plants were selected from F_2 generation onwards and they were evaluated for their sustained yielding ability and homozygosity through pedigree method of breeding. The genotype, SKM 1328 was first evaluated in Preliminary Yield Trial (PYT) at the station level during 2013-14. The genotype was found promising, hence it was evaluated for its potentiality at various locations of Gujarat in a randomized block design in different categories of state trials *viz.,* Small Scale Varietal Trial (SSVT) during 2014-15 and Large Scale Varietal Trial (LSVT) during 2015-16 to 2018-19. Besides, this genotype was also evaluated in Initial Varietal Trial (Timely sown, irrigated) at four different centres of zone IV (comprising the states of Gujarat, Rajasthan and Maharashtra) in the year 2017-18. This genotype was also screened for its reaction to aphid and powdery mildew under field conditions as per standard scale (Anonymous, 2014). The DNA fingerprinting of SKM 1328 along with five checks (Kranti, GM 1, GM 2, GM 3 and GDM 4) was also performed using 18 ISSR primers. The seed yield data was analyzed that is suitable for a randomized block design suggested by Panse and Sukhatme (1985).

RESULTS AND DISCUSSION

The genotype SKM 1328 was tested in preliminary yield trial at Sardarkrushinagar during 2013-14 and found promising, hence it was promoted to multilocation trials from 2014-15 to 2018-19 at different centres of Gujarat state. The gentotype SKM 1328 has been tested at 32 different research stations/centres of Gujarat under irrigated condition. The mean performance of SKM 1328 for seed yield was 2541 kg/ha with a increase of 14.20, 13.98 and 11.94 per cent higher than the check varieties Kranti, GM 3 and GDM 4, respectively (Table 1). Multilocation testing was conducted under both irrigated and limited irrigated condition at different research stations. Under limited irrigation conditions, trials were conducted at ten different locations during *rabi* season from 2015-16 to 2018-19 and genotype SKM 1328 recorded 1758 kg/ha average seed yield with a yield increment of 8.85, 27.21, 9.85 and 17.75 per cent over the check varieties Kranti, GM 1, GM 3 and GDM 4, respectively (Table 2). In All India Co-ordinated Trials, the genotype SKM 1328 was tested in initial varietal trial (timely sown, irrigated) under zone IV during 2017-18 and it recorded 3034 kg/ha of seed yield over two locations which was 23.92 per cent and 12.81 per cent higher than the National check, Kranti and the Zonal check, Bio 902, respectively (Table 3). Yield with good oil quality is also of prime importance in oilseed crops. The genotype SKM 1328 was also found superior in quality traits. It recorded high oil content (38.89 %) with oil yield of 988 kg/ha which was 20.34, 24.75 and 15.02 per cent higher as compared to the check varieties Kranti, GM 3 and GDM 4, correspondingly (Table 4). Besides, it also possessed comparatively high oleic acid (12.51%) than the check varieties (Table 5).

Ancillary observations of economic attributes of SKM 1328 along with the checks are presented in Table 6. The perusal of data showed that SKM 1328 matured in 111 days which was at par with GM 1 and early than GM 3, GDM 4 and Kranti. It also recorded more number of siliquae per plant, siliqua length and number of seeds per siliqua. It exhibited high 1000 seed weight as compared to all three checks except GM 3 (Table 6). Morphological characters of SKM 1328 are furnished in Table 7 and Fig. 1. This genotype possesses long and broad leaf, medium length and width of petal, erect plant type, non-lodging, black colour seed. Siliqua texture is undulated and open angle with main shoot.

The genotype SKM 1328 was screened for resistance to insect-pests and diseases during 2014-15 to 2018-19 under late sown epiphytotic condition at Sardarkrushinagar (Table 8 and 9). Lower incidence of powdery mildew disease was observed under timely sown conditions, but under late sown epiphytotic condition, all the checks and the proposed variety showed susceptible reaction (Table 8). Similarly, lower aphid infestation was observed under timely sown conditions, but under late sown epiphytotic condition, all the checks along with proposed variety exhibited susceptible reaction (Table 9).

DNA fingerprinting of variety SKM 1328 along with five checks (Kranti, GM 1, GM 2, GM 3 and GDM 4) performed using 18 ISSR primers indicated out of 18 primers, 5 primers (ISSR 5, ISSR 13, ISSR 14, ISSR 15 and ISSR 17) exhibited polymorphic bands between SKM 1328 and other five check varieties (Fig. 2).

Considering the superior performance, SKM 1328 has been accepted by 51st State Seed Sub-Committee Meeting held at Conference Hall, Krushi Bhavan, Gandhinagar (Gujarat) during February 15, 2021 and released as Gujarat Mustard 6 (Banas Sona) for commercial cultivation in mustard growing areas of Gujarat State (Fig. 3). The GM 6 has been registered with national identity number (IC 634357) and being conserved under long term storage at NBPGR, New Delhi.

Table 1 Yield performance of SKM 1328 in comparison with check varieties in the Gujarat state

Year/ Season	Name of Trial	Locations	Seed Yield (kg/ha)				SEm. ±	CD at 5%	CV%
			SKM 1328	Kranti (NC) a	GM 3 (LC) b	GDM 4 (LC) c			
2013-14	PYT	SKNagar	2461	2158	2320	2360	163	463	12.49
		% Increase over checks		14.04	6.08	4.28			
2014-15	SSVT	SKNagar	3397a	2830	2995	3163	151	430	9.55
		Junagadh	2465a	2101	2183	2228	112	321	9.52
		Amreli	1771abc	1466	1517	1224	83	236	11.36
		Kothara	2476	2023	2295	2476	216	NS	18.33
		Derol	2322c	2220	1950	1829	148	424	14.69
		Vijapur@	1167	1241	1356	1334	118	NS	18.35
		Mean (5)	2486	2128	2188	2184	-	-	-
		% Increase over checks		16.82	13.62	13.83	-	-	-
2015-16	LSVT	SKNagar	2751ab	2403	2441	2480	106	306	8.44
		Junagadh	1965	1904	1909	2007	100	288	10.12
		Talod	1894	1428	1621	1620	122	NS	13.77
		Jamnagar#	1555	2033	1725	1839	175	NS	20.46
		Anand	1909	2161	2310	2361	144	413	13.30
		Kholwada	2999abc	2564	2528	2289	107	308	8.13
		Ladol	2285a	1586	1968	2167	140	404	13.10
		Bhachau	1757	1441	1419	1469	137	395	17.23
		Mean (7)	2223	1927	2028	2056	-	-	-
		% Increase over checks		15.36	9.62	8.12	-	-	-
2016-17	LSVT	SKNagar	3492a	3009	3169	3271	139	401	8.42
		Junagadh	2816abc	1972	2033	2107	129	370	11.81
		Talod	2293	2508	2110	2337	122	NS	10.16
		Jamnagar	2987bc	2701	2037	2366	135	388	10.50
		Anand	1949abc	1560	1350	1549	103	296	12.60
		Kholwada	2585	2405	2456	2482	107	307	8.33
		Ladol	2047	2077	2083	2125	136	NS	12.92
		Bhachau	2216	2291	1904	1884	189	544	18.10
		Mean (8)	2548	2315	2143	2265	-	-	-
		% Increase over checks		10.06	18.90	12.49	-	-	-
2017-18	LSVT	SKNagar	3377ac	2898	-	2908	147	422	9.65
		Junagadh@	1311c	1187	-	1008	72	207	13.55
		Talod	2254	2432	-	2311	169	NS	14.61
		Jamnagar	2061	1670	-	1835	138	393	14.39
		Anand	2365c	2137	-	1758	122	348	11.46
		Kholwada@	1417ac	876	-	1081	89	253	14.92
		Ladol	1930a	1510	-	1934	97	278	12.28
		Bhachau@#	475	507	-	532	77	NS	27.54
		Mean (5)	2397	2129	-	2149	-	-	-
		% Increase over checks		12.59	-	11.54	-	-	-
2018-19	LSVT	SKNagar	3664ac	3006	-	3024	151	435	9.31
		Junagadh	2595	2474	-	2680	117	336	9.03
		Jamnagar@	1714	1520	-	1949	87	249	10.37
		Anand	2293c	2200	-	1940	105	302	9.92
		Kholwada	2975ac	2226	-	2428	127	369	10.11
		Ladol	3506ac	3037	-	3057	137	395	8.55
		Bhachau@	1314	1715	-	1345	82	239	12.00
		Kothara	3448a	2814	-	2981	173	498	12.12
		Mean (6)	3080	2626	-	2685	-	-	-
		% Increase over checks		17.29	-	14.71	-	-	-
Overall mean (32)			2541	2225					
% Increase over Kranti				14.20					
Overall mean (21)			2421		2124				
% Increase over GM 3					13.98				
Overall mean (32)			2541			2270			
% Increase over GDM 4						11.94			
Frequency in top non-significant groups			23/26	4/26	1/16	10/26			

Note: a, b and c indicate significantly superior than respective check variety for seed yield

NC = National Check and LC = Local Check; #Data were not considered due to high CV%.; @Data were not considered due to below State average seed yield.

Table 2 Yield performance of SKM 1328 with limited irrigations in comparison with check varieties in the Gujarat state

Year/ Season	Name of Trial	Locations	Seed Yield (kg/ha)					SEm. +	CD at 5%	CV%
			SKM 1328	Kranti (NC) a	GM 1 (LC) b	GM 3 (LC) c	GDM 4 (LC) d			
2015-16	LSVT (Lim. Irri)	Vyara	1049	1019	880	957	784	78	232	15.14
		Adiya	1715d	1595	1520	1486	1423	100	289	12.62
		Mean (2)	1382	1307	1200	1222	1104			
		% Increase over checks		5.74	15.17	13.09	25.18			
2016-17	LSVT (Lim. Irri)	Vyara	1587b	1689	1110	1317	1311	105	306	13.80
		Adiya	2118	2093	1940	2126	2190	84	244	7.97
		Dhandhuka*	876	855	745	833	868	47	136	11.00
		Mean (2)	1853	1891	1525	1722	1751			
		% Increase over checks		-2.01	21.51	7.61	5.81			
2017-18	LSVT (Lim. Irri)	Vyara	2337bd	2271	1701	-	1830	99	288	9.97
		Adiya	1989ab	1433	1540	-	1721	101	294	12.13
		Dhandhuka*	387	346	354	-	359	19	56	10.14
		Sihori	1186bd	982	805	-	780	71	206	13.60
		Mean (3)	1837	1562	1349		1444			
		% Increase over checks		17.61	36.17	-	27.22			
2018-19	LSVT (Lim. Irri)	Vyara	1219b	1264	959	-	1192	85	247	14.54
		Adiya	1490bd	1385	1006	-	1288	65	189	9.82
		Dhandhuka*	702abd	414	578	-	513	24	69	7.76
		Sihori	2890abd	2421	2357	-	2411	139	404	10.81
		Mean (3)	1866	1690	1441	-	1630			
		% Increase over checks		10.41	29.49	-	14.48			
Overall mean (10)			1758	1615						
% Increase over Kranti				8.85						
Overall mean (10)			1758		1382					
% Increase over GM 1					27.21					
Overall mean (04)			1617			1472				
% Increase over GM 3						9.85				
Overall mean (10)			1758				1493			
% Increase over GDM 4							17.75			
Frequency in top non-significant groups			8/9	6/9	1/9	1/3	3/9			

a, b, c and d indicate significantly superior than respective check variety for seed yield

* At Dhandhuka centre, LSVT trial in 2015-16 was vitiated due to moisture stress at germination stage.

* The seed yield data of Dhandhuka centre in LSVT 2016-17, 2017-18 and 2018-19 (Limited Irrigations) were not considered due to non availability of irrigation and very low seed yield.

Note: Limited irrigations means two irrigation should be given one irrigation at the time of flowering (50-55 DAS) and second irrigation at the time of pod development and seed filling stage (70-75 DAS).

Table 3 Yield performance of SKM 1328 in comparison with check varieties in the IVT AICRP Trial (Zone IV)

Year/ Season	Name of Trial	Locations	Seed Yield (kg/ha)				SEm. ±	CD at 5%	CV%
			SKM 1328	Kranti (NC) a	GDM 4 (LR) b	Bio 902 (ZC) c			
2017-18	IVT Timely sown (Irrigated)	SKNagar	2873ac	2296	2783	2437	131	373.7	10.00
		Mandor	3194a	2600	3392	2941	160	458.5	9.00
		Jalgaon@	847	764	561	695	62	177.0	16.00
		Nagpur@	1288	1607	1464	1335	173	493.2	26.00
		Overall Mean (2)	3034	2448	3088	2689	-	-	-
		% Increase over the checks		23.92	-1.76	12.81	-	-	-

Note: a, b and c indicate significantly superior than respective check variety for seed yield.

NC = National Check; ZC = Zonal Check and LR = Latest Release; @Data were not considered due to below National average seed yield.

Table 4 Overall mean seed yield (kg/ha) and oil yield (kg/ha) of SKM 1328 in comparison with check varieties

Entry/Varieties	Mean seed yield (kg/ha)	Oil content (%)	Oil yield (kg/ha)	% Oil yield increase over checks
SKM 1328	2541	38.89	988	-
Kranti (NC)	2225	36.90	821	20.34
GM 3 (LC)	2124	37.31	792	24.75
GDM 4 (LC)	2270	37.86	859	15.02

Table 5 Biochemical parameters of SKM 1328 along with checks

Character		SKM 1328	(LC)			(NC)
			GM 1	GM 3	GDM 4	Kranti
Oil content (%)	Mean	38.89	36.66	37.31	37.86	36.90
	Range	36.87-39.69	35.94-37.94	36.51-38.52	35.94-38.54	36.38-37.64
Palmitic acid (%)	Mean	2.30	1.95	2.01	2.25	2.23
	Range	2.16-2.53	1.79-2.17	1.91-2.09	2.15-2.32	2.17-2.28
Stearic acid (%)	Mean	1.31	1.12	1.00	1.20	1.08
	Range	1.07-1.98	1.07-1.17	0.88-1.10	1.10-1.30	1.05-1.11
Oleic acid (%)	Mean	12.51	11.85	11.29	10.74	9.84
	Range	12.04-13.17	10.92-12.77	10.64-11.99	10.35-11.20	9.07-10.30
Linoleic acid (%)	Mean	14.60	14.85	15.02	16.44	16.07
	Range	14.13-15.19	14.31-15.12	14.43-15.41	15.50-16.88	15.38-16.35
Linolenic acid (%)	Mean	14.11	14.55	13.18	13.26	12.82
	Range	13.18-14.99	14.22-14.96	12.57-13.71	13.03-13.55	11.92-13.24
Eicosenoic acid (%)	Mean	6.21	5.73	5.44	6.02	4.98
	Range	6.12-6.37	5.24-7.36	4.92-6.97	5.51-7.55	4.49-6.66
Erucic acids (%)	Mean	48.96	49.95	52.06	50.09	52.98
	Range	46.65-50.90	49.03-50.73	51.02-53.12	48.95-51.07	51.09-54.14

Table 6 Ancillary observation of economic attributes of proposed entry along with checks

Character		SKM 1328	(LC)			(NC)
			GM 1	GM 3	GDM 4	Kranti
Days to flowering (No.)	Mean	41	47	45	45	46
	Range	40-64	44-58	40-51	42-63	41-61
Days to maturity (No.)	Mean	111	109	117	115	116
	Range	104-119	98-115	105-120	107-119	107-121
Plant height (cm)	Mean	170	150	180	172	174
	Range	151-190	131-158	170-195	170-200	172-196
Number of siliquae on main branch (No.)	Mean	44	37	40	42	41
	Range	32-51	31-42	29-47	32-49	32-54
Total number of branches/plant (No.)	Mean	15	10	15	13	14
	Range	12-17	5-19	6-17	10-18	9-17
Number of siliquae/ plant (No.)	Mean	362	300	347	328	313
	Range	198-610	226-374	190-518	188-570	213-606
Siliqua length (cm)	Mean	4.5	4.2	4.1	4.4	4.2
	Range	3.8-5.5	3.8-4.5	3.5-4.5	4.0-4.5	4.0-4.5
Number of seeds/ siliqua (No.)	Mean	15	12	14	14	13
	Range	12-16	9-15	11-15	12-16	12-18
1000 seed weight (g)	Mean	5.66	4.52	5.72	5.44	4.86
	Range	3.94-5.93	3.67-4.57	5.01-6.00	5.07-5.90	3.16-4.91

Table 7 Morphological characters of SKM 1328 along with checks (As per DUS Guidelines)

Descriptors/Characters	SKM 1328	(LC)		
		GM 1	GM 3	GDM 4
Leaf : Hairiness (Absent/Sparse/Dense)	Sparse	Sparse	Sparse	Sparse
Leaf : Colour (Light green/Medium green/Dark Green)	Dark Green	Dark Green	Dark Green	Dark Green
Leaf : Lobes (Absent/Present)	Present	Present	Present	Present
Leaf : Number of lobes (Low/Medium/High)	Medium	Medium	Medium	Medium
Leaf : Dentation of margin (Entire/Dentate/Serrate)	Dentate	Dentate	Dentate	Dentate
Leaf : Length (cm) (Short/Medium/Long)	Long (32-40)	Medium (26-30)	Long (32-39)	Long (32-40)
Leaf : Width (cm) (Narrow/Medium/Broad)	Broad (13-18)	Medium (10-12)	Broad (13-16)	Broad (12-17)
Flower: Time of flowering (50% of the plant with at least one open flower (Early/Medium/Late)	Medium (40-64)	Medium (47-58)	Medium (40-51)	Medium (42-63)
Flower : Colour of petals (White/Light Yellow/Yellow/ Orange)	Yellow	Yellow	Yellow	Yellow
Flower : Length of petals (cm) (Short/Medium/Long)	Medium (1.2-1.4)	Short (0.8-1.1)	Short (0.9-1.1)	Medium (1.2-1.5)
Flower : Width of petals (cm) (Narrow/Medium/Broad)	Medium (0.6-0.7)	Medium (0.6-0.7)	Medium (0.6-0.7)	Broad (0.8-1.0)
Plant : Main shoot length (cm) Short/Medium/Long/Very long)	Very long (70-95)	Very long (80-90)	Very long (60-85)	Very long (70-95)
Plant : Height (cm) (Short/Medium/Tall/Very tall)	Tall (151-190)	Medium (131-158)	Very tall (170-195)	Very tall (170-200)
Siliqua : Length (cm) (Short/Medium/Long)	Medium (3.8-5.5)	Short (3.8-4.5)	Short (3.5-4.5)	Short (4.0-4.5)
Siliqua : Length of beak (cm) Short/Medium/Long)	Medium (0.7-1.2)	Medium (0.8-1.2)	Medium (0.8-1.2)	Long (1.2-1.4)
Siliqua : Number on main shoot (Very few/Few/Medium/Many)	Few	Very few	Very few	Few
Siliqua : Density on main shoot (Low/Medium/High)	Low	Low	Low	Low
Siliqua : Angle with main shoot (Appressed/Semi appressed/Open)	Open	Open	Open	Semi appressed
Siliqua : Texture (Smooth/Undulated/Constricted)	Undulated	Undulated	Undulated	Undulated
Siliqua : Number of seeds per siliqua (Very few/Few/Medium/Many)	Few	Very few	Few	Few
Maturity period (Early/Medium/Late/Very Late)	Medium	Early	Medium	Medium
Seed : Seed colour (Yellow/Reddish brown/Brown/Dark brown/Black)	Black	Dark Brown	Black	Black
Seed : Size (Weight of 1000 seeds) (Small/Medium/Bold)	Medium	Small	Medium	Medium
Seed: Oil content (%) (Low/Medium/High/Very high)	Medium	Low	Low	Low

