Journal of Oilseeds Research

DOR-374

Volume 25
Number 2
December, 2008
ISSN 0970-2776

Indian Society of Oilseeds Research
Directorate of Oilseeds Research
Rajendranagar, Hyderabad-500 030, India

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(Founded in 1983, Registration Number ISSN 0970-2776)

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Overall size 23 cm height (max.) x 17 cm width (max.)
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Indian Society of Oilseeds Research thankfully acknowledges the financial assistance received from INDIAN COUNCIL OF AGRICULTURAL RESEARCH, New Delhi for printing this Journal

Journal of Oilseeds Research is published biannually by the Indian Society of Oilseeds Research

ISSN 0970-2776
Volume 25
Number 2
December, 2008

Journal of OILSEEDS RESEARCH

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Official publication of
The Indian Society of Oilseeds Research, Hyderabad
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Genotype x environmental interactions and stability analysis in large seeded genotypes of groundnut, *Arachis hypogaea* L.

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(Received: May, 2007; Revised: July, 2008; Accepted: August, 2008)

Abstract

Large-seeded groundnut genotypes were evaluated for three years in a single location to examine the existence of genotype x environment (G x E) interaction for pod yield and related traits. Significant G x E interaction was noticed for pod and kernel yield, indicating differential response of the genotypes in different years or environments, while for seed size, shelling percentage and proportion of sound mature kernels the interaction was non-significant. Stability analysis revealed that two genotypes (PBS 29010 and GG 20) had near unity regression coefficient (bi) for pod and kernel yield indicating general adaptation, but only GG 20 had positive phenotypic index. Another released cultivar TKG 19A exhibited significantly low bi, which indicates above average stability and low sensitivity to environmental changes, but had poor mean pod and kernel yield. The genotype ICGV 99101 recorded the highest pod and kernel yield with 21% and 10% yield advantage over the best check, GG 20, respectively. It exhibited the highest phenotypic index for pod and kernel yield, significant bi value and deviation from unity, thereby portraying the highly sensitive nature of the genotype to environmental fluctuations. The 100-seed mass in ICGV 99101 (51.3 g) was numerically superior to TKG 19A that had the highest seed size among the checks.

Key words: Groundnut, large seed size, G x E interaction, stability analysis, AMMI analysis

Introduction

Groundnut (*Arachis hypogaea* L.), being a rich source of protein, minerals and vitamins besides oil, is increasingly finding its use for edible and confectionery purposes since last few decades. Various physical, sensory, chemical and nutritional factors determine the quality of groundnut seed (Dwivedi and Nigam, 2005). Large-seeded groundnut, popularly known as 'hand picked selection (HPS)' is meant for edible purposes, fetches premium price both in domestic and international markets, and holds immense potential for export. Hence, combining high yielding ability with appropriate pod and seed characteristics is one of the important breeding objectives in large-seeded groundnut. Study of genotype x environment (G x E) interactions assume special significance in groundnut as nearly 80% of the crop in India is grown as rainfed, and climatic conditions and seasonal variations have a large bearing on the yield levels. Varietal adaptability to environmental fluctuations is important for yield stabilization. The G x E interaction underlies the very success of a breeding programme related to stability of varieties. Keeping in view the importance of large-seeded groundnut, an attempt was made to evaluate advanced breeding lines with large seed size to assess the stability of the genotypes over the years following Eberhart and Russell's (1966) model. The data obtained were also used to carry out Additive Main effects and Multiplicative Interaction (AMMI) analysis (Zobel *et al.*, 1988; Gauch, 1992).

Material and methods

The experimental material consisted of nine large-seeded groundnut genotypes from Spanish and Virginia habit groups including a National check (M 13) and two zonal checks (GG 20 and TKG 19A). The field trial was conducted in a Randomized Complete Block Design with three replications. Each genotype was grown in a four-row plot of 4m length with an inter-row distance of 60 cm and plant-to-plant distance of 10 cm in a replication. The soil type was medium black and calcareous. The crop was raised during the rainy seasons of 2002 to 2004 by following all the recommended agronomic practices. At maturity, the observations were recorded on pod and kernel yield (kg/ha), shelling percentage (SP), 100-seed mass (HSM) and sound mature kernel (SMK) percentage.

The pooled data of three years were subjected to analysis of variance. Significant genotype x year interaction variance necessitated stability analysis and the stability parameters were computed after verifying the homogeneity of error variances following the model proposed by Eberhart and Russell (1966). The phenotypic index (*Pi*) of each genotype was expressed as deviation of genotypic mean (pooled over years) from the population mean (Sharma, 1998). The *Pi* greatly facilitates identification of poor (negative *Pi*) and highly potential (positive *Pi*) genotypes without referring every time to genotypic mean *vis-à-vis* population mean. The environmental index (*Ij*) of each year was also calculated as deviation of season/year mean from the population mean. The *Ij* helps in identification of favourable and unfavourable environments. The data were also subjected to AMMI analysis (Zobel *et al.*, 1988; Gauch, 1992) in which the model partitions the total variation into genotype main effects, environment main effects, and G x E interaction effects that are further partitioned into several interaction principal component analysis (IPCA) axes and a residual. To apply AMMI, the main effects are first estimated from a standard additive (*i.e.*, no interaction) ANOVA. The residual is then fitted using a principal components analysis, which attempts to find the series of orthogonal axis of a covariance matrix that explain the most variation. The ANOVA model used for phenotypic performance of genotype 'g' tested in environment 'e' is $Y_{ger} = \mu + \alpha_g + \beta_e + \theta_{ge} + E_{ger}$ while the AMMI model is $Y_{ger} = \mu + \alpha_g + \beta_e + {}^N\Sigma_{n=1}\lambda_n\,\gamma_{gn}\,\delta_{en} + \rho_{ge} + E_{ger}$ (Zobel *et al.*, 1988; Ebdon and Gauch, 2002).

Results and discussion

Stability analysis: The analysis of variance revealed that the genotypes differed significantly for all the characters. Also, the seasons (years) were found to differ significantly. The G x E interactions were significant for the traits pod and kernel yield. The pooled analysis of variance for stability revealed that mean squares due to genotypes (G), years (E), G x E, environment (linear) and pooled deviations were significant for these two traits (Table 1). Significant variance due to G x E interaction indicated the differential response of genotypes in expression of the traits to varying environments or years. The existence of significant G x E interaction for pod yield and component traits in groundnut has been well documented (Yadava and Kumar 1979; Yadava *et al.*, 1980; Wynne and Coffelt 1980; Kandaswami *et al.*, 1986; Vindhiyavarman *et al.*, 1989; Raut *et al.*, 1993; Reddy and Gupta, 1994; Reddy *et al.*, 1995; Chuni Lal *et al.*, 1998; Patil *et al.*, 1998; Bentur *et al.*, 2004; Senapati *et al.*, 2004), while absence of G x E interaction for pod yield has also been reported (Veerabadhiran *et al.*, 1990; Vindhiyavarman and Manoharan, 1993). Non-significant G x E interaction observed for HSM, SMK and shelling percentage indicate that these traits are least influenced by the environments or years. The present results are in conformity with the earlier reports on stability of traits like HSM (Reddy and Gupta, 1994; Venkataravana *et al.*, 2000) and shelling percentage (Venkataravana *et al.*, 2000). However, reports are also available on the existence of significant G x E interactions contradicting the results obtained in respect of shelling percentage (Norden *et al.*, 1986; Nigam *et al.*, 1989; Moinuddin *et al.*, 1998; Bentur *et al.*, 2004) and seed size (Kandaswamy *et al.*, 1986; Vindhiyavarman *et al.*, 1989; Bentur *et al.*, 2004). The absence of differential response of the genotypes for seed size in the present study indicates the stable expression of the trait, which in fact is essential in large-seeded groundnuts to maintain requisite seed mass.

Highly significant environmental (linear) variance for pod and kernel yield suggested that variation among the environments or years was linear. A linear environmental variance signifies unit change in environmental index for each unit change in the environmental conditions. The G x E (linear) variance was non-significant implying, thereby, differential performance of genotypes under diverse environments with nearly uniform reaction norms. On the other hand, significant pooled deviations for pod and kernel yield suggest that performance of different genotypes fluctuated significantly from their respective linear path of response to environments. In other words, the unpredictable environment formed the major portion of the G x E interactions. However, on analyzing the individual varietal fluctuation from linearity, it becomes clear that only a few genotypes fluctuated significantly from linearity.

During the years 2002 and 2004, the highest pod and kernel yield was recorded in ICGV 99101, while during 2003 the highest pod and kernel yield was recorded in PBS 29058 (Table 2). The overall performance was highest in 2002 for both pod and kernel yield, while performance was lowest in 2004. The highest and positive environmental index for 2002 indicates that the climatic conditions prevailed during 2002 was most favourable for crop growth. Similarly, highly negative environmental index of 2004 demonstrates that the year was an unfavourable year.

The genotype ICGV 99101 recorded the highest pod and kernel yield on pooled basis with 21.2% (pod) and 10.3% (kernel) yield advantage over the best check, GG 20. The highest mean pod and kernel yield in ICGV 99101 during 2002 also indicates that the genotype performs better under favourable environment. The HSM in ICGV 99101 was numerically superior to the variety TKG 19A that had the highest seed size among the checks.

The stability parameters for pod and kernel yield are presented in Table 2. For pod and kernel yield, GG 20 and PBS 29010 recorded near unity regression coefficient (bi). Bharodia (1997) reported that productivity of GG 20 did not vary significantly in high or low rainfall conditions and the genotype had better stability and adaptability for pod yield under a wide range of soil conditions. The results obtained in the present study also supports the above findings since GG 20 exhibited relatively high mean, near unity regression and least deviations. The genotype ICGV 99101 had the highest bi value for both pod and kernel yield (1.87 and 1.70, respectively), which was significantly higher than the unity. This indicates below average stability of ICGV 99101 or in other words its high sensitive nature and specific adaptation to favourable environments. This genotype had the highest positive phenotypic index, thereby, indicating the potentiality for both pod and kernel yield. Since cultivation of export quality groundnuts has to be under high input and better management conditions in order to realize the full potential of the genotype for seed and other quality traits, ICGV 99101 can be considered as responsive and can give higher yield under such circumstances. Taking into consideration the yield advantage as well as seed size superiority among the tested genotypes, ICGV 99101 holds great promise for production of large-seeded groundnut under high management conditions.

AMMI analysis: The Additive Main Effects and Multiplicative Interaction (AMMI) model (Zobel *et al.*, 1988; Gauch, 1992) is a powerful tool to predict the accuracy of estimates of genotypic yields in across-location trials, especially when trials are conducted at several locations or multi-environments in diverse crop growing zones. Though the present study is restricted to a single location and application of AMMI model is not very essential, the analysis was carried out to see whether the results obtained agree with that of stability analysis of Eberhart and Russell (1966).

The G x E interaction sum of squares for pod yield was divided into two components. The first principal component axis (AMMI-1) captured 82% of the interaction sum of squares with 56% of the degrees of freedom for G x E interaction, while the second principal component axis (AMMI-2) explained the rest. ANOVA for AMMI model indicated that mean square due to AMMI-1 component was significant at 5% level of significance. Thus, the G x E interaction was best predicted by the first principal component.

When contribution of individual genotype towards different components was considered (Table 3) the genotype ICGV 99101 had the highest contribution towards interaction component. Similarly, it also had the highest contribution towards deviations from regression component of interaction indicating its best performance in a favourable environment. Further, The AMMI-1 score was the highest and positive for ICGV 99101, thus indicating significant level of interaction, and thereby its sensitivity to environment. On the other hand variety GG 20 had lowest contribution to the interaction component and least deviation from regression component as well as lower contribution to regression component of the G x E interaction, thus establishing the correspondence between two approaches of stability models.

The interaction biplot with season and genotypes superimposed can also be used to determine the stability of genotype and their adaptation to a given set of environments or locations (Fig. 1). The varieties GG 20 and M 13 are situated close to the center indicating their stability across years, while positions far from the center (ICGV 99101, TKG 19A) represent sensitive nature of the genotypes. The performance of these genotypes bound to vary across seasons/years depending on the environmental conditions or management practices. Fig. 2 gives the genotype map showing best genotypes over the environment scores. Genotype ICGV 99101 (Sl. No. 6 in the figure) occupied larger area among the test entries with better performance under favourable environmental scores. Variety GG 20 occupied the middle position depicting more or less the stable performance, while position of TKG 19A indicated better performance under unfavourable environmental conditions.

Acknowledgment: The authors are grateful to ICRISAT, Hyderabad, India for providing the groundnut breeding lines used in this study.

Table 1 **Analysis of variance for stability (Eberhart and Russell, 1966)**

Source of variation	d.f.	Mean sum of squares				
		Pod yield	Kernel yield	HSM	SMK	SP
Genotypes	8	337961*	211542*	75.6**	247.3*	13.7**
Environments	2	911428**	487043**	350.8**	586.6*	117.3**
G x E	16	130204**	59395*	14.4	95.2	3.4
Environment (linear)	1	2979904**	2090048**	701.6**	1173.1**	234.5**
G x E (linear)	8	80756	42708	14.5	68.9	1.9
Pooled deviation	9	159689*	67629*	12.7	107.9	4.3
Pooled error	48	47483	26602	10.1	64.2	2.7

*, ** Significant at 5% and 1% level of significance, respectively.

Table 2 Mean performance of the genotypes over years and stability parameters for pod and kernel yield

Genotype	Pod yield (kg/ha)							Kernel yield (kg/ha)							HSM (g)	SMK (%)	SP (%)
	2002	2003	2004	Mean	*bi*	S^2di	*Pi*	2002	2003	2004	Mean	*bi*	S^2di	*Pi*			
PBS 29010	1989	1960	1193	1714	0.95	65106	-149.2	1453	1355	772	1193	0.97	27091	-74.4	47.8	48.9	68.8
PBS 29021	2144	1813	1147	1701	1.21	-14973	-162.3	1576	1290	736	1201	1.21	-3625	-66.9	43.0	45.0	69.3
PBS 29026	1884	1815	1147	1615	0.88	28803	-248.1	1373	1214	715	1101	0.94	2876	-166.9	44.4	39.8	67.1
PBS 29058	2297	2080	1224	1867	1.29	46941	3.8	1666	1446	788	1300	1.26	22609	32.7	58.9	44.4	68.9
ICGV 00428	2320	1729	1818	1956	0.65	17808	92.1	1588	1113	1140	1280	0.68	6617	12.8	49.1	31.9	65.2
ICGV 99101	3585	1568	2153	2436	1.87*	949255	572.2	2411	1007	1321	1580	1.70*	390092	312.2	51.3	41.1	64.5
GG 20	2373	2040	1615	2009	0.93	-42499	146.0	1763	1430	1102	1432	0.97	-25601	164.1	45.4	47.9	70.8
M 13	2365	1695	1415	1825	1.18	-33683	-38.2	1623	1164	856	1215	1.13	-26049	-53.0	43.8	20.8	65.8
TKG 19 A	1598	1810	1534	1647	0.06*	-6901	-216.2	1139	1138	1044	1107	0.13*	-24768	-160.6	50.6	33.4	67.2
Popn. mean	2284	1835	1472	1863				1621	1240	942	1268				48.2	39.2	67.5
SE	242.4	261.1	124.5	217.9	0.69	-	-	180.1	193.3	100	163.1	0.54	-	-	3.2	8.0	1.6
Env. index (*Ij*)	420.5	-28.8	-391.7					353.0	-27.7	-325.3							

*, ** Significant at 5% and 1% level of significance, respectively.

Table 3 Contribution of genotypes towards components of stability and scores for AMMI components for genotypes/seasons in respect of pod yield

Genotype/ season	Yield (kg/ha)	Rank	MS-GxE	MS-Reg	MS-Dev	AMMI-1	Rank	AMMI-2
PBS 29010	1714	6	56794	1001	112588	-8.70	8	-4.91
PBS 29021	1701	7	23433	14357	32508	-2.98	5	-7.56
PBS 29026	1615	9	406142	4943	76285	-7.71	7	-2.45
PBS 29058	1867	4	60876	27332	94421	-5.55	6	-11.49
ICGV 00428	1956	3	53376	41463	65290	3.80	3	11.94
ICGV 99101	2436	1	623431	250135	996727	30.91	1	0.01
GG 20	2009	2	3401	1821	4982	-2.28	4	0.26
M 13	1825	5	12425	11053	13798	4.21	2	-1.67
TKG 19 A	1647	8	167267	293954	40580	-11.71	9	15.88
Kharif 2002	2284					23.59	1	-12.18
Kharif 2003	1835					-27.13	3	-7.96
Kharif 2004	1472					3.54	2	20.13

(MS-GxE: Contribution of each genotype to interaction MS; MS-Reg: Contribution of each genotype to the regression component of the G x E interaction; MS-Dev: Deviations from regression component of interaction)

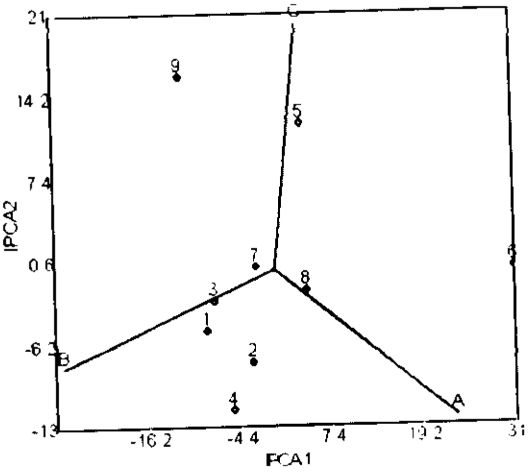

Fig. 1. Interaction biplot for AMMI model

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20.13  9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 5 5 5 5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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14.66  9 9 9 9 9 9 9 9 9 9 9 9 9 5 5 5 5 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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-12.18 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
         ^           ^           ^           ^           ^           ^           ^           ^           ^           ^
       -27.1       -22.0       -16.8       -11.7       -6.5        -1.3         3.8         8.9        14.1        19.3
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Fig. 2. Genotype map showing best genotypes over the range of AMMI-2 site scores

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J. Oilseeds Res., **25**(2) : 132-138 (2008)

Multiple criteria selection of crosses for yield improvement in sesame, *Sesamum indicum* L.

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(Received: March, 2007; Revised: November, 2008; Accepted: December, 2008)

Abstract

The F_1 along with parents of a 12 parent half diallel cross in sesame were studied and seven parameters, i.e., D^2_8 based on 8 characters and D^2_4 based on yield and its 3 direct components and mid-parent value (MP-Y), F_1 mean (F_1-Y), relative heterosis (RH-Y), biparental average GCA (MPGCA-Y) and SCA effect (SCA-Y) for yield were estimated. Thirty selected crosses were studied for segregation for yield in F_2. Thirteen combinations were tried as criteria for selection of crosses. The predictivity of a selection criterion was assessed by correlation and regression of F_2DS_8 on the DS of selection criterion. The usefulness of individual parental and F_1 parameters as selection criteria was also assessed. Among the single-parameter criteria, D^2_4 based on yield and its direct components gave the highest R^2 of 48.28%, followed by MPGCA-Y (45.62%) and F_1-Y (39.98%). Ten of the 13 multiple criteria proved to be better predictor of F_2DS_8 than the best single-parameter criterion D^2_4. The multiple criterion DS(2,4,6) based on D^2_4 and F_1 mean and biparental average GCA for yield was found to be the best criterion for selection of crosses for yield improvement in sesame.

Key words: Sesame, diallel cross, discriminate function

Introduction

The major approach in breeding for yield in autogamous crops is hybridization followed by selection in segregating generations. The basis of improvement by this method is transgressive segregation that results from recombination of desirable genes of the parental varieties. Choice of parents or crosses is a crucial factor determining success from recombination breeding for yield. In absence of any objective method, the breeder selects parents and makes crosses taking into consideration local adaptation, ecogeographic diversity, parental performance *per se* and yield component complementation. The process is subjective and it is a common experience that while some crosses produce superior progeny, others prove disappointing and much effort is expended before such differences become apparent. Though the problem is well recognized, an objective method for choice of parents or crosses is yet to be found. Some workers have assessed the usefulness of D^2, parental performance *per se*, F_1 performance, heterosis and GCA as criteria for choice of parents/crosses in different crops. The present study in sesame evaluates multiple criteria selection based on combinations of parental and F_1 parameters with a view to finding an objective method for choice of parents or crosses of better segregation potential.

Material and methods

The material consisted of a 12-parent half diallel cross of sesame. The parental varieties included 3 improved varieties (Prachi, Uma and Kalika) of Orissa and 9 improved varieties (GT-10, VRI-1, B.67, TKG-22, TC-25, RT-46, Pragati, AKT-64 and HT-1) of nine other states. The F_1 of the half diallel cross along with the parental varieties was grown in Randomised Block Design with 4 replications during summer, 2005. Each entry was represented by one row of 2.5 m. Sowing was done with 35 cm x 10 cm spacing and normal agronomic practices were followed. Observations were taken on days to flowering and maturity on plot basis and on plant height, primary branches, capsules/plant, seeds/capsule, 1000-seed weight and seed yield from 8 random plants/plot.

Analysis of variance and covariance was carried out on the 12 parental varieties and genetic divergence among the varieties estimated by D^2 (Rao, 1952). Two sets of D^2 were estimated, one based on all the 8 characters studied (D^2_8) and another (D^2_4) based on yield and its direct components, i.e., capsules/plant, seeds/capsule and 1000-seed weight. Combining ability analysis was done and GCA and SCA effects estimated following Griffing (1956).

The parental and F_1 parameters evaluated as criteria for choice of parents and crosses were D^2_8, D^2_4, mid-parent value for yield (MP-Y), F_1 performance for yield (F_1-Y), relative heterosis for yield (RH-Y), biparental average GCA for yield (MPGCA-Y) and SCA effect for yield (SCA-Y). These parameters were estimated for the 66 crosses and then 30 crosses were selected such that the selected crosses covered the whole range of each of the seven parameters. This selection was done only to reduce the number of crosses to be handled in F_2 so that large samples of plants could be studied for assessing segregation potential. The selected crosses involved all the 12 parental varieties.

The F_2s of the 30 selected crosses along with the parental varieties were grown in Randomised Block Design with 3 replications during *kharif*, 2005. Each entry was represented by 4 rows of 3 m each in each replication. Agronomic practices were same as in F_1. Single plant observation was taken on seed yield from 70 random plants/cross and 40 random plants/parent variety in each replication. Eight parameters of segregation potential for yield were estimated in F_2. An F_2 plant giving higher yield than the highest yielding plant of the better parent was considered to be a positive transgressive segregant (PTS) and the frequency of such plants was PTSF. PTSM was the average of PTS. MXT was the difference in yield of the highest yielding PTS and the highest yielding plant of the better parent. AVT was estimated as the difference of PTSM and the highest yielding plant of the better parent. All the parameters were estimated replicationwise and then averaged. Weighted average was used in case of PTSM and AVT. The interrelationship of the parental and F_1 parameters, i.e., D^2_8, D^2_4, MP-Y, F_1-Y, RH-Y, MPGCA-Y and SCA-Y and the F_2 segregation parameters, i.e., mean, s^2, T10%M, S10%, PTSF, PTSM, MXT and AVT, was analyzed by simple correlations.

Discriminant analysis by Fisher's linear discriminant function (Mardia *et al.*, 1979) was employed as the method for simultaneous use of multiple parental and F_1 parameters for selection of crosses. The discriminant function, which gives a discriminant score as a linear combination of the variables for each object, is of the following form.

$$y = a_1x_1 + a_2x_2 + a_3x_3 + \dots\dots\dots\dots\dots\dots + a_nx_n \qquad (1)$$

where a_1, a_2, ... an are the weighting coefficients, x_1, x_2, ... x_n are the mean values of the variables of an object and y is the discriminant score. The a's are to be so chosen as to maximize the ratio of between-groups SS to within-groups SS of y. In matrix form, the ratio of between-groups SS to within-groups SS of y is a'Ba/a'Wa, where B is between-groups SS and SP matrix and W is within-groups SS and SP matrix of the original variables x's and a is the vector of unknowns (a's). The vector a of the Fisher's discriminant function is the eigenvector of ($W^{-1}B$) corresponding to the largest eigen value. This method was followed in the present study. Once the weighting coefficients, a's, were estimated, discriminant scores of the crosses were estimated using the function as at (1). It may be noted that the vector a can be re-scaled without affecting the ratio a'Ba/a'Wa. For the purpose of the present study, the discriminant score having the highest numerical value should be positive. Therefore, wherever necessary, the vector a was re-scaled by multiplying it by $^{-1}$.

Discriminant analysis of the crosses was carried out with various combinations of parental and F_1 parameters and the discriminant scores (DS) evaluated as selection criteria. Discriminant analysis was also carried out on the F_2s in order to have a single multivariate measure of segregation potential (F_2DS_8) based on all the 8 segregation parameters estimated for yield in F_2. All variables, both of F_1 and F_2, were standardized as they were in very different units. The predictive value of the selection criteria, i.e., DS based on parental and F_1 parameters, was assessed by simple correlations and regression of F_2DS_8 on DS of selection criterion.

Results and discussion

The present study, which aimed at finding an effective criterion for choice of crosses for yield improvement, envisaged multiple criteria selection is based on a combination of parental and/or F_1 parameters like D_2 and parental performance *per se*, F_1 performance, heterosis (RH), biparental average GCA and SCA for yield. These parameters were estimated from study of the parents and F_1 of a half-diallel cross among 12 varieties of diverse origin. There were significant differences among the parental varieties and among the F_1 hybrids for all the 8 characters studied. D^2_8 estimates among the parental varieties ranged from 8.47 to 125.47 and D^2_4 ranged from 2.19 to 90.77. With D^2_8, the 12 varieties grouped into 5 clusters and with D^2_4, they grouped into 6 clusters. The D^2 values and number of clusters to which the varieties grouped indicated substantial genetic diversity among the varieties for productivity traits.