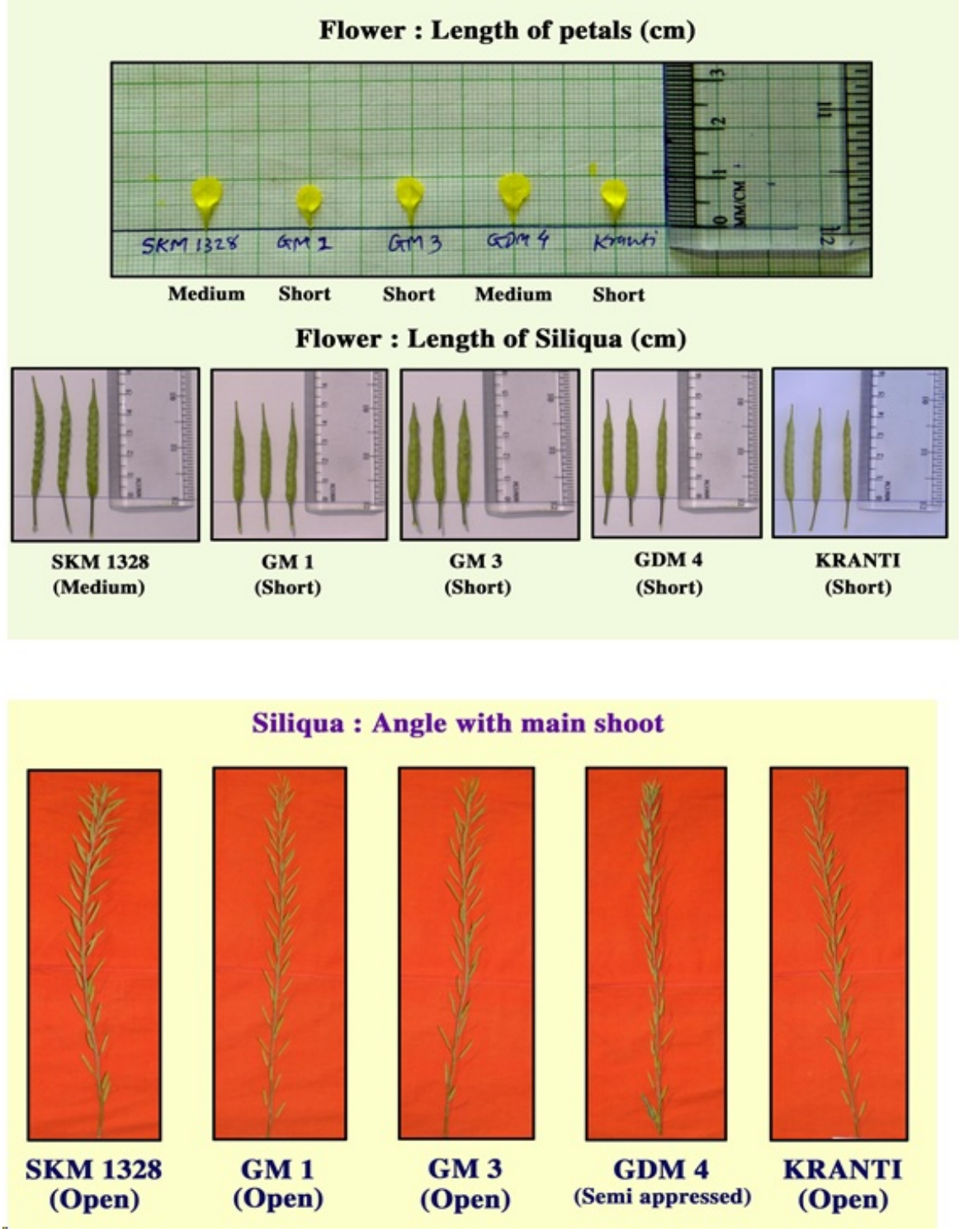

Fig. 1. Important DUS characertistiucs of SKM 1328 along with checks

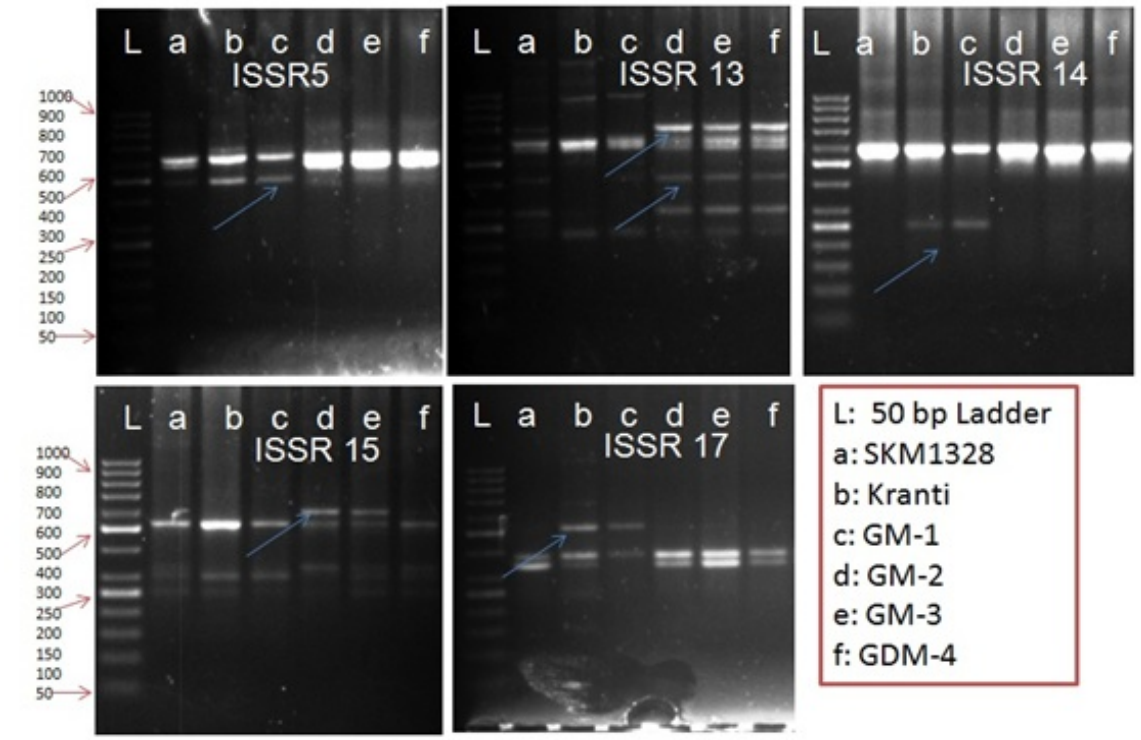

Fig. 2. DNA profiling of SKM 1328 along with checks

Fig. 3. Field view of Gujarat Mustard 6 (SKM 1328)

Table 8 Rating of powdery mildew disease severity (%) at Sardarkrushinagar centre under late sown epiphytotic conditions (After 20th November)

Disease	Year and season	Name of trial	Varieties			
			SKM 1328	(LC)		(NC)
				GM 3	GDM 4	Kranti
Powdery mildew	2014-15	SSVT	88.9	64.4	62.2	66.6
	2015-16	LSVT	73.3	62.2	60.0	73.3
	2016-17	LSVT	85.6	63.3	51.1	74.4
	2017-18	LSVT	95.0	-	92.5	95.0
	2018-19	LSVT	75.0	-	80.0	80.0
	Mean		83.6 (S)	63.3 (S)	69.2 (S)	77.9 (S)

Resistant (R) = ≤ 33.3% severity; Moderately Resistant (MR) = 33.3-55.6 % severity; Susceptible (S) = ≥ 55.6% severity

Table 9 Rating of average aphid infestation index (AAII/plant) at Sardarkrushinagar centre under late sown epiphytotic conditions (After 20th November)

Insect pests	Year and season	Name of trial	Varieties			
			SKM 1328	(LC)		(NC)
				GM 3	GDM 4	Kranti
Aphid	2014-15	SSVT	1.7	1.9	1.8	1.9
	2015-16	LSVT	3.5	3.1	3.4	3.5
	2016-17	LSVT	2.7	2.8	2.8	2.6
	2017-18	LSVT	3.9	-	4.0	3.9
	2018-19	LSVT	3.9	-	3.9	3.9
	Mean		3.1 (S)	2.6 (S)	3.2 (S)	3.2 (S)

Resistant (R) = 0.0-1.0; Moderately Resistant (MR) = 1.1-2.0; Tolerant (T) = 2.1-2.5; Susceptible (S) = 2.6-3.5; Highly Susceptible (HS) = 3.6-5.0

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AMMI analysis of genotype × environment interaction on seed yield of confectionary sunflower (*Helianthus annuus* L.) genotypes

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ABSTRACT

In this study, 60 confectionary sunflower genotypes were grown for three successive years during *kharif* 2018, 2019 and 2020 to determine the seed yield stability and adaptability over years. Yield stability and adaptability were analysed by combined analysis and AMMI model. The significant interaction indicated that the genotypes respond differently across the different environments. In AMMI analysis, the AMMI 1 biplot showed the genotype EC 734790 exhibited highest seed yield with 22.95g and high protein content of 31.23% and low oil content of 21.15% which is favoured for confectionary type of sunflower and is stable than all other varieties over all the three successive years, along with this the genotypes EC 734790, EC 734831, EC 734844 and EC 734814 had higher mean yields with high main (additive) effects. The results of the study further indicated that, the stable genotypes for seed yield over three successive years were G54- EC 734790 (22.95g) >G55- EC 734831(19.57g) >G56- EC 734844(18.15g) >G26- EC 734814(19.38g) with the help of AMMI model of stability analysis. Hence, these genotypes would be considered as more adapted to a wide range of environments over three different years than the rest of genotypes.

Keywords: Confectionary sunflower, G x E interaction, Stability, Seed yield

The cultivated sunflower, *Helianthus annuus* L., has two main types, the oilseed type and the non-oilseed type also known as confectionery. The confectionery non-oil sunflower seed types can be black, white, black with white stripes or colourful and significantly larger than the oil-type sunflower seeds. They have high hull percentage, with thicker hull loosely connected to the kernel, as well as variable seed shape. The hull is easily separated from the kernel and allows the seed to be dehulled as a whole (Hladni, 2016). The most important breeding criteria of confectionery sunflower hybrids is seed yield, seed protein content, mass of 1000 seeds, hull/kernel ratio and dehullability of the seeds; these traits greatly increase their market value. Breeding of confectionery sunflower is characterized by the fact that different markets have different demands regarding the seed size, hull colour and other traits, which makes this process more difficult and costlier. While developing confectionary sunflower hybrids or varieties it is also very important to combine the genes responsible for high yield potential, high protein content and other qualitative traits of the seed (Demurin, 2018).

The nutritional composition of whole confectionery sunflower seed constitutes 900 g/kg of dry matter, 235 g/kg of crude protein, 2.13 g/kg of net energy for lactation, 760 g/kg of total digestible nutrients, 250 g/kg of fat (oil), 285 g/kg of acid detergent fiber, 320 g/kg of neutral detergent fiber, 241 g/kg of crude fiber, 38 g/kg of ash, 3 g/kg of calcium and 6 g/kg of phosphorus (Gholinezhad *et al.,* 2013). The use of confectionery sunflower seeds has a long and rich tradition in Russia, Turkey and Ukraine. Most customers prefer tasty, high-quality and longer confectionery type seeds, but preferences differ according to the region or country. For instance, consumers from Turkey and some other countries require seeds that are at least 2 cm long, whereas Balkan, Ukraine, and Russia consumers prefer big seeds with big kernels and reduced husk content. The buying price for confectionery type hybrids depends on the seed quality, which is defined by seed size and characteristics of the hull.

The quality of confectionery sunflowers is divided into three categories: food-grade, ingredient and bird feed sunflowers. Food-grade category is made up of the highest quality seeds, including the largest and cleanest seeds. The largest seeds, called "in-hull seeds", are marketed salted, roasted and packaged for human consumption. The largest market for food-grade seeds is consumer retail. Packaged sunflowers are primarily a specialty food product and are sold to consumers as a healthy snack either in the hull or hulled. Ingredient category seeds (medium-size seeds) are seeds that are food-grade quality, but they do not contain the highest quality seeds to be in the food-grade category. Medium-size seeds, called "hulling seeds" are dehulled and the kernels are used, either roasted or not, as a snack food or in a number of confectionery or bakery products. Ingredient sunflowers are sold to firms, such as bread companies, that use sunflower seeds in their products. The sunflower seeds

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that cannot be used as food ingredients are used for bird feed. Usually these are smaller, lower quality seeds. High-protein sunflower has a separate market from the oil-type sunflower. Accurate surface and yield information cannot be found in most of the national and international statistic data (Hladni and Miladinovic, 2019).

In comparison to the oil type, presence of confectionery sunflower in India is significantly smaller. In India the potential areas for the cultivation of confectionary sunflower are Haryana, Punjab, Maharashtra, Andhra Pradesh and Karnataka. The demand for confectionery sunflower is slowly increasing in the Indian market. In addition, the export value of this is priced at US $1450-1550/ton as against the oil bearing seeds at US $650-800/ton (Girishraj, 2016).

It could be theoretically desirable that each developed variety will show high performance in all the environments where it is cultivated and in years with different climates although it is not possible in practice. For this reason, the stability analysis of the varieties tested in as many different environments as possible is necessary as, some of the cultivars may show superior performance only in good conditions, while some of them could maintain their performance even in bad conditions (Cvejic *et al.,* 2019). The Genotype x Environment (GxE) interaction is defined as the variation performances of the cultivars developed for long years of intensive studies according to changing environmental conditions. For plant breeders, the fact that GxE interaction causes differences in yield sequences of genotypes in different locations poses a problem in terms of efficiency of selection. However, if this interaction does not change the yield order of genotypes in different environments, then there is no problem in terms of variety recommendation (Rao *et al.,* 2004; Ahmed *et al.,* 2020; Uma *et al.,* 2020).

There are several methods to study stability and genotype × environment interactions of traits through conventional analysis. Different models were proposed on stability variance, ecovalence, regression coefficient analysis or principal component analysis (PCA). However, additive main effects and multiplicative interaction (AMMI) model and the genotype main effects and genotype × environment interaction effects (GGE) model are more popular methods. This method is followed to quantify the genotype environment interaction through PCA and graphical representation and has been widely applied in the multi-environment cultivar trials. The AMMI is more appropriate in the initial statistical analysis of yield trials because it provides an analytical tool to diagnose other models, such as subcases, when these are better for particular data sets and also have a good chance of predicting new sites and new years. The advantages of the AMMI model or its variants are that they use overall fitting, impose no restrictions on the multiplicative terms, and result in a least squares fit (Padmavathi *et al*., 2013).

A panel of 60 confectionary sunflower genotypes were studied with the main objective of identifying the high yielding, promising confectionary sunflower genotypes having wide adaptation and/or specific adaptation to environment and environment interaction for their yield stability and adaptability across different environments over three successive years.

MATERIALS AND METHODS

To assess the stability performance of 60 confectionary sunflower genotypes for relative yield performance, the experiment was conducted in randomized complete block design (RCBD) with two replications at AICRP on Sunflower, Zonal Agriculture Research Station, GKVK, Bangalore, India. Each genotype was sown in two rows of three-meter length each with a row spacing of 60 cm and 30 cm between plants within a row. Observations were recorded in each entry on randomly selected five plants for seed yield/plant. The experiment was laid out across three different environmental conditions *viz.,* successive *kharif* seasons of 2018 (Date of Sowing: 21/07/2018-E1), 2019(Date of Sowing: 23/07/2019 -E2) and 2020 (Date of Sowing: 29/07/2020-E3).

Statistical analysis: The combined analysis of variance was proceeded to observe at GxE and stability of the genotypes across all environments. The AMMI model, which combines standard analysis of variance with PC analysis, was used to investigate of G×E interaction (GEI). In AMMI model the contribution of each genotype and each environment to the GEI is assessed by use of the biplot graph display in which yield means are plotted against the scores of the interaction principal component axis (IPCA).

The AMMI model is:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^{N} \lambda n \gamma_{gn} \delta_{en} + \rho_{ge}$$

Where Y_{ge}= yield of the genotype (g) in the environment (e); μ = grand mean; α_g = genotype mean deviation; β_e= environment mean deviation; N = No. of IPCAs (Interaction Principal Component Axis) retained in the model; λ_n= singular value for IPCA axis n; γ_{gn} = genotype eigenvector values for IPCA axis n; δ_{en} = environment eigenvector values for IPCA axis n and ρ_{ge} = the residuals.

Biplot analysis: Biplot analysis is the most powerful interpretive tool of AMMI models. Biplots are graphs where

aspects of both genotypes and environments are plotted on the same axis so the inter-relationships can be visualized. There are two basic AMMI Biplots, the AMMI1 Biplot where the main effects (genotype mean and environments) are plotted against each other and the AMMI2 Biplot where scores for IPCA 1 and IPCA 2 are plotted.

RESULTS AND DISCUSSION

AMMI Analysis of variance: In terms of yield and yield components, the genotypes planted in *kharif* season over three successive years were analysed and preliminary analysis of variance were performed over the values combined as three environments for the years 2018, 2019 and 2020, the significance of the G x E interaction was tested through statistical analysis. In order to perform stability analysis, G x E interaction should be important so both genotypes and the G x E interactions were significant as indicated in ANOVA Table.

The AMMI analysis of variance for seed yield/plant of 60 confectionary sunflower genotypes tested in three environments showed that 76.28% of the total sum of squares was attributed to genotypic effects, 1% to environment effects and 22.71% given by G x E interaction effects (Table 1). The large sum of squares values for genotypes indicated that the genotypes were diverse with large differences among genotypic means causing most of the variation in seed yield, which is accordance with the findings of Misra *et al.* (2009), Fentie *et al.* (2013) and Uma *et al.* (2018) in confectionary sunflower. The presence of GEI was clearly demonstrated by the AMMI model, when the interaction was portioned among the first interaction principal component axis (IPCA) as they were significant P=0.01 in a postdictive assessment. The IPCA1 explained 89.28% of the interaction sum of squares with the degree of freedom 60, this implied that the interaction of the 60 confectionary sunflower genotypes over three environments was predicted by the first interaction principal components of genotypes and environments which is in line with the recommendation of Sivapalan *et al.* (2010) for wheat. On the other hand, the significant GxE interaction variance is suggestive of different performance of genotypes over three different years.

The mean seed yield value of 60 confectionary sunflower genotypes over three environments is presented in Table 2 along with IPC scores, oil content and protein content. The seed yield/plant among the genotypes varied from 2.35g to 22.95g and the genotype G54 (EC 734790) showed highest seed yield with 22.95g where, oil content varied from 17.33% to 36.61% and protein content varied from 1.63% to 32.87%. When a genotype and environment have the same sign on PCA1 axis, their interaction is positive and if opposite, their interaction is negative. Thus, if a genotype has a PCA1 score near to zero, it has small interaction effect and is considered as stable over wide environments. Conversely, varieties with high mean yield and large PCA scores are considered as explicitly adapted to specific environments.

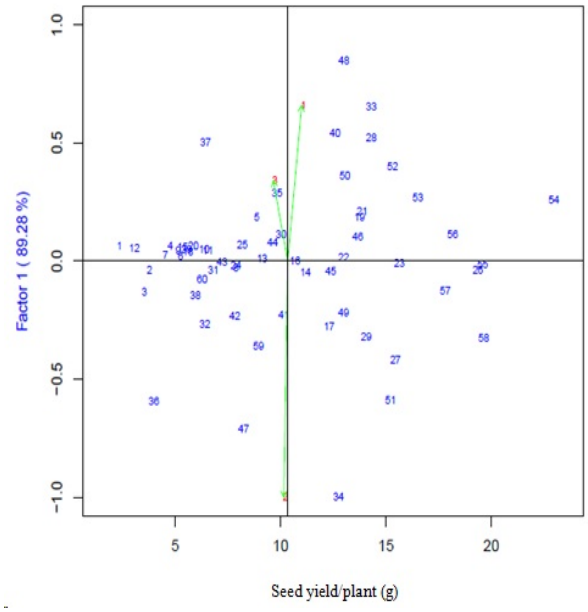
Table 1 AMMI analysis of variance for seed yield/plant of 60 confectionary sunflower genotypes grown at three environments

Source of variation	df	Mean sum of squares	F value	Explained sum of squares (%)
Environment	2	55.37	20.74***	1.00
Genotype	59	142.93	53.53***	76.28
Genotype × Environment	118	21.28	7.97***	22.71
IPCA1	60	37.36	13.98***	89.28
IPCA 2	58	4.64	1.73***	10.71
IPCA 3	56	0	0	0
Residuals	180	2.66	-	-

*** - Significance at P<0.01 probability level; df- degree of freedom

AMMI 1 biplot display: Genotypes and environments on the same parallel line, relative or ordinate have similar yields and a genotype or environment on the right side of the midpoint of this axis has higher yield than those of left hand side. Consequently, from Fig. 1. among the genotypes, G54-EC734790 (22.95g), G55-EC734831(19.57g), and G26-EC 734814 (19.38g) exhibited high yield with small IPCA scores but the genotype, G54 (EC 734790) being the overall best for seed yield of 22.95 g and high protein content of 31.23 % showing positive IPCA1 score near zero and the genotype G54(EC 734790), G26 (EC 734814) and G58 (EC 734849 -II) showed negative IPCA1 score but very close to zero indicating that these varieties were stable and less influenced by the environments. Similar outcomes have been reported by Liovic *et al.* (2021) and Awaad. (2021) and Abdelsatar *et al.* (2020). The genotype G54 was identified as specially adapted culture to the environment E1 (*kharif,* 2018). The genotypes G54 (EC 734790), G26 (EC 734814) and G58 (EC 734849 -II) are considered as the favourable environments for E2 (*kharif*, 2019) whereas the genotypes G36, G37 and G47 were poor yielders and had large negative IPCA score which indicated higher interaction with environments thus they are unstable and genotypes G35 (EC 734809), G30 (EC 734881) and G44 (EC 734798) showed positive IPCA1 score with below average yield and these three genotypes were favourable environments for E3 (*kharif*, 2020). On the other hand, regardless of the positive or negative values, the environment E1 (kharif, 2018) and E2 (*kharif*, 2019) had large IPCA scores which indicated these environments are unstable and higher interaction with genotypes but the environment E3 (*kharif*, 2019) small

positive IPCA score apparently near zero with high mean value and hence had small interaction effects indicating that all the genotypes performed well in this environment. This result is in agreement with the findings of Kindeya *et al.* (2020) and Saremi *et al.* (2020).