Parental and F_1 parameters: The seven parental and F_1 parameters evaluated as selection criteria, i.e., D^2_8 and D^2_4 and MP-Y, F_1-Y, RH-Y, MPGCA-Y and SCA-Y for yield were estimated for all the 66 crosses and 30 crosses were selected for study of segregation for yield in F_2. Range of variation of the parameters among the 30 selected crosses was 9.02 - 124.84 for D^2_8, 2.19 - 90.77 for D^2_4, 4.14 - 7.52 g/pl. for MP-Y, 5.07 -9.75 g/pl. for F_1-Y, -4.38 - 90.60 % for RH-Y, -0.875 - 0.686 g/pl. for MPGCA-Y and -1.870 - 2.231 g/pl. for SCA-Y (Table 1). These ranges of variation of the parameters were the same as of the full set of 66 crosses.

F_2 segregation parameters: Thirty selected crosses were studied for segregation for yield in F_2. Eight parameters, i.e., mean, s^2, T10%M, S10%, PTSF, PTSM, MXT and AVT for yield, were estimated from large samples of 210 plants per F_2. Analysis of variance revealed significant differences among the crosses for all the 8 parameters. Means of the crosses (F_2s) for yield ranged from 3.127 to 5.153 g/pl. with a general mean of 4.139 g/pl., compared to 3.261-4.963 g/pl. of the parental varieties with a general mean of 3.840 g/pl. (Table 2). Range of variation of other parameters of segregation for yield among the 30 F_2s was 0.757 - 3.693 g^2/pl. for variance s^2, 4.880-8.617 g/pl. for T10%M, 1.573 - 4.663 g/pl. for S10%, 1-19 per 210 (0.48

- 9.05 %) for PTSF, 5.39 - 9.60 g/pl. for PTSM, 0.010 - 3.443 g/pl. for MXT and 0.010 - 1.813 g/pl. for AVT.

Correlation among F_2 segregation parameters: All the 28 correlations among the 8 F_2 segregation parameters were positive and 22 of them significant at 1% level (Table 3). Five of the six non-significant correlations were those of mean with other parameters. The parameters s^2, T10%M, S10%, PTSF, PTSM, MXT and AVT showed high positive correlation among them. The segregation parameters estimated in F_2 covered all possible factors determining the segregation and selection potential of a cross. The nature of relationship among the F_2 segregation parameters showed that the parameters are reinforcing rather than counteracting factors and that their use in linear combination for a single measure of the relative segregation and selection potential of the crosses would be straightforward.

Correlation between parental/F_1 and F_2 parameters: Six of the eight F_2 segregation parameters showed significant positive correlation with both D^2_8 and D^2_4, but the correlations with D^2_4 were higher than those with D^2_8 (Table 4). Mean and PTS mean were the two parameters that showed no correlation with either D^2_8 or D^2_4. Chauhan and Singh (1982) examined the relationship between D^2 based on yield and its components and F_2 variance for yield in soybean and found that F_2 variance was higher when the parents were moderately diverse. Dikshit and Swain (2001) found no relationship between D^2 based on 14 characters and F_2 segregation parameters like variance, top 10% mean, PTS frequency, PTS mean and average transgression for yield in sesame. In this study, five F_2 segregation parameters showed significant positive correlation with F_1-Y and six showed significant positive correlation with MPGCA-Y. None of the F_2 segregation parameters showed significant negative correlation with any parental/F_1 parameter. Dikshit and Swain (2001) reported positive relation of F_2 variance with F_1 mean, relative heterosis and biparental average GCA in sesame. In this study, only one F_2 parameter (AVT) showed significant correlation with MP-Y, while none of the F_2 parameters showed significant correlation with RH-Y and SCA-Y. The present results showed that D^2_4, F_1 mean and biparental average GCA were good indicators and RH and SCA were poor indicators of segregation potential.

Parental and F_1 parameters as selection criteria: Fisher's linear discriminant function (Mardia *et al.*, 1979) was used to obtain a single measure of segregation potential of a cross, based on all the aforesaid F_2 parameters. The discriminant score F_2DS_8 based on the 8 F_2 segregation parameters was taken as the measure of segregation potential of a cross and the predictivity of individual parental and F_1 parameters for predicting F_2DS_8 was assessed by correlation and regression analysis. F_2DS_8 showed high positive correlation ® >0.6) with D^2_4, MPGCA-Y and F_1-Y and moderate correlation ($0.5 < r < 0.6$) with D^2_8 and MP-Y (Table 5). Correlations of RH-Y and SCA-Y with F_2DS_8 were low and non-significant. The b-coefficients of the regression of F_2DS_8 on D^2_8, D^2_4, MP-Y, F_1-Y and MPGCA-Y were highly significant, while those of RH-Y and SCA-Y were non-significant. The results showed that D^2_8, D^2_4, MP-Y, F_1-Y and MPGCA-Y have a predictive relationship with F_2DS_8. Between D^2_8 and D^2_4, the latter would be a better indicator of segregation potential for yield. D^2_4 gave the highest R^2 of 48.28%, followed by MPGCA-Y (45.62%), F_1-Y (39.98%), D^2_8 (28.88%) and MP-Y (28.73%). The coefficient of determination (R^2) being generally low in these cases, no single parental/F_1 parameter could be considered to be an adequate criterion for selection of crosses. However, when information is available only on the parental varieties, D^2_4 giving a moderate R^2, can be used as a criterion for choice of parental combinations, to some advantage. Bhatt (1973) reported that choice of parents on the basis of higher D2 was more effective than that based on ecogeographic diversity for yield improvement in wheat.

Combinations of parental and F_1 parameter as selection criteria: The study envisaged multiple criteria selection based on combinations of parental and F_1 parameters. Thirteen combinations of six parental and F_1 parameters, leaving out D^2_8, were tried. These included combinations of parental parameters such as D^2_4 and MP-Y and F_1 parameters like F_1-Y, RH-Y, MPGCA-Y and SCA-Y. Fisher's linear discriminant function (Mardia *et al.*, 1979) was used to obtain discriminant scores (DS) based on each combination. The predictivity of the multiple criteria DS for predicting segregation potential (F_2DS_8) was assessed by correlation and regression analysis. F_2DS_8 showed high positive correlation with DS of all 13 combinations, the r-values ranging between 0.680 and 0.874 (Table 5). Ten of the 13 multiple criteria DS showed higher correlation with F_2DS_8 than the best single parameter D^2_4. The b-coefficients of the regression of F_2DS_8 on the multiple criteria DS of all combinations were significant at 1% level. R^2-values of regressions ranged from 46.25% to 76.31%. Most multiple criteria DS proved to be better predictor of segregation potential as measured by F_2DS_8 than the best single-parameter criterion D^2_4. DS(2,4,6) based on D^2_4, F_1-Y and MPGCA-Y was the best multiple criterion giving an R^2 of 76.31%, followed by DS(2,6) based on D^2_4 and MPGCA-Y giving an R^2 of 70.73% and DS(4,6) based on F_1-Y and MPGCA-Y with R^2 of 62.30%. DS(2,3) based on D^2_4 and MP-Y, DS(4,5) based on F_1-Y and RH-Y and DS(4,5,6,7) based on F_1-Y, RH-Y, MPGCA-Y and SCA-Y proved to be poorer combinations. Generally, inclusion of D^2_4 and biparental average GCA improved predictivity of the predictor DS, while inclusion of relative heterosis and SCA decreased predictivity. Heterotic manifestation in F_1 has been reported to have positive relation with segregation potential (Arunachalam, 1993). As usual, relative heterosis was expressed as percentage of mid-parent value in this study. Only the difference F_1-MP may be a better alternative to RH in the present context.

Selection of crosses and predictivity of selection criteria: The correlations of all selection criteria with F_2DS_8 being positive, selection is to be done for higher values of the selection criteria. F_2DS_8 of the crosses as the measure of segregation potential ranged from -0.028 to 6.065 with a mean of 2.811 (Table 2). The range indicated wide variation in segregation potential of the crosses for yield, offering ample scope for selection. If upper 20% of the crosses are selected on the basis of the best single parameter, i.e., D^2_4 and 3 best multiple criteria, i.e., DS(2,4,6), DS(2,6) and DS(4,6), the selected crosses would be as shown in Table 6. According to F_2DS_8, the best six crosses are VRI-1/AKT-64, GT-10/VRI-1, Kalika/VRI-1, Uma/AKT-64, Prachi/AKT-64 and Uma/Kalika. Selection on D^2_4 picked up 4 of the 6 best crosses according to F_2DS_8. The other two-VRI-1/TC-25 and GT-10/Pragati, ranked 9th and 13th, respectively, for F_2DS_8.

Table 1 Parental and F_1 parameters of 30 selected crosses in sesame

Cross	D^2_8	D^2_4	MP–Y (g/pl.)	F_1–Y (g/pl.)	RH–Y (%)	MPGCA-Y (g/pl.)	SCA–Y (g/pl.)
Prachi / Uma	31.02	24.25	5.93	7.69	29.92	0.337	-0.072
Prachi / B.67	12.81	2.19	4.79	5.07	5.76	-0.078	-1.870
Prachi / TC-25	50.56	10.15	4.37	8.34	90.60	-0.495	2.231
Prachi / Pragati	49.66	25.71	4.85	7.47	53.90	0.040	0.292
Prachi / AKT-64	66.39	45.11	5.22	7.68	47.12	0.196	0.195
Uma/Kalika	29.89	10.08	7.22	8.13	12.60	0.551	-0.072
Uma / GT-10	18.29	10.40	7.52	8.16	8.55	0.686	-0.310
Uma / TKG-22	40.21	13.14	5.69	8.57	50.73	-0.044	1.565
Uma / RT-46	17.42	3.89	6.56	8.49	29.35	0.251	0.888
Uma / AKT-64	26.08	10.25	6.71	9.75	45.34	0.571	1.511
Kalika/GT-10	36.98	12.75	7.32	8.95	22.27	0.524	0.804
Kalika / VRI-1	85.53	51.27	6.43	8.71	35.40	0.281	1.049
Kalika /KG-22	102.89	21.05	5.49	7.04	28.23	-0.206	0.359
Kalika / RT-46	75.40	16.02	6.36	6.51	2.22	0.089	-0.768
Kalika / AKT-64	73.49	31.94	6.51	7.28	11.75	0.410	-0.637
GT-10 / VRI-1	95.01	83.61	6.73	7.41	10.12	0.415	-0.518
GT-10 / RT-46	35.90	18.34	6.66	6.37	-4.38	0.224	-1.173
GT-10 / Pragati	65.29	54.20	6.44	7.17	11.30	0.389	-0.703
GT-10 / HT-1	45.66	23.72	6.43	7.53	17.01	0.148	0.137
VRI-1/ TC-25	104.34	39.84	5.07	6.15	21.27	-0.390	-0.164
VRI-1/ AKT-64	124.84	90.77	5.92	9.48	60.04	0.301	1.780
VRI-1/ HT-1	85.37	25.72	5.54	5.55	0.07	-0.096	-1.356
B.67 / TKG-22	24.53	6.47	4.56	6.13	34.53	-0.459	-0.048
B.67 / TC-25	33.31	7.91	4.73	7.28	53.95	-0.534	1.254
B.67 / AKT-64	38.11	33.22	5.58	8.10	45.14	0.157	0.686
TKG-22 / TC-25	9.02	2.67	4.14	5.44	31.46	-0.875	0.094
TKG-22 / HT-1	14.85	8.00	4.61	5.72	24.24	-0.582	-0.208
RT-46/HT-1	10.82	6.96	5.48	7.37	34.43	-0.287	0.844
Pragati/AKT-64	28.70	17.95	5.64	8.55	51.74	0.275	0.908
Pragati / HT-1	63.50	35.52	5.26	8.79	67.06	-0.123	1.935

Table 2 Segregation parameters for yield and discriminant scores (F_2DS_8) of the 30 crosses in F_2

Cross	Mean (g/pl.)	s^2	T10%M (g/pl.)	S10% (g/pl.)	PTSF	PTSM (g/pl.)	MXT (g/pl.)	AVT (g/pl.)	F_2DS_8 (Rank)
Prachi / Uma	5.15	3.19	8.45	3.30	11	9.17	1.51	1.13	2.97 (12)
Prachi / B.67	5.04	2.26	7.83	2.79	3	9.40	1.57	0.65	1.66 (25)
Prachi / TC-25	4.41	2.33	7.58	3.17	4	8.69	0.95	0.78	2.10 (20)
Prachi / Pragati	4.53	3.03	8.35	3.81	12	9.16	1.83	1.31	3.15 (10)
Prachi / AKT-64	4.19.	3.16	8.27	4.08	14	9.08	2.83	1.19	4.81 (5)
Uma / Kalika	4.65	2.02	7.54	2.89	8	8.72	1.31	1.12	4.71 (6)
Uma / GT-10	4.44	1.49	6.83	2.40	3	8.30	0.72	0.41	3.13 (11)
Uma / TKG-22	4.44	2.14	7.32	2.89	8	8.57	1.37	0.95	2.41 (17)
Uma / RT-46	4.11	2.06	7.07	2.97	8	8.71	1.29	0.98	2.56 (16)
Uma / AKT-64	4.53	2.31	7.66	3.14	10	9.19	1.66	1.04	5.15 (4)
Kalika / GT-10	4.59	1.94	7.71	3.12	9	9.09	2.15	1.81	3.93 (7)
Kalika / VRI-1	4.09	2.75	8.27	4.19	18	8.57	3.04	1.35	5.25 (3)
Kalika /KG-22	4.38	1.92	7.07	2.70	7	8.17	1.58	0.99	2.16 (19)
Kalika / RT-46	4.32	1.29	6.47	2.16	3	8.65	0.75	0.71	1.49 (27)
Kalika /AKT-64	4.37	1.92	7.40	3.05	12	8.28	1.66	1.02	2.88 (14)
GT-10 / VRI-1	4.11	3.63	8.62	4.51	19	8.86	3.43	1.43	6.03 (2)
GT-10 / RT-46	3.62	1.43	6.00	2.39	6	6.91	0.90	0.65	1.70 (23)
GT-10 / Pragati	4.07	2.82	7.90	3.83	19	8.06	3.08	1.45	2.94 (13)
GT-10 / HT-1	3.63	1.59	6.33	2.69	5	7.21	1.15	0.64	1.96 (21)
VRI-1 / TC-25	3.36	2.17	6.70	3.33	8	8.40	1.23	0.91	3.16 (9)
VRI-1/ AKT-64	3.78	3.69	8.45	4.66	17	8.79	3.18	1.42	6.07 (1)
VRI-1/ HT-1	3.47	2.05	6.80	3.33	7	8.26	1.53	0.96	2.68 (15)
B.67 / TKG-22	4.22	2.59	7.67	3.46	5	9.23	1.08	0.94	0.55 (28)
B.67 / TC-25	4.23	2.54	7.41	3.19	2	8.88	0.15	0.15	1.54 (26)
B.67 / AKT-64	4.14	3.11	8.25	4.11	10	9.60	2.10	1.28	2.30 (18)
TKG-22 /TC-25	3.13	0.88	4.96	1.83	2	5.39	0.18	0.15	0.18 (29)
TKG-22 / HT-1	3.31	0.76	4.88	1.57	1	5.72	0.01	0.01	-0.03 (30)
RT-46/HT-1	4.05	1.49	6.29	2.23	8	6.98	1.22	0.83	1.70 (24)
Pragati/AKT-64	4.11	1.23	6.33	2.22	11	7.21	1.08	0.66	1.77 (22)
Pragati / HT-1	3.69	1.91	6.83	3.15	12	7.70	2.00	1.04	3.44 (8)
CD (5%)	0.65	1.23	1.35	0.95	6.633	-	1.39	0.86	-

Table 3 Correlations among F_2 segregation parameters for yield

Parameter	s^2	T10%M	S10%	PTSF	PTSM	MXT	AVT
Mean	.360	.632**	.174	.092	.703**	.170	.342
s^2		.924**	.948**	.683**	.738**	.757**	.677**
T10%M			.873**	.647**	.880**	.746**	.760**
S10%				.765**	.677**	.841**	.750**
PTSF					.313	.920**	.790**
PTSM						.469**	.650**
MXT							.860**

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

Table 4 Correlations between parental and F_1 parameters and F_2 segregation parameters for yield

Parameters	D^2_8	D^2_4	MP-Y	F_1-Y	RH-Y	MPGCA-Y	SCA-Y
Mean	*-.201*	*-.184*	*.265*	*.311*	*.062*	*.460**	*.016*
S^2	.460*	.673**	.037	.335	.280	.306	.166
T10%M	.362*	.511**	.214	.448*	.231	.491**	.157
S10%	.586**	.766**	.106	.374*	.254	.336	.190
PTSF	.551**	.822**	.336	.482**	.124	.537**	.163
PTSM	.240	.206	.208	.353	.144	.428*	.091
MXT	.593**	.820**	.332	.414*	.058	.535**	.082
AVT	.474**	.572**	.423*	.497**	.065	.580**	.147

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

Table 5 Correlation and regression of F_2DS_8 as the measure of segregation potential (y) on parental and F_1 parameters (x) and DS based on their combination (x)

Parental and F_1 parameters		r_{xy}	a	b_{xy}	R^2 (%)
Single parameter					
D^2_8		0.357**	1.472	0.027**	28.88
D^2_4		0.695**	1.582	0.050**	48.28
MP-Y		0.536**	-2.508	0.918**	28.73
F1-Y		0.632**	-3.346	0.821**	39.98
RH-Y		0.095	2.602	0.007	0.90
MPGCA-Y		0.675**	2.659	2.712**	45.62
SCA-Y		0.236	2.704	0.372	5.57
Combination of parameters					
(2) + (3)	$DS_{(2,3)}$	0.680**	-3.720	1.178**	46.25
(4) + (5)	$DS_{(4,5)}$	0.686**	-4.208	1.918**	47.06
(4) + (5) +(6)	$DS_{(4,5,6)}$	0.720**	1.144	1.171**	51.78
(4) + (5) +(6) + (7)	$DS_{(4,5,6,7)}$	0.689**	1.288	1.117**	47.54
(2) + (3) +(4)	$DS_{(2,3,4)}$	0.776**	-5.628	1.209**	60.26
(2) + (3) +(4) + (5)	$DS_{(2,3,4,5)}$	0.740**	-4.787	1.133**	54.81
(2) + (3) +(4) + (5) +(6)	$DS_{(2,3,4,5,6)}$	0.731**	-1.432	0.893**	53.44
(2) +(3) +(4) +(5) +(6) +(7)	$DS_{(2,3,4,5,6,7)}$	0.715**	-1.285	0.871**	51.06
(2) + (4)	$DS_{(2,4)}$	0.781**	-1.446	1.276**	60.92
(2) + (6)	$DS(_{2,6})$	0.841**	1.833	1.334**	70.73
(4) + (6)	$DS_{(4,6)}$	0.789**	0.499	1.315**	62.30
(2) +(4) + (6)	$DS_{(2,4,6)}$	0.874**	-0.082	1.284**	79.31
(2) + (3) +(4) + (6)	$DS_{(2,3,4,6)}$	0.783**	-2.247	0.983**	61.31

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

Table 6 Six top ranking crosses according to the best single parameter and 3 best multiple criteria (DS) of selection

Selection criteria	Selected crosses (Descending order)		F_2DS_8 Rank
D^2_4 (R^2 = 52.71%)	21	(VRI-1/AKT-64)	1
	16	(GT-10/VRI-1)	2
	18	(GT-10/Pragati)	13
	12	(Kalika/VRI-1)	3
	5	(Prachi/AKT-64)	5
	20	(VRI-1/TC-25)	9
$DS_{(4,6)}$ (R^2 = 62.25%)	10	(Uma/AKT-64)	4
	11	(Kalika/GT-10)	7
	21	(VRI-1/AKT-64)	1
	6	(Uma/Kalika)	6
	12	(Kalika/VRI-1)	3
	16	(GT-10/VRI-1)	2
3. $DS_{(2,6)}$ (R^2 = 70.73%)	21	(VRI-1/AKT-64)	1
	16	(GT-10/VRI-1)	2
	6	(Uma/Kalika)	6
	12	(Kalika/VRI-1)	3
	5	(Prachi/AKT-64)	5
	18	(GT-10/Pragati)	13
$DS_{(2,4,6)}$ (R^2 = 76.36%)	21	(VRI-1/AKT-64)	1
	16	(GT-10/VRI-1)	2
	12	(Kalika/VRI-1)	3
	6	(Uma/Kalika)	6
	10	(Uma/AKT-64)	4
	11	(Kalika/GT-10)	7

The multiple criterion DS (4,6) picked up 5 of the 6 best crosses according to F_2DS_8. The different one (Kalika/GT-10) ranking 7th for F_2DS_8 substituted Prachi/AKT-64 of rank 5. DS(2,6) also picked up 5 of the 6 best crosses according to F_2DS_8. The different one (GT-10/Pragati) ranking 13th for F_2DS_8 substituted Uma/AKT-64 of rank 4. DS(2,4,6) picked up the same set of crosses as DS(4,6). But the correspondence between ranking of the selected crosses according to DS(2,4,6) and the ranking for F_2DS_8 was much better than it was with DS(4,6), which meant that DS(2,4,6) would make a much better criterion than DS(4,6). The crosses selected on different criteria and their ranking for F_2DS_8 reflected significant differences in predictivity of the criteria. The multivariate criterion DS(2,4,6), which made use of D^2_4 based on yield and its direct components and F_1 mean and biparental average GCA for yield, was found to be the best criterion for selection of crosses. The crosses selected on this basis are expected to give more high-yielding lines in later generations.

The results of the study showed that a linear combination of certain parental and F_1 parameters could provide an effective criterion for choice of crosses for recombination breeding for yield. A multiple criterion (DS) that made use of D^2_4 based on yield and its direct components and F_1 mean and biparental average GCA for yield was found to be the best criterion for choice of crosses for improvement of yield in sesame. The study has thrown light on multiple criteria selection as a method for choice of crosses for recombination breeding for yield, which can be used for other autogamous crops.

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J. Oilseeds Res., **25**(2) : 139-144 (2008)

Line x tester analysis for yield and powdery mildew resistance in sesame, *Sesamum indicum* L.

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(Received: December, 2007; Revised: March, 2007; Accepted: July, 2008)

Abstract

The combining ability of the parents as well as hybrids of sesame, *Sesamum indicum* (L.) involving six lines and four testers was studied. The parents and their resultant 24 hybrids were evaluated in line x tester mating design and observations were recorded for eight quantitative and one qualitative traits. The GCA/SCA ratio has indicated that all the traits studied were found to be predominantly controlled by non additive genes. Based on mean performance and *gca* effect, two parents *viz.*, VS 9510 and Co 1 were found to be the best general combiner for seed yield/plant. The hybrid VS 9510 x Co 1 was found to be superior for more than a trait based on *per se* performance, *sca* effect and standard heterosis. This cross yields about 44.1% of standard heterosis over the best check Co 1 for seed yield/plant. Besides a heterotic potential, this hybrid was found to be moderately resistant to powdery mildew.

Key words: GCA variance, SCA variance, *per se*, gene action, heterosis, powdery mildew

Introduction

The average productivity of sesame is low as compared to other oilseed crops due to the lack of high yielding genotypes and susceptibility of the genotypes to major pest and diseases, of which powdery mildew, *Oidium acanthospermi* Childarwar inflicted considerable economic damage in post-rainy/severe winter season. Shambarkar *et al.* (1997) reported that powdery mildew alone could cause yield loss up to 45%. Hence, there is paramount importance to improve the yield potential along with resistance/tolerance to pests and diseases and the yield potential can be overcome by commercial exploitation of heterosis and reshuffling of genes in order to get better recombinants or transgressive segregants, by hybridization of suitable parents. The combining ability analysis is useful to find out the general combiners for yield and its components, promising cross combinations, nature and magnitude of gene action governing the expression of yield and its components which in turn helps in identification of proper breeding methodology. In this context, present investigation was carried out to estimate general and specific combining ability effects, which help in selecting parents for developing hybrids and for exploitation of heterosis in this crop.

Material and methods

The experimental materials chosen for this study consisted of 10 genotypes including six lines *viz.*, VS 9701, VS 9510, NIC 7907, NIC 7937, Cianno 13/10 and Si 1115/1 and four testers *viz.*, TMV 3, Co 1, SVPR 1 and VRI 1. Each genotype was accommodated in two rows of 3 m length with a spacing of 30 cm x 30 cm. Two staggered sowings were taken up at 10 days interval to have synchronization in flowering to facilitate crossing work.

In the crossing block, crosses were effected between six lines and four testers in a line x tester mating design (Kempthorne, 1957). In order to obtain parental seed materials the above genotypes were raised separately and selfing was done to ensure self pollination. The selfing and the crossing works were effected as described by Thangavelu and Nallathambi (1982). The resulting 24 F_1 hybrids and their parents were grown in a Randomized Block Design with three replications at Agricultural College and Research Institute, Madurai, during *rabi*, 2003-04. Each genotype was accommodated in two rows of 3m length with a spacing of 30 cm x 30 cm. Observations were recorded for nine traits *viz.*, days to maturity, plant height, number of branches/plant, number of capsules/plant, capsule length, 1000 seed weight, oil content, powdery mildew resistance and seed yield/plant in five randomly selected plants. Border plants were avoided for taking up observations.

During post rainy season 2003-04, eight hybrids that were obtained by crossing two powdery mildew resistant /tolerant lines *viz.*, VS 9701 and VS 9510 with four testers *viz.*, TMV3 , Co 1, SVPR 1 and VRI 1 were evaluated in a Randomized Block Design with five replications separately for screening against powdery mildew disease in unprotected conditions in two rows of 3m length. Three rows of susceptible check TMV 3 were raised all around the experimental plot two weeks before the test entries in order to facilitate easy spreading of the fungal air borne species. During vegetative and first flowering stages, the spores from the infected plants were collected and sprayed to the test entries.

The disease intensity (score) was recorded on 10 leaves of the middle and bottom portion from each of five plants/replication, selected at random during maximum disease incidence (60 days after sowing or capsule formation state).

The disease score was registered in each plant and the mean was arrived at 0-5 scale (AICORPO, 1989) used for disease scoring as detailed below:

Score	Description	Category
0	No infection	Immune
1	1-10% of the leaf area infected	Resistant
2	11-25% of the leaf area infected	Moderately resistant
3	26-50% of the leaf area infected	Moderately susceptible
4	51-70% of the leaf area infected	Susceptible
5	More than 70% of the leaf area infected	Highly susceptible

The per cent disease index (PDI) was calculated by adopting the following formula (Mc Kinney, 1923)

$$\mathrm{PDI} = \frac{\text{Sum of individual grade recorded}}{\text{Total number of leaves assessed}} \times \frac{100}{\text{Maximum disease grade}}$$

Results and discussion

The analysis of variance showed significant differences between the genotypes for all the traits indicating wider genetic variability among genotypes (Table 1). The analysis of variance for combining ability revealed significant differences in the variance due to lines, testers and line x tester for all the traits and non additive variance component was higher than the additive variance.

The higher estimate of dominance variance as compared to additive variances for all the traits was probably due to predominance of non-additive gene action suggesting that these traits can be improved through heterosis breeding. Non-additive genetic components for plant height, number of branches/plant, capsule length, 1000-seed weight and seed yield/plant was reported earlier by Krishnadoss *et al.* (1987), Mishra and Yadav (1996) and Padmavathi (1999).

As the choice of the parents assumes greater importance in heterosis breeding the potentiality of a genotype might be judged by it's *per se* performance and *gca* effects. So the parents should posses high order of expression, genetically it should have accumulated large additive gene action and complementation effect and it should express high gca effect..

Regarding the *per se* performance of parents (Table 2) the lines *viz.*,VS 9510, NIC 7907 and NIC 7937 and among testers TMV 3 and SVPR 1 recorded desirable lower *per se* performance for days to maturity. NIC 7907 and NIC 7937 showed high *per se* performance for number of capsules/plant. VS 9510, NIC 7907, NIC 7937, Co 1 and VRI 1 showed significant mean performance for seed yield/plant. The highest oil content was registered in Co 1 (44.4%) and the minimum was recorded by VRI 1 (39.6%).Lines NIC 7907, NIC 7937 and VRI 1 exhibited the highest *per se* but registered negative *gca* effects for seed yield, whereas Cianno 13/10 and TMV 3 registered significant *gca* but non-significant mean performance for yield.

The *gca* effect of parents suggested that VS 9701, VS 9510, Cianno 13/10, TMV 3 and Co 1 were good general combiners for different yield components (Table 3). The lines NIC 7907, NIC 7937, SVPR 1 and VRI 1 recorded desirable negative *gca* effects for maturity. VS 9510 and Co 1 exhibited high *gca* effects for six yield contributing traits.

The lack of relationship between parental *per se* performance and *gca* effects could be possibly due to predominance of non-allelic interaction in governing these traits and the findings were in consonance with Saravanan and Nadarajan (2003). The parents NIC 7907, NIC 7937 and SVPR 1 might be utilized in breeding for earliness as they recorded low mean with negative *gca* effects. Two genotypes *viz.*, Co1 and VRI 1 were emerged as good combiners as they showed negative and significant *gca* effects and low *per se* performance for powdery mildew disease, so the parents would be utilized as donors in the hybridization programme in order to infuse the disease resistance against powdery mildew.None of the parent was found to be good for all the traits. Similar finding was reported by Haripriya and Reddy (1993) and Ram 1995. The above results indicated that it would be desiarable to have multiple crosses to isolate desiarable segregants in advanced generations for yield and yield attributing traits as no parents was a good combiner for all the traits.

Among the 24 cross combinations studied only ten crosses recorded high *per se* performance for more than one trait in favorable direction (Table 2). The hybrid NIC 7937 x VRI 1 was the earliest (73.7) to mature and Si 1115/1 x Co1 was found to be late (109.43). Si 1115/1 x TMV 3 recorded the highest seed yield of 32.6g/plant followed by VS 9510 x Co1 and Cianno 13/10 x VRI 1 with seed yield of 31.9 and 30.2g, respectively. Among the eight hybrids studied for powdery mildew disease resistance, only two hybrids VS 9510 x Co1 and VS 9510 x VRI 1 registered significant lower mean value for this trait.

The hybrid VS 9510 x Co1 recorded significant *sca* effect for seven traits, Cianno 13/10 x VRI 1 for six traits followed by Si 1115/1 x TMV 3 for five traits. Three hybrids *viz.*, VS 9510 x TMV 3, VS 9701 x Co 1 and VS 9510 x SVPR 1 recorded desirable negative *sca* effects for powdery mildew disease resistance (Table 3).

Table 1 Analysis of variance for combining ability

Source of variation	df	Mean squares								
		Days to maturity	Plant height	Number of branches/ plant	Number of capsules/plant	Capsule length	1000 seed weight	Oil content	Seed yield/ plant	Powdery mildew
Hybrids	23	357.29*	646.38*	1.37*	2256.98*	0.054*	0.508*	16.50*	45.95	39.03
Line	5	1336.07*	1021.95*	1.40*	670.85	0.05*	1.209*	12.01*	56.66*	1.17
Tester	3	165.54*	593.07*	4.18*	6535.79*	0.13*	0.507*	32.74*	79.58	5.49
Line x Tester	15	69.38*	531.85*	0.80*	1929.94*	0.04*	0.274*	14.75*	35.66*	13.89
Error	46	1.53	0.84	0.04	0.917	0.002	0.011	0.06	0.12	1.00

* Significant at 5% level.

Table 2 ***Per se*** **performance of parents and hybrids**

Genotypes	Days to maturity	Plant height (cm)	No. of branches/plant	No. of capsules/plant	Capsule length (cm)	1000-seed weight (g)	Oil content (%)	Seed yield/plant (g)	Powdery mildew
L_1	91.57	84.58	2.37	49.73	2.26	2.87*	39.79	18.41*	0.73*
L_2	76.56*	106.24*	3.87*	67.03	2.53*	2.64	40.45	20.44*	0.60*
L_3	75.78*	91.17	2.67	103.33*	2.58*	2.96*	42.55*	16.82*	-
L_4	72.97*	93.62	3.70*	118.23*	2.70*	2.71	41.63*	17.81*	-
L_5	90.30	105.10*	2.93	72.00	2.11	2.51	38.44	11.52	-
L_6	93.16	86.25	4.90*	81.33	1.95	2.21	40.49	12.42	
T_1	89.32*	86.92	3.57	86.30	2.51*	3.01	43.32*	20.09	4.80*
T_2	94.14	121.00*	5.53*	111.80*	2.47*	3.00	44.44*	22.18*	0.53*
T_3	88.89*	86.12	3.87	75.53	2.17	2.90	40.39	13.17	2.40
T_4	92.69	92.95	4.47*	95.03*	2.51*	3.02	39.61	24.48*	1.40
L_1 x T_1	92.16	101.37	4.13	122.13	2.87	3.03	42.75*	28.29*	4.20
L_1 x T_2	90.34	118.62*	5.20	155.20*	2.70	2.99	40.65	29.61*	1.80
L_1 x T_3	90.86	93.44	5.40*	107.90	3.04*	2.12	42.44*	28.67*	3.60
L_1 x T_4	90.85	101.99	4.97	107.00	2.68	3.07	37.30	27.38*	1.40
L_2 x T_1	98.19	109.40	4.23	102.27	2.76	3.90*	40.71	23.62	1.80
L_2 x T_2	99.07	140.03*	6.20*	196.33*	3.16*	3.70*	45.45*	31.94*	0.33*
L_2 x T_3	91.17	94.51	4.30	90.80	2.94	3.32	41.49*	22.75	3.60
L_2 x T_4	92.92	104.63	5.10	126.77*	2.99*	3.61*	39.58	25.66*	0.60*
L_3 x T_1	75.01*	103.51	4.53	114.33	2.82	3.24	43.08*	28.96*	-
L_3 x T_2	75.18*	106.24	5.87*	151.33*	3.01*	2.77	41.51*	24.37	-
L_3 x T_3	75.59*	95.95	4.40	106.17	2.81	2.97	38.43	23.44	-
L_3 x T_4	75.48*	104.59	5.90*	119.2	2.84	3.11	38.32	18.68	-
L_4 x T_1	74.19*	84.22	4.07	108.67	2.82	3.81*	42.51*	22.07	-
L_4 x T_2	76.00*	78.71	4.44	121.67	3.01*	3.81*	39.52	24.71	-
L_4 x T_3	74.18*	103.37	4.07	116.77	3.18*	3.66*	43.52*	22.71	-
L_4 x T_4	73.68*	128.73*	4.60	115.40	2.98*	2.87	35.26	19.54	-
L_5 x T_1	90.78	120.12*	4.13	103.60	2.91	3.03	40.37	24.2	-
L_5 x T_2	101.69	128.65*	5.70*	120.00	2.96*	3.12	41.60*	27.64*	-
L_5 x T_3	92.46	122.48*	4.77	106.00	2.96*	3.14	42.66*	24.49	-
L_5 x T_4	95.59	125.18*	5.80*	164.7*	2.97*	3.43*	43.97*	30.17*	-
L_6 x T_1	106.25	113.66*	5.87*	177.90*	2.74	3.47*	40.38	32.61*	-
L_6 x T_2	109.43	121.65*	5.50*	162.10*	3.00*	3.11	39.13	28.85*	-
L_6 x T_3	88.89	109.78	5.17	103.60	3.08*	2.89	40.30	21.57	-
L_6 x T_4	87.47	106.42	5.00	107.83	2.85	2.81	38.31	19.53	-
Grand mean	88.23	109.05	4.99	125.33	2.92	3.21	40.80	25.20	2.57
SEd	0.71	0.52	0.11	0.55	0.01	0.06	0.15	0.19	0.75
CD (P=0.05)	1.43	1.05	0.22	1.10	0.02	0.12	0.30	0.38	1.51

* Significant at 5% level

L_1 VS 9701 L_2 VS9510 L_3 NIC 7907 L_4 NIC 7937 L_5 Cianno 13/10, L_6 Si 1115/1.
T_1 - TMV 3 T_2 - Co 1 T_3 - SVPR 1 T_4 - VRI 1

Table 3 Combining ability effects of parents and hybrids for different economic traits

Genotypes	Days to maturity	Plant height	No. of branches/plant	No. of capsules/plant	Capsule length	1000-seed weight	Oil content	Seed yield/plant	Powdery mildew
L_1	2.83*	-5.20*	-0.06	-2.27*	-0.10*	-0.40*	-0.02	3.01*	1.81
L_2	7.11*	3.09*	-0.03	3.71*	0.04*	0.43*	1.00*	0.51*	-1.81
L_3	-12.91*	-6.48*	0.19*	-2.52*	-0.05*	-0.18*	-0.47*	-1.61*	-
L_4	-13.71*	-10.29*	-0.61*	-9.70*	0.08*	0.33*	-0.59*	-3.22*	-
L_5	6.90*	15.06*	0.11	-1.75*	[illegible]	-0.03	1.35*	1.15*	-
L_6	9.78*	3.82*	0.40*	12.53*	0.01	-0.14*	-1.27*	0.16	-
SE	0.36	0.26	0.05	0.28	0.004	0.03	0.07	0.09	1.64
T_1	1.20*	1.20*	-3.67*	-0.49*	-3.84*	-0.10*	0.21*	0.83*	1.15*
T_2	3.73*	3.73*	6.60*	0.55*	25.81*	0.05*	0.04	0.51*	2.37*
T_3	-2.70*	-2.70*	-5.80*	-0.30*	-20.12*	0.08*	-0.19*	0.68*	-1.54*
T_4	-2.23*	-2.23*	2.87*	0.24*	-1.84*	-0.04*	-0.06*	-2.01*	-1.98*
SE	0.29	0.22	0.05	0.23	0.003	0.03	0.06	0.08	2.33
L_1 x T_1	-0.10	1.19*	-0.30*	2.92*	0.15*	0.02	1.14**	-1.35*	7.35*
L_1 x T_2	-4.44*	8.17*	-0.28*	6.33*	-0.18*	0.15*	-0.64*	-1.25*	-12.11*
L_1 x T_3	2.51*	-4.62*	0.78*	4.96*	0.13*	-0.49*	0.98*	1.72*	6.07*
L_1 x T_4	2.02*	-4.73*	-0.20	-14.21*	-0.11*	0.32*	-1.47*	1.65*	-0.31
L_2 x T_1	1.64*	0.93	-0.23*	-22.93*	-0.10*	0.06	-1.92*	3.95*	-7.35*
L_2 x T_2	0.01	21.29*	0.69*	41.48*	0.14*	0.03	3.14*	1.87*	12.11*
L_2 x T_3	-1.46*	-11.83*	-0.36*	-18.12*	0.10*	-0.12	-1.00*	1.12*	-6.10*
L_2 x T_4	-0.19	-10.39*	-0.10	-0.43	0.06*	0.03	-0.22	-3.20*	0.31
L_3 x T_1	-1.51*	4.60*	-0.15	-4.63*	0.05*	0.01	1.92*	-1.34*	-
L_3 x T_2	-3.86*	-2.93*	0.14	2.91*	0.09*	-0.29*	0.67*	0.07	-
L_3 x T_3	2.97*	-0.82	-0.47*	3.48*	-0.14*	0.14*	-2.58*	1.99*	-
L_3 x T_4	2.39*	-0.85	0.48*	-1.76*	0.01	0.14*	-0.01	-0.73*	-
L_4 x T_1	-1.53*	-10.86*	0.18	-3.11*	-0.08*	0.07	1.46*	-1.34*	-
L_4 x T_2	-2.24*	-26.64*	-0.16	-19.77*	-0.04*	0.23*	-1.20*	0.07	-
L_4 x T_3	2.37*	10.41*	-0.01	21.26*	0.10*	0.32*	2.68*	1.99*	-
L_4 x T_4	1.39	27.10*	-0.02	1.62*	0.02	-0.61*	-2.94*	-0.73*	-
L_5 x T_1	-5.55*	-0.31	-0.47*	-16.13*	0.06*	-0.35*	-2.61*	-3.57*	-
L_5 x T_2	2.83*	-2.06*	0.05	-29.39*	-0.04*	-0.11	-1.0*	-1.36*	-
L_5 x T_3	0.03	4.17*	-0.03	2.55*	-0.07*	0.15	-0.17	-0.60*	-
L_5 x T_4	2.69*	-1.80*	0.46*	42.97*	0.06*	0.31**	3.84*	5.53*	-
L_6 x T_1	7.04*	4.45*	0.98*	43.89*	-0.08*	0.19*	0.02	5.82*	-
L_6 x T_2	7.70*	2.18*	-0.44*	-1.57*	0.03*	0.01	-0.91*	0.83*	-
L_6 x T_3	-6.42*	2.70*	0.09	-14.14*	0.08*	0.01	0.09*	-2.53*	-
L_6 x T_4	-8.31*	-9.33*	-0.63*	-28.18*	0.03*	-0.20*	0.8*	-4.13*	-
SE	0.71	0.53	0.11	0.55	0.01	0.06	0.15	0.19	3.30

Hybrid NIC 7937 x VRI 1 recorded desirable negative heterosis over better parent for days to maturity (-21.7%) (Table 4). A large number of crosses (18 out of 24) exhibited positively significant standard heterosis for seed yield. NIC 7937 x SVPR 1 recorded highest standard heterosis for capsule length of 29.1% and Si 1115/1 x TMV 3 recorded 47.1% for seed yield/plant. Except VS 9510 x Co 1 all other hybrids recorded negative heterosis for oil content. VS 9510 x Co1 had high heterotic vigour for plant height, number of branches/plant, number of capsules/ plant, capsule length, 1000-seed weight, oil content, powdery mildew resistance and seed yield/plant. Si 1115/1 x TMV 3 for number of branches/plant, number of capsules/plant, capsule length, 1000-seed weight and seed yield/plant.

In general there was a good agreement between *per se* performance, *sca* effects and standard heterosis. Based on the *gca* status of parents, crosses were classified into HH (both the parents in a cross with high *gca* status) HL (one parent with high and other parent with low *gca* status) and LL (both parents with low *gca* status). The promising crosses resulted from the combinations of high x low *gca* parents could be possibly due to complimentary gene action of divergent genes in the hybrids and additive type of gene interaction (Table 5).

Heterotic hybrids found in case of high x high *gca* parental combinations and with significant *sca* effects were due to accumulation of additive genes in hybrid from both the parents and additive x additive type of gene interaction. Low x low *gca* parental combinations showed higher *sca* effects and also evidenced high standard heterosis indicating the importance of dominance x dominance gene interactions.

Table 4 Standard heterosis of hybrids for different economic traits

Genotypes	Days to maturity	Plant height	No. of Branches/plant	No. of Capsules/plant	Capsule length	1000-seed weight	Oil content	Seed Yield/plant	Powdery mildew
$L_1 \times T_1$	-2.11*	-16.22*	-25.30*	9.24*	16.49*	-3.82*	1.11	27.55*	381.86*
$L_1 \times T_2$	-4.04*	-1.97*	-6.02*	38.82*	9.46*	-8.54*	-0.22	33.50*	-1.55
$L_1 \times T_3$	-3.48*	-22.78*	-2.41	-3.49*	23.11*	-4.52*	-29.22*	29.26*	353.64*
$L_1 \times T_4$	-3.50*	-15.71*	-10.24*	-4.29*	8.51*	-16.0*	2.33	29.26*	69.91*
$L_2 \times T_1$	4.30*	-9.58*	-23.49*	-8.50*	12.03*	-8.40*	30.11*	6.51*	519.15*
$L_2 \times T_2$	5.24*	15.72*	12.05*	75.61*	27.97*	2.26*	23.44*	44.01*	-28.50*
$L_2 \times T_3$	-3.15*	-21.89*	-22.29*	-18.78*	19.19*	-6.65*	10.67*	2.59*	315.94*
$L_2 \times T_4$	-1.29	-13.53*	-7.83*	13.39*	21.08*	-10.95*	20.22*	15.72*	18.57*
$L_3 \times T_1$	-20.32*	-14.46*	-18.07*	2.27*	14.32*	-3.07*	8.11*	30.60*	-
$L_3 \times T_2$	-20.14*	-12.20*	6.02*	35.54*	22.16*	-6.61*	-7.56*	9.89*	-
$L_3 \times T_3$	-19.71*	-20.70*	-20.48*	-5.04*	14.05*	-13.52*	-0.89	5.70*	-
$L_3 \times T_4$	-19.82*	-13.56*	6.63*	6.62*	15.27*	-13.78*	3.67	-15.75*	-
$L_4 \times T_1$	-21.20*	-30.39*	-26.51*	-2.80*	14.19*	-4.36*	27.00*	-0.47	-
$L_4 \times T_2$	-19.27*	-34.95*	-13.86*	8.83*	22.16*	-11.07*	26.89*	11.4*	-
$L_4 \times T_3$	-21.20*	-14.57*	-26.51*	4.44*	29.05*	-1.94*	22.00*	2.42*	-
$L_4 \times T_4$	-21.74*	6.39*	-16.84*	3.22*	20.68*	-20.66*	-4.44	-11.87*	-
$L_5 \times T_1$	-3.57*	-0.72	-25.30*	-7.33*	17.84*	-9.17*	1.11	9.14*	-
$L_5 \times T_2$	8.02*	6.32*	3.01	7.33*	20.14*	-6.39*	3.89	24.65*	-
$L_5 \times T_3$	-1.79	1.22	-13.86*	-5.19*	20.14*	-4.02*	4.67	10.42*	-
$L_5 \times T_4$	1.54	3.45*	4.82	47.32*	20.41*	-1.06	14.33*	36.03*	-
$L_6 \times T_1$	12.80*	-6.07	6.02*	59.12*	10.95*	-9.14*	15.56*	47.06*	-
$L_6 \times T_2$	16.25	0.54	-0.60	44.99*	21.62*	-11.96*	3.78	30.08*	-
$L_6 \times T_3$	-5.58*	-9.27*	-6.63**	-7.33*	25.00*	-9.33*	-3.78	-2.74*	-
$L_6 \times T_4$	-7.09*	-12.05*	-9.64*	-3.55*	15.41*	-13.79*	-6.22*	-11.93*	-
SE	0.71	0.75	0.14	0.77	0.02	0.25	0.07	0.27	2.67

* Significant at 5% level; Standard check Co 1 (T_2)

Table 5 Best three cross combinations exhibiting high *per se* performance, standard heterosis and their *gca* status

Character	Crosses	F_1 mean	Standard heterosis	sca effect	*gca* status
Days to maturity	NIC 7937 x VRI 1	73.68*	-21.74*	1.39	H x H
	NIC 7937 x SVPR 1	74.18*	-21.20*	2.37*	H x H
	NIC 7937 x TMV 3	74.19*	-21.20*	-1.53*	H x H
Plant height	VS 9510 x CO 1	140.03*	15.72*	21.29*	H x H
	NIC 7937 x VRI 1	128.73*	6.39*	27.10*	H x H
	Cianno 13/10 x CO 1	128.65*	6.32*	-2.06*	H x H
Number of branches/plant	VS 9510 x CO 1	6.20*	12.05*	0.69*	L x L
	NIC 7907 x VRI 1	5.90*	6.63*	0.48*	L x L
	Si 1115/1 x TMV 3	5.87*	6.02*	0.96*	L x L
Number of capsules/plant	VS 9510 x CO 1	192.33*	75.61*	41.48*	H x H
	Si 1115/1 x TMV 3	177.90*	59.12*	43.89*	H x H
	Cianno 13/10 x VRI 1	164.70*	47.32*	42.97*	L x H
Capsule length	NIC 7937 x SVPR 1	3.18*	29.05*	0.10*	L x L
	VS 9510 x CO 1	3.16*	27.97*	0.14*	L x L
	Si 1115/1 x SVPR 1	3.08*	25.00*	0.08*	L x L
Oil content	VS 9510 x CO 1	45.45*	2.26*	3.14*	H x L
	Cianno 13/10 x VRI 1	43.97*	-1.06	3.84*	L x H
	NIC 7937 x SVPR 1	43.52*	-1.94*	2.68*	L x L
1000-seed weight	VS 9510 x TMV 3	3.90*	30.11*	0.06	L x L
	NIC 7937 x TMV 3	3.81*	27.00*	0.07	L x L
	NIC 7937 x CO 1	3.81*	26.89*	0.23*	L x L
Powdery mildew	VS 9510 x CO 1	0.33*	12.11*	-28.50*	L x H
Seed yield/plant	Si 1115/1 x TMV 3	32.64*	47.06*	5.82*	H x L
	VS 9510 x CO 1	31.94*	44.01*	1.87*	L x L
	Cianno 13/10 x VRI 1	30.17*	36.03*	5.53*	L x L

It was showed that the desirable *sca* effects of any cross combinations need not necessarily depend on the level of *gca* effects of the parents involved (Sumathi and Kalaimani, 2000). It indicated the role of additive and non-additive gene action for the traits studied and also signify the importance of both the types of gene action for improvement in seed yield.

It was observed that the parents VS 9510 and Co 1 were the good general combiners for yield and powdery mildew disease resistance, and these parents can be used advantageously in the crossing programme of practical plant breeding like pedigree breeding etc., for the development of superior sesame varieties and three hybrids *viz*., VS 9510 x Co 1, Cianno 13/10 x VRI 1 and Si 1115/1 x TMV 3 were found to be the best hybrid combinations for yield and other contributing traits and these hybrids can be utilized for exploitation of heterosis as well as to select desirable transgressive genotypes in the subsequent generations.

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J. Oilseeds Res., **25**(2) : 145-149 (2008)

Inheritance of self-incompatibility, branching and anthocyanin pigmentation in sunflower, *Helianthus annuus* L.[1]

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(Received: November, 2006; Revised: October, 2008; Accepted: October, 2008)

Abstract

Six generation mean analysis was designed to study inheritance pattern of self-incompatibility, branching and anthocyanin pigmentation in sunflower. Three inbreds *viz.*, ARM 243, ARM 245 and HA 336 with non branching, green plant parts and high self-fertility were used as ovule parent whereas, line HA 1652 was used as male parent having profound branching, pigmentation on all plant parts with high self-incompatibility. The behavior of self-incompatibility character in F_1 and subsequent F_2, BC_1P_1 and BC_1P_2 generation clearly indicated that self-incompatibility was dominant over self-compatibility and it is controlled by single dominant gene. For anthocyanin pigmentation and branching, the observed segregation in F_2 and backcross progeny indicated that the inheritance of these two characters is controlled by two dominant genes with duplicate gene action.

Key words: Self-incompatibility, anthocyanin pigmentation, branching, duplicate dominant gene, inheritance

Introduction

Sunflower is known to exhibit different levels of self-incompatibility. The open-pollinated varieties of Russian origin exhibit high degree of self-incompatibility. Sporophytic self-incompatibility system is reported to be present in cultivated sunflower. At least two multi-allelic loci are known to govern self-incompatibility and its expression is influenced by physiological factors (Habura, 1957). However, it is to be recognized that the genetics of self-incompatibility in sunflower is still not fully understood. During germplasm maintenance, wide variability is observed for seed set and extent of self-fertility (seed set on selfing) among the accessions. Pollen self-incompatibility is the main biological reaction of sunflower plants against self-fertilization. Foreign pollen germinates on stigma much faster than its own pollen. Seed set is the culmination of the vegetative phase and is affected by gametogenesis, pollination, fertilization and embryogenesis. All these processes are influenced by genetic and environmental factors and their interaction. The inheritance of self-incompatibility in sunflower has not been investigated.

The inheritance of branching is a complex phenomenon with both dominant and recessive genes controlling this trait. The branching in wild species of sunflower is often controlled by dominant genes whereas, the branching utilized in some restorer lines for hybrid seed production is controlled by recessive genes. The information on the heritability of self-incompatibility, anthocyanin pigmentation and branching habit in sunflower may provide valuable information to plant breeder for developing new cultivars by altering plant architecture that may lead to increase in yield or yield components. The objective of present investigation was to study the inheritance of self-incompatibility, anthocyanin pigmentation and branching habit in sunflower.

Material and methods

Six generation mean analysis was designed to study the genetics of self-incompatibility, branching habit and anthocyanin pigmentation in sunflower. Four inbreds *viz.*, ARM 243, ARM 245, HA 336 and HA 1652 were utilized in this genetical study. Inbred lines ARM 243, ARM 245 and HA 336 were non-branching having green plant parts with high self-fertility whereas, line HA 1652 was distinct from all other three inbreds and it has profound branching (branching over the entire stem, central head larger than any secondary heads), pigmentation on all plant parts and is highly self-incompatible. The self-incompatible line HA 1652 obtained from USA, was used as male parent and crossed with all the three self-compatible lines during rainy season of 1998. To facilitate easy crossing, the female parents were made male sterile by applying Gibberlic acid of 100 ppm to the just forming flower buds (star bud stage) continuously for three days at the rate of 4-5 drops/day/ plant.