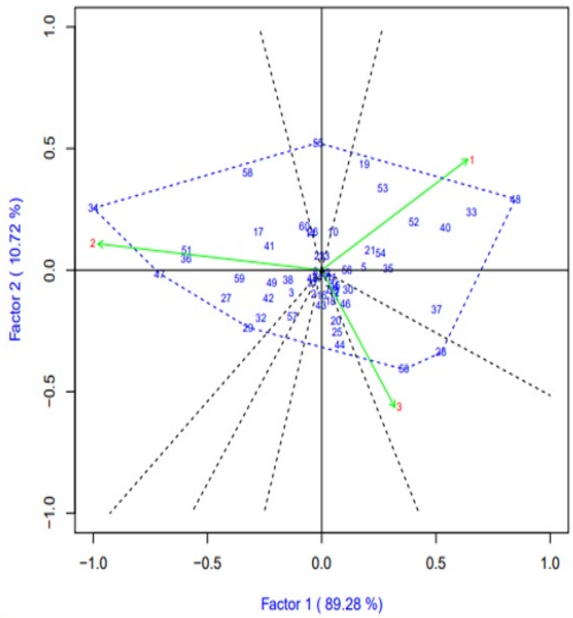


*1, 2 and 3 are environments *viz., kharif* 2018, 2019 and 2020, respectively' *1-60 are genotypes

Fig. 1. AMMI 1 Biplot for seed yield/plant of 60 sunflower genotypes and 3 environments using genotypic and environmental scores

AMMI 2 biplot display: In AMMI 2 biplot, the environmental scores are joined to the origin by side lines. Sites with short spokes do not exert strong interactive forces. Those with long spokes exert strong interaction. An example of this is shown in Figure 2 where the points representing the environments E1, E2 and E3 are connected to the origin. The environment E3 had short spokes and this environment do not exert strong interactive forces but the environments E1 and E2 had long spokes and they exert the most discriminating environments in Figure 2. Hence, the genotypes near the origin are not sensitive to environmental interaction and those distant from the origins are sensitive and have large interaction. In this case, the genotypes, G34 (EC 734879) and G48 (EC 734842) had more responsive since they were away from the origin. In multivariate approach, the AMMI model is better for partitioning the G x E into the causes of variation, which is easier identify environments potential and used to identify superior genotypes for specific adaptation.

From the present investigation it is concluded that stability analysis provided a good understanding of the adaptation level of confectionary sunflower genotypes over three successive growing years. The yield stability across different years varied among genotypes. AMMI statistical model could be a great tool to select the most suitable and stable high yielding hybrids for specific as well as for diverse environments. As a result, almost all of the evaluated genotypes were affected by the genotype x environment interaction effects and no genotype had superior performance in all the three years. In this study, the combined analysis of variance indicated that the genotypes (G), environments (E) and G x E interaction were significant at P<0.01 level. It is noted that the genotype G54 showed higher seed yield (22.95g) with high protein content of 31.23% and less oil content of 21.15 % which is favoured for confectionary sunflower and is stable than all other varieties over all the three successive years. Hence from this study, it could be concluded that among the evaluated confectionary sunflower genotypes; the genotypes G54 (EC 734790) along with the genotypes G55 (EC 734831), G56 (EC 734844) and G26 (EC 734814) with their sustained performance of seed yield over three different years could be considered as most stable and their performance can be further tested across different locations for commercial cultivation.



*1, 2 and 3 are environments *viz., kharif* 2018, 2019 and 2020 respectively; *1-60 are genotypes

Fig. 2. AMMI 2 Biplot for seed yield/plant showing the interaction of IPCA2(Factor 2) against IPCA1 (Factor 1) scores of 60 confectionary sunflower genotypes (G) in three environments (E)

Table 2 Average seed yield, oil content, protein content and IPC scores of confectionary sunflower genotypes

Genotype No.	Genotype Name	Seed Yield/plant(g)	IPC1	IPC2	Oil content (%)	Protein content (%)
G1	EC 734812	2.35	0.15552	-0.2709	31.63	17.69
G2	EC 734888	3.77	-0.0869	-0.2374	26.97	21.71
G3	EC 734870	3.52	-0.3191	-0.2218	29.24	25.78
G4	EC 734874	4.75	0.15125	-0.1514	30.07	18.32
G5	EC 734872	8.85	0.44437	0.0314	34.84	26.43
G6	EC 734887	5.24	0.0445	-0.0441	35.79	19.83
G7	EC 734877	4.53	0.06627	-0.2008	34.26	22.58
G8	EC 734826	7.87	-0.0645	-0.0069	33.14	19.68
G9	EC 734876	5.14	0.10295	-0.0972	36.61	24.06
G10	EC 734841 –I	6.36	0.11842	0.38341	33.67	23.32
G11	EC 734841 –II	6.53	0.10398	-0.0712	25.44	20.37
G12	EC 734811	3.046	0.13288	-0.2216	31.27	27.5
G13	EC 734816 –I	9.11	0.02746	0.13638	23.62	30.38
G14	EC 734839	11.17	-0.1189	0.36471	24.71	19.63
G15	EC 734884	5.33	0.14245	-0.1465	25.5	30.15
G16	EC 734821	10.67	-0.0014	-0.2557	25.1	20.15
G17	EC 734880	12.29	-0.6679	0.37905	23.92	18.74
G18	EC 734810	5.59	0.09194	-0.3049	25.42	21.8
G19	EC 734837	13.73	0.44756	1.04782	26.16	18.06
G20	EC 734828	5.84	0.14924	-0.5012	24.19	24.7
G21	EC 734820	13.86	0.51099	0.1995	23.68	22.3
G22	EC 734867	12.97	0.03751	-0.0325	26.42	23.23
G23	EC 734883	15.62	-0.024	0.13453	33.63	18.58
G24	EC 734822 -I	7.86	-0.0452	-0.0742	31.42	20.3
G25	EC 734824	8.17	0.16294	-0.6131	23.13	21.91
G26	EC 734814	19.38	-0.0938	0.38114	26.92	19.49
G27	EC 734825	15.43	-1.0061	-0.2794	28.41	23.51
G28	EC 734864	14.28	1.25885	-0.8174	34.21	21.81
G29	EC 734881	14.053	-0.7759	-0.5677	29.57	26.19
G30	EC 734869	10.01	0.27686	-0.1938	25.29	23.25
G31	EC 734835	6.8	-0.096	-0.1258	33.35	32.87
G32	EC 734818	6.39	-0.641	-0.4716	34.32	22.54
G33	EC 734879	14.28	1.57917	0.57382	22.87	19.03
G34	EC 734809	12.74	-2.4095	0.61308	22.03	17.8
G35	EC 734817 -II	9.82	0.70056	0.01571	22.22	30.1
G36	EC 734823	3.98	-1.4309	0.11724	20.99	24.7
G37	EC 734843	6.43	1.21269	-0.3924	24.88	16.8
G38	EC 734865	5.94	-0.3559	-0.0984	26.48	27.5
G39	EC 734803	5.52	0.11823	-0.2012	27.13	29.38
G40	EC 734840	12.58	1.30415	0.42231	29.44	1.63
G41	EC 734799	10.13	-0.5525	0.24271	19.6	29.15
G42	EC 734819	7.82	-0.5623	-0.2714	31.41	20.6
G43	EC 734798	7.21	-0.0067	-0.3479	22.81	19.74
G44	EC 734863 -I	9.61	0.19104	-0.7411	26.7	22.8
G45	EC 734817 -I	12.37	-0.099	-0.0837	17.33	30.15
G46	EC 734866	13.64	0.25119	-0.3314	28.95	21.25
G47	EC 734842	8.24	-1.7103	-0.035	25.42	19.74
G48	EC 734850	12.98	2.04345	0.70418	32.78	22.8
G49	EC 734804	12.97	-0.5274	-0.1282	18.68	19.56
G50	EC 734816 –II	13.04	0.86889	-0.9836	28.42	23.7
G51	EC 734849 –I	15.21	-1.4248	0.20295	30.08	18.55
G52	EC 734807	15.98	0.97108	0.47997	19.95	17.87
G53	EC 734802	16.5	0.64432	0.80796	31.46	26.5
G54	EC 734790	22.95	0.62269	0.16775	21.15	31.23
G55	EC 734831	19.57	-0.0387	1.26101	27.3	29.55
G56	EC 734844	18.15	0.26672	-0.0059	29.92	29.23
G57	EC 734813 –I	17.805	-0.3098	-0.4611	21.62	30.87
G58	EC 734849 –II	19.62	-0.7798	0.96915	24.54	16.53
G59	EC 734792	8.945	-0.8692	-0.0815	22.12	17.32
G60	EC 734796	6.27	-0.1828	0.43427	34.24	22.55

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Assessment of *Bacillus thuringiensis* var. *kurstaki* (Bt-127) SC formulation as a component of IPM in soybean through farmer's participatory approach

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ABSTRACT

Insect pests are major biotic constraints limiting soybean production and quality. Soybean growers rely heavily on synthetic chemical insecticides to combat insect pests. Increasing concern for environmental awareness about the use of chemical insecticides has sparked interest in eco-friendly pest management alternatives. An experiment was conducted to assess Bt-127 suspension concentrate (SC) formulation as a component of IPM under real farm situation in Hegdoli village of Kotgiri Mandal, Nizamabad District, Telangana during *kharif* 2017-18. Incidence of semiloopers (*Chrysodeixis acuta* and *Mocis undata*) and tobacco caterpillar (*Spodoptera litura*) was lowered by 99.5% and 92.9% with the first spray of Bt-127 SC formulation while their incidence was lowered by 99.6% and 97.3%, respectively in farmer's practice with spray of emamectin benzoate. After second spray of Bt-127 SC formulation, incidence of *S. litura* was lowered by 91.3% and found on par with 91.5% lowering from spray of chlorantraniliprole in farmer's practice. Incidence of natural enemies in IPM field after first and second spray was higher at 0.84 and 0.72 per meter row length in comparison to 0.12 and 0.40, respectively in farmer's practice. The IPM module resulted in higher cost-benefit ratio (1: 2.36) as compared with farmer's practice (1: 1.61).

Keywords: Bt-127 SC, Economics, Insect Pests, IPM, Soybean

Soybean [*Glycine max* (L.) Merrill] is one of the important oilseed crops of the world and contributes 25% of the global vegetable oil production, about two thirds of the world's protein concentrates for livestock feeding and is an ingredient in making feeds for poultry and fish. Because of its wide range of applications in food, feed, and non-food applications, soybean is often referred to as the "miracle bean". Its products are virtually a boon to mankind because of rich source of protein (40%) and oil content (20%), as well as a variety of neutraceutical components like isoflavones, tocopherol, and lecithin. In India, soybean is grown over an area of 12.81 m ha with a production of 12.90 m tonnes and the productivity of 1007 kg/ha (DAC & FW, 2021). Soybean cultivation is mostly confined to Madhya Pradesh, Maharashtra, Rajasthan, Telangana, Andhra Pradesh, Karnataka, Chhattisgarh and Gujarat. Even though the country witnessed a spectacular increase in area and production, the productivity of the crop has remained low at one tonne per ha as compared to world average productivity of 2.31 tonnes per ha. The lower yield of soybean in India is attributed to many factors, but the insect pests play an important role in lowering the productivity (Rathod and Bhosle, 2014; Ramesh Babu *et al.*, 2018). The luxuriant crop growth, soft and succulent foliage attracts many insects. About 48 insect pest species reported to attack on different plant parts throughout the growth stages of soybean (Patil, 2002; Basappa and Duraimurugan, 2018). The most important insect pests are tobacco caterpillar *(Spodoptera litura*), green semiloopers (*Chrysodeixis acuta*, *Gesonia gemma* and *Diachrysia orichalcea*), gram pod borer (*Helicoverpa armigera*), stem fly (*Melanagromyza sojae*), girdle beetle (*Obereopsis brevis*) and whitefly (*Bemisia tabaci*). Yield losses due to these pests range from 20 to 50% (Singh and Singh, 1990). Insecticides have been used widely to control the pests on soybean because of their easy adaptability, effectiveness and immediate control. Injudicious use of chemical pesticides has led to development of several problems like development of resistance by insects, destruction of natural enemies and pollinators, pollution of the environment etc. Increasing environmental concerns coupled with requirement of residue free produce have necessitated search for alternate techniques that are eco-friendly for management of insect pests. Hence, it is necessary to adopt holistic approach with integrated pest management (IPM) in order to avoid economic damage. In ICAR-IIOR, a suspension concentrate (SC) formulation of a novel local isolate of *Bacillus thuringiensis* (Bt) var. *kurstaki* Bt-127 was developed and the formulation found effective in reducing the lepidopteran pests in soybean (AICRP on Soybean, 2017; Vimala Devi *et al*., 2020). With this background, an IPM module was formulated using Bt-127 SC formulation as a component and assessed in farmer's field for the management of insect pests in soybean.

MATERIALS AND METHODS

Field experiment was conducted in farmer's field at Hegdoli village, Kotgiri Mandal, Nizamabad District,

Telangana (Latitude 18.60°N and Longitude 77.77°E) during *kharif* 2017-18 to evaluate IPM module for the management of insect pests of soybean in comparison with farmer's practice. The soybean cultivar, JS-335 was sown on 18th June 2017 in one acre each for IPM and farmer's practices with a spacing of 30 x 10 cm. All agronomic practices were followed as per the recommendations except for pest management. The IPM module was formulated based on the benchmark survey conducted among the farmers of Hegdoli village which showed that semilooper, tobacco caterpillar, stem fly, girdle beetle, whitefly, leafhopper and pod borer are the major insect pests of soybean. The synthesized IPM module comprised of monitoring of tobacco caterpillar, *Spodoptera litura* using pheromone trap (4 traps/acre), ETL based application of Bt-127 SC formulation @ 3 ml/l against lepidopteran pests (ETL of 2 larvae of semilooper or 4 larvae of *S. litura* per metre row length), application of phorate 10CG @ 4 kg/acre at the time of sowing against stem fly and girdle beetle, destruction of YMV infected plants and foliar spray of diafenthiuron 50WP@ 1 g/l against sucking pests. The farmer's practice involved spray of chemical insecticides *viz.,* emamectin benzoate 5SG and chlorantraniliprole 18.5SC. The insecticide sprayings were given with a high volume knapsack sprayer using 500 litres of spray fluid per hectare. In each module, pre-treatment and post-treatment populations of insect pests and natural enemies were recorded. Per cent infestation of stem flies and girdle beetle was assessed in 50 randomly selected spots at 30 and 60 days after sowing, respectively. The number of tobacco caterpillar and semilooper larvae and population of natural enemies were assessed in 25 randomly selected areas of one metre row length of the crop and the average number per metre row was worked out. In case of sucking insect pests (whitefly and leafhopper), three leaves were selected one each from top, middle and bottom, total number of nymphs and adults from 50 randomly selected plants (10 plants each in five spots) were counted and average population was estimated. At harvest, per cent pod damage was assessed in 50 randomly selected spots. Seed yield was also recorded from each treatment. The data on numbers were transformed into square root values and per cent transformed into arc sine values and subjected to statistical analysis using AGRES statistical software. Finally, monetary returns and cost-benefit ratios of treatments were assessed.

RESULTS AND DISCUSSION

Effectiveness of IPM module on the incidence of insect pests: The data on population of insect pests and natural enemies before imposing each treatment and after each treatment are presented in Table 1. Two foliar sprays of Bt-127 SC formulation were carried out in the IPM module for the management of lepidopteran pests *viz.,* semiloopers (*Chrysodeixis acuta* and *Mocis undata*), tobacco caterpillar (*Spodoptera litura*) and pod borer (*Helicoverpa armigera*), while chemical insecticides were sprayed in farmer's practice. At 60 days after sowing (DAS), first spray of Bt-127 SC @ 3 ml/l in IPM module effectively reduced the population of semiloopers (0.56 and 0.04 larvae per metre row length at 7 and 14 days after spray, respectively) and tobacco caterpillar (0.48 and 0.44 larvae per metre row length at 7 and 14 days after spray, respectively) and was on par with farmer's practice of spraying of emamectin benzoate 5SG @ 0.4 g/l (0.36 and 0.04 semiloopers larvae per metre row length at 7 and 14 days after spray, respectively and 0.40 and 0.16 tobacco caterpillars per metre row length at 7 and 14 days after spray, respectively). Incidence of semiloopers and tobacco caterpillar was lowered by 99.5% and 92.9% with the first spray of Bt-127 SC while their incidence was lowered by 99.6% and 97.3%, respectively in farmer's practice with spray of emamectin benzoate. Similarly, second spray of Bt-127 SC @ 3 ml/l in IPM at 80 DAS was effective in reducing the population of tobacco caterpillar (1.12 larvae per metre row length at 14 days after spray) and on par with farmer's practice of spraying of chlorantraniliprole 18.5 SC @ 0.3 ml/l (1.04 larvae per metre row length at 14 days after spray). After second spray of Bt-127 SC, incidence of *S. litura* was lowered by 91.3% and on par with 91.5% lowering from spray of chlorantraniliprole in farmer's practice. The Bt-127 spray also resulted in low pod damage due to pod borer, *Helicoverpa armigera* (1.57% pod damage) as compared to 3.56% pod damage in farmer's practice. In the IPM module, soil incorporation of phorate10CG during sowing was efficient against stem fly and girdle beetle (4.0% and 6.0% infestation at 30 DAS and 60 DAS, respectively) when compared to farmer's practice (18.0% and 10.0% infestation at 30 DAS and 60 DAS, respectively) of using no plant protection measures. At 45 DAS, application of diafenthiuron 50WP @ 1g/l in IPM module was the best in reducing the population of sucking pests *viz*., whitefly (0.84 and 0.36 whiteflies/3 leaves/plant) and leafhopper (0.52 and 0.24 leafhoppers/3 leaves/plant), while higher population of whiteflies (2.20 and 2.32 whiteflies/3 leaves/plant) and leafhopper (3.32 and 1.88 leafhoppers/3 leaves/plant) was observed in farmer's practice, where no plant protection measures have been implemented. The findings of present study are in close conformity with many research workers in respect of effectiveness of different components used in IPM modules. Rathod and Bhosle (2014) and Motaphale *et al.* (2016) reported effectiveness of IPM module for soybean pests comprised of biocontrol agents *viz., Nomuraea rileyi, Beauveria bassiana* along with need based use of recommended chemical insecticides over spray of chemical insecticides alone. Shirale *et al.* (2010),

Knight *et al.* (2000) and AICRP on Soybean (2017) reported effectiveness of Bt insecticide formulations against various lepidopteran pests including *S. litura*. The present findings on effectiveness of soil application of phorate against stem borers (stem fly and girdle beetle) are in accordance with the findings of Motaphale *et al.* (2016). Effective management of sucking pests in IPM module was supported by Singh *et al.* (2017), who reported superior efficacy, higher yield and benefit cost ratio obtained with diafenthiuron in soybean.

Impact of IPM module on the occurrence of natural enemies: The data on impact of modules on the natural enemies revealed that IPM module was safer and recorded significantly more number of natural enemies compared to farmer's practice (Table 2). The application of Bt-127 SC formulation @ 3 ml/l in IPM module at 60 DAS and 80 DAS recorded higher number of predators *viz*., spiders and chrysopids (0.84 and 0.72 per meter row length at 14 days after first and second spray, respectively) as compared to chemical insecticides *viz*., emamectin benzoate 5SG @ 0.4 g/l and chlorantraniliprole 18.5 SC @ 0.3 ml/l sprayed in the farmer's practice (0.12 and 0.40 per meter row length at 14 days after first and second spray, respectively). The results on the safety of IPM module to potential natural enemies are in accordance with the findings of Kumar *et al.* (2019) and Motaphale *et al.* (2017) who reported significantly higher population of spiders, chrysopa and lady bird beetles in IPM module over farmer's practice involving foliar application of chemical insecticides. Thus the foliar sprays of Bt-127 SC formulation against lepidopteran pests as a component of IPM resulted in increased biodiversity of spiders and chrysopids as this is safer to natural enemies.

Table 1 Effectiveness of IPM module against major insect pests in soybean

Module	Semiloopers (larvae/plant)*			*Spodoptera litura* (larvae/plant)*		
	PTC	7 DAT	14 DAT	PTC	7 DAT	14 DAT
IPM module	8.36 (2.82)	0.56 (0.98)	0.04 (0.73)	6.20 (2.44)	0.48 (0.95)	0.44 (0.92)
Farmer's practice	9.12 (2.99)	0.36 (0.89)	0.04 (0.73)	5.88 (2.32)	0.40 (0.90)	0.16 (0.76)
CD(P=0.05)	NS	NS	NS	NS	NS	NS
Module	*Spodoptera litura* (larvae/plant)@			No. of whitefly/3 leaves/plant#		
	PTC	7DAT	14 DAT	PTC	7DAT	14 DAT
IPM module	12.92 (3.40)	1.32 (1.29)	1.12 (1.21)	2.12 (1.51)	0.84 (1.08)	0.36 (0.87)
Farmer's practice	12.16 (3.15)	0.48 (0.94)	1.04 (1.12)	2.44 (1.54)	2.20 (1.49)	2.32 (1.56)
CD(P=0.05)	NS	0.27	NS	NS	0.35	0.31
Module	No. of leafhoppers/3 leaves/plant#			Stem fly damage (%)	Girdle beetle damage (%)	Pod damage (%)
	PTC	7 DAT	14 DAT	30 DAS	60 DAS	At harvest
IPM module	3.52 (1.80)	0.52 (0.96)	0.24 (0.83)	4.0 (9.64)	6.0 (11.97)	1.57 (7.01)
Farmer's practice	3.08 (1.69)	3.32 (1.71)	1.88 (1.29)	18.0 (24.50)	10.0 (18.08)	3.56 (10.67)
CD(P=0.05)	NS	0.47	0.40	2.53	2.42	0.83

PTC- Pre treatment count; DAT- Days after treatment; DAS- Days after sowing; Figures in parentheses are transformed values; * - Observations before and after application of Bt-127SC in IPM module and emamectin benzoate in farmer's practice; @ - Observations before and after application of Bt-127SC in IPM module and chlorantraniliprole in farmer's practice; #- Observations before and after application of diafenthiuron in IPM module and no plant protection measures implemented farmer's practice

Table 2 Impact of IPM module on natural enemies in soybean

Module	No. of natural enemies (spiders and chrysopids) per m row*			No. of natural enemies (spiders and chrysopids) per m row@		
	PTC	7DAT	14 DAT	PTC	7DAT	14 DAT
IPM module	1.28 (1.26)	1.16 (1.21)	0.84 (1.09)	0.88 (1.11)	0.92 (1.12)	0.72 (1.08)
Farmer's practice	1.52 (1.32)	0.44 (0.92)	0.12 (0.77)	0.72 (1.05)	0.32 (0.87)	0.40 (0.91)
CD(P=0.05)	NS	0.23	0.18	NS	0.21	0.15

PTC- Pre treatment count; DAT- Days after treatment; Figures in parentheses are transformed values; * - Observations before and after application of Bt-127SC in IPM module and emamectin benzoate in farmer's practice; @ - Observations before and after application of Bt-127SC in IPM module and chlorantraniliprole in farmer's practice

Table 3 Seed yield and economics of IPM module in soybean

Module	Seed yield (kg/acre)	Gross returns (₹/acre)	Cost of cultivation (₹/acre)	Net returns (₹/acre)	BC ratio
IPM module	700	21350	9038	12312	1: 2.36
Farmer's practice	450	13725	8530	5195	1: 1.61

Cost of seed - Rs. 30.50/kg

Impact of IPM module on yield and economics: Significant impact of IPM module over farmer's practice in consideration of seed yield was noted. IPM module exhibited higher mean seed yield (700 kg/acre) as against 450 kg/acre in farmer's practice (Table 3). Net profit of soybean raised under IPM module was relatively higher (₹12312/acre) than farmer's practice (₹5195/acre). The cost effectiveness of IPM module was high with cost-benefit ratio of 1:2.36 as compared to farmer's practice (1: 1.61). The results were in accordance with the findings of Vinayagam and Dupare (2019) and Kumar *et al*. (2019), who also reported highest seed yield and highest return per rupee with the IPM module as compared to chemical intensive farmer's practice in soybean. Use of action economic thresholds and conservation of occurring natural enemies are fundamental component of a sound IPM programme. Similarly, inclusion of novel biopesticides or botanicals or insecticide molecules in the IPM strategy is a healthy sign as it will lead to the reduced selection pressure on the limited number of efficacious products. The results established that Bt-127 SC formulation @ 3 ml/l had the economic potential to substitute chemical insecticides for the management of lepidopteran pests without any adverse effects on environment, natural enemies and human health. The present study thus revealed that IPM practice involving monitoring of tobacco caterpillar (*S. litura*) using pheromone trap (4 traps/acre), destruction of YMV infected plants, ETL based application of Bt-127 SC formulation @ 3 ml/l against lepidopteran pests, application of phorate 10CG @ 4 kg/acre at the time of sowing against stem fly and foliar spray of diafenthiuron 50WP @ 1 g/l against sucking pests can be used for effective and economic management of insect pests in soybean.

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Identification of potential districts for technology transfer in sesame (*Sesamum indicum* L.)

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ABSTRACT

India is the largest producer of sesame in the world with an area of 16.22 lakh ha and production of 6.57 lakh t and contributing to 10.5% and 11.1% of the Worlds' area and production, respectively. The AICRP-sesame centres have developed location-specific improved technologies, which can enhance sesame productivity significantly, but the awareness and adoption of these technologies among farmers is very low. Hence, focused efforts are required to transfer the existing technologies from the AICRP system to the farmers' fields through effective and efficient technology transfer programmes. To have focussed efforts for productivity enhancement and area expansion of sesame, state-wise most efficient sesame cropping districts were identified by estimating the Relative Spread Index (RSI) and Relative Yield Index (RYI). Frontline demonstrations conducted in selected districts in the most efficient, efficient, and moderately efficient districts indicated a huge yield gap and vast potential to improve the sesame productivity under real farm situations. The extension strategies to be followed in technology transfer in various categories of districts for enhancing the productivity and area expansion of sesame crop are mentioned.

Keywords: FLDs, Most Efficient Districts, Sesame, Technology transfer

Sesame (*Sesamum indicum* L.) is cultivated over an area of 16.22 lakh ha with a production of 6.57 lakh t and productivity of 405 kg/ha (Directorate of Economics and Statistics, 2019). Even though India ranks first in the area and second in sesame production by contributing to 10.5% and 11.1% of the Worlds' area and production respectively, the productivity is low (FAO, 2019). Sesame contains 50% oil, 25% protein, and 15% carbohydrates. The oil contains about 40% oleic and 40% linoleic acid. Oil has a long shelf-life due to the presence of an antioxidant called sesamol. Sesame is also called gingelly, til, benne seed and popularly known as "Queen of Oilseeds" due to its high degree of resistance to oxidation and rancidity (Pathak *et al.,* 2014). Oil is used in the manufacture of soaps, paints, perfumes, pharmaceuticals, and insecticides. In India, it is grown mainly in the states of Madhya Pradesh, Rajasthan, Uttar Pradesh, Maharashtra, Gujarat, Karnataka, Odisha, West Bengal, and Tamil Nadu.

The yield levels of sesame in India are low due to non-adoption of good agronomic management practices by the farmers, cultivation of old varieties with low yields, cultivation of the crop on marginal lands without proper nutrient management, lack of mechanization, delayed harvesting due to labour shortages resulting in seed shattering, biotic and abiotic stresses (Raikwar and Srivastava, 2013). Farmers generally allocate soils with poor nutrients and low fertility status, and marginal lands for the cultivation of sesame crop. Identification of efficient districts and adoption of good management practices for cultivation of sesame are important to improve productivity levels.

Enhancing and maintaining sustainability in crop productivity is possible only when efficient locations are identified for crops. Efficient zone is an area which has a high spread and high productivity of the crop. Spread of a crop is directly related to market prices and availability of specific infrastructure facilities, but the spread may not be the same over a period in a particular area. Further, crop productivity depends on suitable bio-physical characteristics and management practices adopted by the farmers (Ramamurthy *et al.,* 2018).

The present study was conducted to identify efficient districts and map the performance of improved technologies (IT) under FLDs in these districts.

MATERIALS AND METHODS

For identifying efficient districts, Relative Yield Index (RYI) and Relative Spread Index (RSI) were estimated based on the methodology of Kanwar (1972). These were calculated based on the district-wise area and productivity of sesame for the past 10 years.The district-wise secondary data related to area, production, productivity, and total cultivable area of sesame and other crops in all states were collected for the period, 2008-09 to 2018-19 from the respective states (Directorate of Economics and Statistics, 2020).

The following formulae were used for the estimation of RSI and RYI.

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$$RSI = \frac{\text{Area of the particular crop expressed as \% of the total cultivable area in the district}}{\text{Area of that crop expressed as \% to the total cultivable area in the country}} \times 100$$

$$RYI = \frac{\text{Mean yield of a particular crop in a district}}{\text{Mean yield of that particular crop in the country}} \times 100$$

Based on the RSI and RYI values, the districts were categorized into most efficient (RSI > 125 and RYI > 125), efficient (RSI < 125 and RYI > 125), moderately efficient (RSI > 125 and RYI <125), and inefficient districts (RSI < 125 and RYI <125) as per the methodology suggested by Ramamurthy *et al.* (2018). The idea was to narrow down the number of districts for more focus and impact.

Most efficient cropping districts are areas, where a particular crop has high spread and high productivity and these areas are bio-physically suitable for the cultivation of the crop. Efficient cropping districts are areas, where there is low spread but high productivity and are biophysically suitable to a particular crop. Moderately efficient cropping districts are areas, where there is high spread but low productivity and are biophysically suitable to cultivate the crop. Inefficient cropping districts are areas, where both spread and productivity are low and substitution of the crop is necessary and should not be recommended to grow the crop in these districts.

To show the productivity potential and profitability of improved technologies, frontline demonstrations (FLDs) were conducted by the scientists of AICRP's voluntary centres, KVKs, and NGOs in various categories of districts during 2017-18 to 2019-20. Each demonstration on whole package was conducted in an area of 0.4 ha with improved technologies such as new cultivar, optimum seed rate, and spacing, nutrient management, and management of pests and diseases. In the remaining area, sesame was grown with farmers' practices. FLDs were conducted in two most efficient, one efficient, and twelve moderately efficient districts prior to actual categorization of districts and the FLDs data was mapped over districts post-categorization. The various yield gaps (I, II, III and IV) were estimated.

RESULTS AND DISCUSSION

In all, 102 districts were identified as potential districts for sesame cultivation in India based on RSI and RYI values. Thirteen most efficient districts spread over different states of West Bengal, Gujarat, Tamil Nadu and Karnataka were identified. Twenty seven efficient districts spread in West Bengal, Tamil Nadu, Maharashtra, Gujarat, Madhya Pradesh, and Karnataka, and 62 moderately efficient districts spread in Gujarat, Uttar Pradesh, Rajasthan, Madhya Pradesh, Tamil Nadu, Andhra Pradesh, and Karnataka were identified (Table 1). In most efficient districts emphasis should be placed on the use of improved production technologies for increasing productivity and profitability and the transfer of advanced and niche technologies such as INM, IPM and mechanical harvesting. In efficient districts, the major focus should be placed on area expansion by conducting several extension programmes. In moderate districts, the focus should be on transfer of improved technologies and hastening the adoption process by the farmers through intensive campaigns. The inefficient districts may not be considered for promoting sesame cultivation and the possibilities for crop substitution should be explored.

Table 1 Categorization of districts based on RSI and RYI

Efficient District	Number	Districts
Most efficient districts	13	West Medinipur, Hooghly, Bankura, Nadia, Howrah, Jhargram, Purbabardhaman, Murshidabad, South 24 Paraganas, Jamnagar, Junagadh, Villupuram, Chikmagalur
Efficient districts	27	Birbhum, Paraganas north, Paschimbardhaman, Jalpaiguri, Coochbehar, Medinipur east, Dinajpurdakshin, Darjeeling, Salem, Jalgaon, Nandurbar, Bharuch, Panchmahals, Girsomnath, Navsari, Narmada, Alipurduar, Tapi, Balaghat, Rajgarh, Guna, Ashoknagar, Narsinghpur, Dewas, Ratlam, Davangere, Chikballapur
Moderately efficient districts	62	Botad, Surendranagar, Kachchh, Morbi, Bhavnagar, Amreli, Dohad, Rajkot, Mahesana, Banaskantha, Patan, Jhansi, Hamirpur, Jalaun, Banda, Hardoi, Sonbhadra, Fatehpur, Unnao, Lalitpur, Sitapur, Chitrakoot, Pali, Sawaimadhopur, Sirohi, Karauli, Tonk, Bhilwara, Kota, Dausa, Bundi, Ajmer, Jalore, Jodhpur, Rajsamand, Baran, Dholpur, Datia, Sidhi, Gwalior, Tikamgarh, Singrauli, Sheopur, Umaria, Bhind, Morena, Katni, Satna, Shivpuri, Shajapur, Karur, Erode, Cuddalore, Virudhunagar, Ariyalur, Prakasam, Anantapur, Kadapa, Mandya, Koppala, Ramanagara, Mysore

Table 2 State-wise suitable cultivars of sesame

State	Variety
Andhra Pradesh	YLM-66, Swetha til
Gujarat	GJT-5, GT-6, GT-10, RT-372, RT-351
Rajasthan	RT- 346, RT- 351, RT-372
Maharashtra	PKV-NT-11, JLT-408, RT-351
Madhya Pradesh	Jawahar Til –12, (PKDS-12), Jawahar Til –14, TKG-308 (PKDS-8)
West Bengal	Suprava (CUMS-17), Savitri
Tamil Nadu	TMV(SV)-7, VRI 3
Karnataka	DSS-9, DS-5, RT-372, RT-351, Suprava
Uttar Pradesh	RT-372, RT-351
All India	GT-10, RT-351

At present, the district-wise varieties were not recommended and hence state-wise improved varieties and technologies for sesame to be demonstrated in the selected districts are given in Table 2 and 3, respectively. The frontline demonstrations conducted in most efficient districts showed that the seed yield of sesame was 26% higher as compared to farmers' practice. Twenty six per cent of yield gap -I was observed in these districts as compared to farmers' practices (Table 4). The districts are highly suitable for sesame cultivation and concerted efforts in these districts will result in a huge jump in the productivity (1574 kg/ha) of the crop. Further, the emphasis in these districts should be on value addition, developing value added products of sesame so that complete value chain may be created for increasing the income of farmers. In efficient districts, the productivity improvement was to the tune of 17% (Yield gap-I). Huge productivity improvement of up to 40% is possible in moderately efficient districts by bridging the yield gap-I. The yield gaps-I observed in these districts ranged from 29 to 117.5%. These districts have a high potential for area expansion and productivity improvement. The FLDs had clearly indicated that in a few of the districts, significant improvement in productivity (544 kg/ha) is possible with the adoption of improved technologies by the farmers. The focus in these districts has to be on conducting large scale cluster FLDs, capacity building of farmers, farmer participatory seed production, and rapid technology transfer efforts in convergence with other stakeholders.

In most efficient districts, the productivity with improved technology was higher as compared to district average yield. High yield gap-II of 82.5% and 99.2 % were observed in West Medinapur and Bankura, respectively. This clearly indicates the possibility of doubling the production of sesame in these districts with concerted extension efforts. In efficient districts the yield increment due to improved technology was 54.8% (Yield gap-II) observed in Jalgaon. In moderately efficient districts huge yield gap was noticed and ranged from 6 % to 256.5% (Yield gap-II) and negative yield gap of 10 and 32% was observed in Kadapa and Banda respectively due to aberration in rainfall during the period of demonstrations. It indicates there is a need to increase the productivity in moderately efficient districts.

The yield gap-III indicates the increase in productivity with improved technology as compared to state average yield. In most efficient districts, the yield gap-III was 69% and 68% in West Medinapur and Bankura, respectively. In efficient district, huge gap of 156% was seen in Jalgaon. In moderately efficient districts, the yield gap-III ranged from 2% to 169% in Amreli and Hamirpur, respectively.

The yield gap-IV as a result of the demonstration of improved technology over the national average yield was very high to the tune of 231% in most efficient district and 4% in efficient district. In moderately efficient districts, the yield gap was ranged from -.47.76% to 74.5% in Banda and Vriddhachalam, respectively. The productivity potentials and economics of improved sesame production technologies showed that there exists a vast potential to improve the sesame productivity under real farm situations through conduct of various extension programmes such as, cluster FLDs, awareness campaigns, result and method demonstration, field days, use of location specific technology, capacity building of farmers and agricultural department staff and convergence of efforts of all stakeholders.

Table 3 Strategies for dissemination of technology

State/districts	Recommended Technology	Extension strategy
All identified districts	Crop management technologies One hand weeding at 15 DAS + vegetative mulching (4 t/ha organic waste) was the best *in-situ* moisture conservation technique for maximum seed and oil yield of sesame.	Voice advisories, information dissemination through folders, leaflets,
	Application of zinc (20 kg $ZnSO_4$/ha) and iron (25 kg $FeSO_4$/ha) and with RDF and 2.5 t FYM gave the maximum seed yield and economic returns.	Specific crop advisory, Radio, TV channels, Farmer meeting
	Terminal nipping at 30 DAS followed by spraying of Salicylic acid (SA) @ 100 ppm/ha and DAP 2% enhances the plant growth and gave higher seed yield.	Social media, tele-advisories through telephone services
	Application of FYM @ 12.5 t/ha + *Azospirillum* + Phosphobacteria + PGPR each @ 600 g/ha + soil application of biofertilizer (*Azospirillum* + Phosphobacteria + PGPR each @ 2 kg/ha) and foliar application of panchagavya 3% spray at 30 and 45 DAS for organic sesame production.	Group meetings, method demonstrations, result demonstrations
Identified districts in Tamil Nadu	Sowing of sesame after harvest of rice under till condition with combined nutrient spray of 1% urea and 2% DAP,	WhatsApp group of targeted farmers, information dissemination through local Radio and local newspaper. TV channels.
Identified distircts in Tamil Nadu and Madhya Pradesh	Seed pelleting with neem leaf powder @ 760 g + 120 g *Azotobacter* + 120 g phosphobacteria for 1 kg seed with 1.5 % combined nutrient spray at 30 & 45 DAS for early pest control and nutrient management	Use of mass media, method demonstration, group meetings,
All identified districts	Crop protection technologies Management of sesame phyllody vectors through newer molecules indicated that the minimum vector incidence (leafhopper), higher seed yield, and BC ratio was recorded from seed treated with imidacloprid 70 WS (7.5 g/kg seed) and two foliar sprayings of thiamethoxam 25 WG @ 0.25 g/l or imidacloprid 17.8 SL@ 0.3 ml/l at 30 and 45 DAS.	Advisory services through Toll-free Number, ICT based information Dissemination
	For the management of *Tribolium castaneum* in stored sesame spinosad 45 SC (0.5 ml/kg seed) was found most effective and gave 100% mortality of beetles at 5 days after release. However, among plant products, NSK powder (5g/kg seed) was found most effective and gave 90% mortality at 25 days after treatment.	Creating and distributing program materials, such as flyers, guides, pamphlets, and DVDs
	Application of IPM module comprising seed treatment with imidacloprid 600 FS @ 5 ml/kg seed + intercropping with green gram (3:3) along with yellow sticky traps then one foliar spray of profenofos (2 ml/l) at 30 days after sowing, if a needed second foliar spray of NSKE 5% was effective to manage insect pests of sesame.	Method demonstrations, result demonstrations, use of mass media, advisory services, Awareness programme, Distribution of leaflets Web portal,
	Integrated management of foliar disease of sesame: seed treatment with *T. viride* @ 10 g/kg, furrow application of enriched *T. viride* (2.5 kg in 100 kg of FYM) @ 250 kg/ha followed by foliar spray of combi-product (Tebuconazole 50% + Trifloxystrobin 25%) @ 0.5 g/l was found effective	Advisory service through SMS, Watts app group chat, Group discussion, Farmers and scientist interaction meetings
	Integrated management of stem and root rot of sesame: Seed treatment with *T. viride*+ *Pseudomonas fluorescens* @ 10g/kg +soil application of *T. viride+P. florescence* before sowing @2.5 kg/ha (enriched with 100 kg of FYM + neem cake) @ 250 kg/ha, followed by foliar spray of combi-product (Tebuconazole 50% + Trifloxystrobin 25%) @ 0.5 g/l.	
Identified districts in Odisha	For the management of rice moth (*Corcyra cephalonica*) in stored sesame, seed treated with neem seed kernel powder (5g/kg of seed) and neem leaf powder (5g/kg of seed) were found most effective treatment.	Group meeting, Method demonstration, Use of mass media

Table 4 Productivity potential and various yield gaps in sesame with improved technologies