The F_1s of the three crosses were raised along with their parents during summer 1999 and back crossed with respective parents to generate BC_1P_1 and BC_1P_2 populations. In the same season, F_2 seeds were collected from the selfed F_1 plants. Thus the seeds of six generations namely P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 for all the three crosses were obtained. This material was grown in a ratio of 1:1:1:8:4:4 in Randomised Complete Block Design with three replications, respectively during rainy season of 1999. The data were recorded for self-incompatibility, anthocyanin pigmentation in the plant parts and branching. For recording self-incompatibility, the capitula of all plants were covered with cloth bags before opening of the ray florets to avoid cross pollination. Plants were separately harvested and per cent seed set was calculated for individual plants. The plants showing 0-20 per cent seed set under bagging were considered as self-incompatible. To record presence or absence of pigmentation, visual observation of pigmentation on plant parts *viz.*, stem, petiole, leaf margin, ray florets and disc flowers was made at flowering stage.

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[1] Part of the Ph.D. Thesis submitted to the University of Agricultural Sciences, Bangalore by the first author.

Observations on branching and non-branching were recorded at full flowering. Only one type of branching pattern was observed i.e. branching seen over the entire stem with central head larger than any other secondary heads (IBPGR Descriptor, 1985). Data collected from individual plants in various generations were subjected to goodness of fit with the expected genetic ratio using chi-square test.

Results and discussion

Inheritance of self-incompatibility: The inheritance pattern was studied in three crosses - ARM 243 x HA 1652, ARM 245 x HA 1652 and HA 336 x HA 1652. Per cent seed set on selfing was considered for forming frequency distribution in F_1 and other segregating generations namely F_2, BC_1P_1 and BC_1P_2 (Table 1). The two parents involved in three crosses showed distinctly different pattern for seed set on selfing. The segregation for self-compatibility and self-incompatibility in different generations of the three crosses is given in Table 2. It is evident from the data that self-incompatibility was dominant over self-compatibility. In F_2, the segregation pattern of 3:1 (3 self-incompatibility : 1 self-compatibility) was observed in all the three crosses and showed very good fit with the expected ratio. The segregation in BC_1P_1 and BC_1P_2 generations also showed good fit with the expected ratio and chi-square values were non-significant.

The self-incompatible parent HA 1652 did not set any seed on selfing indicating that the line was unique for this character. The other parents ARM 243, ARM 245 and HA 336 used in crossing were highly self-compatible showing good seed set on selfing. However, the seed set between plants varied with majority showing more than 60%. The behavior of self-incompatible character in F_1 and subsequent F_2, BC_1P_1 and BC_1P_2 generation clearly indicated that self-incompatibility was dominant over self-compatibility. The segregation pattern was similar in all the three crosses suggesting that this is controlled by single dominant gene.

Sunflower is reported to show different levels of self-incompatibility. The open pollinated varieties of Russian origin show high levels of self-incompatibility (judged by the extent of seed set on selfing) under Indian conditions (Seetharam, 1981). Soare and Vranceanu (1996) in their study with large number of inbred lines observed self-compatibility to be dominant. However, based upon generation mean analysis they observed both additive and non-additive gene action for this character. Skaloud and Kovacik (1996) observed that self-compatibility was reflected in different degrees in autogamous pollination. The self-incompatibility showed partial dominance over self-compatibility.

Inheritance of anthocyanin pigmentation: The plants in different generations could be classified as pigmented or green based on the presence or absence of anthocyanin pigmentation (Table 3). In all the three crosses anthocyanin pigmentation was found dominant over green showing a segregating pattern of 15:1 (15 pigmented : 1 green) in F_2 generation. The BC_1P_1 and BC_1P_2 data also confirmed the observed ratio with the expected ratio. In all the three crosses the chi-square values were low and non-significant.

There was complete expression of anthocyanin in F_1 in all the three crosses suggesting the character was controlled by dominant genes. The observed segregation 15:1 (15 pigmented : 1 green) in F_2 generation in all the three crosses further indicated the involvement of two dominant genes with duplicate gene action. The segregation in BC_1P_1 and BC_1P_2 also confirmed the involvement of two duplicate dominant genes. Velkov, 1970 and Luczkiewicz, 1975 reported the involvement of single dominant gene in controlling this character. In this study, although it is inferred that the presence of pigmentation is controlled by duplicate dominant genes, there was variation for the intensity of pigmentation among the pigmented plants ranging from deep pigmentation to light pigmentation. However, for genetic analysis purposes all pigmented plants were clubbed together irrespective of the intensity of the pigmentation.

Inheritance of branching: In all the three crosses branching was dominant over non-branching. F_2 plants segregated in a ratio of 15:1 (15 branching : 1 non-branching) and showed good fit. The behaviour in BC_1P_1 and BC_1P_2 was in conformity with the expected ratio. The chi-square values were non-significant (Table 4).

As regards inheritance of branching is concerned, in F_1 generation, branching was dominant over non-branching in all the three crosses. In F_2 generation, a segregating ratio of 15:1 (15 branching : 1 non-branching) was observed suggesting the operation of dominant duplicate genes. The test cross results also confirmed this.

The inheritance of branching character has been studied in great detail by Putt (1940), Hockett and Knowles (1970) and Kovacik and Skaloud (1990). In these studies both single as well as two dominant genes control have been reported. Although branching is dominant over non-branching in most instances, there were instances of recessive branching and this was first reported by Putt (1964). Again in spite of this character being controlled by major genes one could expect differences in type and intensity of branching between plants in F_2 and back cross generation. This suggested the likely involvement of additional minor genes in determining branching behaviour.

Table 1 Frequency distribution for per cent seed set on selfing in different generations of crosses involving self-compatible and self-incompatible parents

Generations / Class interval	P_1	P_2	F_1	F_2	BC_1P_1	BC_1P_2
			Cross-I (ARM 243 x HA 1652)			
0- 10	-	33	48	78	84	158
10- 20	-	-	2	19	23	3
20- 30	-	-	-	6	16	4
30- 40	1	-	-	8	17	-
40- 50	4	-	-	2	10	-
50- 60	2	-	-	4	7	-
60- 70	9	-	-	2	11	-
70- 80	10	-	-	2	14	-
80- 90	5	-	-	2	7	-
90-100	10	-	-	1	16	-
Total	41	33	50	124	205	165
			Cross-II (ARM 245 x HA 1652)			
0- 10	-	25	83	259	96	207
10- 20	-	-	6	27	24	7
20- 30	6	-	-	26	15	2
30- 40	3	-	-	5	9	1
40- 50	4	-	-	13	16	1
50- 60	6	-	-	8	15	-
60- 70	5	-	-	9	14	-
70- 80	5	-	-	8	9	-
80- 90	1	-	-	4	14	-
90-100	8	-	-	4	14	-
Total	38	25	89	363	226	218
			Cross-III (HA 336 x HA 1652)			
0- 10	-	32	82	238	91	195
10- 20	-	-	-	60	21	6
20- 30	4	-	-	32	11	-
30- 40	9	-	-	18	13	-
40- 50	4	-	-	17	25	-
50- 60	13	-	-	13	16	-
60- 70	14	-	-	4	10	-
70- 80	5	-	-	4	12	-
80- 90	3	-	-	4	10	-
90-100	4	-	-	8	1	-
Total	56	32	82	398	210	201

Table 2 Segregation for self-compatibility and self-incompatibility in different generation of three crosses of sunflower

Crosses/ Generations	No. of plants						Test ratio	Chi-square value	Table Value
	Observed			Expected					
	SI*	SC*	Total	SI*	SC*	Total	SI:SC		
				Cross-I (ARM 24 x HA 1652)					
P_1	0	41	41	-	-	41	-	-	-
P_2	33	0	33	-	-	33	-	-	-
F_1	50	0	50	-	-	50	-	-	-
F_2	97	27	124	93	31	124	3:1	0.69	3.841
BC_1P_1	107	98	205	103	102	205	1:1	0.39	3.841
BC_1P_2	161	4	165	165	0	165	1:0	0.09	3.841
				Cross-II (ARM 245 x HA 1652)					
P_1	0	38	38	0	38	38	-	-	-
P_2	25	0	25	25	0	25	-	-	-
F_1	89	0	89	89	0	89	-	-	-
F_2	286	77	363	272	91	363	3:1	2.87	3.841
BC_1P_1	120	106	226	113	113	226	1:1	0.86	3.841
BC_1P_2	214	4	218	218	0	218	1:0	0.07	3.841
				Cross-III (HA 336 x HA 1652)					
P_1	0	56	56	0	56	56	-	-	-
P_2	32	0	32	32	0	32	-	-	-
F_1	83	0	83	83	0	83	-	-	-
F_2	298	100	398	299	99	398	3:1	0.84	3.841
BC_1P_1	112	98	210	105	105	210	1:1	0.92	3.841
BC_1P_2	199	2	201	201	0	201	1:0	0.02	3.841

SI : Self-incompatibility; SC = Self-compatibility

Table 3 Segregation pattern for anthocyanin pigmentation in different generations of three crosses of sunflower

Crosses/ Generations	No. of plants						Test ratio	Chi-square value	Table value
	Observed			Expected					
	P*	A*	Total	P*	A*	Total	P:A		
				Cross-I (ARM 243 x HA 1652)					
P_1	-	42	42	-	42	42	-	-	-
P_2	35	-	35	35	-	35	-	-	-
F_1	52	-	52	52	-	52	-	-	-
F_2	174	48	222	208	14	222	15:1	1.52	3.841
BC_1P_1	195	68	263	197	66	263	3:1	0.08	3.841
BC_1P_2	171	0	171	171	0	171	1:0	0.00	3.841
				Cross-II (ARM 245 x HA 1652)					
P_1	-	40	40	-	40	40	-	-	-
P_2	25	-	25	25	-	25	-	-	-
F_1	89	-	89	89	-	89	-	-	-
F_2	390	22	412	386	26	412	15:1	0.65	3.841
BC_1P_1	195	80	275	206	69	275	3:1	2.33	3.841
BC_1P_2	279	0	279	279	0	279	1:0	0.00	3.841
				Cross-III (HA 336 x HA 1652)					
P_1	-	56	56	-	-	56	-	-	-
P_2	32	-	32	-	-	32	-	-	-
F_1	83	-	83	-	-	83	-	-	-
F_2	439	24	463	434	29	463	15:1	0.92	3.841
BC_1P_1	178	66	244	183	61	244	3:1	0.53	3.841
BC_1P_2	241	0	241	241	0	241	1:0	0.00	3.841

P = Presence of anthocyanin pigmentation on plant parts; A = Absence of anthocyanin pigmentation on plant parts

Table 4 **Segregation pattern for branching and non-branching in three different crosses of sunflower**

Crosses/ Generations	No. of plants						Test ratio	Chi-square value	Table value
	Observed			Expected					
	Br*	NB*	Total	Br*	NB*	Total	Br:NB		
				Cross-I (ARM 243 x HA 1652)					
P_1	-	42	42	-	42	42	-	-	-
P_2	35	-	35	35	-	35	-	-	-
F_1	52	-	52	52	-	52	-	-	-
F_2	207	15	222	208	14	222	15:1	0.075	3.841
BC_1P_1	149	56	205	154	51	205	3:1	0.65	3.841
BC_1P_2	167	4	171	171	0	171	1:0	0.09	3.841
				Cross-II (ARM 245 x HA 1652)					
P_1	-	40	40	-	40	40	-	-	-
P_2	25	-	25	25	-	25	-	-	-
F_1	89	-	89	89	-	89	-	-	-
F_2	369	24	393	368	25	393	15:1	0.042	3.841
BC_1P_1	202	78	280	210	70	280	3:1	1.21	3.841
BC_1P_2	263	8	271	271	0	271	1:0	0.23	3.841
				Cross-III (HA 336 x HA 1652)					
P_1	-	56	56	-	56	56	-	-	-
P_2	32	-	32	32	-	32	-	-	-
F_1	83	-	83	83	-	83	-	-	-
F_2	423	25	448	420	28	448	15:1	0.34	3.841
BC_1P_1	188	56	244	183	61	244	3:1	0.53	3.841
BC_1P_2	237	3	240	240	0	240	1:0	0.03	3.841

Br = Branching; NB = Non-branching

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J. Oilseeds Res., **25**(2) : 150-153 (2008)

Multi-environment testing, estimates of stability parameters and sustainability index for comparing varieties in linseed

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(*Received:* December, 2007; *Revised:* June, 2008; *Accepted:* July, 2008)

Abstract

Multilocation trials on ten released varieties of linseed were conducted in a number of states during three consecutive years, 2001-02 to 2003-04 to study the genotype x environment interaction and stability of genotypes for seed yield and oil content. Significant genotype and environment interaction was observed. Both linear and non-linear components of GxE interaction were significant with preponderance of the linear components were non-significant. Based on statistics of stability parameters, four genotypes Shubhra, Sweta, Shekhar and Sheela were found to be most stable in different years for varied agronomic conditions. For oil content, Shubhra and Shekhar were identified as most stable variety. Contrary findings were observed based on Eberhart and Russel model and sustainability index model in the present set of materials for seed yield and oil content.

Key words: G x E interaction, stability, sustainability index, linseed

Introduction

Linseed, *Linum usitatissimum* L. is the second important *rabi* oilseed crop after rapeseed-mustard both in area and production at national level as well as in the state of Uttar Pradesh. It is cultivated in varied agroclimatic conditions ranging from moisture stress and input starved condition to fragile ecosystem like *utera* which is certainly accountable for the low national productivity (329 kg/ha). Selection and yield testing are the two major phases of varietal development and the later one is highly influenced by the locations and years of testing. The magnitude of G x E interaction and its components has a direct bearing on the environmental domain of the varieties to be recommended for commercial cultivation. Jensen (1988) emphasized the significance of G x E interaction as it is not to much to say that genotype x environment interaction, not the genotype, is the cultivar.

Linseed breeders look forward for widely adapted genotypes responsive to input intensive as well as input deficient agriculture in order to enhance production and productivity of the crop. The success and effectiveness of an evaluation trial largely depends upon standard check varieties against whom the tested genotypes are compared. In All India Coordinated Linseed Breeding Trials, T-397, an old linseed variety developed in 1960 at Kanpur under Central Oilseed Scheme is still used as national check. During Annual Group Meeting on Linseed held at PDKV, Akola in 2001, it was decided to replace this old national check which has become susceptible to diseases like rust and powdery mildew. With this background, the present study was undertaken under rainfed situation for three consecutive years to identify stable genotypes of linseed for seed yield and oil content.

Material and methods

Ten released varieties of linseed recommended for various agroclimatic zones and with differences in their seed size, colour, maturity and reactions to powdery mildew and rust diseases, comprised the experimental material for present study. The trials were conducted in a Randomized Complete Block Design with three replications at ten locations each year representing diverse agroclimatic conditions during *rabi* season of 2001-02, 2002-03 and 2003-04. The plot size was ten rows of 5m length, spaced 30 cm apart. Replication-wise seed yield data for ten locations per year on plot basis were recorded for three years whereas, oil content of seed samples collected from 9 and 10 locations were estimated following NMR technique during 2002-03 and 2003-04, respectively. The breakup of these locations were one from zone I (Himachal Pradesh), three from zone II (UP, Jharkhand and West Bengal), two from zone III (Rajasthan and Madhya Pradesh) and four from zone IV (Chhatisgarh, Orissa, Maharashtra and Karnataka). All the ten locations were common for the first two years (2001-02 and 2002-03) and 9 were common for the third year in case of seed yield. Nine locations were common during both years for oil content. Genotypes and locations were assumed as fixed and years as random in the combined analysis of variance. The Bartletts test was employed to test the homogeneity of error variances of different environments. Stability analysis for seed yield and oil content were performed for locations within individual years and on pooled basis over 30 environments for seed yield following Eberhart and Russell (1966) and the sustainability indices were calculated following the formula **suggested by** Singh and Agarwal (2003).

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Results and discussion

The mean squares due to genotypes (G), environments (E), E+(GxE) and E (linear) were tested against both pooled error and pooled deviation whereas, G x E, interactions and G x E (linear) component were tested against pooled error (Table 1 and 2).

The analysis of variance for individual years showed that the mean squares for genotypes, environments, G x E interactions and environment (linear) were found to be highly significant for seed yield and oil content. This suggested that broad range of diversity existed among genotypes and among locations and that the performance of genotypes was differential over locations. This was expected because the locations were diverse for soil type, fertility, rainfall and temperature regime. Both linear and non-linear components of GxE interaction were significant for both seed yield and oil content. Limited studies on phenotypic stability with local cultivars in India and abroad indicated that GxE interaction for seed yield was highly significant and that most interactions were linear (Yadav *et al.*, 2000; Adunga and Labuschagne, 2002 and 2004). However, substantial non-linear component was also observed and has been reported inn past by several workers like Rai *et al.* (1989), Mishra and Rai (1993) and Yadav *et al.* (2000). The predominance of linear component noticed for seed yield except the year 2002-03 would help in predicting the performance of the genotypes across environments. Overwhelming effect of locations/environment on genotypic performance along with GxE interaction suggests that linseed varieties bread for one region may not do well in other regions. These findings call for widening the genetic base used in breeding programmes.

However, pooled analysis of variance for seed yield indicated the non-significance of G x E interaction and so stability parameters were not estimated on pooled basis. Different measures of stability have been used by various workers e.g., Finlay and Wilkinson (1963) considered linear regression as a measure of stability whereas, Eberhart and Russell (1966) emphasized that both linear (bi) and non-linear (S^2di) components of GxE interaction be considered while judging the phenotypic stability of a genotype. Subsequent studies on this aspect suggested that bi could simply be regarded as measure of response whereas, S^2di should be considered as measure of stability. Accordingly, a variety is considered to be stable if it shows high mean performance, unit regression coefficient (bi=1) and non-significant deviation from the regression line (S^2di). The perusal of stability parameters for seed yield presented in Table 3 revealed that out of ten released varieties tested only Sheela and Shubhra in 2001-02; Sweta in 2002-03, Shekhar, Sweta and Shubhra in 2003-04 were found stable over locations as indicated by their non-significant deviation from regression (S^2bi). Among these stable varieties Shukhar and Shubhra manifested above unity regression coefficient (bi>1). This implies that both varieties recommended for irrigated condition are adapted to more favourable growing conditions and will show decline in performance under unfavourable condition. Under intensive agriculture with high inputs, both varieties can yield maximum returns. Whereas, Sweta seems to be responsive for favourable as well as unfavourable environment. For oil content, linseed var. Shekhar and Shubhra were found stable by virtue of their non-significant deviation from regression over locations in both individual years (Table 4). Like seed yield, *rabi* season 2003-04 seems to favourable for this quality parameters as most of the varieties yielded more than 40% oil. Further more, it was observed that Shubhra with regression coefficient less than unity will be suitable for realising high oil content under unfavourable conditions. The high value of sustainability index coupled with high *per se* performance may be considered as indicator of close proximity between the best performance and the average performance over the years. Linseed var. Padmini and LC-54 recorded high sustainability index (73%) along with mean seed yield of 799 and 732 kg/ha, respectively indicating consistent performance over the years for seed yield (Table 3).

Table 1 Analysis of variance of multi-environment seed yield data in linseed following Eberhart and Russell (1966) model

Source	d.f.	Mean sum of squares			d.f.	Pooled MSS
		2001-02	2002-03	2003-04		
Genotypes	9	27755.67*	10027.56*	43431.04*+	9	4599.42*
Environment	9	934452.23*+	2985557.1*+	2249168.40*+	2	139144.36*+
G x E	81	15864.36*	30460.18*	387444.61*	18	2035.87
E+(G x E)	90	107723.15*+	325969.88*+	259786.90*+	20	15746.72*+
E (Linear)	1	8410071.9*+	26872210.00*+	2024252.00*+	1	278290.12*+
G x E (Linear)	9	19323.92*	26756.79*	73180.07*	9	1601.69
Pooled deviation	80	13888.71*	27830.84*	30996.09*	10	2222.90*
Pooled error	180	2020.34	2955.54	3748.42	54	1423.74

* = Significant against pooled error at 1% level; + = Significant against pooled deviation at 1% level

Table 2 Analysis of variance of multi-environment oil content data in linseed following Eberhart and Russell (1966) model

Source	2002-03		2003-04	
	d.f.	MSS	d.f.	MSS
Genotypes	9	40.46*+	9	36.84*+
Environment	8	43.03*+	9	36.00*+
G x E	72	1.78*	81	2.87*
E+(G x E)	80	5.91*+	90	6.18*+
E (Linear)	1	344.23*+	1	324.02*+
G x E (Linear)	9	3.57*	9	1.79*
Pooled deviation	70	1.37*	80	2.70*
Pooled error	162	0.28	180	0.29

* = Significant against pooled error at 1% level; + = Significant against pooled deviation at 1% level

Table 3 Estimates of stability parameters and sustainability index (SI for seed yield in linseed)

Entry	2001-02			2002-03			2003-04			SI (%) mean of 2 years
	Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di	
LC-54	658.20	0.98	14298.05**	714.40	0.91	35775.72**	830.40	0.63**	22494.11*	73.14
Sheela	622.80	0.83	7016.78	697.90	1.11	20178.50**	840.00	1.09	33402.57**	67.17
T-397	648.50	1.08	11847.71*	727.10	1.04	18893.86**	939.40	0.72*	54822.73**	61.35
Shekhar	617.20	1.01	10029.81*	679.30	1.00	13144.70*	910.50	1.15	5935.31	56.79
Shubhra	585.90	1.10	6089.25	708.30	1.01	16350.81*	808.20	1.07	12553.43	67.23
Garima	577.70	0.90	8911.71*	734.90	1.03	22663.09**	752.80	0.98	63447.30**	70.31
Padmini	711.50	1.00	12626.20*	786.60	0.80	72262.73**	900.30	1.13	23397.45*	73.87
J 23	689.10	1.03	24398.53**	674.60	0.95	22754.62**	975.40	1.19	30777.12**	55.34
Kiran	592.70	0.76	14432.11**	726.60	1.00	38187.88**	877.00	1.13	41339.09**	60.54
Sweta	725.30	1.30*	22502.47**	717.60	1.16	8244.78	894.80	0.91	9297.14	71.25
GM	642.89	1.00	-	716.73	1.00	-	872.88	1.00	-	-
SEm±	39.28	0.13	-	55.61	0.10	-	58.68	0.13	-	-

*, ** Significant at 5% and 1% levels, respectively.

Table 4 Estimates of stability parameters and sustainability index (SI) for oil content (%) in linseed

Entry	2002-03			2003-04			SI (%) mean of 2 years
	Mean	bi	S^2di	Mean	bi	S^2di	
LC-54	37.45	0.88	2.76**	39.69	1.13	4.60**	77.25
Sheela	39.32	1.27	2.78**	40.10	0.95	3.95**	78.40
T-397	36.42	0.55*	0.81	40.76	0.80	1.30*	82.53
Shekhar	39.95	1.01	0.87	42.93	0.83	0.86	82.60
Shubhra	35.81	0.65	0.42	44.48	0.85	0.83	79.14
Garima	38.65	1.27	0.50	43.19	1.31	3.28**	75.20
Padmini	43.06	1.10	1.60*	45.55	1.34	2.17**	79.602
J-23	39.56	0.90	0.72	42.19	1.24	3.88**	78.83
Kiran	39.14	0.76	1.16*	41.22	0.88	3.24**	82.12
Sweta	40.80	1.61**	1.17*	43.55	0.68	1.96**	78.35
GM	39.02	1.00	-	42.36	1.00	-	-
SEm±	0.41	0.19	-	0.55	0.29	-	-

*, ** Significant at 5% and 1% levels, respectively.

However, as per the Eberhart and Russell model, these two varieties were found to be unstable for seed yield. For oil content, all the linseed varieties recorded very high sustainability index indicating least influence of environmental factors on all the ten varieties (Table 4). These results are contrary to the findings based on Eberhart and Russell model hence, sustainability index model may not be useful for the selection of stable genotypes in the present set of materials. It was observed that these two attributes i.e., seed yield and oil content appear to be specific for a given genotype and any generalization regarding the stability of a genotype for both traits together is quite difficult. Considering the norms of *stability parameters, it may be concluded that Sweta and* Sheela for seed yield whereas, for both seed yield and oil content, Shubhra, Shekhar are the stable linseed varieties. Shekhar exhibited consistent performance for seed yield as well as oil content both under favourable and unfavourable conditions while Shubhra responded differently for these traits.

Acknowledgement: We are thankful to linseed breeders of the different AICRP (Linseed) centres *viz.*, Palampur, Kanke, Kanpur, Berhampore, Kota, Sagar, Nagpur, Jashipur, Raipur and Raichur who conducted the trials and recorded the data nicely.

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J. Oilseeds Res., **25**(2) : 154-156 (2008)

Combining ability studies in linseed, *Linum usitatissimum* L.

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(Received: October, 2007; Revised: September, 2008; Accepted: October, 2008)

Abstract

Six well adapted lines and three testers of linseed (*Linum usitatissimum* L.) were crossed in Line x Tester fashion to elicit information regarding the desirable parents and crosses for their use in crop improvement programme. The material was raised in Randomized Block Design with three replications. Sufficient genetic variability was observed among the parents, lines and crosses for all quantitative traits. Non-additive gene action predominated for all the traits except days to 50% flowering. The estimates of *gca* effects revealed that the genotypes Ayogi among the lines and Kiran among the testers were the best general combiner for seed yield/plant and its components and could be utilized in future breeding programme. Significant *sca* effect was exhibited by three crosses *viz.*, Ayogi x Kiran, Solin x T-397 and Y-Kiran x Kiran for seed yield and could be used for exploitation of heterosis for seed yield and its components.

Key words: Line x Tester analysis, combining ability, heterosis, linseed

Introduction

Linseed in an important non edible oilseed crop grown in *rabi* season. Seed yield of linseed is low in India as compared to developed countries. In India, for enhancing linseed yield, the research efforts made mostly being concentrated towards individual plant selection of land races and progeny selection followed by hybridization of parents having higher *per se* performance. Therefore, present investigation was undertaken to study the combining ability for identification of good combiners and promising crosses for future better accomplishment in linseed.