State	District/Centre	FLDs (No.)	Improved technology	Mean seed yield (kg/ha)		Yield gap-I (%)	DAY	SAY	NAY	Yield gap-II (%)	Yield gap-III (%)	Yield gap-IV (%)
				IT	FP							
Most Efficient Districts												
West Bengal	West Medinipur	121	Savitri variety, seed treated with imidacloprid 70 WS @ 7.5 g/kg seed and two foliar sprays of imidacloprid 17.8 SL@ 0.3 ml/l at 30 and 45 DAS and soil test based fertilizer application	1575	1275	23.5	863	932	475	82.5	69.0	231.6
	Bankura	90		1572	1214	29.5	789	932	475	99.2	68.7	230.9
Mean		211		1574	1249	26						
Efficient Districts												
Maharashtra	Jalgaon	60	RT-351 variety and line sowing	495	422	17.5	320	193	475	54.8	156.2	4.3
Moderately Efficient Districts												
Uttar Pradesh	Jhansi/Mauranipur	41	RT-351 variety, seed treatment with *T. viride* @ 10 g/kg, line sowing and management of phyllody	453	254	78.1	127	235	475	256.5	92.7	-4.7
	Mahoba	60		459	354	29.6	313	235	475	46.5	95.2	-3.4
	Hamirpur	15		633	474	33.5	197	235	475	221.3	169.4	33.3
	Banda	15	RT-351 variety	249	193	29.0	368	235	475	-32.3	6.0	-47.6
Madhya Pradesh	Tikamgarh	30	TKG-308 variety, line sowing, soil test based fertilizer application and integrated pest management	633	291	117.5	389	467	475	62.5	35.6	33.3
	Sidhi	5		632	310	103.9	378	467	475	67.1	35.4	33.1
	Satna	60		547	353	55.0	360	467	475	51.9	17.1	15.2
Rajasthan	Mandor	31	RT-351 variety,	479	370	29.5	411	315	475	16.6	52.1	0.9
Gujarat	Amreli	44	GT-10 variety, seed treatment with imidacloprid 70 WS @ 7.5 g/kg seed, line sowing, soil test based fertilizer application	591	456	29.7	558	580	475	6.0	2.0	24.5
Andhra Pradesh	Kadapa	24	GT-10 variety and line sowing, soil test based fertilizer management and seed treatment with with imidacloprid 70 WS @ 7.5 g/kg seed	543	450	20.7	603	292	475	-10.0	86.0	14.3
	Prakasam	77		490	403	21.6	282	292	475	73.8	67.8	3.2
Tamil Nadu	Vriddhachalam	45	VRI-3 variety, line sowing of sesame after harvest of rice under till conditions, integrated management of pests and diseases	829	592	40.1	649	577	475	27.7	43.6	74.5
Mean		447		544	387	40.5						

Yield gap-I (%)=Increase in seed yield of IT over FP; Yield gap-II (%)=Increase in seed yield of IT over District average yield;Yield gap- III (%)=Increase in seed yield of IT over state average yield; Yield gap- IV (%)=Increase in seed yield of IT over National average yield; IT=Improved practices; FP=Farmers' practices

Table 5 Economic returns of sesame cultivation in efficient districts

State	District/Centre	Cost of cultivation (₹/ha)		Gross returns (₹/ha)		Additional net returns (₹ ha)	B:C ratio	
		IT	FP	IT	FP		IT	FP
Most Efficient Districts								
West Bengal	West Medinapur	23867	22567	60092	52833	5958	2.52	2.34
	Bankura	22950	20000	58050	48000	7100	2.53	2.40
Mean		23476	21472	59221	50772	6445	2.52	2.36
Efficient Districts								
Maharashtra	Jalgaon	18257	17456	43458	36556	6101	2.38	2.09
Moderate Efficient Districts								
Uttar Pradesh	Jhansi/Mauranipur	19872	15965	38590	22282	12401	1.94	1.40
	Mahoba	16750	15500	47138	30973	14915	2.81	2.00
	Hamirpur	13743	13343	39602	29637	9565	2.88	2.22
	Banda	5100	4500	13537	10615	2322	2.65	2.35
	Tikamgarh	21254	11660	56640	27045	20001	2.66	2.32
Madhya Pradesh	Sidhi	11475	9200	40972	20117	18580	3.57	2.19
	Satna	17864	14717	57496	35900	18449	3.22	2.44
Rajasthan	Jodhpur/Mandor	17098	16226	29845	23030	5943	1.75	1.42
Gujarat	Amreli	24121	21681	63636	50201	10995	2.64	2.32
Andhra Pradesh	Kadapa	11946	10575	27367	20880	5116	2.29	1.94
	Prakasam	10850	9500	24713	18738	4625	2.29	1.97
Tamil Nadu	Vriddhachalam	23555	23361	65548	45363	19991	2.78	1.94
Mean		17098	14820	44286	29865	12143	2.59	2.02

Profitability of FLDs in various categories of districts: The cost of cultivation in all the districts was higher with improved technologies as compared to farmers' practice. The average cost of cultivation was higher in most efficient districts compared to other districts in both IT and FP. The gross monetary returns were also higher in most efficient districts compared to other districts indicating the higher profitability with improved technologies. The additional net returns were lower in efficient districts and most efficient districts compared to moderately efficient districts indicating higher cost of cultivation in most efficient districts.

In most efficient districts, the average cost of cultivation with improved practice and technologies was maximum in Bankura, West Bengal (₹22,950/ha) in comparison with farmer's practice (₹20,000/ha). The maximum average gross monetary returns with improved technology was ₹ 65,548/ha in moderately efficient districts. The maximum net returns observed were ₹20,001/ha in Tikamgarh followed by ₹19,991 in Vridhhachalam, ₹18,580 in Sidhi, ₹18,449 in Satna and ₹14,915 in Mahoba (Table.5).

Even though the cost of cultivation is high in most efficient district, the gross monetary returns (GMR) and B:C ratios were also higher than other districts indicating high profitability of the crop. In moderately efficient districts, the additional net returns (ANR) were higher compared to other districts indicating high profitability to farmers with additional investment, which will go a long way in sustaining the profitability of the crop in the district.

The study clearly brought out the efficient districts for area expansion and productivity improvement to have a focused and mission mode approach. The study also indicated the possibility of productivity enhancement in different districts through FLDs. The recommended technologies and the extension strategies to be adopted were indicated. Focused efforts and convergence of all the stakeholders will go a long way in area expansion and productivity of sesame crop in India.

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Role of phosphorus and molybdenum on root growth, nodulation and nutrient uptake of soybean [*Glycine max* (L.) Merr.]

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ABSTRACT

A field investigation was carried out during *kharif* 2015 to study the response of soybean to phosphorus and molybdenum nutrition. Results revealed that the interaction effect of phosphorus application (60 kg P_2O_5/ha) and molybdenum seed treatment @ 6 g/kg seed recorded significantly higher vigour index-I (2305), vigour index- II (90), root length (21.26 cm), root volume (12.70 cm^3), effective nodules/plant (37), nodule dry weight (50.73 mg), oil content (19.43 %) and molybdenum uptake by seed (4.10 g/ha). The leghaemoglobin content was highest (249 µg/g fresh weight) with P application @ 60 kg/ha and it was unaffected due to Mo seed treatment and interaction of P and Mo. Among the P levels, protein content and seed yield were significantly higher (41 % and 1784 kg/ha) with 60 kg/ha and with Mo seed treatment @ 6 g/kg seed (40.2 % and 1572 kg/ha).

Keywords: Molybdenum, Nodulation, Nutrient uptake, Phosphorus, Root growth, Soybean

Vegetable oils are critical for the nutritional security of an economy. Annual production of oilseeds in India is experiencing a high degree of fluctuation mainly due to the poor input management, declining factor productivity in drylands and rainfed tracts. Soybean popularly known as 'Golden or miracle bean' is the foremost important oilseed crop known for its excellent protein (42-45%), oil (20%) and starch content (21%). Contribution of soybean to total oilseed production and acreage during 2019-20 was 33.6% and 44.7%, respectively. Madhya Pradesh is the leading state in area (6.2 m ha) and production (5.2 m t) of soybean in the country with a contribution of 47.9% to area and 48.5% to production (Chauhan *et al.,* 2021). During 2019-20, among the states having substantial area under this crop, Telangana state had the highest seed yield (1808 kg/ha) followed by Maharashtra (1138 kg/ha) and Karnataka (1137 kg/ha) (Chauhan *et al.,* 2021).

Phosphorus nutrition is pivotal for sustained legume productivity and sub-optimal phosphorus application is one of the major and the most common constraints behind poor soybean productivity in India. Indian soils are beset with a higher degree of variability in crop response to different doses and sources of phosphatic fertilizers in different agro-climatic zones due to wide variations in fixation of applied fertilizer material owing to variations in soil pH, organic matter, calcium status and a complex chain of processes and factors that govern the ultimate phosphorus availability to crop plants.

Phosphorus plays a crucial role in root growth and development of seed, energy transformations, improvement of oil content, metabolic processes and aids in symbiotic nitrogen fixation by increasing the nodulation (Raghuveer and Hosmath, 2018). Among the micronutrients, molybdenum is an important nutrient for legumes which is most significant for nodulating bacteria in the process of atmospheric nitrogen fixation for the conversion of the atmospheric inorganic nitrate form into organic (amino acid) form and is involved in the synthesis of ascorbic acid. It is a co-factor of enzymes like nitrogenase, nitrate reductase, xanthine oxidase / dehydrogenase and sulphite reductase (Mendel, 2013). Since molybdenum is required in small quantity, application of this nutrient particularly through seed treatment at optimum concentration would increase root elongation with greater root proliferation and nodulation apart from reducing the cost of application. Further, the effect of molybdenum application in soils which are low or deficient in nitrogen has marked influence on nodulation, nitrogen fixation, yield attributes and yield.

Keeping these points in view, a field study was conducted on Alfisols of College Farm, College of Agriculture, Professor Jayashankar Telangana State Agricultural University, (PJTSAU) Rajendranagar, Hyderabad during *kharif* 2015. The experiment consisted of 12 treatments *viz.,* three levels of phosphorus application (0, 30 and 60 kg/ha) and four levels of seed treatment with molybdenum (0, 2, 4 and 6 g/kg seed) laid out in randomized block design with factorial concept (Table 1) and replicated thrice. The experimental site is geographically located at 170 19' N latitude, 780 28' E longitude an altitude of 542.3 m above mean sea level. The soil of the experimental site was sandy loam in texture, with pH of 7.4, electrical conductivity of 0.23 dS/m, low in organic carbon (0.39 %), low in available nitrogen (218.0 kg/ha) and medium in available phosphorus

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(33.3 kg P_2O_5/ha), high in available potassium (410.0 kg/ha) and the available molybdenum was (0.28 ppm) above critical level. Entire phosphorus (DAP), as basal dose and seed treatment with molybdenum (Ammonium molybdate, 54% Mo) was done as per the treatments. Remaining fertilizers i.e., 20 kg N/ha (urea) and K_2O (muriate of potash @ 40 kg/ha) were applied as basal placement at 5 cm depth and 5 cm apart by the side of seed row. Seed treatment was done with Bavistin @ 2 g/kg seed followed by molybdenum as per the treatments and finally with biofertilizer (*Rhizobium japonicum*). Sowing (variety JS-335) was done on 6th July, 2015 adopting a spacing of 45 cm between rows and 5 cm between plants. The gross and net plot size were 5.85 m x 3.0 m and 4.95 m x 2.9 m, respectively. Pre-emergence herbicide Pendimethalin 30% EC @ 1 kg a.i./ha was sprayed next day after sowing under optimum soil moisture conditions. At later stages of crop, weeds were controlled by manual weeding at 20-25 DAS. Bio-metric observations were taken on five representative plants selected randomly treatment wise from net plot and the mean values were presented. The data were statistically analyzed duly following the analysis of variance technique for randomized block design with factorial concept as suggested by Gomez and Gomez (1984). The oil content of seed for each treatment was determined by using continuous type Pulsed Nuclear Magnetic Resonance (NMR oxford MQC). For calculating vigour indices, on the same day of sowing in main field, simultaneously seed was also sown in pot culture (12 x 3=36 No.) as per the treatments (Table 1) and replicated thrice following recommended package of practices. After 15 days, seedling length (cm) and dry weight (g) were recorded treatment wise and the seedling vigour indices (I and II) were calculated as per the formula (Abdul-Baki and Anderson, 1973).

Seedling vigour index- I = Germination (%) x Seedling length (cm)
Seedling vigour index- II = Germination (%) x Seedling dry weight (g)

Root volume was measured using water displacement method (Burdett, 1979). Effective nodules from the destructive plant samples were counted by observing the pink colour when they were pressed with fingers and the nodules were oven dried at 65°C for 24 hours and the final dry weights were recorded. The leghaemoglobin content in fresh nodules (40 DAS) was quantified (µg/g fresh weight) calorimetrically as haemochromogen as outlined by (Hartee *et al.,* 1957).

It could be inferred from the data that all the parameters were significantly influenced due to P and Mo application. The interaction effect of varying levels of P and seed treatment with Mo was significant on vigour indices I and II (Table 1). Among the treatment combinations, application of P_2O_5 @ 60 kg/ha and molybdenum seed treatment @ 6 g/kg recorded greater vigour index-I (2305 and vigour index-II (90) over rest of the treatment combinations. Increased vigour index-I recorded with this treatment combination was due to improved germination (%) and seedling length (cm) over rest of the treatments. Similarly, highest vigour index-II was due to the adequate nutrition that produced higher initial energy resulting in good seed germination (%) besides greater seedling dry weight (g) over rest of the treatment combinations. Similar results on improved vigour indices with phosphorus and Mo application were reported by Prashanth *et al.* (2006) and Sreedhara *et al.* (2012).

Root parameters at 60 DAS (Table 2) *viz.,* root length and volume were significantly higher (21.26 cm and 12.70 cm3) with the combined application of P_2O_5 @ 60 kg/ha and seed treatment with molybdenum @ 6 g/kg over corresponding lower level of P (30 and 0 kg/ha) and Mo (4, 2 and 0 g kg/seed) interaction. Improved root length and volume associated with this treatment was probably due to adequate phosphorus availability that promoted better cell division and cell enlargement reflecting in better root elongation and higher rootlets (Raghuveer and Hosmath, 2018).

Similarly, the nodule parameters (effective nodules/plant and nodule dry weight) were significantly higher with the application of phosphorus @ 60 kg P_2O_5/ha and molybdenum seed treatment @ 6 g (Table 3) and this improvement could be attributed to the beneficial effect of phosphorus and molybdenum on nodule growth and development, energy transformation and enhanced root activity (Alben Awomi *et al.,* 2012; Marcos *et al.,* 2016).

With respect to the leghaemoglobin content the interaction effect of P and Mo as well molybdenum seed treatment was non-significant. Contrary to this, varying levels of P application significantly influenced leghaemoglobin content. Among the phosphorus treatments, application of 60 kg P_2O_5/ha significantly improved the leghaemoglobin content (249 µg/g fresh weight) over 30 (232 µg/g fresh weight) and 0 kg P_2O_5/ha (207 µg/g fresh weight). Significantly higher leghaemoglobin content in nodule with the corresponding increase in P_2O_5 levels might be attributed to enhanced P uptake and profuse nodulation leading to increased N fixation (Ismail and Bodke, 2013).

From the data on seed yield (Table 4) it is evident that that there was a linear and significant increase with a corresponding increase in P application from 0 (1212 kg/ha) up to 60 kg P_2O_5/ha (1784 kg/ha). The improvement in seed yield with 60 kg P_2O_5 was to the tune of 19.97 and 47.19 % over 30 and 0 kg P_2O_5/ha, respectively. Among the varying levels of Mo seed treatments, 6 g/kg seed recorded significantly higher seed yield (1572 kg/ha) over 4 (1521 kg/ha), 2 g (1467 kg/ha) and no seed treatment (1418 kg/ha). The improvement in seed yield with Mo seed treatment @ 6 g was to the extent of 10.86, 7.15, 3.35% over 0, 2 and 4 g/kg seed. Higher seed yield with the application of 60

P_2O_5/ha and Mo seed treatment @ 6 g was due to the improved root growth, nodulation and nodule activity and higher nutrient uptake under adequate nutrient availability. Similar results of improved seed yield with optimum application of P and Mo in lentil were reported by Togay *et al.* (2008) and Spandana *et al.* (2021). Improved oil content (18.90 and 18.7%) with application of phosphorus @ 60 kg P_2O_5/ha along with seed treatment molybdenum @ 6 g/kg seed could be attributed to the adequate P that help in synthesis of fatty acids and their esterification by acceleration of biochemical reactions in glyoxalate cycle (Myo *et al*., 2010) apart from the fact that P is a constituent of phospholipids and is highly essential for oil synthesis (Sharma *et al*., 2012).

Table 1 Vigour index -I and II as influenced by the interaction of phosphorus and molybdenum nutrition

Factor –A P levels (kg/ha)	Factor – B Molybdenum seed treatment (g/kg)										
Vigour index-I	Mo1-0	Mo2-2	Mo3-4	Mo4-6	Mean (P)	Vigour index-II	Mo1-0	Mo2-2	Mo3-4	Mo4-6	Mean (P)
P1-0	1220	1256	1298	1361	1284	P1-0	62.0	63.0	68.0	72.0.	66.2
P2-30	1414	1510	1647	1812	1596	P2-30	73.0	75 .0	79 .0	82.0	77.2
P3-60	1910	2020	2121	2305	2089	P3-60	84 .0	86 .0	80 .0	90 .0	85.0
Mean (Mo)	1515	1596	1689	1826		Mean (Mo)	73 .0	74.6	75.6	81.3	
P x Mo	S.Em ±	34				P x Mo	S.Em ±	3.4			
	CD (p=0.05)	99					CD (p=0.05)	8.5			

Table 2 Root length (cm) and volume (cm^3) at 60 DAS as influenced by the interaction of phosphorus and molybdenum nutrition

Factor -A P levels (kg/ha)	Factor – B Molybdenum seed treatment (g/kg)										
Root length (cm)	Mo1-0	Mo2-2	Mo3-4	Mo4-6	Mean (P)	Root volume (cm^3)	Mo1-0	Mo2-2	Mo3-4	Mo4-6	Mean (P)
P1-0	13.06	14.30	15.53	16.10	14.75	P1-0	7.00	7.20	8.10	8.60	7.72
P2-30	16.76	17.23	17.80	18.50	17.57	P2-30	9.20	9.40	10.10	10.40	9.77
P3-60	18.96	19.40	20.23	21.26	19.96	P3-60	11.16	11.50	12.23	12.70	11.90
Mean (Mo)	16.26	16.97	17.85	18.62		Mean (Mo)	9.12	9.36	10.14	10.56	
Interaction (P x Mo)											
	S.Em ±	0.19	-	-	-	P x Mo	S.Em ±	0.06	-	-	-
	CD (p=0.05)	0.57	-	-	-	-	CD (p=0.05)	0.18		--	-

Table 3 Effective nodules/plant and nodule dry weight (mg/plant) at 60 DAS as influenced by the interaction of phosphorus and molybdenum nutrition

Factor -A P levels (kg/ha)	Factor – B Molybdenum seed treatment (g/kg)										
Effective nodules/ plant	Mo1-0	Mo2-2	Mo3-4	Mo4-6	Mean (P)	Nodule dry weight (mg/plant)	Mo1-0	Mo2-2	Mo3-4	Mo4-6	Mean (P)
P1-0	20.6	22.3	22.0	25.0	22.5	P1-0	26.13	28.86	31.33	33.26	29.90
P2-30	26.6	28.6	30.0	31.0	29.0	P2-30	34.66	36.33	38.26	41.33	37.65
P3-60	32.3	33.6	35.6	37.0	34.6	P3-60	43.26	45.93	48.53	50.73	47.11
Mean (Mo)	26.5	28.2	29.2	31.0	-	Mean (Mo)	34.68	37.04	39.37	41.77	-
Interaction (P x Mo)											
	S. Em±	0.24	-	-	-	P x Mo	S. Em±	0.22	-	-	-
	CD (p=0.05)	0.71	-	-	-		CD (p=0.05)	0.67	-	-	-

Table 4 Leghaemoglobin content, quality parameters, yield and nutrient uptake of soybean (seed) as influenced by phosphorus and molybdenum nutrition

Treatment	Leghaemoglobin content (µg/g fresh weight)	Seed yield (kg/ha)	Oil content (%)	Protein content (%)	N uptake (kg/ha)	P uptake (kg/ha)	Mo uptake (g/ha)
P1-0	207	1212	18.0	39.0	75.2	4.4	2.52
P2-30	232	1487	18.4	40.0	95.0	7.0	3.07
P3-60	249	1784	18.9	41.0	117.0	9.7	3.82
S.Em ±	6 .0	11	0.10	0.08	0.6	0.09	0.03
CD (p=0.05)	16	31	0.30	0.24	1.8	0.27	0.09
Mo1-0	224	1418	18.0	39.5	90.0	6.2	2.83
Mo2-2	228	1467	18.4	39.8	93.7	6.6	3.01
Mo3-4	233	1521	18.5	39.5	97.7	7.4	3.25
Mo4-6	232	1572	18.7	40.2	101.6	7.9	3.43
S.Em ±	6.0	12	0.04	0.10	0.7	0.1	0.03
CD (p=0.05)	NS	36	0.12	0.25	2.1	0.31	0.09
Interaction (P x Mo)							
S.Em ±	11.0	22	0.07	0.18	1.3	0.18	0.06
CD (p=0.05)	NS	NS	0.21	NS	NS	NS	0.18

With respect to protein content, phosphorus application @ 60 kg P_2O_5/ha recorded higher protein content (41.0%) over 30 (40.0%) and 0 kg P_2O_5/ha (39.0%). Among molybdenum seed treatment, 6g recorded significantly higher protein content (40.2%) over 4 (39.5%), 2 g (39.8%) and no seed treatment (39.5%). Improved protein content associated with phosphorus application @ 60 kg/ha and Mo seed treatment @ 6 g might be due to the improved nodulation and nitrogen fixation that resulted due to higher seed N uptake (117.0 and 101.6 kg N/ha) over corresponding lower levels (Table 4). These results are in accordance with Singh *et al.* (2013). P and Mo uptake by seed (Table 4) was significantly influenced by varying levels of P and seed treatment with Mo and application of 60 kg P_2O_5 and seed treatment with Mo @ 6 g/kg recorded highest P (9.7 and 7.9 kg/ha) and Mo uptake (3.82 and 3.42 g/ha) which could be ascribed to the increased root growth and nodulation that reflected in higher seed yield and improved phosphorus and Mo concentration apart from the synergism between these nutrients Shankar *et al.* (2014).