Material and methods

The experimental material, consisting of eighteen crosses in Line x Tester design involving six diverse lines and three well adapted testers of lines were grown along with parents in the randomized block design with three replication at Research farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during *rabi*, 2004-05. Each treatment in a replication has a single row of 4 m length, with 30x10 cm spacing between and within the row, respectively. All the recommended cultural practices were followed. Data were recorded on five randomly competitive plants from each genotype/replication for days to 50% flowering days to maturity, plant height (cm), primary branches/plant, secondary branches/plant, capsules/plant, seeds/capsule, seed/plant (g), 1000 seed weight (g) and seed yield/plant (g). The analysis of variance was worked out as per procedure given by Sukhatme and Amble (1985), whereas combining ability analysis was done as per Kempthorne (1957).

Results and discussion

The analysis of variance for combining ability revealed highly significant differences of the Line x Tester component for all the characters, indicating that the material chosen was variable with respect to traits under investigation. The lines showed significant differences for *days 50% flowering, days to maturity, plant height*, secondary branches/plant, capsules/plant, seeds/capsule and seeds/plant. While, the testers exhibited significant differences for day to maturity, plant height, capsules/plant and seeds/plant (Table 1).

Partitioning of combining ability variances into fixable additive genetic variance and non-fixable dominance variance indicated that non-additive gene action play a significant role in inheritance of all the traits except for days to 50% flowering. Therefore, it would be beneficial to build up a population by inter-mating these parents inter se before initiating random mating in F_2 to allow higher recombination (Rawat, 1982). Preponderance of dominance gene action for majority of traits, observed was found in agreement with Bhateria *et al.* (2001), Swarnakar *et al.* (2003) and Tiwari *et al.* (2004).

The estimates of *gca* effect revealed that the genotypes Ayogi among the lines and Kiran among the testers would prove the good general combiner for seed yield/plant (Table 2). Parents Ayogi and Kiran were also found good general combiners for secondary branches/plant, capsules/plant, seeds/capsule and seeds/plant. In addition to these Ayogi was a good general combiner for primary branches/plant whereas, Kiran for early maturity. Polf 22 was the good general combiner for days to 50 % flowering days to maturity, plant height, secondary branches/plant and seeds/plant. The *gca* effects for other characters showed that Y-Kiran for plant height, Solin for 1000-seed weight. R 552 for primary branches/plant and secondary branches/plant. T-397 for plant height and 1000-seed weight, were the good general combiners. Crosses involving these parents might produce heterotic hybrids with high mean performance for respective traits.

High *sca* effects mostly from the dominance and epistatic interaction effects existed between the hybridizing parents. In the present study, significant *sca* effects were exhibited by three crosses *viz.*, Ayogi (H) x R-552 (L), Solin (L) x T-397 (L) and Y-Kiran (L) x Kiran (H) for seed yield/plant (Table 3). All the three crosses having *significant sca effects, recorded higher per se* performance, where both of the parents involved in the combination having either high x low or low x low *gca* effects. In addition to seed yield/plant, these crosses exhibited significant and positive *sca* effects for different traits like cross Ayogi x R-552 for tallness, primary branches/plant, secondary branches/plant, capsules/plant and seeds/plant; Solin x T-397 for tallness, secondary branches/plant, seeds/capsule, seeds/plant and 1000-seed weight; Y-Kiran x Kiran for primary branches/plant, secondary branches/plant, capsules/plant and 1000-seed weight. It was observed that crosses involving either one low or the other high or low general combining parents would produce heterotic hybrids. Earlier workers like Kusalkar *et al.* (2002), Bhateria and Pathania (2003) and Ratnaparkhi *et al.* (2004) also reported similar results for grain yield and yield attributing traits in linseed. It is concluded that non-additive gene effects were found important in the inheritance of most of the traits. The good general combiner parent *viz.*, Ayogi and Kiran could be utilized in future breeding programmes. The crosses Ayogi x R-552, Solin x T-397 and Y-Kiran x Kiran could be used for isolating superior genotypes from segregation generation.

Table 1 Analysis of variance of combining ability for different characters in linseed

Source	D.F.	Days to 50% *flowering*	Days to maturity	Plant height	Primary branches/ *plant*	Secondary branches/ *plant*	Capsules/ plant	Seeds/ capsule	Seeds/ plant	1000 seed weight	Seed yield/ plant
Replication	2	3.679*	2.654	51.666*	0.700	3.719*	105.623**	0.213	4532.54**	0.251	0.118
Lines	5	7.25**	19.672**	1131.253**	2.182	12.06**	276.698**	2.965*	18346.28**	1.385	1.142
Testers	2	1.89	18.084	12.492**	0.031	0.231	81.604**	0.174	17989.32**	0.617	0.201
Line x tester	10	5.87**	7.132**	91.832**	4.625**	54.587**	1018.301**	4.407**	100636.20**	1.342	2.849**
Error	52	2.500	1.073	12.860	0.174	1.479	28.814	0.202	6028.140	0.079	0.247
Additive genetic variance	σ^2A	4.016	0.762	7.145	0.0747	0.42	27.143	-0.0667	-1363.707	-0.0713	-0.0739
Dominance variance	σ^2D	1.123	2.019	26.300	1.4800	17.70	329.829	1.4010	31536.020	0.4200	0.8670
Degree of dominance	σ^2A/σ^2D	3.576	0.377	0.271	0.0504	0.0237	0.0822	-0.0476	-0.0432	0.1697	0.0852

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

Table 2 Estimates of *gca* effects for different parents for various traits in linseed

Cross	Days to 50% flowering	Days to maturity	Plant height	Primary branches/ *plant*	Secondary branches/ *plant*	Capsules/ plant	Seeds/ capsule	Seeds/ plant	1000 seed weight	Seed yield/ plant
Lines										
Polf 22	-4.80**	-104**	-5.77**	-0.20	1.07**	-1.86	-0.64**	53.56**	-0.73*	-0.03
Y-Kiran	2.14**	0.54*	-6.13**	-0.17	-0.64*	-7.46**	-0.29**	-32.33	0.41**	0.05
Solin	*1.63***	*0.84***	*2.52***	*0.94***	*-2.07***	*-10.00***	*-0.60***	*-56.00***	*0.84***	*0.05*
Ayogi	3.49**	1.63**	10.12**	1.25**	5.58**	32.78**	0.90**	219.89**	-0.35**	1.03**
SIKO 10	0.16	0.92**	1.32	-0.84**	-0.62**	3.38**	0.35**	-100.67**	0.48**	-0.33**
JRF 3	-2.62**	-1.04**	-2.06**	-1.15**	-3.31**	-16.84**	-2.62**	-84.44**	-0.65**	-0.77**
SE (gi)	0.45	0.25	0.83	0.12	0.32	1.37	0.09	23.42	0.06	0.15
Testers										
Kiran	0.63*	-1.30**	1.71**	-0.10	0.62**	1.11	0.50**	42.50**	-0.13**	0.18**
R 552	0.89	0.63**	-0.43	0.46**	0.94**	-.34	-0.37**	1.44	-0.10**	-0.02
T 397	-1.52**	0.67**	-1.28*	-0.36**	-1.57**	-0.79	-0.13*	-43.94**	0.20**	-0.16
SE(gi)	0.28	0.16	0.52	0.07	0.20	0.86	0.06	14.81	0.04	0.09

*, ** Significant at 5% and 1% levels, respectively.

Table 3 Estimates of *sca* effects of crosses for different characters in linseed

Cross	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Capsules/ *plant*	Seeds/ *capsule*	Seeds/ *plant*	1000 seed weight (g)	Seed yield/ plant (g)
Polf 22 x Kiran	-0.14	-1.39**	3.56**	0.30	3.87**	6.22*	-1.02**	57.94	-0.07	0.24
Polf 22 x R-552	-0.74	-0.12	-5.37**	-0.86**	-2.66**	-10.80**	0.01	-104.33**	0.39**	-0.36
Polf 22 x T-397	0.87	1.51**	1.81	0.56**	-1.21**	4.59**	1.01**	46.39	-0.32**	0.12
Y-Kiran x Kiran	-0.07	0.24	-1.35	0.92**	2.51**	9.82**	-0.04	50.83	0.56**	0.63**
Y-Kiran x R-552	0.20	-0.10	2.45**	-1.17**	-1.74**	-6.40**	1.27**	19.89	-0.34**	-0.06
Y-Kiran x T-397	-0.13	-0.14	-1.10	0.25	-0.77	-3.41	-1.24**	-70.72**	-0.22**	-0.57**
Solin x Kiran	*0.37*	*1.74***	*0.80*	*-0.06*	*0.80*	*13.22***	*-0.99***	*4.17*	*-0.39***	*-0.10*
Solin x R-552	-0.43	-1.30**	-7.73**	0.85**	-2.59--	-16.74**	0.15	-98.11**	0.00	-0.62**
Solin x T-397	0.05	-0.44	6.93**	-0.79**	1.79**	3.52	0.84**	93.94**	0.39**	0.72**
Ayogi x Kiran	1.29*	0.61	-1.06	-1.97**	-7.24**	-32.23**	0.84**	-294.72**	0.20**	-1.47**
Ayogi x R-552	-0.96	-0.12	8.27**	2.34**	8.37**	38.02**	-1.62**	373.33**	0.12	2.01**
Ayogi x T-397	2.25**	-0.49	-7.21	-0.37*	-1.12**	-5.76**	0.78	-78.61*	-0.32**	-0.54**
SIKO-10 x Kiran	-0.43	0.92*	-2.93*	0.39*	-0.58	-2.96	0.69**	16.17	0.84**	0.46*
SIKO-10 x R-552	1.64**	1.16**	0.94	-0.44**	1.30**	1.89	-0.67**	-11.44	-0.35**	-0.22
SIKO-10 x T-397	-1.21	-2.08**	1.99	0.05	-0.72	1.07	-0.01	-4.72	-0.48**	-0.24
JRF-3 x Kiran	1.55**	-2.12**	0.98	0.43**	0.64	5.93**	0.52**	165.61**	-1.13**	0.24
JRF-3 x R-552	0.29	0.48	1.45	-0.73**	-2.68**	-5.96**	0.86**	-179.33**	0.18*	-0.74*
JRF-3 x T-397	-1.84**	1.64	-2.43*	0.30	2.03**	0.03	-1.38**	13.72	0.95**	0.50*
Sij	*0.63*	*0.36*	*1.17*	*0.16*	*0.45*	*1.93*	*0.13*	*33.13*	*0.08*	*0.21*
CD (0.05)	1.2348	0.7050	2.2930	0.3136	0.8820	3.7800	0.2540	64.9033	0.1560	0.4116
CD (0.01)	1.6220	0.9300	3.0100	0.4120	1.1590	4.9700	0.3340	85.3400	0.2060	0.5400

*, ** Significant at 5% and 1% levels, respectively.

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J. Oilseeds Res., **25**(2) : 157-160 (2008)

Effect of integrated nutrient management practices on growth and yield of rainfed groundnut, *Arachis hypogaea* L. intercropped with guava, *Psidium guajava*

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(Received: October, 2007; Revised: June, 2008; Accepted: July, 2008)

Abstract

A field study was conducted during *kharif* seasons of 2005 and 2006 at Students' Farm on red sandy loam soil to find the effect of different integrated nutrient management practices on groundnut in guava plantation. The pod yield of groundnut was significantly higher in sole cropping than the intercropping either in nutritioned or unnutritioned guava. Application of recommended dose of NPK + vermicompost and enriched FYM with recommended dose of NPK recorded significantly higher pod yield during both the years. Lower pod yield was observed with application 50% recommended dose of fertilizer + FYM. Similar response was observed in LAI and dry matter production. Soil physical and chemical properties like bulk density and nutrient status were improved before and after cropping in guava plantation when compared to sole cropping.

Key words: Guava, groundnut, intercropping, sole cropping

Introduction

The small and marginal farmers who are dependent on rainfed sole crop farming rarely get remunerative returns. Hence they are shifting towards other production systems particularly fruit trees compared to fodder and fuel wood trees. These shifts are essentially driven by the market forces and social factors. Further, the economic returns are found to be in favour of agrihorticultural system compared to traditional farming in low rainfall areas. Under such situations, agrihorticultural system with dryland fruit trees as basic component is readily acceptable as an alternate land use, which provides stability and sustainability to the resource poor farmers in semi arid tropics. (Dass, 1983).

Traditional agriculture is organic based everywhere. In the modern agriculture, as the chemicals fancied the farmers, organic farming is neglected. To maintain soil health and to supply nutrients in balanced proportion for higher crop yields, it is imperative to practice integrated nutrient supply system through the combined use of organic, biological and chemical sources of nutrients. Soil fertility buildup through agroforestry and practice of integrated nutrient management were suggested as potential means to increase the soil fertility especially in drylands (Subba Reddy *et al.*, 1991). Application of commercial fertilizers in large quantities is not only expensive and often results in imbalance of soil reserves. Adoption of intercropping and integrated nutrient management practices of soil fertility build of is highly imperative to achieve self-sufficiency in oilseed production.

Material and methods

A field experiment was conducted during *kharif* seasons of 2005 and 2006 at Students' Farm, College of Agriculture, Rajendranagar, Hyderabad. The experimental site was under eight years old guava plantation spaced at 8m x 8m with curry leaf [*Murraya koenigii* (L.)] as filler plant. The soil in guava plantation was red sandy loam, medium in organic carbon (0.50 and 0.51%), available N (221.6 and 223.5 kg/ha), available P (34.4 and 35.2 kg/ha) and available K (231.4 and 232.8 kg/ha) respectively during 2005 and 2006, whereas the open area was low in organic carbon (0.28 and 0.30%) and available N (189.8 and 190.3 kg/ha), medium in available P (26.4 and 26.8 kg/ha) and available K (216.5 and 217.4 kg/ha) respectively during 2005 and 2006. The treatments comprised of 3 cropping situations and seven integrated nutrient management practices (Table 1). The experiment was laid out in Split Plot Design with three replications. The plot sizes were 8m x 4m and 4m x 4m intercropping and solecropping respectively. Guava trees were fertilized with 210 g N, 160 g, P_2O_5, 300 g K_20 and 60 kg FYM/tree under the treatment of intercropping of groundnut in nutritioned guava during both the years of study. The groundnut variety TMV-2 was selected as intercrop and sown at recommended spacing both in intercropping and solecropping situations on 15th July 2005 and 4th July 2006. Groundnut was grown as rainfed crop in the system. The total rainfall was received in the cropping season was 800 mm rainfall distributed in 41rainy days during 2005 and 498 mm rainfall distributed in 35 rainy days 2006.

Results and discussion

Growth: Growth of groundnut in terms of leaf area index (LAI) and drymatter production at harvest was significantly influenced by cropping situations which were higher in solecropping of groundnut than intercropping of groundnut either in nutritioned guava or unnutritioned guava during both the years (Table 1). This might be due to competition from the trees on natural resources like light, water and nutrient resulting in decline trend in these growth parameters. Similarly results were obtained by Okoria *et al.* (1994). The highest LAI and drymatter production per plant were obtained in enriched FYM with recommended dose of NPK as well as recommended dose of NPK + vermicompost in both the years when compared to the other integrated nutrient management practices. However recommended dose of NPK + FYM and also recommended dose of NPK proved to be effective in enhancement of LAI and drymatter production in both the years compared to 50% recommended dose of NPK with combination of organic manure. The added advantage from the application of enriched FYM or vermicompost was one of the beneficial factor which might have contributed in improvement of soil physical properties as well as soil moisture status resulting in complementary effects on growth of groundnut. Similar results were obtained by Shivaprasad and Sheelavanter (1996).

Yield and yield attributes: Pod weight and shelling percentage were more under solecropping situation compared to intercropping of groundnut either nutritioned guava or unnutritioned guava (Table 2). The better performance of these attributes in groundnut when grown as solecrop was clearly understood from the fact that the plant growth was attained due to transmission of light reaching to the crop resulting in effective utilization of light for assimilation of photosynthates. These results were in accordance with the findings of Okoria *et al.* (1994). These results are in conformity with Anonymous (1992) and Bheemaiah and Subrahmanyam (2001). Though the haulm yields under cropping situations did not show any significant variations harvest index was found increased considerably under solecropping situation when compared to groundnut as intercrop in nutritioned or unnutritioned guava, it was mainly due to wide range between pod and haulm yield observed under solecropping situation.

The yield attributing characters of groundnut like 100-pod weight and shelling percentage were found improved to the maximum extent with the application of recommended dose of N, P and K either with the combination of vermicompost or enriched FYM among the integrated nutrient management practices studied. It might be mainly due to adequate supply of nutrients to the crop grown under marginal soils of dry lands. Further, application of vermicompost as well as enrichment of FYM also might have helped in improvement of yield attributing characters and groundnut because of better improvement in soil properties as well as moisture availability for better crop growth. Similar findings were obtained by Chaithanya Devi *et al.* (2003), Devaranavadgi *et al.* (2005). Application of recommended dose of NPK with combination of vermicompost as well as enrichment of FYM recorded the maximum pod and haulm yields. However application of FYM along with recommended dose of NPK also was found effective to increase the pod and haulm yields when compared to application of 50 % recommended dose of NPK with the combination of different organic manures. Higher pod and haulm yields obtained with recommended dose of NPK along with organic manures could be due to adequate supply of essential nutrients and also application of vermicompost and enrichment of FYM might have helped steady supply of nutrients because of favourable soil properties maintained throughout the crop growth period. Sagare *et al.* (1992) stated that the increase in pod yield of groundnut due to recommended dose of fertilizer application with combination of organic manures which might be attributed to enhanced synthesis of carbohydrates and proteins. Similar results were obtained by Taha *et al.* (1999), Khatik and Dikshit (2001), Singh *et al.* (2001) and Das (2002). The similar trend was observed in harvest index under integrated nutrient management practices studied.

Economics: The highest profit per rupee investment (3.28) was obtained with enriched FYM with recommended dose of NPK under intercropping situation in unnutritioned guava (Table 3), which was followed by enriched FYM with recommended dose of NPK under intercropping situation in nutritioned guava (3.10). Similar results were obtained by Sunanda Rani *et al.* (2006).

The analysis of physical and chemical properties of soil before and after cropping revealed that in general soil properties with respect to physical and chemical were improved in guava plantation when compared to treeless area i.e. open area under solecropping. Bulk density was reduced considerably in plantation area before cropping and after cropping when compared to that of open area. This was mainly due to the increase in porosity because of addition of leaf litter over the years. There was reduction in soil pH and EC under intercropping situation in guava trees when compared to solecropping situation (open area). This might be due to production of organic acids during biological decomposition of leaf litter. Whereas, organic carbon content was found increased in soils of tree planted areas when compared to open area. There was not much variation in organic carbon content of soil before and after cropping. Similarly there was considerable improvement in available N, P and K in soils, where guava plantation was there when compared to open area. These chemical properties of soil were found improved after cropping when compared to before cropping. This might be better explained with beneficial effects of trees possessing the deep and extension root system and leaf fall resulting in site improvement. Similar findings were observed by Jha *et al.* (2000).

Table 1 Effect of cropping situations and integrated nutrient management practices on yield attributes and yield of groundnut in guava based agrihorticultural system

Treatment	Leaf area index		Drymatter production/plant (g)		100-pod weight (g)		Shelling (%)		Pod yield (kg/ha)		Haulm yield (kg/ha)		Harvest index	
	2005	*2006*	*2005*	*2006*	*2005*	*2006*	*2005*	*2006*	*2005*	*2006*	*2005*	*2006*	*2005*	*2006*
Cropping situations (CS)														
Intercropping of groundnut in nutritioned guava	3.8	4.1	13.3	12.9	45.4	44.6	59.3	58.2	656.9	521.2	3104	3273	15.7	13.7
Intercropping of groundnut in unnutritioned guava	3.7	4.0	13.3	12.8	43.2	42.3	58.6	57.5	629.4	509.5	3216	3273	16.4	13.9
Sole cropping	4.6	5.0	15.2	14.4	6.6	45.9	62.9	61.5	948.2	875.1	3152	3336	22.5	21.6
SEm±	0.05	0.10	0.41	0.26	0.77	0.66	0.57	0.55	26.76	15.62	65.0	52.9	0.55	0.59
CD (P=0.05)	0.15	0.28	1.61	1.02	0.16	1.82	1.59	1.52	74.29	43.36	NS	NS	1.53	1.64
Integrated nutrient management practices														
Recommended dose of NPK (20:40:40 kg/ha)	4.2	4.5	14.0	13.2	45.4	44.2	63.3	62.1	750.9	639.5	3146	3304	18.5	16.8
Recommended dose of NPK+FYM (10 t/ha)	4.4	4.7	14.5	13.8	46.5	45.2	64.5	63.2	870.9	730.5	3336	3497	19.9	17.9
Recommended dose of NPK + Vermicompost (2 t/ha)	4.7	5.0	15.7	14.7	47.9	46.9	66.5	65.4	955.7	847.1	3600	3789	20.1	19.0
Enrichment of FYM (750 kg/ha) with recommended dose of NPK	4.7	5.1	15.5	14.7	48.1	46.7	66.4	65.2	943.1	584.0	3654	3817	19.7	18.8
50% recommended dose of NPK + FYM (10 **t/ha**)	3.3	3.6	12.0	11.8	41.6	41.3	52.5	51.7	519.3	415.9	2628	2771	15.4	13.3
50% recommended dose of NPK + Vermicompost (2 t/ha)	3.5	3.8	13.1	12.6	43.0	42.5	54.1	52.7	587.5	477.9	2773	2924	16.4	14.3
Enrichment of FYM (750 kg/ha) with 50% recommended dose of NPK	3.5	3.8	12.7	12.8	43.0	42.6	54.1	53.1	586.6	482.1	2754	2954	16.3	14.6
SEm±	0.09	0.06	0.24	0.23	0.16	0.28	0.35	0.50	23.36	22.67	46.4	29.8	0.52	0.56
CD (P=0.05)	0.19	0.11	0.68	0.65	0.32	0.57	0.70	1.01	45.37	45.99	94.2	60.5	1.06	1.14

Table 2 Profit per rupee investment from the system (tree + crop) as influenced by cropping situations and integrated nutrient management practices in agrihorticultural system

Treatment	Profit/rupee investment					
	Intercropping in nutritioned guava		Intercropping in unnutritioned guava		Sole cropping	
	2005	2006	2005	2006	2005	2006
Recommended dose of NPK (20:40:40 kg/ha)	2.9	2.7	3.0	2.7	1.9	1.8
Recommended dose of NPK + FYM (10 t/ha)	2.7	2.4	2.7	2.4	1.8	1.6
Recommended dose of NPK + Vermicompost (2 t/ha)	2.0	1.8	1.9	1.6	1.2	1.1
Enriched FYM (750 kg/ha) with recommended dose of NPK	3.1	3.0	3.3	3.0	2.3	2.3
50% recommended dose of NPK + FYM (10 t/ha)	2.1	1.9	1.9	1.8	1.2	1.0
50% recommended dose of NPK + Vermicompost (2 t/ha)	1.5	1.3	1.2	1.0	0.7	0.6
Enriched FYM (750 kg/ha) with 50% recommended dose of NPK	2.6	2.3	2.5	2.1	1.7	1.5
Mean	2.4	2.2	2.3	2.1	1.6	1.4

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J. Oilseeds Res., **25**(2) : **161-164** (2008)

Studies on spatial distribution of thrips on sunflower, *Helianthus annuus* L.

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(Received: June, 2008; Revised: October, 2008; Accepted: October, 2008)

Abstract

Investigations were made to study the spatial distribution of thrips (*Thrips palmi* Karny and *Scirtothrips dorsalis* Hood) on Sunflower (*Helianthus annuus* L.). Based on the variance-mean ratio, chi-square test and dispersion indices thrips have shown aggregated distribution and negative binomial model fitted the population pattern. Intra plant distribution studies indicated that the upper strata of plant provided the most reliable estimate of the thrips population on sunflower.

Key words: Spatial distribution, thrips, sunflower

Introduction

Sunflower (*Helianthus annuus* L.) is an important edible oilseed crop in India with an area of 2.00 m. ha and a production of 0.99 million tonnes (Anonymous, 2005). Apart from capitulum borers and defoliators, some sucking pests *viz*., whitefly (*Bemesia tabaci* Gennadius), leaf hopper (*Amrasca biguttula biguttula* Ishida) and thrips (*Thrips palmi* Karny and *Scirtothrips dorsalis* Hood) are potential pests causing around 46% loss to sunflower crop (Basappa *et al*., 1999).Thrips cause enormous loss indirectly by facilitating the transmission of tobacco streak virus, which causes necrosis disease in sunflower. Thrips assist in transmission of this virus by carrying the infected pollen but not by acquiring the virus in their body (Sonali *et al*., 2005). A detailed study of spatial distribution of thrips would be helpful in formulating an optimum sampling size to arrive at an appropriate population estimate.

Material and methods

To study the distribution of thrips, popular variety Morden was sown in an area of 25 x 20 m^2 adopting a spacing of 60 cm x 30 cm during *rabi*, 2000-2001. The crop was raised as per the recommended crop production practices. However, the plot was left unsprayed through out the crop period. The experiment was repeated in *rabi*-summer 2000-2001.

Observations on incidence of thrips were made at weekly interval starting from the appearance of individual pests up to flowering. The population of thrips was counted on two top, two middle and two bottom leaves of the plant canopy, on 30 randomly selected plants (Rathore and Tiwari, 1999). The observations were made during early hours of day when there was minimum movement of the pest. Each leaf was gently tapped on a tray lined with white paper and the thrips (nymphs and adults) population, were counted.

The first step in confirming the nature of distribution of thrips population was to arrange the data in frequency distribution. Mean and variance were then worked out for all the weekly observations (Snedecor and Cochran, 1967). On the basis of X and S^2, statistical tests were applied to confirm the distribution of thrips.

Variance-Mean ratio (S^2 - X Ratio): The data of thrips population was summarized in frequency distribution and the mean (X) and variance (S^2) and dispersion parameter were calculated and inspected for fit to negative binomial distribution (Elliot, 1979 and Southwood, 1978).

A common dispersion parameter 'K' (K$_c$) for the negative binomial distribution was estimated by moment and regression method given by Bliss and Owen (1958). χ (Chi Square) test for "Goodness-of-Fit" for agreement with a negative binomial distribution was also done (Anscombe, 1950; Bliss and Fischer, 1953). The pattern of dispersion (random/aggregated/contagious) was studied by calculation of Cole's Index (Cole, 1946),

Cole's Index = I = $\Sigma(X)^2 / \Sigma X)^2$, where X= Mean

and Lloyd's Index of mean crowding (Lloyd, 1967),

$X^* / X = 1 + 1/K$, where X= Mean and K=Common dispersion parameter.

In order to understand which stratum of the plant provides the most reliable estimate of thrips population, relative variation (RV) values were calculated by the formula.

RV = (SX / X) 100,

Where, SX = Standard error of mean and X = Sample mean (Walgenbach *et al*., 1985).

The coefficient of variation or relative variation indicates the degree of precision and is a good index of reliability of the experiment. It expresses the experimental error as a percentage of mean; thus the lower the RV value, the higher is the reliability of the experiment. RV is unit less and hence comparable regardless of the sample unit use (Ruesink, 1980).

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Results and discussion

Variance - Mean ratio: The upper strata recorded variance to mean ratio ranged from 1.3 to 2.0 during *rabi* and 1.0 to 2.1 during *rabi*-summer. The variance to mean ratio of thrips in the middle strata ranged in between 1.1 to 2.1 during rabi and 1.5 to 2.5 during *rabi*-summer. No incidence of thrips was recorded on crop from 49 DAS to 63 DAS during both the seasons on lower strata. At 35 DAS, the variance to mean ratio was 1.7 in *rabi* and 2.0 in *rabi*-summer. At 45 DAS, the variance to mean ratios was 2.8 and 2.2 for *rabi* and *rabi*-summer, respectively. The values were always greater than unity in all the observations, which indicates aggregated population of thrips, (Table 1, 2).

Dispersion parameters 'K' of the negative binomial:

Upper strata: The value of dispersion parameter K, (K_1) ranged from 2.2 to 12.3 for *rabi* and 2.5 to 7.9 for *rabi-summer. The K values calculated from proportion of* zeroes (K_2) ranged from 5.1 to 8.0 for *rabi* and 6.4 to 7.1 for *rabi*-summer. The K values calculated from trial and error method (K_3) ranged from 4.4 to 7.6 for *rabi* and 5.0 to 8.0 for *rabi*-summer. Thus 'K' values never went beyond 8 in calculations from trial and error method confirming aggregate distribution of thrips in the upper strata (Tables 1 and 2).

Middle strata: For the middle strata the value of dispersion parameter K (K_1) showed a wide range of 1.0 to 49.5 for *rabi*. The values were ranging from 0.6 to 3.8 *during rabi-summer. The 'K_2' values were in between* 5.1 to 7.9 for *rabi* and 6.4 to 7.7 for *rabi*-summer. In the trial and error method the 'K' (K_3) value ranged between 3.1 to *7.3 for rabi and 5.4 to 7.4 for rabi-summer.* As the 'K' values were never more than 8 in the trial and error method, the aggregated distribution of thrips is confirmed, (Tables 1 and 2).

Lower strata: No thrips were recorded on lower strata at 49 DAS and beyond, during both the seasons. The values of dispersion K (K_1) at 35 DAS and 42 DAS were 0.6 and 1.4 and 0.5 and 0.3 during *rabi* and *rabi*-summer respectively. The 'K_2' values were 7.9 and 5.1 and 6.4 and 7.1 for *rabi* and *rabi*-summer respectively. The K_3 values were 5.9 and 5.8 and 7.2 and 7.1 for *rabi* and *rabi*-summer respectively, which were always less than 8 indicating aggregated population of thrips on lower strata (Tables 1 and 2).

Common K (K_c): During *rabi*, the thrips population exhibited aggregated distribution as the K_c values of upper (0.4), middle (0.3) and lower (0.1) strata were never more than one. Similar results were obtained during *rabi*-summer also where upper, middle and lower strata recorded K_c values of 0.4, 0.3 and 0.4, respectively (Tables 1 and 2).

Chi-Square (χ^2) test: During *rabi*, the upper strata recorded χ^2 values in the range of 18.9 to 160.2. The calculated values of Chi-square (χ^2) ranged between 14.1 to 51.2 and 52.4 to 59.3 for middle and lower strata respectively. The calculated values of Chi-square (χ^2) were always greater than the table value of Chi-square, χ^2 (1.96), confirming the negative binomial distribution of thrips.

During *rabi*-summer, the calculated values of Chi-square (χ^2) ranged from 10.7 to 77.3, 16.5 to 136.4 and 4.0 to 44.0 *for upper, middle and lower strata respectively.* The calculated values of Chi-square (χ^2) were always greater than the table value of Chi-square, χ^2 (1.96), which confirmed the negative binomial distribution of thrips (Tables 1 and 2).

Dispersion Indices

Cole Index of Dispersion: On the upper strata, the values of Cole Index of Dispersion ranged from 0.1 to 0.3 for *rabi* season and 0.2 for *rabi*-summer season (Cole, 1946). *With regard to middle strata, during rabi, the Cole Index of* Dispersion values were in between 0.1 to 0.3. The indices were 0.2 for *rabi*-summer. On the lower strata, the values ranged from 0.1 to 0.2 for *rabi* and 0.2 for *rabi*-summer. As the values were always more than 0.1, it confirmed aggregated distribution of thrips, (Tables 1 and 2).

Index of mean crowdiness: For the upper strata the indices ranged from 1.3 to 4.0 for *rabi* and 2.9 to 5.3 for *rabi*-summer. The values ranged from 1.0 to 5.7 for *rabi* and 1.0 to 3.7 for *rabi*-summer on the middle strata. These values were more than 1 in all the observations, which proved the aggregated distribution of thrips for both the seasons. However, for the lower strata, the values of index of mean crowdiness ranged from 0.5 to 2.9 for *rabi* and 0.5 to 0.6 for *rabi*-summer, (Tables 1 and 2).

Intra-plant distribution: *For rabi, with regard to thrips the* upper strata exhibited the least mean relative variation (15.0) followed by middle strata (15.1). The lower strata *recorded comparatively high mean relative variation of* 27.9 (Table 3). During *rabi*-summer, the mean relative variation was again lowest for upper strata (12.0). The middle strata recorded mean relative variation of 19.1, whereas, the lower strata showed a high mean relative variation of 39.1 (Table 3).

In the present study thrips have shown aggregated distribution and negative binomial model fitted the population pattern. This is in concordance with the results obtained by Rathore and Tiwari (1999), Cho ki-Jong *et al.* (2000) and Deligeorgidis *et al.* (2002) .Thrips have shown preference towards upper and middle strata in the intra-plant distribution studies. Cho ki-Jong *et al.*(2000) also obtained similar results. Thrips might have preferred fresher succulent upper and middle leaves compared to lower leaves. Hence, based on these observations on various aspects of spatial distribution further studies can be made to arrive at an appropriate sampling technique and sample size for estimating thrips population on sunflower.

Table 1 Variance-mean ratio (s^2/x), dispersion parameter (k), chi-square (χ^2) values and dispersion indices for thrips population (*rabi*) on sunflower

Crop Age (DAS)	S^2/X	K_1	K_2	K_3	χ^2	Cole index	Index of Mean Crowdiness
Upper strata							
35	1.9	3.8	8.0	4.4	18.9	0.1	4.0
42	2.0	3.0	8.0	6.0	93.2	0.2	3.4
49	1.3	7.0	5.1	4.6	77.2	0.2	2.7
56	1.3	12.3	5.1	5.0	160.2	0.2	3.9
63	1.5	2.2	7.1	7.6	27.8	0.3	1.3
							Common K (K_C) = 0.4
Middle strata							
35	2.1	4.5	7.9	7.3	43.7	0.1	5.7
42	1.1	49.5	7.9	4.3	42.6	0.2	5.3
49	2.0	4.2	5.1	6.6	51.2	0.2	4.6
56	1.9	2.5	7.1	7.1	14.1	0.2	2.5
63	1.8	1.0	7.1	3.1	47.7	0.3	1.0
							Common K (K_C) = 0.3
Lower strata							
35	1.7	0.6	7.9	5.9	52.4	0.1	0.5
42	2.8	1.4	5.1	5.8	59.3	0.2	2.9
49	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
63	0	0	0	0	0	0	0
							Common K (K_C) = 0.11

K_1 = Dispersion parameter (K); K_2 = K calculated from proportion of zeroes;
K_3 = K obtained from trial and error method; n = Number of plants sampled

Table 2 Variance-mean ratio (s^2/x), dispersion parameter (k), chi-square (χ^2) values and dispersion indices for thrips population (*rabi*-summer) on sunflower

Crop Age (DAS)	S^2/X	K_1	K_2	K_3	χ^2	Cole index	Index of Mean Crowdiness
Upper strata							
35	1.4	6.3	6.4	6.7	10.7	0.2	2.9
42	2.1	2.5	6.4	5.0	77.3	0.2	3.4
49	1.0	7.7	7.1	6.6	13.2	0.2	4.9
56	2.1	4.5	7.1	8.0	38.5	0.2	5.3
63	1.1	7.9	7.7	4.1	20.6	0.2	5.0
							Common K (K_C) = 0.4
Middle strata							
35	1.7	3.8	6.4	7.4	24.1	0.2	3.1
42	2.0	3.4	6.4	5.4	136.4	0.2	3.7
49	1.5	3.5	7.1	6.2	25.8	0.2	2.1
56	2.5	0.6	7.7	6.6	16.5	0.2	1.0
63	1.6	2.3	7.7	4.5	34.2	0.2	1.7
							Common K (K_C) = 0.3
Lower strata							
35	2.0	0.5	6.4	7.2	44.0	0.2	0.6
42	2.2	0.3	7.1	7.1	4.0	0.2	0.5
49	0	0	0	0	0	0	0
56	0	0	0	0	0	0	0
63	0	0	0	0	0	0	0
							Common K (K_C) = 0.4

K_1 = Dispersion parameter (K); K_2 = K calculated from proportion of zeroes;
K_3 = K obtained from trial and error method; n = Number of plants sampled

Table 3 **Mean standard error of mean (±SEM) and relative variation of thrips population on sunflower**

Stratum	Crop age (DAS)	*Rabi*			*Rabi*-summer		
		Mean	±SEM	*Relative variation*	*Mean*	±SEM	Relative variation
Upper	35	3.3	0.5	13.7	2.5	0.3	13.7
	42	2.9	0.4	14.9	2.9	0.5	15.7
	49	2.2	0.3	14.0	4.3	0.4	9.0
	56	3.3	0.4	11.4	4.7	0.6	12.0
	63	1.2	0.3	21.1	4.0	0.4	9.4
	Mean			**15.0**			**12.0**
Middle	35	5.0	0.6	11.8	2.8	0.4	14.5
	42	4.3	0.4	9.1	3.1	0.5	14.4
	49	4.0	0.5	12.8	1.8	0.3	16.7
	56	2.2	0.4	17.1	0.9	0.3	30.2
	63	0.8	0.2	24.7	1.4	0.3	19.6
	Mean			**15.1**			**19.1**
Bottom	35	0.4	0.2	35.9	0.5	0.2	35.8
	42	2.5	0.5	19.3	0.4	0.2	42.4
	49	-	-	-	-	-	-
	56	-	-	-	-	-	-
	63	-	-	-	-	-	-
	Mean			**27.6**			**39.1**

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J. Oilseeds Res., **25**(2) : 165-168 (2008)

Incidence of bud fly, *Dasyneura lini* and gram pod borer, *Helicoverpa armigera* on linseed, *Linum usitatissimum* in relation to crop geometry and fertilizer application

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(Received: August, 2008; Revised: December, 2008; Accepted: December, 2008)

Abstract

Field studies on the effect of two row spacings (25 and 30 cm), three plant distances (no thinning, 4 cm and 8 cm apart) and four doses of fertilizer ($N_{90}P_{45}K_{30}$, $N_{60}P_{30}K_{20}$, $N_{30}P_{15}K_{10}$ and $N_0P_0K_0$ kg/ha) were carried out against the incidence of bud fly (*Dasyneura lini*) and gram pod borer (*Helicoverpa armigera*), crop growth and production of linseed during 2005-06 and 2006-07 following factorial Randomized Block Design with three replications at the research farm of the university. Row spacing (25 and 30 cm) in linseed had only numerical impact on plant vigour, insect-pests and seed yield, while plant distance at 8 cm reduced plant height significantly and enhanced the number of branches and capsules/plant over no thinning. Bud fly infestation exhibited non-significant impact of plant distance ranging between 38.7-43.2 and 37.6-40.6% bud infestation in respective years, while capsule infestation by gram pod borer was significantly higher in closer spacing. Higher seed yield being 1641 and 1684 kg/ha was harvested from linseed raised with 4 cm plant distance over no thinning and 8 cm distant plants in respective years. Plant height, branches and capsules/plant, infestation of bud fly as well as gram pod borer and seed yield were significantly higher in nutrients applied crop in comparison to no fertilizers application during both the years. Highest additional net monetary return of Rs 14064/ha along with good incremental benefit cost ratio (IBCR) of 10.07 was fetched from linseed grown at 30 cm row spacing with out thinning crop applied $N_{60}P_{30}K_{20}$ kg/ha fertilizer.

Key words: *Spatial distribution, thrips, sunflower*

Introduction

Linseed (*Linum usitatissimum* Linn.) faces heavy yield losses due to bud fly (*Dasyneura lini* Barnes) ranging 17-49% in different linseed growing prominent states with an average of 40% at national level (Malik, 2006), while gram pod borer (*Helicoverpa armigera* Hubner) is also emerging as a major pest in some area of its cultivation (Patnaik and Lenka, 2000 and Kumar *et al.*, 2008). However, the chemical method for the management of these insect-pests in linseed is available, but the other possible components of IPM like cultural practices need to be evaluated for cost effective pest management strategies for the resource starved farmers. Hence, present studies on the incidence of bud fly and gram pod borer in relation to crop geometry and fertilizer application in linseed were undertaken for evolving the economic as well as feasible technique of pest management.

Material and methods

Twenty four treatment combinations of two row spacing (25 cm -S_1 and 30 cm -S_2); three plant distance (no thinning -P_0, 4 cm -P_2 and 8 cm apart -P_3) and four fertilizer doses ($N_{90}P_{45}K_{30}$-F_1, $N_{60}P_{30}K_{20}$-F_2, $N_{30}P_{15}K_{10}$-F_3 and $N_0P_0K_0$ kg/ha-F_4) *were replicated thrice in Randomized* Block Design. Linseed cv Neelum was sown during first week of November in each year. Full quantity of the fertilizers except half of the nitrogen dose as per treatments was applied in furrows before seeding and remaining half quantity was given after first irrigation. Plant spacing was maintained by thinning after 20 days of sowing and *no insect-pests management was adopted.* Observations on yield attributes (plant height, number of branches and capsules/ plant) and infestation of bud fly as well as gram pod borer were recorded at dough stage of the crop on five randomly selected plants in each plot. Seed yield was recorded after harvesting of the crop. The data obtained on various parameters were computed for *their critical differences. Economic analysis for various* treatments was also carried out considering the crop grown at 30 cm row spacing without thinning and fertilizers ($S_2P_0F_4$) as control treatment being the farmers practice.

Results and discussion

Crop vigour: Linseed sown at 25 (S_1) and 30 cm (S_2) row spacing showed no impact on plant height being 56 and 49-50 cm in first and second year (Table 1). Significantly taller plants of 58 and 52 cm were observed in the crop grown without thinning (P_0) in comparison to spaced planting during both the years. Higher dose of fertilizer ($N_{90}P_{45}K_{30}$ *kg/ha) produced significantly taller plants of* 58 and 53 cm height against the shortest plants of 50 and 46 cm height in linseed raised without fertilizer application (F_4)

during respective years. This indicated that row spacing had no effect on plant height in linseed, while dense crop and fertilizer application produced taller plants. Impact of row spacing on branching was non-significant, while effect of plant distance improved branching in linseed being 7 branches/plant in 8 cm plant distance (P_2) and 6 branches/plant in crop without thinning during respective years. Significantly higher number of 8 and 7 branches/ plant were observed in highly fertilized crop with $N_{90}P_{45}K_{30}$ kg/ha (F_1) in respective years, against the minimum number of 5 branches/plant recorded in nutrient stressed crop (F_4). Insignificant effect of row spacing on capsule bearing was noticed during both the years. Capsules/plant were found to increase with the enhancement in plant spacing, as 103, 120 and 136 capsules/plant in first year and 95, 98 and 115 capsules/plant in second year were counted in no thinning (P_0), 4 cm (P_1) and 8 cm (P_2) apart plants, respectively. Spaced planting showed significantly higher capsules over with out thinning in linseed. Higher dose of fertilizer ($N_{90}P_{45}K_{30}$ kg/ha) proved to be the best bearing significantly higher numbers of 139 and 120 capsules/plant in comparison to the least numbers being 100 and 90 capsules/plant recorded in without nutrients applied crop in respective years. Row spacing (25 and 30 cm) in linseed showed only numerical variations in plant height and number of branches as well as capsules/plant, while wider plant distance (8 cm) increased the branches and capsules/plant with reduction in plant height. Only numerical difference in plant height of linseed grown with different row spacing reported by Chauhan *et al.* (1993) and more branch as well as capsule/plant in wider row spacing than narrow ones observed by Singh and Verma (1993), support fully these results. The observations of better crop growth in spaced planting by Singh and Husain (2003), confirms these findings.

Insect-pests infestation: Numerically higher bud fly infestation being 41.3 and 39.9% was recorded in closer row spacing of 25 cm (S_1) against 40.5 and 38.1% bud infestation noticed in 30 cm (S_2) row distance during 2005-06 and 2006-07, respectively. Similarly, closer row spacing (25 cm) showed insignificant higher capsule damage being 16.2 and 12.8% in comparison to 14.5 and 10.5% capsule damage by gram pod borer recorded in wider row spacing (30 cm) during respective years. The impact of plant distance on bud fly was insignificant, while it was significant on gram pod borer infestation in both the years. Maximum bud fly infestation being 43.2 and 40.6% was observed on linseed grown without thinning (P_0) during respective years, which was on par with 38.7 and 37.6% bud infestation noticed in 8 cm plant spaced (P_2) crop during these years. Significantly lower capsule damage by H. armigera being 8.3 and 5.7% was recorded in linseed with 8 cm plant distance in respective years against 12.4 and 9.1% capsule infestation noticed in without thinning crop. Application of higher dose of fertilizer ($N_{90}P_{45}K_{30}$ kg/ha) in linseed increased bud fly infestation significantly being 49.8 and 48.1% against the lowest bud infestation of 33.8 and 32.1% noticed on the crop grown without fertilizers in respective years. Similarly, capsule damage by gram pod borer was found to increase with the enhancement in fertilizers exhibiting 4.1-11.2 and 2.7 9.3% infestation in each year proving statistical superiority in higher dose of fertilizer over no application. These observations indicated that crop geometry of linseed had no effect on bud fly infestation, while closer spacing received higher capsule infestation by gram pod borer. Bud fly infestation in relation to row spacing in linseed is still an untouched aspect, but the results on the impact of plant distance on this pest are in accordance with Malik *et al.* (2008). Higher infestation of capsules in linseed by gram pod borer in closer spacing may be argued with those of Ahmad and Rai (2005). Positive response of fertilizer application on insect- pests in linseed received full support of Malik *et al.* (1996) and Kumar *et al.* (2008).

Seed yield: Row spacing had no impact on linseed production, while plant distance at 4 cm produced higher yield than other distances. Positive relationship between fertilizer application and seed yield was noticed in linseed (Table 1). Application of $N_{60}P_{30}K_{20}$ kg/ha (F_2) fertilizer was found to be optimum dose in linseed providing at par yields with higher dose. However, mean maximum seed yield of 1880 kg/ha was obtained from the linseed sown at 30 cm row spacing with 4 cm plant distance applied $N_{60}P_{30}K_{20}$ kg/ha fertilizer dose ($S_2P_1F_2$), which was closely followed by 1874, 1869 and 1863 kg/ha production from $S_1P_1F_1$, $S_1P_2F_1$ and $S_2P_0F_2$ inputs against the lowest of 1090 kg/ha yield harvested from farmers practice ($S_2P_0F_4$), respectively (Table 2). Views of Singh and Husain (2003) and Malik *et al.* (2008), who reported higher seed yield of linseed at 4 cm plant distance without any effect of row spacing. However, higher incidence of insect-pests was noticed in higher dose of fertilizer applied crop in comparison to low/no application of nutrients, which was nullified by the better crop growth resulting in enhanced seed production. Earlier observations of Malik *et al.* (1996), Choubey *et al.* (2002) and Kumar *et al.* (2008) on the positive response of fertilizer application in linseed justify fully these results.

Economic: Analysis of input investment in linseed provided highest additional gross monetary return (AGMR) of Rs.15800/ha from $S_2P_1F_2$ inputs applied linseed closely followed by Rs.15680, 15580, 15460, 15100 and 15000/ha from $S_1P_1F_1$, $S_1F_2F_1$, $S_2P_0F_2$, $S_1F_1F_2$ and $S_2F_1F_1$ combination of inputs over farmers practice ($S_2P_0F_4$), respectively (Table 2). However, maximum additional net monetary return (ANMR) of Rs.14064/ha was realized from linseed crop grown at 30 cm row spacing without thinning applied $N_{60}P_{30}K_{20}$ kg/ha fertilizer dose ($S_2P_0F_2$) followed by Rs.13667 and 13136/ha from $S_2P_1F_2$ and $S_1P_0F_2$ treatments, respectively.

Table 1 Effect of crop geometry and fertilizer application on crop growth, infestation of insect-pests and seed yield of linseed

Factors	Plant height (cm)		Branch/ plant		Capsule/ plant		Bud fly infestation (%)		Gram pod borer infestation (%)		Seed yield (kg/ha)	
	2005-06	2006-07	2005-06	2006-07	2005-06	2006-07	2005-06	2006-07	2005-06	2006-07	2005-06	2006-07
I. Row Spacing (cm)												
25 cm (S_1)	56	50	7	6	115	95	41.3 (40.0)	39.9 (39.2)	16.2	12.8	1594	1641
30 cm (S_2)	56	49	7	6	124	111	40.5 (39.5)	38.1 (38.1)	14.5	10.5	1563	1609
SEm ±	1.1	0.9	0.23	0.1	6.4	5.5	0.3	0.5	0.7	0.9	13.9	14.1
CD (P = 0.05)	*NS*	*NS*	*NS*	*NS*	*NS*	*NS*	*NS*	*NS*	*NS*	*NS*	*NS*	*NS*
ii. Plant distance (cm)												
No thinning (P_0)	58	52	6	6	103	95	43.2 (41.1)	40.6 (39.6)	12.4	9.1	1582	1631
4 cm (P_1)	53	49	7	6	120	98	40.5 (39.5)	38.4 (38.3)	10.0	8.5	1641	1684
8 cm (P_2)	51	47	7	7	136	115	38.7 (38.5)	37.6 (37.8)	8.3	5.7	1512	1559
SEm ±	1.92	1.21	0.23	0.17	7.9	6.7	0.81	0.66	1.3	1.1	15.2	17.6
CD (P = 0.05)	5.4	3.4	0.65	0.48	22.4	19.0	NS	NS	3.7	3.1	43.2	50.0
iii. Fertilizer dose (kg/ha)												
$N_{90}P_{45}K_{30}$ (F_1)	58	53	8	7	139	120	49.8 (44.9)	48.1 (43.9)	11.2	9.3	1796	1845
$N_{60}P_{30}K_{20}$ (F_2)	56	50	7	7	128	108	44.2 (41.7)	41.1 (39.9)	9.1	6.1	1777	1830
$N_{30}P_{15}K_{10}$ (F_3)	53	49	6	6	111	95	37.5 (37.8)	35.7 (36.7)	6.3	5.2	1604	1642
$N_0P_0K_0$ (F_4)	50	46	5	5	100	90	33.8 (35.5)	32.1 (34.5)	4.1	2.7	1136	1182
SEm ±	*1.5*	*1.3*	*0.34*	*0.20*	*6.7*	*7.5*	*1.1*	*0.8*	*1.3*	*1.1*	*18.7*	*20.6*
CD (P = 0.05)	4.3	3.8	0.96	0.56	19.2	21.4	3.2	2.2	3.7	3.1	53.1	58.5

Figures in parentheses are angular transformed values

Table 2 Economic analysis of input investment for the management of insect-pests in linseed

Treatment combination	Seed yield (kg/ha)	*Yield increased* over control (kg/ha)	Cost of treatment (Rs/ha)	Additional cost of treatment (Rs/ha)	*Additional gross* monetary return (Rs/ha)	*Additional net* monetary return (Rs/ha)	Incremental benefit: cost
$S_1P_0F_1$	*1808*	*718*	*2889*	*2222*	*14360*	12138	*5.46*
$S_1P_0F_2$	1823	733	2191	1524	14660	13136	8.62
$S_1P_0F_3$	1621	531	1494	827	10620	9793	11.84
$S_1P_0F_4$	1204	114	795	128	2280	2152	16.81
$S_1P_1F_1$	1874	784	3996	3329	15680	12351	3.71
$S_1P_1F_2$	1845	755	3298	2631	15100	12469	4.74
$S_1P_1F_3$	1761	671	2600	1933	13420	11487	5.94
$S_1P_1F_4$	1173	83	1902	1235	1660	425	0.34
$S_1P_2F_1$	1869	779	3812	3145	15580	12435	3.95
$S_1P_2F_2$	1726	636	3113	2446	12720	10274	4.20
$S_1P_2F_3$	1583	493	2416	1749	9860	8111	4.64
$S_1P_2F_4$	1151	61	1717	1050	1220	170	0.16
$S_2P_0F_1$	1784	694	2761	2094	13880	11786	5.63
$S_2P_0F_2$	1863	773	2063	1396	15460	14064	10.07
$S_2P_0F_3$	1670	580	1365	698	11600	10902	15.62
$S_2P_0F_4$	1090	-	667	-	-	-	-
$S_2P_1F_1$	1840	750	3499	2832	15000	12168	4.30
$S_2P_1F_2$	1880	790	2800	2133	15800	13667	6.41
$S_2P_1F_3$	1758	668	2103	1436	13360	11924	8.30
$S_2P_1F_4$	1201	111	1404	737	2220	1483	2.01
$S_2P_2F_1$	1728	638	3376	2709	12760	10051	3.71
$S_2P_2F_2$	1717	627	2677	2010	12540	10530	5.24
$S_2P_2F_3$	1345	255	1980	1313	5100	3787	2.88
$S_2P_2F_4$	*1166*	*76*	*1281*	*614*	*1520*	*906*	*1.48*

Linseed price @ Rs.20/kg

Highest gain of Rs.16.81/Re investment was realized from the crop sown at 25 cm row spacing grown without thinning and fertilizer ($S_1P_0F_4$), but the input combination of $S_2P_0F_2$ providing maximum ANMR of Rs.14064/ha showed a good incremental benefit cost ratio of Rs.10.07/Re investment also. Thus, it can be inferred that row spacing and thinning had no significant impact on production of linseed, while application of fertilizer @ $N_{60}P_{30}K_{20}$ kg/ha proved superior over maximum dose ($N_{90}P_{45}K_{30}$ kg/ha). These results are in conformity with those of Badiyala and Kumar (2003) and Kumar *et al.* (2008), who reported better economic returns from optimum dose of fertilizer application in linseed.