From the present study, it could be concluded that in soybean soil application of 60 kg/ha and Mo seed treatment @ 6g/kg seed significantly improved the root growth, nodulation, nodule activity, quality parameters, nutrient uptake (N, P and Mo) and seed yield.

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Performance of sunflower (*Helianthus annuus* L.) hybrids to boron levels in sandy loam soils of Odisha

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ABSTRACT

Field experiment conducted to find out the effect of soil applied boron on the yield attributes, yield and economics of sunflower (*Helianthus annuus* L.) at OUAT, Bhubaneswar revealed that boron @ 1.5 kg/ha recorded highest yield attributing characters such as head diameter (18.6 cm), total number of seeds/capitulam (830), seed (2.10 t/ha), stover (5.28 t/ha) and oil yield (743.6 kg/ha) over B applied @ 1kg/ha. Among the hybrids tested, the productivity was in the descending order of KBSH-44 < KBSH-53 <RSFH-1887 < LSFH-171. However, oil yield (764.9 kg/ha) was highest with KBSH-53 followed by RSFH-1887 (715.1 kg/ha). Among the hybrids, KBSH-44 recorded highest B:C ratio of 1.94 and lowest (1.67) was with LSFH-171. In case of boron levels, highest B: C ratio was recorded due to application of Boron @1.5 kg/ha.

Keywords: Acid soils, Soil application of boron, Sunflower

Oilseed crops continue to remain as the backbone of agricultural economy of the country and sunflower (*Helianthus annuus* L.) an important oilseed crop of the world has emerged as an important crop of the state of Odisha with an average productivity of 1193 kg/ha (Mahapatra *et al.,* 2021b; Mahapatra *et al.,* 2021a; Ramesh *et al.,* 2019). The crop has gained popularity in the recent past because of its excellent quality oil due to richness with high degree of polyunsaturated fatty acids, anticholesterol properties, short duration, wide adaptability to soil and climatic conditions, photo and thermo-insensitiveness, drought tolerance and higher oil yield per unit area. Poor selection of appropriate hybrid for a particular agro climatic zone, improper nutrient managements, bird attack and major diseases and pests are few deterrents for the successful cultivation of sunflower in the country. Continuous and indiscriminate use of chemical fertilizers containing only the major nutrients has led to secondary and micronutrient deficiencies (Sudhakar *et al.,* 2020) in several soils and hence a validated balanced fertilizer prescription and its application (Ramesh *et al.,* 2017) is necessary to harvest optimum crop yields (Patel *et al.,* 2020). Among the emerging micronutrient deficiencies, boron (B) is the second most deficient micro-element globally and soil is the primary source for boron. B is required for normal growth and plant development of many crops. Sunflower is sensitive to boron deficiency and fairly responds for boron application (Oyinlola, 2007) and several crops demand B at reproductive growth stage and if supplied, improves grain yield (Zahoor *et al.,* 2011) including sunflower.

A field study was conducted during summer season of 2019-20 at Instructional Farm of the Department of Agronomy, College of Agriculture, OUAT, Bhubaneswar, which lies at 20°15' N latitude, 85°52' E longitude, respectively with an altitude of 25.9 m above the mean sea level. The farm is located at about 64 km away from the Bay of Bengal. The soil was sandy loam in texture with pH (5.89), organic carbon (0.22%), total nitrogen (165 kg/ha) and available phosphorus (23.3 kg/ha). The experiment was conducted with four genotypes (G1: KBSH-44, G2: KBSH-53, G3: RSFH-1887 and G4: LSFH-171) and four levels of boron (B0: 0 kg/ha, B2: 0.5 kg/ha, B3: 1.0 kg/ha and B4: 1.5 kg/ha) tested in a factorial randomized block design (FRBD) with three replications. Sowing was done at 5cm depth in furrows drawn by hand-hoe and covered manually, following the recommended seed rate i.e. 5 kg/ha. The size of each plot was 4.2 m × 4.2 m and the spacing adopted was 60 cm × 30 cm. Well decomposed FYM @ 5t/ha was incorporated into the soil at final ploughing. Liming was done @ 0.2LR. Recommended fertilizer dose of 60: 80:60 kg N, P_20_5 and K_20/ha were applied uniformly to all the plots through Urea, SSP and MOP. Full P and K + half N were applied as basal, 25% N was top dressed at 30days after sowing and rest 25% N at 45 DAS. Boron was also applied as per the treatment in the form of borax. Intercultural operations were done as and when required. Totally 5 irrigations, including pre-sowing irrigation, were given at 12 days interval. The mature flower heads were harvested when the thalamus drooped down and when the colour changed to lemon-yellow.

The results revealed that boron levels had significant influence on yield and yield attributes (Table 1) of sunflower hybrids. Highest head diameter was recorded in KBSH-44 (17.84 cm), which was statistically at par with RSFH-1887 (17.61cm) and KBSH-53(17.45 cm). KBSH-44 recorded the maximum number of total seeds/capitulam (848.1), which was significantly superior to other hybrids, KBSH-53 (794) and RSFH-1887 (774), whereas LSFH-171 recorded the

minimum of 706 seeds/capitulam. KBSH-44 recorded the highest seed (1.99 t/ha) and stover (5.02 t/ha) yield while the lowest was recorded in LSFH-171 (1.73 and 4.19 t/ha respectively). Shukla *et al.* (2019) was of the opinion that boron deficiency is one of the serious nutritional problems in acid soils and soil application of borax is used to correct its deficiency. The plausible reason could be genotypic variation for partitioning in the remobilization of assimilates from stem and thalamus to seed yield (Hall *et al.,* 1989) and yield components of sunflower hybrids responding to management practices (Barmaki *et al.,* 2009). The highest oil yield (764.9 kg/ha) was obtained with KBSH-53 which was due to more oil content than KBSH-44 and RSFH-1887. The results obtained are in agreement with Kalaiyarasan *et al.* (2019) who reported maximum oil content (33.61 %) with KBSH-53.The treatment B @ 1.5 kg/ha gave highest head diameter (18.6 cm), which might be due to stimulated photosynthetic activity contributing towards the increase of higher head diameter. Boron is known to influence cell development and elongation of cells through control of polysaccharide formation which prevents the excessive conversion of sugars into starch, continued growth of the head might have resulted in bigger size of capitulum (Hegde and Sudhakarababu, 2004). Soil application of boron@1.5 kg/ha recorded maximum number of total seeds (830.9) per head, which might be due to better development of pollen tubes and was on par with other boron levels. This corroborates the findings of Silva *et al*. (2011). In addition, boron levels caused significant variation in test weight with a maximum of 49.3 g when Boron was applied on soil @ 1.5 kg/ha, which was on par with B @ 1.0 kg/ha (47.4 g). This might be due to better translocation of photosynthates due to boron application. Results obtained are in line with Kala *et al.* (2017) who determined that highest 100 grain weight was obtained with B @ 1.0 kg/ha when compared to B @ 0.5 kg/ha. Highest seed (2.10 t/ha) and stover (5.28 t/ha) yields were recorded with B @ 1.5 kg/ha which remained at par with1.0 kg/ha and the lowest values were observed with control. The results obtained are in agreement with the findings of Renuka devi *et al.* (2002), who reported that the soil application of boron fertilizer increased the sunflower seed yield (15.8%) and stalk yield (18.9%) due to B @ 2.0 kg/ha over the control. Highest oil yield (743.6 kg/ha) was obtained with application of B @ 1.5 kg/ha which remained at par with B@ 1.0 kg/ha (726.4 kg/ha) and significantly higher than other boron levels. Zahoor *et al.* (2011) reported that soil application of boron resulted in significantly increased oil contents. Similarly, Renuka devi and Savithri (2003) reported that enhanced uptake of boron resulted in significant increase in seed oil contents. The gross returns (₹1,12,315/ha), net returns (₹54,389/ha) and B:C ratio (1.94) were highest for KBSH-44 which might be due to its enhanced productive response over other genotypes (Table 2). The higher seed yield of the hybrid, KBSH-44 along with low cost of cultivation was responsible for highest gross return, net return and B:C ratio (Sher *et al*., 2018). Among different boron levels imposed, the maximum gross returns (₹1,18,527/ha), net returns (₹59,383/ha) and benefit-cost ratio (2.0) were found to be with B@ 1.5 kg/ha, which was on par with B @ 1.0 kg/ha and the least was recorded with control (B0). Similar results were found by Jyothi and Anjaiah (2018).

From the study, it is concluded that sunflower hybrid KBSH-44 may be cultivated in the spring season at Odisha along with soil application of boron @ 1.5 kg/ha for maximum seed yield with monetary returns.

Table 1 Yield attributes and yield of sunflower hybrids as influenced by boron levels

Treatment		Head diameter (cm)	Test weight (g)	Seeds/ capitulam	Seed yield (t/ha)	Stover yield (t/ha)	Harvest Index (%)	Oil yield (kg/ha)
Genotype								
G1	KBSH-44	17.8	47.0	848.1	1.99	5.02	28.38	685.8
G2	KBSH-53	17.5	46.8	793.9	1.91	4.86	28.25	764.9
G3	RSFH-1887	17.6	46.0	773.6	1.85	4.69	28.30	715.1
G4	LSFH-171	14.6	41.9	705.9	1.73	4.19	29.25	540.5
SEm ±		0.64	0.82	24.69	0.06	0.15	0.13	23.64
CD (p=0.05)		1.8	2.4	71.3	0.18	0.43	0.38	68.28
Boron level								
Bo	No boron	14.4	41.1	726.0	1.64	4.07	28.7	600.1
B1	0.5 kg	16.6	44.1	769.7	1.77	4.44	28.5	636.2
B2	1.0 kg	17.9	47.4	794.8	1.98	4.97	28.5	726.4
B3	1.5 kg	18.6	49.3	830.9	2.10	5.28	28.5	743.6
SEm ±		0.64	0.82	24.69	0.06	0.15	0.13	23.64
CD (p=0.05)		1.8	2.4	71.3	0.18	0.43	NS	68.28
Interaction								
SEm ±		0.24	1.64	49.38	0.12	0.30	0.27	47.29
CD (0.05)		NS	NS	NS	NS	NS	NS	NS

Table 2 Economics of sunflower hybrids influenced by boron levels

Treatment		Cost of cultivation (₹/ha)	Gross returns (₹/ha)	Net returns (₹/ha)	B:C ratio
Genotype					
G1	KBSH-44	57926	112315	54389	1.94
G2	KBSH-53	57926	107952	50026	1.86
G3	RSFH-1887	57776	104578	46802	1.81
G4	LSFH-171	58451	97850	39399	1.67
Boron level					
B0	No boron	56895	92679	35784	1.63
B1	0.5 kg	57645	99816	42171	1.73
B2	1.0 kg	58395	111673	53278	1.91
B3	1.5 kg	59145	118527	59383	2.00

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Impact of KVK training on knowledge and adoption levels of soybean growers in Maharashtra State

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ABSTRACT

The study was conducted in ten selected villages of Washim District of Maharashtra to study the impact of training programs conducted by KVK, Karda on knowledge and adoption levels of soybean growers. The sample comprised of 150 trainees and 150 non-trainees from the KVK operated villages. The results of the study revealed that the trainee farmers had higher knowledge and adoption levels on improved soybean cultivation practices than the non-trainee farmers. The scores of knowledge and adoption indices for various soybean cultivation practices were also found to be more for trainee farmers than their counterparts. This indicated that KVK played a significant role in increasing the knowledge and adoption levels of soybean growers.

Keywords: Adoption level, Impact, Knowledge level, Soybean growers, Training

Soybean [*Glycine max* (L) Merrill] is the world's most important seed legume, which contributes to 25% of the global edible oil and about two-thirds of the world's protein concentrate, which is used for livestock feeding. In India, soybean is cultivated in an area of 11.0 million ha, with a production of 9.30 million tonnes and productivity of 865 kg/ha under rainfed condition in Madhya Pradesh, Rajasthan, Karnataka, Chhattisgarh and Telangana. There is a wide variation in the productivity ranging from 950 kg/ha in Karnataka and Chhattisgarh to 1480kg/ha in Telangana. In Maharashtra, soybean is cultivated in an area of 3.73 million ha with a production of 3.94 million tonnes and productivity of 1055 kg/ha with second rank in India (SOPA Databank, 2019). However, low productivity of the crop remains a major problem of soybean cultivation.

KVKs conduct training programs for farmers to update their knowledge and skills on modern technologies. They play a vital role in conducting on-farm testing to assess the suitability and location specificity of the technology. KVKs conduct demonstrations to show the productivity potential of various crops at farmers' fields. They also conduct need based training programs for the benefit of farmers, farm women, and rural youths. KVKs are creating awareness about improved agricultural technologies through large number of extension programs. KVK, Karda organizes regular training programs for soybean growers on improved soybean production technology. The present study was undertaken to assess the impact of training on knowledge and adoption levels of soybean growers.

The study was conducted in Washim district of Maharashtra state during 2018-19. The list of farmers who attended the training on improved soybean cultivation practices was obtained from KVK, Karda. Out of six taluks of Washim district, three taluks namely, Risod, Washim and Malegaon were selected as these taluks had highest number of soybean trainees. Six villages from Risod, two villages from Washim and two villages from Malegaon were selected purposively based on the availability of number of trainees. The selected villages were Bhapur, Tandalwadi, Belkhed, Gobhani, Warud Tofa and Karda from Risod taluk, Shelgaon bagade and Tiwali from Malegaon taluk, Hiwara rohila and Sawargaon Jire from Washim taluk. A sample of 150 trainee farmers were selected from all these ten villages by following the proportionate random sampling technique and considered as an experimental group. In order to study the impact of training among the trainees, a sample size of 150 non-trainee farmers were also selected as control group. The non-trainees were also selected from the same villages following the proportionate random sampling method. Thus, a total of 300 farmers were selected for the study.

The list of improved soybean production technologies imparted during training organized by KVK, Karda were prepared for studying the knowledge and adoption levels of both the trainees and non-trainees. The data were collected with the help of pre-tested and structured interview schedule by personal interview method. Independent 't' test was applied to test the significant difference between mean knowledge and adoption scores of trainees and non-trainees.

Knowledge was crucial factor for an adoption of an innovation so the extent of knowledge among trainee and non-trainee farmers was studied and the results are presented in Table 1.

The mean knowledge score of trainee farmers was more than that of non-trainee farmers. Further, the difference between the means of trainee and non-trainee farmers was highly significant. Based on the mean scores, it may be stated that the trainee farmers possessed higher knowledge than non-trainee farmers. Hence, it may be concluded that the

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trainee farmers possessed more knowledge about improved soybean cultivation practices than, non-trainee farmers. Majority of the trainee farmers (70.0 per cent) were with higher level of knowledge, whereas majority of non-trainee farmers (47.33 per cent) were with low level of knowledge. The proportion of respondents under medium level of knowledge was 30.0 per cent for trainee farmers and 36.0 per cent for non-trainee farmers (Table 1).

The trainee farmers have attended training programs organized by Krishi Vigyan Kendra on improved soybean cultivation practices, which enabled them to gain more knowledge about soybean cultivation compared to non-trainee farmers.

The adoption level of trainee and non-trainee farmers on improved soybean cultivation practices are presented in Table 2.

It was interesting to see that majority of the trainee farmers (62.67 per cent) were high adopters of improved soybean cultivation practices, whereas majority of the non-trainee farmers (56.00 per cent) were low adopters. Around 30.00 per cent of the trainee farmers (26.00 per cent) and non-trainee farmers (28.67 per cent) were in medium adoption category. Only less than one-fifths of the non-trainee farmers (15.33 per cent) were high adopters and only 11.33 per cent of non-trainee farmers were low adopters.

Analysis further showed that the mean score of trainee farmers was more than that of non-trainee farmers. The difference between the means was significant at 5.00 per cent level. Based on the mean scores, it may be concluded that the trainee farmers were high adopters, compared to non-trainee farmers.

The trainee farmers underwent training program on soybean cultivation practices organized by Krishi Vigyan Kendra, gained more knowledge. The higher knowledge level of respondents coupled with their best extension contact, media exposure, scientific orientation, economic motivation and innovativeness would have enabled the trainee farmers to adopt more practices.

In order to study the impact of training, the mean knowledge and adoption indices were worked out for all the selected technologies and for trainees and non-trainees.

The results (Table 3) showed that the mean knowledge score was higher for the trainee farmers (97.59 per cent) rather than non-trainee farmers (52.41 per cent). Cent per cent of the trainee farmers had knowledge on the practices namely, recommended varieties, seed rate, spacing, broad bed and furrow system, application of FYM and time of harvest, whereas the corresponding knowledge level for the same practices for the non-trainee farmers were 45.33 per cent, 46.67 per cent and 80.67 per cent, 94.67 per cent and 84.00 per cent respectively. Vast majority of trainee farmers had knowledge on the remaining practices namely, seed germination test (94.67 per cent), chemical seed treatment (98.00 per cent), bio-fertilizer seed treatment (98.67 per cent), weed management (98.67 per cent), application of chemical fertilizer (94.67 per cent), pest management (92.00 per cent) and disease management (92.00 per cent). In case of non-trainee farmers, less than half the proportion of the respondents had knowledge on recommended varieties (45.33 per cent), seed rate (48.00 per cent), spacing (46.67 per cent) and weed management (43.33 per cent). About 40.00 per cent of the respondents had knowledge on pest management. The practices namely, chemical seed treatment (34.67 per cent), bio-fertilizer seed treatment (32.00 per cent) and disease management (36.00 per cent) were known by only less than 40.00 per cent of the respondents. Only a smaller proportion of the respondents had knowledge on seed germination test (14.00 per cent).

The mean adoption score was greater for the trainee farmers (96.05 per cent) compared to the non-trainee farmers (44.92 per cent). In case of adoption, the practices namely, recommended varieties, seed rate, spacing, broad bed and furrow system, application of FYM and time of harvest were adopted by all the trainee farmers, whereas in the case of non-trainee farmers, these practices were found to be adopted by 42.67 per cent, 46.67 per cent, 46.67 per cent, 71.33 per cent and 73.33 per cent of the respondents. Majority of the trainee farmers had adopted the remaining practices namely, seed germination test (87.33 per cent), chemical and bio-fertilizer seed treatment (95.33 per cent), weed management (92.67 per cent), application of chemical fertilizer (98.00 per cent) and pest and disease management (90.00 per cent). In the case of non-trainee farmers, about 70.00 per cent of the farmers adopted application of chemical fertilizer. Less number of non-trainee respondents had adopted chemical and bio-fertilizer seed treatment (22.67 per cent) and pest and disease management (28.00 per cent). None of them had adopted the seed germination test.

The mean knowledge and adoption scores were found to be 98.59 per cent and 96.05 per cent for the trainee farmers, whereas for the non-trainee farmers it was 52.41 per cent and 44.92 per cent respectively. It clearly showed that the trainee farmers had greater knowledge and adoption levels compared to the non-trainee farmers.

Therefore it could be stated that there was a remarkable impact of training on those respondents who attended the training program conducted by KVK, Washim in terms of knowledge and adoption of improved soybean cultivation practices as compared to their counterparts.

The study showed that the trainee farmers had higher knowledge and adoption levels with regard to improved soybean cultivation practices compared to the non-trainee farmers. The mean knowledge index and mean adoption index were higher for the trainee farmers than non-trainee farmers. The impact of KVK training was observed to be 48.15 Per cent. Hence it may concluded that the Krishi Vigyan Kendra contributed positively in enhancing the

knowledge and extent of adoption of improved soybean cultivation practices among the trainee farmers. It is suggested that more number of training programs on soybean production may be organized for all the non-trainee farmers in the KVK operated villages so as to ensure better knowledge and adoption among all the farmers.