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J. Oilseeds Res., **25**(2) : **169-172 (2008)**

Short communication

Genetics of yield and its components in Indian mustard, *Brassica juncea* (L.) Czern & Coss. under normal and late sown conditions

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(Received: March, 2008; Revised: September, 2008; Accepted: October, 2008)

Abstract

The results on gene action and mean analysis revealed that all the three types of gene actions i.e., additive, dominance and epistasis were responsible in varying proportions for all the crosses for four characters in Indian mustard. Among the epistatic interactions, dominance x dominance interaction was more important than additive x additive in both the situations and such a genetic situation it is suggested that reciprocal recurrent selection might be most efficient for utilization of all three types of gene effects for improving the characters under study.

Keywords: Indian mustard, genetics of yield

Yield is one of the most important economic characters and is the product of multiplicative interaction of contributing characters. Indian mustard is generally grown under timely sown condition, however, a sizeable area is under late sown condition after harvest of late maturity paddy varieties. For such situations, identification of promising crosses and subsequent handling of segregating material, through appropriate breeding procedures is urgently required. The developments in statistical genetics have made possible to study the various facts of the operation of quantitative genes and to use this information in formulating appropriate breeding strategy to effect genetic improvement of traits under normal and late sown conditions. The estimation of gene effects involved in the inheritance of yield contributing or quantitative characters are helpful in planning breeding programs. Hence, in the present investigation, an effort has been made to study the inheritance of yield and its components for further utilization in the breeding programme.

The experimental materials for the present investigation comprised of a set of six generations, *viz*.,, P_1, P_2, F_1, F_2, BC_1 and BC_2 of each of these crosses planted in compact Family Block Design with three replications under normal and late sown conditions during *rabi* 2006-07. NPK ratio of irrigated condition was 120:40:40 and rainfed condition was 60:20:20. Each non- segregating generations (P_1, P_2 and F_1) was sown in one row. Among the segregating generations back crosses were sown in four rows and F_2s were sown in six rows. Rows were 3 m long with spacing of 30 cm between rows and 15 cm between plants. Five randomly selected plants each of P_1, P_2 and F_1, 20 plants of F_2 and 15 plants each of BC_1 and BC_2 generations per replication, were utilized for recording observations on seeds/siliqua (SPS), 1000-seed weight (TW), seed yield/plant (SYP) and oil content (OC). The data were subjected to scaling tests (Mather, 1949) to detect the presence of epistasis. In case of significance of scaling tests, data were then subjected to the estimation of various genetic components (Hayman, 1958). More precise estimates of there parameters were then obtained by using weighted joint scaling tests. In the event of the scaling test being non-significant (i.e., absence of non-allelic interactions), the three parameter model, which is based on least square estimates (joint scaling test) was used to estimate main effects (m), (d) and (h). The significance of the parameters was tested against their corresponding standard errors.

The scaling tests showed inadequacy of additive-dominance model indicating the presence of non-allelic interactions for SPS, SYP and OC in all the eight crosses under NS and LS conditions and for TW in most of the crosses under both situations except in C_1 under NS and LS conditions and C_5 under LS condition showing absence of inter allelic interactions in genetic control of these characters. Additive effect was most important for SPS, being significantly higher in magnitude and in +ve direction in both NS and LS (Table 1). Among the interactions additive x additive (I) and dominance x dominance (1) were relatively more important because of their higher magnitude and +ve direction. Opposite sign of (h) and (1) effects indicated the presence of duplicate epistasis for SPS, which would hinder the progress in selection whereas complementary epistasis in cross 3 under LS would act as aid in improving response of selection.

Additive as well as dominant effects were important for the inheritance of TSW, SYP and OC dominant effects being more in magnitude. The interactions additive x additive (I) and dominance x dominance (1) were relatively more important components and in +ve direction. This suggested that selection of SYP and OC would be more fruitful if selection is delayed till dominance component is reduced due to selfing. Opposite sign of (h) and (1) component indicated duplicate epistasis for all three characters. Inadequacy of additive-dominance model for only SYP in C_2 under LS condition, C_3 under NS, C_7 under LS and C_8 under LS, indicated presence of gene interaction in the expression of SYP.

The estimate of gene effects showed that in all the crosses, additive gene effect (d) had significant contribution in the inheritance of SYP and OC, whereas the other fixable component additive x additive (I) is important for SPS, TW, SYP and OC in most of the crosses. The results are in agreement with the earlier studies in mustard (Kant and Gulati, 2001). It should be possible to select for the increased manifestation of higher seed yield/plant, higher 1000-seed weight and higher oil content. Dominance effect (h) being important role in governing the inheritance of SPS, SYP and OC. Dominance x dominance (1) interaction component is important for SPS, SYP and OC. These results are in agreement with the findings in mustard (Pal and Kumar, 1993, Kumar *et al.* (2002); Goswami, 2005 and Yadav *et al.*, 2005).

The present study suggests that the nature and magnitude of gene effects varied with different crosses for different characters under both conditions. So, specific breeding strategy has to be adopted for a particular cross to get improvement. In some crosses, pure lines can be developed through hybridization following the pedigree method of selection. In other crosses, although high magnitude of dominance gene effects and dominance x dominance interactions were present, it is difficult to exploit them due to presence of duplicate epistasis, in such cases diallel selective or biparental mating may be an effective approach.

Table 1 Estimates of gene effect and epistasis based on six parameter model for four characters in Indian mustard

Crosses	Conditions	m	d	h	I	j	l	Types of epistasis
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Seeds/siliqua								
NDR-190 X NDRE-4	NS	13.98 ± 0.34	- 0.40 ± 0.52	- 3.07 ± 1.73	- 2.93 ± 1.71	6.67** ± 0.56	0.93 ± 2.55	-
	LS	11.90 ± 0.15	1.43 ± 3.89	1.93 ± 1.02	0.73 ± 0.99	1.70** ± 0.42	6.67** ± 1.74	-
NDR-190 X NDYR-8	NS	12.40 ± 0.23	0.70 ± 0.43	1.80 ± 1.32	0.87 ± 1.26	1.10* ± 0.47	1.19 ± 2.11	-
	LS	12.20 ± 0.10	- 0.87** ± 0.27	6.40** ± 0.71	6.80** ± 0.67	- 1.13 ± 2.85	- 12.00** ± 1.23	D
NDR-8208 X NDRE-4	NS	13.30 ± 0.12	-0.70 ± 0.26	- 2.13** ± 0.72	-2.33** ± 0.69	-0.70* ± 0.29	3.07** ± 1.19	D
	LS	14.63 ± 0.19	- 0.80** ± 0.11	- 6.17** ± 0.79	-4.27** ± 0.77	-0.03 ± 0.17	-1.93* ± 0.91	C
NDR-8208 X PHR-1	NS	13.00 ± 0.15	1.57** ± 0.32	5.67** ± 0.94	8.33** ± 0.89	2.27** ± 0.35	- 18.07** ± 1.56	D
	LS	11.87 ± 0.18	- 1.50 ± 1.59	7.13** ± 0.79	7.27** ± 0.77	-2.09** ± 0.20	- 15.33** ± 1.01	D
Urvashi x PHR-1	NS	12.07 ± 0.09	- 0.40** ± 0.12	2.83** ± 0.48	4.80** ± 0.43	0.49* ± 0.21	- 8.33** ± 0.74	D
	LS	11.47 ± 0.09	1.50** ± 0.24	2.33** ± 0.63	2.73** ± 0.59	0.63* ± 0.26	- 4.67** ± 1.09	D
Urvashi x Vardan	NS	13.60 ± 0.15	0.33 ± 0.24	-5.70 ± 0.86	- 5.60** ± 0.77	0.49 ± 0.26	6.87** ± 1.37	D
	LS	15.90 ± 0.35	0.03 ± 0.42	-13.07** ± 1.63	- 14.47** ± 1.62	0.43 ± 0.44	20.67** ± 2.20	D
Vardan x NDRE-4	NS	14.23 ± 0.12	- 0.33** ± 0.11	-5.87** ± 0.55	-7.07** ± 0.52	-0.20 ± 0.18	9.73** ± 0.71	D
	LS	14.20 ± 0.03	- 2.53** ± 0.23	-3.67** ± 0.52	- 4.00** ± 0.47	- 2.73** ± 0.29	4.80** ± 1.02	D
NDYR-8 x PHR-1	NS	13.40 ± 0.42	0.10 ± 0.12	- 4.57** ± 1.70	- 4.60** ± 1.68	0.47* ± 0.19	1.00** ± 1.82	D
	LS	13.10 ± 0.21	1.10** ± 0.23	3.00** ± 0.99	-0.07 ± 0.95	0.77** ± 0.25	1.33 ± 1.34	-

Table 1 (Contd...)

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
1000-seed weight								
NDR-190 X NDRE-4	NS	4.85 ± 0.08	-0.50* ± 0.20	- 0.89 ± 0.53	- 0.83 ± 0.51	-0.51* ± 0.23	0.95 ± 0.91	-
	LS	4.38 ± 0.07	0.60** ± 0.19	- 0.31 ± 0.55	- 0.18 ± 0.48	-4.33** ± 0.24	-0.55 ± 0.98	-
NDR-190 X NDYR-8	NS	4.94 ± 0.08	0.14 ± 0.15	2.49** ± 0.48	1.12* ± 0.45	0.37* ± 0.18	33.30** ± 0.74	C
	LS	4.97 ± 0.11	0.76** ± 0.11	- 1.94** ± 0.58	- 1.83** ± 0.48	0.58** ± 0.19	2.49** ± 0.89	D
NDR-8208 X NDRE-4	NS	4.84 ± 0.15	0.74** ± 0.13	- 3.88** ± 0.69	- 2.85** 0.65	0.63** ± 0.17	3.46** ± 0.90	D
	LS	4.75 ± 0.26	0.82** ± 0.23	- 2.33** ± 1.18	-2.98** ± 1.13	0.94** ± 0.26	2.29 ± 1.55	-
NDR-8208 X PHR-1	NS	4.12 ± 0.09	-0.50** ± 0.14	1.58** ± 0.49	2.96** ± 0.47	-0.85** ± 0.17	-6.99** ± 0.73	D
	LS	4.91 ± 0.08	-1.01** ± 0.29	1.67* ± 0.75	0.72 ± 0.67	-0.61 ± 0.35	-3.56** ± 1.38	D
Urvashi x PHR-1	NS	3.57 ± 0.22	0.92** ± 0.19	1.43 ± 0.97	2.87** ± 0.96	0.61** ± 0.21	-4.05** ± 1.19	-
	LS	4.38 ± 0.14	0.55** ± 0.20	- 1.32 ± 0.75	-0.59 ± 0.68	0.36 ± 0.29	0.25 ± 1.17	-
Urvashi x Vardan	NS	5.16 ± 0.05	0.26 ± 0.18	- 1.56** ± 0.44	-2.16** ± 0.42	0.22 ± 0.20	4.32** ± 0.79	D
	LS	5.18 ± 0.07	0.51** ± 0.18	- 0.71 ± 0.53	-1.41** ± 0.46	-0.61** ± 0.23	2.36* ± 0.94	-
Vardan x NDRE-4	NS	5.02 ± 0.05	-0.50** ± 0.18	- 0.82 ± 0.45	-1.41** ± 0.42	-0.57** ± 0.21	2.91** ± 0.82	-
	LS	4.96 ± 0.12	0.28 ± 0.15	- 4.61** ± 0.60	3.89** ± 0.56	-0.29 ± 0.18	3.18** ± 0.88	D
NDYR-8 x PHR-1	NS	4.94 ± 0.08	0.37* ± 0.18	- 3.88** ± 0.49	-2.34** ± 0.48	0.11 ± 0.21	0.59 ± 0.83	-
	LS	5.15 ± 0.06	1.48** ± 0.17	0.13 ± 0.47	-0.23 ± 0.41	1.42** ± 0.21	-1.23 ± 8.61	-
Seed yield/plant								
NDR-190 X NDRE-4	NS	11.07 ± 0.15	-1.81** ± 0.30	-8.90** ± 0.88	-8.06** ± 0.85	-0.82* ± 0.35	8.54** ± 1.42	D
	LS	9.66 ± 0.21	2.43** ± 0.39	-1.93 ± 1.25	-0.57 ± 1.16	0.71 ± 0.49	-2.48 ± 2.02	-
NDR-190 X NDYR-8	NS	12.24 ± 0.12	1.36** ± 0.36	-4.96** ± 0.92	-7.89** ± 0.87	2.68** ± 0.40	12.73** ± 1.65	D
	LS	7.15 ± 0.07	-2.19** ± 0.18	8.26** ± 0.69	8.69** ± 0.44	-3.77** ± 0.19	-8.50** ± 1.29	D
NDR-8208 X NDRE-4	NS	13.92 ± 0.45	-1.57** ± 0.37	-3.26 ± 1.95	-3.25 ± 1.95	-0.82* ± 0.39	-9.85** ± 2.34	-
	LS	9.43 ± 0.11	-1.29** ± 0.34	8.17** ± 0.84	-0.29 ± 0.81	-1.71 ± 0.35	-5.20** ± 1.49	D
NDR-8208 X PHR-1	NS	8.17 ± 0.19	1.99 ± 0.52	12.34** ± 1.34	12.08** ± 1.28	0.97 ± 0.55	-22.51** ± 2..36	D
	LS	10.47 ± 0.15	-2.09** ± 0.19	-4.75** ± 0.79	-6.13** ± 0.72	-2.60** ± 0.28	5.03** ± 1.17	D
Urvashi x PHR-1	NS	10.54 ± 0.18	1.66** ± 0.51	4.85** ± 1.33	4.52** ± 1.25	-0.37 ± 0.55	-12.24** ± 2.35	D
	LS	6.87 ± 0.26	1.43** ± 0.26	3.80** ± 1.18	9.69** ± 1.15	-0.13 ± 0.29	-12.32** ± 1.55	D
Urvashi x Vardan	NS	9.56 ± 0.32	0.26 ± 0.67	10.67** ± 1.85	8.90** ± 1.84	-0.14 ± 0.68	-8.80** ± 2.98	D
	LS	9.41 ± 0.18	-0.31 ± 0.21	-4.64** ± 0.90	-5.74** ± 0.85	-1.40** ± 0.23	15.10** ± 1.27	D
Vardan x NDRE-4	NS	8.22 ± 0.09	-1.43** ± 0.38	15.61** ± 0.88	16.73** ± 0.85	-1.23 ± 0.39	-25.65** ± 1.63	D
	LS	10.50 ± 0.17	4.23** ± 0.39	-5.49** ± 1.09	-5.31 ± 1.03	3.60** ± 0.43	1.29 ± 1.85	-

Table 1 (Contd...)

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
NDYR-8 x PHR-1	NS	9.72 ± 0.25	-0.69* ± 0.32	-5.75** ± 1.23	-4.71** ± 1.20	-2.61** ± 0.36	6.68** ± 1.72	D
	LS	10.29 ± 0.21	-4.79** ± 0.59	4.30** ± 1.47	2.90* ± 1.45	-5.11** ± 0.59	-12.19** ± 2.55	D
Oil content								
NDR-190 X NDRE-4	NS	40.13 ± 0.18	0.70* ± 0.31	-5.55 ± 0.98	-4.02** ± 0.94	1.33** ± 0.33	2.74 ± 1.52	-
	LS	41.32 ± 0.12	1.47** ± 0.21	-9.17** ± 0.79	-8.41** ± 0.65	0.40 ± 0.29	8.75** ± 1.34	D
NDR-190 X NDYR-8	NS	40.99 ± 0.13	1.27** ± 0.15	-2.66** ± 0.66	-0.99 ± 0.59	3.99** ± 0.22	0.19 ± 0.95	-
	LS	40.23 ± 0.30	-1.97** ± 0.33	4.67** ± 1.39	5.35** ± 1.38	-0.50 ± 0.39	-3.41 ± 1.86	-
NDR-8208 X NDRE-4	NS	39.84 ± 0.12	1.13** ± 0.21	5.78** ± 0.75	4.76** ± 0.65	1.33 ± 0.24	-6.67** ± 1.22	D
	LS	40.54 ± 0.14	1.59** ± 0.09	-5.06** ± 0.67	-3.90** ± 0.59	0.42** ± 0.20	2.32* ± 0.20	D
NDR-8208 X PHR-1	NS	38.73 ± 0.26	1.56** ± 0.25	10.85** ± 1.18	8.59** ± 1.15	1.26** ± 0.29	-11.80** ± 1.54	D
	LS	41.81 ± 0.17	1.25** ± 0.11	-5.93** ± 0.77	-6.99** ± 0.69	0.53 ± 0.29	8.48** ± 1.01	D
Urvashi x PHR-1	NS	38.43 ± 0.13	-1.07 ± 0.27	3.48** ± 0.78	5.17** ± 0.74	-1.36** ± 0.32	-11.94** ± 1.28	D
	LS	40.70 ± 0.21	0.69** ± 0.18	-8.06** ± 1.02	-7.15** ± 0.91	0.17 ± 0.26	8.90** ± 1.43	D
Urvashi x Vardan	NS	38.36 ± 0.11	-0.50** ± 0.16	3.92** ± 0.61	6.23** ± 0.57	0.99** ± 0.22	-9.88** ± 0.89	D
	LS	40.67 ± 0.29	-0.90** ± 0.14	-0.69 ± 1.19	0.23 ± 1.19	-1.38** ± 0.25	-3.29* ± 1.45	-
Vardan x NDRE-4	NS	41.11 ± 0.10	0.75** ± 0.15	-5.73** ± 0.53	-4.88** ± 0.49	5.99** ± 0.79	7.45** ± 0.21	D
	LS	41.27 ± 0.11	0.91** ± 0.24	-2.04* ± 0.87	-4.64** ± 0.65	0.20 ± 0.38	7.82** ± 1.57	D
NDYR-8 x PHR-1	NS	40.92 ± 0.19	2.79** ± 0.23	-0.95 ± 0.92	0.68 ± 0.91	0.29 ± 0.26	-2.86* ± 1.26	-
	LS	41.49 ± 0.08	1.28 ± 0.17	-6.80** 0.66	-4.87 ± 4.99	-1.03** ± 0.24	4.86** ± 1.20	-

*, ** Significant at 5% and 1% level, respectively; C = complementary epistasis and D = Duplicate epistasis; NS = Normal sown and LS = Late sown

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J. Oilseeds Res., **25**(2) : 173-174 (2008)

Short communication

Combining ability study for seed yield and its components in taramira (*Eruca sativa* Mill.)

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(Received: March, 2007; Revised: September, 2008; Accepted: September, 2008)

Among different winter oilseed crops, taramira (*Eruca sativa* Mill.) occupies an important position for cultivation in arid and semi arid parts of the country. The information on combining ability effects and their estimating variances provides the way to choose an appropriate breeding strategy for improvement of the crop. In the present study, an attempt has been made to identify better genotypes on the basis of combining ability study through diallel analysis involving 7 parents.

A field experiment was carried out at RRS, Bawal, Haryana, The experiment is based on a diallel set of 7 genetically diverse lines *viz.*, 'RTM-314', 'TC-31', 'BTM-1', 'DITA-1', 'TC-15', 'TC-22' and 'BTM-2' developed by 3 subsequent selfing (bud pollination). The 21 crosses along with 7 parents were grown in Randomized Block Design with three replications under rainfed conditions. Each genotype was sown in two rows of 5 m length. The rows and plants within rows were spaced at 45 cm and 15 cm apart, respectively. Observations were recorded on five randomly selected plants in each entry, for days to 50% flowering, plant height, siliquae on primary branches, siliquae on secondary branches, siliquae on main shoot, total siliqua/plant and seed yield. Combining ability analysis was carried out according to Method 2, Model 1 of Griffing (1956).

Significant *gca* and *sca* variances for all the characters except days to 50 % flowering, plant height and siliquae on main shoot for *sca*, suggesting the importance of additive and non-additive gene actions for the expression of these traits. In this study higher magnitude of *gca* variances than the *sca* variances were recorded for all the characters which indicated a predominant role of additive and additive x additive components of genetic variance which are fixable. Non-additive gene effects (dominance and epistatic components of variation) are also important in the present material. Kumar and Yadav (1986) also reported importance of additive and non-additive components in taramira.The estimates of *gca* effects (Table 1) showed that the parent 'TC-15' is a good general combiner for seed yield, days to 50% flowering, plant height, siliquae on primary branches, siliquae on secondary branches. 'TC-22' was good general combiner for seed yield, siliquae on primary branches, siliquae on secondary branches and total siliquae/plant and 'BTM-1' was good general combiner for days to 50% flowering, siliquae on primary branches, siliquae on secondary branches and total siliquae/plant.

The specific combining ability (*sca*) effects of crosses (Table 2) for different characters have been grouped in three categories; i.e., those involving parents with high x high, high x poor, and poor x poor *gca*. The cross 'TC-31' x 'TC-15' showed high *sca* effects for seed yield and belongs to the category of high x high *gca* parents and cross 'BTM-1' x 'TC-15' for siliquae on primary branches. Obviously, high *sca* effects in such a case can be attributed to additive type of interaction between the parents and thus can be utilized in a variety of ways to improve the crop. The importance of additive x additive effects and possibility of their fixation, single plant selection may be practiced in segregating generations for isolating superior inbreds. On the other hand, 'BTM-1' x 'TC-22' with high *gca* effects did not give equally high *sca* effects for siliquae on primary branches. This is probably due to mutual cancellation of gene effects for this character. High *sca* effects for days to 50 % flowering in the cross 'TC-31' x 'TC-15' involving one parent with desirable high *gca* for early maturity and the other with low *gca* was probably due to dominant x recessive interaction. Overall, cross 'BTM-1 x TC-15' was the best specific cross combination for seed yield, days to 50% flowering, siliquae on primary branches, siliquae on secondary branches and total siliquae/plant; cross 'RTM-314' x 'TC-22' for seed yield, siliquae on primary branches, siliquae on secondary branches and total siliquae/plant and cross 'RTM-314' x 'BTM-2' for seed yield, plant height and total siliquae/plant. Under the present situation, where both additive and non-additive variances are important, it is suggested that reciprocal recurrent selection may be adopted.

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Table 1 Estimates of general combining ability effects for yield and its components in taramira

Parents	Seed yield/ plant	Days to 50 % flowering	Plant height	Siliquae on primary branches	Siliquae on secondary branches	Siliquae on main shoot	Total siliqua/ plant
'RTM-314'	0.639 (29.1)	0.175 (59)	-9.532*(131)	-22.34*(161)	-29.96*(183)	-1.889*(22)	-29.27*(416)
'TC-31'	2.231*(38.2)	1.159*(57)	7.635*(144)	0.937 (204)	6.262 (292)	1.722 (26)	7.452 (579)
'BTM-1'	-2.984*(33.8)	1.270*(55)	0.690 (136)	13.38*(160)	46.10*(249)	-2.278*(23)	77.40*(480)
'DITA-1'	-3.098*(40.8)	-0.008 (60)	0.635 (136)	-12.99*(242)	-36.41 (295)	0.389 (25)	-82.60*(612)
'TC-15'	0.494* (39.6)	-1.175*(57)	4.913*(140)	13.16*(208)	8.151*(289)	-3.917*(25)	13.68 (592)
'TC-22'	3.946* (34.1)	0.270 (59)	-1.810*(133)	22.55*(209)	17.54*(252)	-2.306*(21)	37.34*(512)
'BTM-2'	-1.228* (34.4)	-1.341*(60)	-2.532 (136)	-14.79*(193)	-11.68*(223)	0.250 (22)	-23.99*(487)
S.E.(gi) ±	0.6715	0.4626	1.8033	4.4188	8.0741	0.9834	17.034
S.E.(gi-gj) ±	1.0257	0.7066	2.7546	6.7499	12.333	1.5022	26.020

Values in parenthesis are the parental means. *P=0.05

Table 2 Estimates of specific combining ability effects for yield and its components in taramira

Cross	Days to 50 % *flowering*	Plant *height*	Siliquae on primary *branches*	Siliquae on *secondary branches*	Siliquae on *main shoot*	Total siliqua/ plant	Seed yield/plant
'RTM-314' x 'TC-31'	3.819*	-11.39*	-28.54*	-78.57*	-2.583	-127.74*	-8.064*
'RTM-314' x 'BTM-1'	-1.792	-4.444	-17.99	55.09*	-1.583	71.819	5.251*
'RTM-314'x 'DITA-1'	-1.514	2.611	-5.208	54.09*	2.750	44.819	0.166*
'RTM-314' x'TC-15'	-1.847	1.333	-5.764	-14.96	3.361	-17.458	-2.327
'RTM-314' x 'TC-22'	2.708*	-6.944	81.35*	120.2*	-2.528	258.88*	12.59*
'RTM-314' x 'BTM-2'	-0.681	21.28*	8.681	20.88	-0.472	192.71*	16.40*
'TC-31' x 'BTM-1'	3.875*	14.89*	-42.26*	-68.13*	-1.194	-130.40*	-10.01*
'TC-31' x 'DITA-1'	-0.847	-3.056	12.01	9.875	1.139	19.597	-11.89*
'TC-31' x 'TC-15'	-3.681*	5.667	20.46	30.32	1.750	44.319	8.314*
'TC-31' x 'TC-22'	-3.125*	-1.611	-17.93	-36.07	-6.139*	-14.347	-2.938
'TC-31' x 'BTM-2'	-0.014	1.611	10.90	36.15	-0.583	24.486	11.04*
'BTM-1'x 'DITA-1'	-0.458	-3.611	-14.43	-42.46	1.139	-86.847	-3.212
'BTM-1'x 'TC-15'	-3.292*	-9.389	71.51*	93.99*	3.250	293.38*	9.629*
'BTM-1'x 'TC-22'	-0.736	1.833	12.13	81.55*	-5.639*	99.208*	10.04*
'BTM-1'x 'BTM-2'	1.875	15.06*	-54.54*	-43.18	0.417	-160.49*	-1.316
'DITA-1' x 'TC-15'	-1.014	4.667	-39.21	-15.51	-3.917	53.125	-4.256
'DITA-1'x 'TC-22'	0.542	-3.611	16.90	25.60	-2.306	58.208	3.992*
'DITA-1' x 'BTM-2'	-0.347	-1.889	14.24	-18.68	0.250	-27.258	-12.33*
'TC-15' x 'TC-22'	3.208*	1.611	-40.65*	-79.96*	-5.194	-180.57*	-5.768*
'TC-15' x 'BTM-2'	0.319	-0.667	-43.82*	-67.74*	-3.639	-149.74*	0.973
'TC-22' x 'BTM-2'	-0.125	5.056	-19.71	46.38*	-3.028	22.097	-6.345*
S.E.(Sij) ±	1.3220	5.1534	12.6228	23.0737	2.8104	48.6793	1.919
S.E.(Sij-sik) ±	1.9987	7.7912	19.0916	34.8812	4.2489	73.5962	2.901

*P=0.05

Acknowledgment: The authors are grateful to the Indian Council of Agricultural Research, New Delhi, for the financial support provided through NATP to carry out this research.