Table 1 Distribution of respondents on their knowledge about improved soybean cultivation practices

Category	Trainee farmers (n=150)		Non-trainee farmers (n=150)	
	Number	Per cent	Number	Per cent
Low	-	-	71	47.33
Medium	45	30.00	54	36.00
High	105	70.00	25	16.67
Total	150	100.00	150	100.00
Mean		77.60		45.50
Difference between means		32.1		
't' value		34.49**		

** - Significant at 0.01 level of probability

Table 2 Distribution of respondents on their extent of adoption of improved soybean cultivation practices

Category	Trainee farmers (n=150)		Non-trainee farmers (n=150)	
	Number	Per cent	Number	Per cent
Low	17	11.33	84	56.00
Medium	39	26.00	43	28.67
High	94	62.67	23	15.33
Total	150	100.00	150	100.00
Mean		77.30		47.20
Difference between means		30.10		
't' value		25.31**		

** - Significant at 0.01 level of probability

Table 3 Knowledge and adoption indices of trainees and non-trainees for soybean cultivation practices

Soybean cultivation practices	Item-wise knowledge score (%)		Item-wise adoption score	
	Trainees (n=150)	Non-trainees (n=150)	Trainees (n=150)	Non-trainees (n=150)
Recommended varieties	100.00	45.33	100.00	42.67
Seed germination test	94.67	14.00	87.33	0
Chemical seed treatment	98.00	34.67	95.33	22.67
Bio-fertilizer seed treatment	98.67	32.00	95.33	22.67
Seed rate	100.00	48.00	100.00	46.67
Spacing	100.00	46.67	100.00	46.67
Broad bed and furrow system	100.00	80.67	100.00	93.33
Weed management	98.67	43.33	92.67	39.33
Application of FYM	100.00	94.67	100.00	71.33
Application of chemical fertilizer	94.67	82.67	98.00	69.33
Pest management	92.00	39.33	90.00	28.00
Disease management	92.00	36.00	90.00	28.00
Time of harvest	100.00	84.00	100.00	73.33
Mean score	97.59	52.41	96.05	44.92

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Yield response and pathological characterization of promising genotypes of soybean against major diseases in Madhya Pradesh

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ABSTRACT

The yield potential along with multiple disease resistance in 38 promising soybean genotypes including four checks i.e. JS 20-34, JS 335, JS 20-98 and NRC 86 was assessed under field condition of JNKVV, Jabalpur which is one of the hot spot locations for major diseases of soybean like Charcoal rot, Aerial blight and Yellow mosaic. Significant differences were observed for days to 50 per cent flowering, days to maturity, yield (kg/h) and 100 seed weight. The highest yield was obtained from JS 21-72 (2650 kg/h) followed by Himso 1689 (2255 kg/h) and JS 21-71 (2222 kg/h). Maximum 100 seed weight of 14.37g was recorded in JS 21-72 followed by JS 21-71 (14.2g) and JS 20-34 (14.16g). Out of thirty eight, the yield of seven genotypes i.e. Himso 1688, MAUS 734, DSb 33, NRC 139, SL 1171, VLS 97 and BAUS 100 could not be recorded due to complete mortality of the plants by charcoal rot. Eight genotypes *viz.,* JS 21-71, MACS 1566, JS 21-72, DS 3110, MACS 1620, JS 20-34(C), RSC 11-15 and Himso 1689 against charcoal rot, seven genotypes against aerial blight, eighteen genotypes against YMV and thirty-three (33) against bacterial pustule disease showed high resistance. Overall, three genotypes *viz.,* JS 21-71, JS 21-72 and Himso 1689 exhibited absolute to moderate resistance against charcoal rot plus absolute/highresistance to YMV, RAB and bacterial pustule.

Keywords: Aerial blight, Bacterial pustule, Charcoal rot, Disease, Soybean, Yield, YMV

Soybean [*Glycine max* (L.) Merrill] also known as "Golden bean" grows across the world for its high nutritional values. The seed of soybean contains high protein (40%) along with considerable amount of edible oil (20%) (Mehra *et al.,* 2020). In India, it is mainly grown in *kharif* season in an about 12 m.ha. Madhya Pradesh is a key state for soybean cultivation in the country. Soybean is affected by many diseases and among the diseases, charcoal rot (*Macrophomina phaseolina*) which usually causes complete mortality of plant during reproductive stages, and Rhizoctonia aerial blight (RAB) (*Rhizoctonia solani*) that produces light to dark brown blighting on foliage, respectively are the major fungal diseases in Madhya Pradesh (Amrate *et al.,* 2018). Most of the Indian soybean varieties are completely susceptible to charcoal rot disease (Amrate *et al.,* 2019). Apart from this, Yellow mosaic virus which is caused by a single stranded DNA virus from geminiviridae family transmitted by whitefly *Bemisia tabaci* (Kumar *et al.,* 2014) is also a major disease which can cause as high as 85.7% yield reduction, if the plants affected severely in earlier stage of the crop (Amrate *et al.,* 2020a). Among the bacterial diseases, bacterial pustule (*Xanthomonas campestris* pv. *glycines*) is an important disease of soybean in India and can cause yield reduction of 15-53 per cent depending upon severity (Shukla, 1994). Looking at the seriousness of complex of disease in soybean, the present investigation was undertaken to identify multiple disease resistant genotypes coupled with high seed yield which can be utilized as resistant donors in developing resistant cultivars.

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Thirty eight promising genotypes (including four checks viz., JS 20-98, JS 335, JS 20-34 and NRC 86) from different agro ecological zones of the country were evaluated for maturity duration, yield and 100 seed weight in the field of AICRP on Soybean at JNKVV, Jabalpur during *kharif* 2018. These genotypes were sown in the plot of 3.0 x 1.35 m^2 (4.35 m^2) in randomized block design with three replications. All recommended package of practices were followed of the soybean crop. Days to 50 per cent flowering was recorded from ten randomly selected plants, days to maturity was noted at maturity of crop, yield and 100 seed weight was taken after the harvesting of the entries.

As the location is hot spot for all the major diseases of soybean, all the thirty eight genotypes were thoroughly observed for the severity of charcoal rot, Yellow mosaic, Aerial blight and Bacterial pustule disease of soybean (Fig. 2). The characterization for resistance was done by assigning the ratings/grades as per the earlier reports for different diseases (Anonymous, 2016; Amrate *et al.,* 2018). Charcoal rot mortality was observed during reproductive stages of crop and it was expressed in terms of per cent mortality and accordingly genotypes were classified as 0 = No Mortality-Absolutely resistant (AR), 1= 1% mortality-Highly resistant (HR) 3 = 1.1 to10% mortality-Moderately Resistant (MR), 5 = 10.1 to 25% mortality-Moderately susceptible (MS), 7= 25.1 to 50% -Susceptible (MS), 9 = more than 50% mortality-Highly Susceptible (HS). For the reaction of genotypes to YMV, observations on the percent disease incidence (percentage of number of infected plants to the total number of plants in a given accession) and disease severity (number of leaves having symptom over total

number of leaves in a single plant and averaged from 10 such plants) was recorded. Based on disease symptom severity grades (designated with numerical values of 0-4) and a scale of response value (0-1) corresponding to such grades, the coefficient of infection (CI) calculated by multiplying the percent disease incidence to the response value assigned for each severity grade following standard methodology as per the scale given below (Singh and Singh, 2000; Amrate *et al.,* 2018).

Symptoms	Severity grade	Response value	Coefficient of Infection (CI)	Disease reaction
Symptoms absent	0	0	0-4	Highly resistant
Very mild symptoms up to 25% leaves	1	0.25	5-9	Resistant
Appearance of symptoms in 26-50% leaves	2	0.50	10-19	Moderately resistant
Appearance of symptoms in 51-75% leaves	3	0.75	20-39	Moderately susceptible
Severe disease infection in symptoms (>75% leaves)	4	1.00	40-69	Susceptible
			70-100	Highly susceptible

Reaction of the genotypes to RAB and Bacterial pustules observed on ten randomly selected plants from each genotype. Selected plants were approximately divided into three positions as bottom, middle and top. From each position two to four leaves were graded. All the infected leaves were assigned 0-9 ratings orgrades where 0=No lesions, 1= 1% leaf area with lesions/spots, 3= 1.1 to 10% leaf area affected, 5= 10.1 to 25% area affected, 7= 25.1 to 50% area affected, 9 = more than 50% area affected. These grades were then utilized for the calculation of PDI by using the following formula of Wheeler (1969);

Per cent Disease Index (PDI) =

$$\frac{\text{Sum of individual rating}}{\text{No. of leaves examined}} \times \frac{100}{\text{Max. Disease rating}}$$

On the basis of PDI, the genotypes/varieties were classified as absolutely resistant (no diseases), highly resistant (0.1-1.0), moderately resistant (1.1-10), moderately susceptible (10.1 - 25), susceptible (25.1 - 50) and highly susceptible (> 50).

The days to 50% flowering (DFF) differed significantly among all the thirty eight genotypes and it ranged from 31.7 to 48.0 days. The minimum DFF was observed in JS 20-34 (31.7) followed by NRC 138 (32.7) and NRC 146 (33.7), whereas the maximum was recorded in KDS 1009 (48.0). Days to maturity varied significantly from 86.3 to 97.7 days. The minimum maturity period was recorded in JS 20-34 (86.3 days) followed by NRC138, RVS 2011-10 and RVMS 2011-35. The maximum maturity duration was recorded in MAUS 732 (97.7 days).

The genotype JS 21-72 (14.37 g) followed by JS 21-71 (14.21g), JS 20-34 (14.1g) and MACS 1620 (13.29) recorded maximum 100 seed weight whereas PS 1634 (7.6 g) recorded lowest 100 seed weight. The maximum yield was recorded from JS 21-72 (2650kg/h) followed by Himso 1689 (2255kg/h) and JS 21-71 (2222kg/h). The seed yield could not be recorded from seven genotypes *viz.,* Himso 1688, MAUS 734, DSb 33, NRC 139, SL 1171, VLS 97 and BAUS 100 as nearly 50% plant stand was affected due to Charcoal rot (Fig. 1). The seed yield among various genotypes differed significantly and ranged between 238 and 2650 kg/ha. It was recorded that the genotypes which yielded less than 1000.0 kg/ha were severely affected by major diseases of soybean (Fig.1).

Out of the total thirty eight genotypes, eight genotypes viz., JS 21-71, MACS 1566, JS 21-72, DS 3110,MACS 1620, JS 20-34(c), RSC 11-15 and Himso 1689 were absolutely resistant/highly resistant against charcoal rot disease of soybean. Remaining was found to be moderately resistant (7), moderately susceptible (8), susceptible (5) and highly susceptible (10) against charcoal rot of soybean.

Total eighteen genotypes namely; DS 3109, JS 21-71, SL 1191, Himso 1688, JS 20-98 (c), RSC 11-17, MAUS 734, DSb 33, NRC 138, JS 21-72, PS 1637, NRC 148, RSC 11-15, Himso 1689, CAUMS -1, RVSM 2011-35, RVS 2007, and BAUS 100 were highly resistant (HR) to YMV of soybean.Seven genotypes were moderately resistant, twelve were resistant and the remaining one was moderately susceptible to YMV of soybean.

The genotypes NRC 46, JS 21-71, JS 21-72, S 3110, JS 20-34(c), NRC 148 and Himso 1689 showed absolute/high resistivity against aerial blight. In addition to this, nineteen genotypes were found to be moderately resistant, eleven moderately susceptible and only one was found susceptible to aerial blight disease of soybean.

Thirty three genotypes exhibited absolute/ highly resistant reaction against bacterial pustule disease of soybean. Two genotypes KDS 1073 and KS 113 showed moderate susceptibility and susceptibility against it, respectively.

Eight genotypes *viz.,* DS 3109, JS 21-71, SL 1191, JS 20-98(c), RSC 11-17, JS 21-72, RSC 11-15 and Himso 1689 were found to be absolute to moderate resistant against

Charcoal rot and highly resistant to YMV. Whereas, five genotypes *viz.,* JS 21-71, JS 21-72, DS 3110, JS 20-34(c) and Himso 1689 were absolutely to moderately resistant against Charcoal rot and highly resistant to RAB (Table 1). Altogether, out of thirty eight only three genotypes viz., JS 21-71, JS 21-72 and Himso 1689 exhibited absolute to moderate resistance to charcoal rot plus absolute/high resistance to YMV, RAB and bacterial pustule.

Similar works has been carried out by many workers, Ansari (2007) found absolute resistance to highly susceptible reactions in different elite soybean genotypes under field conditions of Madhya Pradesh. Pancheshwar *et al.* (2016) screened seventy two germplasm against YMV under Madhya Pradesh conditions and recorded highly resistant, moderately resistant and susceptible reactions. Recently, Amrate *et al.,* (2018) evaluated large number of germplasm under Madhya Pradesh condition and out of one hundred and nineteen genotypes only seventeen showed resistance against all the three diseases charcoal rot, aerial blight and YMV. Amrate *et al.,* (2020b) also screened sixty important soybean genotypes for charcoal rot and aerial blight and reported five genotypes as highly resistant against both the diseases under high disease pressures conditions.

Table 1 Genotypes exhibited absolute to moderate resistance against Charcoal rot coupled with highly resistance to other diseases

Diseases	Resistant Genotypes
Charcoal rot (AR to MR)	DS 3109, PS 1634, JS 21-71, MACS 1566, SL 1191, JS 20-98(c), RSC 11-17, JS 21-72, DS 3110, JS 335(c), MACS 1620, MAUS 732, JS 20-34(c), RSC 11-15, Himso 1689 (15)
Charcoal rot (AR to MR) + YMV (HR)	DS 3109, JS 21-71, SL 1191, JS 20-98(c), RSC 11-17, JS 21-72, RSC 11-15, Himso 1689 (8)
Charcoal rot (AR to MR) + RAB (HR)	JS 21-71, JS 21-72, DS 3110, JS 20-34(c), Himso 1689 (5)
Charcoal rot (AR to MR) + Bacterial pustules (HR)	DS 3109, PS 1634, JS 21-71, MACS 1566, SL 1191, JS 20-98(c), RSC 11-17, JS 21-72, JS 335(c), DS 3110, MACS 1620, MAUS 732, JS 20-34(c), RSC 11-15, Himso 1689 (15)
Charcoal rot (AR to MR) + YMV (HR) + RAB (HR)	JS 21-71, JS 21-72, Himso 1689 (3)
Charcoal rot (AR to MR) + YMV (HR) + RAB (HR) + Bacterial pustules (HR)	JS 21-71, JS 21-72, Himso 1689 (3)

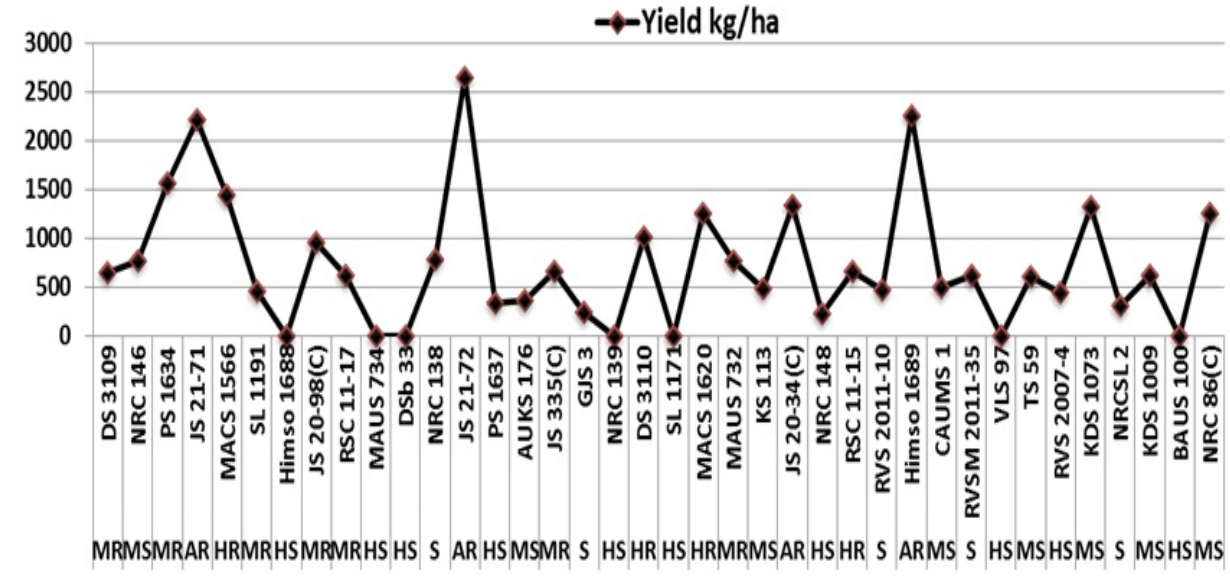

Fig. 1. Influence of Charcoal rot severity on yield of soybean genotypes

Fig. 2. (A) Close up view of Charcoal rot affected root, (B) YMV severity in affected line, (C) Aerial blight affected foliage; (D) Bacterial pustules severity in susceptible genotype

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General

Full-length articles, short communications, book reviews and review articles are published in the Journal. Review articles and book reviews are published usually by invitation. Full length articles and short communications should report results of original investigations in oilseeds, oil bearing plants and relevant fields of science. Choice of submitting the paper(s) either as full length paper or short communication rests with the authors. The Editor(s) or Reviewer(s) will examine their suitability or otherwise only in that specific category. Each article should be written in English correctly, clearly, objectively and concisely. All the statements made in the manuscript should be clear, unambiguous, and to the point. Plagiarism is a crime and therefore, no part of the previously published material can be reproduced exactly without prior permission from the original publisher or author(s) as deemed essential and the responsibility of this solely rests on the authors. Also, authors shall be solely responsible for the authenticity of the results published as well as the inferences drawn thereof. Telegraphic languages should be avoided. The data should be reported in a coherent sequence. Use active voice. Active voice is clear, unambiguous and takes less space. Use past tense while reporting results. Do not repeat ideas in different forms of sentences. Avoid superfluous sentences such as `it is interesting to note that', `it is evident from the table that' or `it may be concluded that' etc. Use % for percent, %age for percentage, / for per, @ for at the rate of hr for hours, sec for seconds. Indicate date as 21 January 2010 (no commas anywhere). Spell out the standard abbreviations when first mentioned eg. Net assimilation rate (NAR), general combining ability (GCA), genetic advance (GA), total bright leaf equivalents (TBLE), mean sum of squares (MSS).

Manuscript

Language of the Journal is English. Generally, the length of an article should not exceed 3,000 words in the case of full-length article and 750 words in the case of short communication. However completeness of information is more important. Each half-page table or illustration should be taken as equivalent to 200 words. It is desirable to submit manuscript in the form of soft copy either as an e-mail attachment to editorisor@gmail.com (preferred because of ease in handling during review process) or in a **compact disk (CD) (in MS Word document; double line space; Times New Roman; font size 12).** In exceptional cases, where the typed manuscript is being submitted as hard copy, typing must be done only on one side of the paper, leaving sufficient margin, at least 4 cm on the left hand side and 3 cm on the other three sides. Faded typewriter ribbon should not be used. Double space typing is essential throughout the manuscript, right from the **Title** through **References** (except tables), foot note etc. Typed manuscript complete in all respects, is to be submitted to the Editor, Journal of Oilseeds Research, Directorate of Oilseeds Research, Rajendranagar, Hyderabad-500 030. Every page of the manuscript, including the title page, references, tables, etc. should be numbered. Punctuation marks help to show the meanings of words by grouping them into sentences, clauses, and phrases and in other ways. These marks should be used in proper manner if the reader of a paper is to understand exactly the intended meaning. Receipt of the manuscript (in the form of either soft or hard copy) will be acknowledged by the editorial office of the Society, giving a manuscript number which should be quoted in all subsequent correspondence regarding that particular article.

Full-length Articles

Organization of the Manuscript

Before reading the instructions given below, the author(s) would better have a close look at the latest issue of the Journal.

Full-length article comprises the following sections.

(a) Short title
(b) Title
(c) Author/Authors
(d) Institution and Address with PIN (postal) code
(e) Abstract (along with key words)
(f) Introduction
(g) Materials and Methods
(h) Results and Discussion
(i) Acknowledgments (if any)
(j) References
(k) Tables and figures (if any)

Guidelines for each section are as follows:

All these headings or matter thereof should start from left hand side of the margin, without any indent.

Short Title

A shortened title (approximately of 30 characters) set in capital letters should convey the main theme of the paper.

Title

Except for prepositions, conjunctions, pronouns and articles, the first letter of each word should be in capital letter. The title should be short and should contain key words and phrases to indicate the contents of the paper and be attractive. Jargons and telegraphic words should be avoided. In many cases, actual reading of the paper may depend on the attractiveness of the title.

Author/Authors

The name(s) of author(s) should be typed in capital letters a little below the title, starting from the left margin. Put an asterisk on the name of the corresponding author. **Give the Email ID of the corresponding author** as a footnote.

Institution and Address

This matter will come below the name(s) of the author(s). Name of the Laboratory/Department, followed by the name of the Institution/Organization/University where the work reported in the paper was carried out shall come below the name(s) of author(s). Complete postal address, which should include city/town, district, and state, followed by PIN (postal) code is to be furnished. In case any author has left the above address, this should be indicated as a footnote.

Abstract

The paragraph should start with the word Abstract (in bold font). The abstract should comprise brief and factual summary or salient points of the contents and the conclusions of the investigation reported in the paper and should refer to any new information therein. As the abstract is an independent entity, it should be able to convey the gist of the paper in a concise manner. It will be seen by many more people than will read the paper. The abstract, as concise as possible, should not exceed 250 words in length. Everything that is important in the paper must be reflected in the abstract. It should provide to the reader very briefly the rationale, objectives or hypothesis, methods, results and conclusions of the study described in the paper. In the abstract, do not deflect the reader with promises such as 'will be discussed' or 'will be explained'. Also do not include reference, figure or table citation. At first mention in the abstract, give complete scientific name for plants and other organisms, the full names of chemicals and the description of soil order/series. Any such names or descriptions from the abstract need not be repeated in the text. It must be remembered that the abstracting journals place a great emphasis on the abstract in the selection of papers for abstracting. If properly prepared, they may reproduce it verbatim.

"Key words" should, follow separately after the last sentence of the abstract. "Key words" indicate the most important materials, operations, or ideas covered in the paper. Key words are used in indexing the articles.

Introduction (To be typed as side-heading, starting from the left-hand margin, a few spaces below the key words)

This section is meant to introduce the subject of the paper. Introduction should be short, concise and indicate the objectives and scope of the investigation. To orient readers, give a brief reference to previous concepts and research. Limit literature references to essential information. When new references are available, do not use old references unless it is of historical importance or a landmark in that field. Emphasis should be given among other things on citing the literature on work done under Indian conditions. Introduction must include: (a) a brief statement of the problem, justifying the need for doing the work or the hypothesis on which the work is based, (b) the findings of others that will be further developed or challenged, and (c) an explanation of the approach to be followed and the objectives of the research described in the paper. If the methods employed in the paper are new, it must be indicated in the introduction section.

Materials and methods (To be typed as side-heading, starting from the left-hand margin, a few spaces below the introduction)

This part of the text should comprise the materials used in the investigation, methods of experiment and analysis adopted. This portion should be self-explanatory and have the requisite information needed for understanding and assessing the results reported subsequently. Enough details should be provided in this section to allow a competent scientist to repeat the experiments, mentally or in fact. The geographical position of soil site or soils used in the experiment or site of field trial should be identified clearly with the help of coordinates (latitude & longitude) and invariably proper classification according to Soil Taxonomy (USDA), must be indicated to the level of Great-group, Suborder or Order as far as possible. Specify the period during which the experiment(s) was conducted. Send the article after completion of the experiment(s) not after a gap of 5 years. Instead of kharif and rabi use rainy and winter season respectively. Please give invariably the botanical names for local crop names like raya, bajra moong, cholam etc. Botanical and zoological names should confirm to the international rules. Give authorities. Go through some of our recent issues and find out the correct names. Give latest correct names from authentic source. For materials, give the appropriate technical specifications and quantities and source or method of preparation. Should a product be identified by trade name, add the name and location of the manufacturer or a major distributor in parenthesis after the first mention of the product. For the name of plant protection chemicals, give popular scientific names (first letter small), not trade names (When trade name is given in addition, capitalize the first letter of the name). Known methods of analysis should be indicated by referring to the original source, avoiding detailed description. Any new technique developed and followed should be described in fair detail. When some specially procured or proprietary materials are used, give their pertinent chemical and physical properties. References for the methods used in the study should be cited. If the techniques are widely familiar, use only their names in that case.

Results and Discussion (To be typed as a side-heading, a few spaces below the matter on "Materials and Methods")

This section should discuss the salient points of observation and critical interpretation thereof in past tense. This should not be descriptive and mere recital of the data presented in the tables and diagrams. Unnecessary details must be avoided but at the same time significant findings and special features should be highlighted. For systematic discussion, this section may be divided into sub-sections under side-heading and/or paragraph side heading. Relate the results to your objectives. While discussing the results, give particular attention to the problem, question or hypothesis presented in the introduction. Explain the principles, relationships, and generalizations that can be supported by the results. Point out any exceptions. Explain how the results relate to previous findings, support, contradict or simply add as data. Use the Discussion section to focus on the meaning of your findings rather than recapitulating them. Scientific speculation is encouraged but it should be reasonable and firmly founded in observations. When results differ from previous results, possible explanations should be given. Controversial issues should be discussed clearly. References to published work should be cited in the text by the name(s) of author(s) as follows: Mukherjee and Mitra (1942) have shown or It has been shown (Mukherjee and Mitra, 1942)..... If there are more than two authors, this should be indicated by et al. after the surname of the first author, e.g., Mukherjee et al. (1938).

Always conclude the article by clearly crystallizing the summary of the results obtained along with their implications in solution of the practical problems or contribution to the advancement of the scientific knowledge.

Acknowledgments (To be typed as given above, as a side-heading, well below the concluding portion of Conclusions)

The author(s) may place on record the help, and cooperation, or financial help received from any source, person or organization. This should be very brief, and omitted, if not necessary.

References (To be typed as above, as side heading below Acknowledgement)

The list of references must include all published work referred to in the text. Type with double line spacing. Do not cite anonymous as author; instead cite the name of the institute, publisher, or editor. References should be arranged alphabetically according to the surnames of the individual authors or first authors. Two or more references by the same author are to be cited chronologically; two or more in the same year by the letters a, b, c, etc. All individually authored articles precede those in which the individual is the first or joint author. Every reference cited in the article should be included in the list of References. This needs rigorous checking of each reference. Names of authors should not be capitalized.

The reference citation should follow the order: author(s), year of publication, title of the paper, periodical (title in full, no abbreviations, italics or underlined), volume (bold or double underlining), starting and ending pages of the paper. Reference to a book includes authors(s), year, title (first letter of each word except preposition, conjunction, and pronouns in capitals and underlined), the edition (if other than first), the publisher, city of publication. If necessary, particular page numbers should be mentioned in the last. Year of publication cited in the text should be checked with that given under References. Year, volume number and page number of each periodical cited under "References" must be checked with the original source. The list of references should be typed as follows:

Rao C R 1968. *Advances in Statistical Methods in Biometrical Research*, pp.40-45, John Wiley & Sons, New York.

Kanwar J S and Raychaudhuri S P 1971. *Review of Soil Research in India*, pp 30-36. Indian Society of Soil Science, New Delhi.

Mukherjee J N 1953. The need for delineating the basic soil and climatic regions of importance to the plant industry. *Journal of the Indian Society of Soil Science*, **1** : 1-6.

Khan S K, Mohanty S K and Chalam A B, 1986. Integrated management of organic manure and fertilizer nitrogen for rice. *Journal of the Indian Society of Soil Science*, **34** : 505-509.

Bijay-Singh and Yadvinder-Singh 1997. Green manuring and biological N fixation: North Indian perspective. In: Kanwar J S and Katyal J C (Ed.) *Plant Nutrient Needs, Supply, Efficiency and Policy Issues 2000-2025*. National Academy of Agricultural Sciences, New Delhi, India, pp.29-44.

Singh S, Pahuja S S and Malik R K 1992. Herbicidal control of water hyacinth and its effect on chemical composition of water *(in) Proceedings of Annual Weed Science Conference*, held during 3-4 March 1992 by the Indian Society of Weed Science, at Chaurdhary Charan Singh Haryana Agricultural University, Hisar, 127p.

AICRP on Soybean 1992. *Proceedings of 23rd Annual Workshop of All-India Co-ordinated Research Project on Soybean*, held during 7-9 May 1992 at University of Agricultural Sciences, Bangalore, Karnataka, National Research Centre for Soybean, Indore, pp.48.

Devakumar C. 1986. Identification of nitrification retarding principles in neem (*Azadirachta indic*a A.Juss.) seeds. Ph D Thesis, Indian Agricultural Research Institute, New Delhi.

Reference to unpublished work should normally be avoided and if unavoidable it may be mentioned only in the text.

Short Communication

Conceptually short communication is a first report on new concept, ideas and methodology which the author(s) would wish to share with the scientific community and that the detailed paper would follow. Short Communication is akin to an advance booking for the report on the findings. Short communications may include short but trend-setting reports of field or laboratory observation(s), preliminary results of long-term projects, or new techniques or those matters on which enough information to warrant its publication as a full length article has still not been generated but the results need to be shared immediately with the scientific community. The style is less formal as compared with the "full-length" article. In the short communications, the sections on abstract, materials and methods, results and discussion, and conclusion are omitted; but the material is put concisely in the same sequence but without formal sections. The other instructions are the same as in the case of the full-length articles.

Tables

Tables should not form more than 20% of the text. Each table should be typed on separate sheet and should have on the top a table number (in Arabic numerals *viz*. 1, 2, 3 etc.) and a caption or title which should be short, but sufficiently explanatory of the data included in the table. Information in the table should never duplicate that in the text and vice versa. Symbols (asterisks, daggers, etc. or small letters, *viz*., a, b, etc.) should be used to indicate footnotes to tables. Maximum size of table acceptable is what can be conveniently composed within one full printed page of the journal. Over-sized tables will be rejected out-right. Such tables may be suitably split into two or more small tables.

The data in tables should be corrected to minimum place of decimal so as to make it more meaningful. Do not use full stop with CD, SEm $\pm$, NS (not C.D., S.E.m $\pm$, N.S.). Do not put cross-rules inside the table. Tables should be numbered consecutively and their approximate positions indicated in the margin of the manuscript. Tables should not be inserted in the body of the text. Type each table on a separate sheet. Do not use capital letters for the tabular headings, do not underline the words and do not use a full-stop at the end of the heading. All the tables should be tagged with the main body of the text i.e. after references.

Figures

Figures include diagrams and photographs. Laser print outs of line diagrams are acceptable while dot-matrix print outs will be rejected. Alternatively, each illustration can be drawn on white art card or tracing cloth/ paper, using proper stencil. The lines should be bold and of uniform thickness. The numbers and letterings must be stenciled; free-hand drawing will not be accepted. Size of the illustrations as well as numbers, and letterings should be sufficiently large to stand suitable reduction in size. Overall size of the illustrations should be such that on reduction, the size will be the width of single or double column of the printed page of the Journal. Legends, if any, should be included within the illustration. Each illustration should have a number followed by a caption typed/ typeset well below the illustration.

Title of the article and name(s) of the author(s) should be written sufficiently below the caption. The photographs (black and white) should have a glossy finish with sharp contrast between the light and the dark areas. Colour photographs/ figures are not normally accepted. One set of the original figures must be submitted along with the manuscript, while the second set can be photocopy. The illustrations should be numbered consecutively in the order in which they are mentioned in the text. The position of each figure should be indicated in the margin of the text. The photographs should be securely enclosed with the manuscript after placing them in hard board pouches so that there may not be any crack or fold. Photographs should preferably be 8.5 cm or 17 cm wide or double the size. The captions for all the illustrations (including photographs) should be typed on a separate sheet of paper and placed after the tables.

Expression of Plant Nutrients on Elemental Basis

The amounts and proportions of nutrient elements must be expressed in elemental forms e.g. for ion uptake or in other ways as needed for theoretical purposes. In expressing doses of nitrogen, phosphatic, and potassic fertilizers also these should be in the form of N, P and K, respectively. While these should be expressed in terms of kg/ha for field experiments, for pot culture studies the unit should be in mg/kg soil.

SI Units and Symbols

SI Units (System International d 'Unities or International System of Units) should be used. The SI contains three classes of units: (i) base units, (ii) derived units, and (iii) supplementary units. To denote multiples and sub-multiples of units, standard abbreviations are to be used. Clark's Tables: Science Data Book by Orient Longman, New Delhi (1982) may be consulted.

Some of these units along with the corresponding symbols are reproduced for the sake of convenience.

Names and Symbols of SI Units

Physical Symbol for SI Unit Symbol Remarks quantity physical quantity for SI Unit

Primary Units

length	l	time	t
metre	m	second	s
mass	m	electric current	I
kilogram	kg	ampere	A

Secondary Units

plane angle	radian	rad	Solid angle	steradian	sr

Unit Symbols

centimetre	cm	microgram	µg
cubic centimetre	cm^3	micron	µm
cubic metre	m^3	micronmol	µmol
day	d	milligram	mg
decisiemens	dS	millilitre	mL
degree-Celsium	°C [=(F-32)x0.556]	minute	min

gram	g	nanometre	nm
hectare	ha	newton	N
hour	h	pascal	Pa
joule J	(= 10^7 erg or 4.19 cal.)	second	s
kelvin	K (= °C + 273)	square centimetre	cm^2
kilogram	kg	square kilometre	km^2
kilometre	km	tonne	t
litre	L	watt	W
megagram	Mg		

Some applications along with symbols

adsorption energy	J/mol (=cal/molx4.19)	leaf area	m^2/kg
cation exchange capacity	cmol (p+)/kg (=m.e./100 g)	nutrient content in plants (drymatter basis)	µg/g, mg/g or g/kg
Electrolytic conductivity	dS/m (=mmhos/cm)	root density or root length density	m/m^3
evapotranspiration rate	$m^3/m^2/s$ or m/s	soil bulk density	Mg/m^3 (=g/cm^3)
heat flux	W/m^2	specific heat	J/kg/K
gas diffusion	$g/m^2/s$ or $m^3/m^2/s$ or m/s	specific surface area of soil	m^2/kg
water flow	$kg/m^2/s$ (or) m^3m^2s (or) m/s	thermal conductivity	W/m/K
gas diffusivity	m^2/s	transpiration rate	$mg/m^2/s$
hydraulic conductivity ion uptake	m/s	water content of soil	kg/kg or m^3/m^3
(Per kg of dry plant material)	mol/kg	water tension	kPa (or) MPa

While giving the SI units the first letter should not be in capital i.e cm, not Cm; kg not Kg. There should not be a full stop at the end of the abbreviation: cm, not cm. kg, not kg.; ha, not ha.

In reporting the data, dimensional units, viz., M (mass), L (length), and T (time) should be used as shown under some applications above. Some examples are: 120 kg N/ha; 5 t/ha; 4 dS/m etc.

Special Instructions

I. In a series or range of measurements, mention the unit only at the end, e.g. 2 to 6 cm2, 3, 6, and 9 cm, etc. Similarly use cm2, cm3 instead of sq cm and cu m.

II. Any unfamiliar abbreviation must be identified fully (in parenthesis).

III. A sentence should not begin with an abbreviation.

IV. Numeral should be used whenever it is followed by a unit measure or its abbreviations, e.g., 1 g, 3 m, 5 h, 6 months, etc. Otherwise, words should be used for numbers one to nine and numerals for larger ones except in a series of numbers when numerals should be used for all in the series.

V. Do not abbreviate litre to` l' or tonne to `t'. Instead, spell out.

VI. Before the paper is sent, check carefully all data and text for factual, grammatical and typographical errors.

VII. Do not forget to attach the original signed copy of `Article Certificate' (without any alteration, overwriting or pasting) signed by all authors.

VIII. On revision, please answer all the referees' comments point-wise, indicating the modifications made by you on a separate sheet in duplicate.

IX. If you do not agree with some comments of the referee, modify the article to the extent possible. Give reasons (2 copies on a separate sheet) for your disagreement, with full justification (the article would be examined again).

X. Rupees should be given as per the new symbol approved by Govt. of India.

Details of the peer review process

Manuscripts are received mainly through e-mails and in rare cases, where the authors do not have internet access, hard copies of the manuscripts may be received and processed. Only after the peer review the manuscripts are accepted for publication. So there is no assured publication on submission. The major steps followed during the peer review process are provided below.

Step 1. ***Receipt of manuscript and acknowledgement***: Once the manuscript is received, the contents will be reviewed by the editor/associate editors to assess the scope of the article for publishing in JOR. If found within the scope of the journal, a Manuscript (MS) number is assigned and the same will be intimated to the authors. If the MS is not within the scope and mandate of JOR, then the article will be rejected and the same is communicated to the authors.

Step 2. ***Assigning and sending MS to referees***: Suitable referees will be selected from the panel of experts and the MS (soft copy) will be sent to them for their comments - a standard format of evaluation is provided to the referees for evaluation along with the standard format of the journal articles and the referees will be given 4-5 week time to give their comments. If the comments are not received, reminders will be sent to the referees for expediting the reviewing process and in case there is still no response, the MS will be sent to alternate referees.

Step 3. ***Communication of referee comments to authors for revision***: Once the referee comments and MS (with suggestions/ corrections) are received from the referees, depending on the suggestions, the same will be communicated to the authors with a request to attend to the comments. Authors will be given stipulated time to respond and based on their request, additional time will be given for attending to all the changes as suggested by referees. If the referees suggest no changes and recommend the MS for publication, then the same will be communicated to the authors and the MS will be taken up for editing purpose for publishing. In case the referees suggest that the article cannot be accepted for JOR, then the same will be communicated to the authors with proper rationale and logic as opined by the referees as well as by the editors.

Step 4. ***Sending the revised MS to referees***: Once the authors send the revised version of the articles, depending on the case (like if major revisions were suggested by referees) the corrected MS will be sent to the referees (who had reviewed the article in the first instance) for their comments and further suggestions regarding the acceptability of publication. If only minor revisions had been suggested by referees, then the editors would look into the issues and decide take a call.

Step 5. ***Sending the MS to authors for further revision***: In case referees suggest further modifications, then the same will be communicated to the authors with a request to incorporate the suggested changes. If the referees suggest acceptance of the MS for publication, then the MS will be accepted for publication in the journal and the same will be communicated to the authors. Rarely, at this stage also MS would be rejected if the referees are not satisfied with the modifications and the reasoning provided by the authors.

Step 6. ***Second time revised articles received from authors and decision taken***: In case the second time revised article satisfies all the queries raised by referees, then the MS will be accepted and if not satisfied the article will be rejected. The accepted MS will be taken for editing process where emphasis will be given to the language, content flow and format of the article.

Then the journal issue will be slated for printing and also the pdf version of the journal issue will be hosted on journal webpage.

Important Instructions

- Data on field experiments have to be at least for a period of 2-3 years
- Papers on pot experiments will be considered for publication only as short communications
- Giving coefficient of variation in the case of field experiments Standard error in the case of laboratory determination is mandatory. For rigorous statistical treatment, journals like Journal of Agricultural Science Cambridge, Experimental Agriculture and Soil Use and Management should serve as eye openers.

SPECIAL ANNOUNCEMENT

In a recently conducted Executive Committee meeting of the Indian Society of Oilseeds Research, it was decided to increase the scope of the Journal of Oilseeds Research by accommodating vibrant aspects of scientific communication. It has been felt that, the horizon of scientific reporting could be expanded by including the following types of articles in addition to the Research Articles, Shor Communications and Review Articles that are being published in the journal as of now.

Research accounts (not exceeding 4000 words, with cited references preferably limited to about 40-50 in number): These are the articles that provide an overview of the research work carried out in the author(s)' laboratory, and be based on a body of their published work. The articles must provide appropriate background to the area in a brief introduction so that it could place the author(s)' work in a proper perspective. This could be published from persons who have pursued a research area for a substantial period dotted with publications and thus research account will provide an overall idea of the progress that has been witnessed in the chosen area of research. In this account, author(s) could also narrate the work of others if that had influenced the course of work in authors' lab.

Correspondence (not exceeding 600 words): This includes letters and technical comments that are of general interest to scientists, on the articles or communications published in Journal of Oilseeds Research within the previous four issues. These letters may be reviewed and edited by the editorial committee before publishing.

Technical notes (less than 1500 words and one or two display items): This type of communication may include technical advances such as new methods, protocols or modifications of the existing methods that help in better output or advances in instrumentation.

News (not exceeding 750 words): This type of communication can cover important scientific events or any other news of interest to scientists in general and vegetable oil research in particular.

Meeting reports (less than 1500 words): It can deal with highlights/technical contents of a conference/ symposium/discussion-meeting, etc. conveying to readers the significance of important advances. Reports must

Meeting reports should avoid merely listing brief accounts of topics discussed, and must convey to readers the significance of an important advance. It could also include the major recommendations or strategic plans worked out.

Research News (not exceeding 2000 words and 3 display items): These should provide a semi-technical account of recently published advances or important findings that could be adopted in vegetable oil research.

Opinion (less than 1200 words): These articles may present views on issues related to science and scientific activity.

Commentary (less than 2000 words): This type of articles are expected to be expository essays on issues related directly or indirectly to research and other stake holders involved in vegetable oil sector.

Book reviews (not exceeding 1500 words): Books that provide a clear in depth knowledge on oilseeds or oil yielding plants, production, processing, marketing, etc. may be reviewed critically and the utility of such books could be highlighted.

Historical commentary/notes (limited to about 3000 words): These articles may inform readers about interesting aspects of personalities or institutions of science or about watershed events in the history/development of science. Illustrations and photographs are welcome. Brief items will also be considered.

Education point (limited to about 2000 words): Such articles could highlight the material(s) available in oilseeds to explain different concepts of genetics, plant breeding and modern agriculture practices.

Note that the references and all other formats of reporting shall remain same as it is for the regular articles and as given in Instructions to Authors

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