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J. Oilseeds Res., **25**(2) : 175-177 (2008)

Short communication

Genetic variability in induced mutants of soybean, *Glycine max* (L.) Merrill

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(Received: December, 2007; Revised: April, 2008; Accepted: July, 2008)

Abstract

Genetic variability can be created in selected mutants from three soybean varieties i.e., JS-93-05, JS-335 and MRC-37 through gamma rays.

Keywords: Genetic variability, soybean, X-rays

Soybean has experienced an unprecedented growth rate during last three decades in terms of area, production and productivity in India. However, in spite of substantial increase in area and total production, productivity appeared stagnated after 1995 basically due to the narrow genetic base of varieties released. In this situation, there is a strong need to broaden the genetic base of soybean. Use of mutagens has been a practical tool, especially where natural variability is not available. Mutation techniques are the best methods to enlarge the genetically conditioned variability and have played a significant role in the development of many crop varieties (Micke, 1988).

To broaden the genetic base of soybean, mutation breeding has already been started and several mutants, induced by gamma rays have been isolated from JS 335, JS 93-05 and NRC 37. In the present study X rays induced mutants and their parents were evaluated for various characters.

The investigation was carried out during the *kharif* season 2005-2006, under All India Co-ordinate Research Project on Soybean. The experimental material was comprised of selected mutants from the three varieties *viz.*, JS 93-05, JS 335 and NRC 37. Total 72 treatments including three parents were studied with the observation of days to 50% flowering, days to maturity, plant height (cm.), number of primary branches/plant, number of pods/plant, number of seeds/plant, number of seeds/pod, 100 seed weight and yield/plant. The data were subjected to analysis as per Panse and Sukhatme (1967).

The phenotypic and genotypic coefficient of variation in percent was computed by formulae given by Burton (1952). Heritability in percent in broad sense was estimated by the formula given by Hanson *et al.* (1956). The estimates of expected genetic advance from selection, G(s), was obtained by the formula suggested by Johnson *et al.* (1956). Estimation of genetic variability created through induced mutations was one of important aims of this research programme. This information is necessary for selections and breeding plans to be followed in future.

Among the mutants of three sets no difference for mean was observed for days to 50% flowering however, wider range was observed for mutants of JS 93-05. Early maturing genotypes were generally found among the mutants of JS 93-05 showing the largest range. Mean value for plant height was the highest among the mutants of NRC37 having the largest range also. The mean did not show difference among the mutant sets however, the largest range was observed in the mutants of JS 93-05 for number of branches. The highest mean and range for number of pods/plant and number of seeds/plant was exhibited by mutants of NRC 37. Mutants of JS 93-05 have shown the highest mean for number of seeds/pod whereas mutants of JS 335 showed largest range for this trait. For 100 seed weight the highest mean and range was observed by mutants of JS 93-05. Mutants of NRC 37 exhibited the highest mean for yield/plant while mutants of JS 93-05 showed the largest range.

These findings suggest that for the improvement of any trait the breeding lines (mutants) can be selected from different set of mutants where mean and range have been found desirable and substantial for the concerned trait.

The relative magnitudes of CV also indicated that sufficient variability was induced among the mutants for all the characters except days to 50% flowering and 100 seed weight.

As usual in all the three sets of mutants PCV estimates were, found higher than GCV estimates (Table 1) for all the nine characters indicated that variation was not only due to genotypes but also due to the influence of environment. The present analysis revealed that higher variability is present in mutant bulks of the three varieties under study.

A relative comparison of the magnitude of phenotypic and genotypic coefficient of variation for different traits revealed that higher values of PCV and GCV were depicted for number of pods per plant followed by number of seeds/plant and yield/plant by all the three sets of mutants. Where as mutants of JS93-05 and NRC 37 showed high magnitude for number of branches and plant height in addition to above mentioned traits.

These results are in conformity with the finding of Upadaya (1985), Mehetre *et al.* (1994), Geetha and Vaidyanathan, (1998), Patel (2004) and Mishra (2005) in gamma rays treated population of soybean.

These estimates varied from character to character and variety to variety (Table 2). Heritability estimates along with genetic advance are normally more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance.

If high heritability in broad sense is accompanied with high genetic advance, it indicates that the heritability is most likely to be due to additive gene effect and selection may be effective, while high **heritability in broad sense coupled** with low genetic advance, **indicates predominance of non** - additive gene action.

The high heritability estimates were recorded for days to 50% flowering and days to maturity by all the sets of mutants. However, for plant height and number of seeds, the mutants of JS 93-05 and NRC 37 both recorded high heritability. For number of primary branches/plant, number of pods/plant, 100 seed weight and yield/plant mutants of JS 93-05 exhibited high heritability. Similarly, the remaining magnitudes of heritability fluctuated for different characters in different sets of mutants from moderate to low. These results revealed the influence of genotype and irradiation interactions in the expression of heritability.

Table 1 Estimates of PCV and GCV among nine characters in gamma rays induced mutants obtained from JS 93-05, JS-335 and NRC 37

Mutants of Varieties	Characters																	
	Days to 50% flowering		Days to maturity		Plant height (cm)		No. of primary branches/ plant		No. of pods/ plant		No. of seeds/plant		No. of seeds/pods		100 seed wt. (g)		Yield/ plant (g)	
	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV	PCV	GCV
JS 93-05	4.89	4.52	4.66	4.39	21.07	19.11	29.55	25.00	31.75	27.05	26.90	21.35	11.24	10.67	9.52	8.97	23.97	20.54
JS 335	4.10	3.54	2.64	2.26	18.10	14.26	11.69	8.85	22.50	16.20	16.38	13.53	18.68	1.27	12.20	9.31	19.60	15.75
NRC 37	4.26	3.74	3.35	3.17	26.40	24.52	22.97	18.37	26.92	20.76	24.47	16.69	10.77	9.46	11.55	7.55	25.34	17.32

Table 2 Heritability and genetic advance in gamma rays induced mutants obtained from JS 93-05, JS 335 and NRC 37

Mutants of Varieties	Characters																	
	Days to 50% flowering		Days to maturity		Plant height (cm)		No. of primary branches/ plant		No. of pods/ plant		No. of seeds/plant		No. of seeds/pods		100 seed wt. (g)		Yield/ plant (g)	
	h^2%	GA	h^2%	GA	h^2%	GA	h^2%	GA	h^2%	GA	h^2%	GA	h^2%	GA	h^2%	GA	h^2%	GA
JS 93-05	85	3.1	89	8.1	82	14.5	71	1.6	72	17.35	62	28.27	90	0.47	89	2.20	73	3.87
JS 335	71	2.39	73	3.93	62	8.9	57	0.53	52	11.06	68	21.9	0.4	0.003	58	1.74	64	2.97
NRC 37	77	2.59	89	6.07	86	20.63	63	1.19	59	16.99	46	24.98	77	0.36	43	1.17	47	2.97

The fluctuations in the magnitudes of genetic advance were also found from moderate to low for different traits and sets of mutants indicated the influence of genotype and irradiation interactions in this case also.

There was no combination of high heritability high genetic advance. However, incase of mutants of JS 93-05 moderate heritability coupled with moderate genetic advance was observed for number of seed/plant indicated the preponderance of additive gene action. Remaining traits showed either high to low heritability coupled with low genetic advance indicated the predominance of non-additive gene action in the expression of these traits.

High heritability after irradiation was reported by number of workers for number of pods and number of seeds per plant, Mohammad and Kady 1978, for yield, seeds and pods/plant in fababean, Singh *et al.* (1980) for days to flowering, days to maturity, plant height, primary branches, pods/plant, seeds/pod and yield/plant, Mehetre *et al.* (1994) for plant height, yield/plant, pods/plant and branches/plant, Geetha and Vaidyanathan (1988) for 100-seed weight and yield/plant and Patel (2004) for plant height, branches/plant, pods/plant, number of seeds/plant, 100-seed weight and seed yield/plant) supports the present findings except for pod/plant, seeds/plant and 100-seed weight.

This study clearly indicated that through gamma rays irradiation sufficient variability can be created as highly significant variance and high estimates of PCV and GCV for various traits have been observed. The differential magnitudes of estimates shown by different genotypes and characters revealed the difference in the sensitivity of genotypes and characters to the gamma rays.

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J. Oilseeds Res., **25**(2) : 178-180 (2008)

Short communication

Studies on genetic divergence in soybean, *Glycine max* (L.) Merrill

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(Received: September, 2008; Revised: October, 2008; Accepted: October, 2008)

Abstract

Studies on genetic divergence in soybean, *Glycine max* (L.) Merrill were carried out at BARC, Trombay, Mumbai. PK-472, JS-335, IC-118268, EC-390981 and EC-106992 were found distinct and can be used in breeding programme.

Keywords: Soybean, diversity, genotypes

Soybean [*Glycine max* (L.) Merril] is one of the important oilseed crops of India. The crop occupies an area of about 7.0 m.ha with a production of over 7.0 m. tonnes. The average yield of soybean in India is about 1 t/ha as compared to the world average of 2.2 t/ha. The narrow genetic base of the released soybean varieties is responsible for low average yields in India (Satyavathi *et al.*, 2003). Improvement in yield is normally attained through exploitation of the genetically diverse genotypes in breeding programmes. The degree of genetic variability available for selection can play an important role in overcoming yield barriers. Germplasm is the most valuable and essential basic raw material to meet the current and future needs of crop improvement programme. Multivariate analysis has been found to be a potent biometrical tool in quantifying the degree of divergence in the germplasm (Mahalanobis, 1936). The soybean germplasm collection has many useful traits and can be utilized efficiently and systematically in the breeding programme for increasing soybean productivity (Verma and Thomas, 1991). The present investigation was carried out to know the genetic divergence using 55 soybean genotypes including 15 released varieties.

Fifty-five genotypes of soybean were grown in a Randomised Block Design with three replications at the experimental field of Nuclear Agriculture and Biotechnology Division, Bhabha Atomic Research Centre, Trombay during *kharif*, 2002. The foundation seeds of the released varieties were obtained from Dr. Punjabrao Deshmukh Krishi Vidyapeeth, Akola and the seeds of germplasm lines from National Research Centre for soybean, Indore and National Bureau of Plant Genetics Resources, Akola. Soybean crop was grown as a rainfed crop in vertisol soil following normal cultural practices. Two seeds per hill, 10 cm apart, were sown in 3 m long rows with a distance of 30 cm between rows. The data of ten randomly selected plants from the middle rows of each plot per replication were recorded for various characters like days to 50% flowering, days to maturity, plant height, number of branches/plant, number of pods/plant, number of seeds/pod, hundred seed weight, seed yield/plant and harvest index. Multivariate analysis was done using Mahalanobis generalized distance D^2 (Mahalanobis, 1936) and clustering of genotypes was done by Tocher's method (Rao, 1952).

The analysis of variance revealed significant differences among the genotypes for all the traits studied. The multivariate analysis suggested that the 55 genotypes can be grouped into 10 clusters (Table 1). The maximum number of genotypes were included in cluster II (18 genotypes) followed by cluster I (12 genotypes), cluster III (11 genotypes) and Cluster V (8 genotypes) and the other 6 clusters had one genotype each. Among the 15 released soybean varieties, JS 335 & PK-472 were included in cluster VII and cluster IX respectively indicating their distinctness from the other varieties and genotypes. Grouping of genotypes based on multivariate analysis have also been reported by Bhatt (1970), Sharma *et al.* (2005), Ramana and Satyanarayana (2006).

Average intra and inter cluster D^2 values among the 55 genotypes (Table 2) revealed that cluster I had the minimum intra cluster value (14.45) indicating that genotypes within this cluster were similar. The maximum intra cluster value was observed in cluster V (17.51) followed by cluster III (16.17) and cluster II (16.07) indicating the presence of diverse genotypes in these clusters. The inter cluster D^2 values ranged from 14.31 to 38.06. Minimum inter cluster D^2 values (14.31) were observed between cluster VII and IX indicating the similarity among the genotypes included in these clusters. Maximum inter cluster value (38.06) was observed between cluster IV (EC-390981) and cluster X (IC-118268). Bhatt (1970) reported that the crosses between genotypes belonging to the clusters having maximum inter cluster distance will yield better recombinants. This indicates that germplasm accessions EC-390981 and IC-118268 are genetically diverse and may give rise to high heterotic response when used in hybridization programme. The selection of diverse parents for crossing programme in soybean has also been reported by Jaylal (1994).

The cluster means and contribution of each trait towards divergence are presented in Table 3. The highest yield was recorded by cluster IX (PK-472), cluster VII (JS -335), *and cluster* VI (UM-21). *Along with high seed yield,* cluster VI (UM-21) also recorded high harvest index (43.24%), *more number of seeds/pod* (3.33) *and highest seed weight* (15.77g). High harvest index (54.24%) was observed in the variety JS-335. The highest number of pods/ plant (54.60) and more number of branches (3.47) was observed in cluster X (IC 118268). The germplasm accessions IC-18758, IC-118047, IC-118058, IC-118041, IC-118054, EC-280132 and EC-241755 grouped in cluster IV recorded early maturity (78.75 days) and maximum days to maturity were observed in cluster VIII (108 days). It is always desirable to utilise genotypes in crossing programme having more number of good agronomic traits. The genotypes UM-21, PK-472, JS-335, IC-118268, EC-390981 *and* EC-106992 *are distinct and diverse and* can be utilised in the breeding programme. The variety PK-472 was also identified as distinct and diverse by Sharma *et al.* (2005). Verma and Thomas (1991) also reported significant variability for all the economically important qualitative and quantitative traits in the soybean germplasm.

Table 1 Clustering pattern of soybean genotypes on the basis of genetic divergence

Cluster's Number	Genotypes	Number of genotypes
I	IC-118183, EC-389400, JS-220, P-4-2, IC-202, EC-389170, IC-96297, EC-341755, EC-391172, EC-389165, EC-18735, EC-7724	12
II	EC-280125, EC-389148, IC-96245, EC-39076, VLS-2, PUJAB-1, PK-1042, EC-113394, PK-1024, EC-251523, EC-251358, Jawa-16, Monetta, EC-389392, NRC-7, Ankur, VLS-47, NRC-12	18
III	C0-1, EC-389178, IC-118296, EC-389159, JS 90-41, JS 90-41, EC-389166, MACS-58, JS 80-21, EC-389179, IC-96382, EC-391181	12
IV	EC-390981	12
V	IC-18758, IC-118047, IC-118058, IC-118041, IC-118054, EC-280132, EC-241755	7
VI	UM-21	1
VII	JS-335	1
VIII	EC-106992	1
IX	PK-472	1
X	IC-118268	1

Table 2 Average intra and inter cluster distance (D^2 values) of 55 soybean genotypes

Cluster	I	II	II	IV	V	VI	VII	VII	IX	X
I	14.45	26.10	21.89	30.19	30.39	31.68	33.42	22.93	28.60	25.06
II		16.07	22.03	20.71	26.60	19.32	22.55	22.38	20.79	33.14
III			16.17	29.26	32.77	24.01	23.73	22.01	24.03	22.65
IV				0.00	16.68	30.22	32.58	34.42	30.31	38.06
V					17.51	37.19	34.96	36.70	33.10	37.67
VI						0.00	19.73	20.60	16.39	35.12
VII							0.00	25.56	14.31	29.04
VIII								0.00	23.91	32.14
IX									0.00	28.56
X										0.00

Table 3 Cluster means and per cent contribution of characters towards divergence

Cluster	Days to 50% Flowering	Day to maturity	Plant height (cm)	No. of branches	No. of pods/ plant	No. of seeds/pod	100 seed weight (g)	Yield/ Plant (g)	Harvest index (%)
I	37.08	100.67	53.09	2.55	30.39	2.14	8.14	8.25	11.17
II	32.83	94.89	26.68	2.44	21.51	2.38	11.14	15.3	36.14
III	36.82	101.55	54.57	3.23	29.73	2.27	9.01	17.31	34.65
IV	26.00	81.00	39.61	2.67	18.73	2.83	11.80	10.70	30.58
V	27.63	78.75	34.01	2.82	22.70	2.18	6.70	7.46	22.71
VI	39.0	102.00	22.00	3.53	27.33	3.33	15.77	21.43	43.24
VII	36.0	98.00	18.71	3.00	37.53	2.16	7.13	22.00	54.24
VIII	45.0	108.00	22.18	2.40	19.83	2.35	7.77	10.25	30.60
IX	36.0	98.00	17.34	1.63	43.13	2.73	11.33	22.67	36.68
X	42.0	98.00	77.40	3.47	54.60	2.01	7.77	12.35	31.13
Per cent contribution	2.49	32.19	17.64	0.13	7.68	0.67	9.43	3.64	26.13

The characters contributing maximum to D^2 values are given greater emphasis for deciding the clusters for the purpose of future selection and choice of parents for hybridization. Among the characters studied, days to maturity (32.19%) contributed maximum towards the genetic divergence, followed by harvest index (26.13%), plant height (17.64%) and 100 seed weight (9.43). Similar results have also been reported by Kumar and Nadarajan (1994), Jaylal (1994), Ramana and Satyanarayana (2006), Sharma *et al.* (2005). Satyavathi *et al.* (2003) studied the genetic base of 66 soybean varieties of India and reported that the narrow genetic base of the Indian soybean varieties is because of repetitive use of the same parents for the development of the genetic stock or breeding material. The efficient use of unexploited variability available in the germplasm in the crossing programmes can help to overcome the problem of narrow genetic base and simultaneously improve the average soybean productivity. Based on the present study the genotypes UM-21, PK-472, JS-335, IC-118268, EC-390981 and EC-106992 were found to be distinct and diverse. These genotypes can be utilised in the breeding programme for developing better varieties of soybean.

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J. Oilseeds Res., **25**(2) : 181-182 (2008)

Short communication

Identification of fertility restorers/maintainers in sunflower, *Helianthus annuus* L.

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(Received: June, 2008; Revised: September, 2008; Accepted: September, 2008)

Abstract

The studies resulted in identification of restorer lines for different background CMS lines will help in developing hybrids with broad cytoplasmic base for more heterosis.

Keywords: Restorer lines, sunflower

Majority of the presently grown commercial hybrids in the world, possess the cytoplasm of *Helianthus petiolaris* (PET 1). Prevalence of genetic uniformity of this kind over a large area could result in genetic vulnerability of hybrids, if the cytoplasm becomes susceptible to a new strain of disease or insect pest. It is evident from earlier experiments that dependency on single source of cytoplasm posed a threat to the cultivation of the crops, maize and bajra as they became susceptible to leaf blight and downy mildew, respectively. The association of Texas sterile cytoplasm with susceptibility to southern corn leaf blight has shown the genetic vulnerability of Cytoplasmic male sterility system in maize hybrids (Hooker *et al.*, 1970).

Since the start of the hybrid development in sunflower, PET 1 cytoplasmic male sterility source and few restorer genes have been utilized in commercial production of hybrids. This narrow genetic base may limit the future progress in sunflower breeding programmes. Therefore, sunflower researchers accelerated their efforts to develop new diverse sources of Cytoplasmic male sterility to widen the genetic base and to reduce the genetic vulnerability of sunflower hybrids. Besides developing new sources of male sterility, identification of new restorer lines will enhance the genetic diversity. Considering the fact, about 60 additional sources of Cytoplasmic male sterility have been identified from the progenies of crosses between wild Helianthus species and cultivated as well as induced mutant lines (Anashchenko *et al.*, 1974).

The F_1s obtained from crossing four diverse CMS lines *viz.*, CMS 234A, CMS 7-IA (PET I), DCMS 6 (PET 2), DCMS 36 (ARG), DCMS 1 and DCMS 15 (GIG 1), with 20 inbreds were planted during *kharif* 2004-05. Each entry was sown in a single row of 4.5 m length with a spacing of 60 x 30cm in three replications. All the F_1s planted were studied for maintainer/restorer behaviour of the inbreds. The plants were classified as male fertile or male sterile based on anther exertion and pollen production during flowering. The pollen fertility was confirmed in the laboratory by using 1% Acetocarmine staining (Chaudhary *et al.*, 1981). In case of no pollen production, conspicuous stigma projection coupled with pale yellow disc florets, the plants were termed as to be sterile. Based on the data, the lines were classified as restorers or maintainers for the different CMS sources. Identification of effective fertility restorers to these cytoplasmic male sterile lines helps in utilizing them for developing hybrids with diverse cytoplasm and the identified maintainers with good combining ability along with suitable genetic background can be converted into new CMS lines for further exploitation in developing new hybrids.

Out of the 120 F_1s evaluated, 64 hybrids were found fertile and 50 hybrids were found sterile with no pollen production. The remaining six hybrids showed partial restoration. Sixteen inbreds behaved as restorers, three inbreds behaved as maintainers and the remaining one inbred behaved as partial restorer for the lines CMS 7-1A and CMS 234A. Out of 20 inbreds studied, twelve inbreds behaved as restorers, eight inbreds behaved as maintainer lines for the CMS line DCMS 6. For the CMS line DCMS 36, fourteen inbreds behaved as restorer lines and six inbreds behaved as maintainers. For the CMS lines DCMS 1 & DCMS-15, three inbreds behaved as restorers and fifteen inbreds as maintainer lines and two inbreds behaved as partial restorers.

These findings are in accordance with the reports of Serieys and Vincourt (1987), Whelan (1980), Virupakshappa *et al.* (1991), Vishnuvardhan Reddy (2002) and Gourishankar *et al.* (2006). It could be noted that most of the lines, which acted as restorers for the traditional PET 1 cytoplasm behaved as maintainers for GIG 1 and ARG Cytoplasmic male sterility sources.

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The inbred line PS 1021 could not restore fertility on any CMS line and behaved as a maintainer for all the CMS lines. The inbred line DRS 45 could restore fertility on four CMS lines CMS 234 A, CMS 7-IA, DCMS 6 and DCMS 36 and behaved as a maintainer for DCMS 1 and DCMS 15.The inbreds DRS 9 and DRS 34 restored fertility on all the six different cytoplasmic male sterile lines. Only 10 inbreds in common restored fertility on four cytoplasmic male sterile lines of three CMS sources.

Among the 20 inbreds tested for fertility restoration and maintainer reaction, ten inbreds restored fertility on four CMS lines. The 10 inbred lines that restored fertility successfully on all the four CMS lines were DRS 5, DRS 9, DRS 16, DRS 22, DRS 34, DRS 45, DRS 52, DRS 102, RHA 340 and R83R6.

The inbred line DSI 257 and DSI 99 restored fertility on CMS lines CMS 234A, CMS 7-1A and DCMS 36 and behaved as a maintainer on the remaining three CMS lines like DCMS 6, DCMS 1 and DCMS 15. The inbred line RHA 340 could restore fertility on CMS 234 A, CMS 7-1A, DCMS 6 and DCMS 36 but behaved as a maintainer of DCMS 1 and DCMS 15.

The line RHA 341 could not restore fertility on any CMS line but behaved as a partial restorer on CMS 234A and CMS 7-1A, DCMS 1 and DCMS 15. The inbred line RHA 348 could restore fertility only on DCMS 6 and behaved as a maintainer on CMS 234A, CMS 7-IA, DCMS 36, DCMS 1 and DCMS 15.The inbred line DRS 102 could restore fertility on CMS 234A, CMS 7-1A, DCMS 6 and DCMS 36. The line DRS 63 could restore fertility on DCMS 6 and DCMS 36 and acted as a maintainer on the remaining four CMS lines.

The line DRS 5 could restore fertility on CMS 234 A, CMS 7-1A, DCMS 6 and DCMS 36 behaved as a maintainer on the remaining two CMS lines. The inbred line R83R6 could restore fertility on CMS 234A, CMS 7-1A, DCMS 6 and DCMS 36 and behaved as a maintainer on the remaining two CMS lines. Only two inbreds i.e., DRS 34 and DRS 22 restored fertility on all the six CMS lines. The differential behaviour of the above inbreds in restoring fertility/maintaining sterility may be attributed to genetic contribution especially of number of genes involved in fertility restoration and their interaction with different cytoplasm which could be confirmed from inheritance studies carried out. In the study, the specificity displayed by several inbred lines for fertility restoration further indicated that loci of restorer genes in an inbred line might vary from each other, which revealed the capacity to restore fertility. All the four CMS sources utilized in the experiment showed diversity among themselves, thus broadening the genetic base of the CMS lines, which could be safely included in breeding programmes thereby mitigating the vulnerability of the lines to various insect pests and diseases.

Against PET 1 cytoplasm 16 restorers, against PET 2 cytoplasm 12 restorers against ARG cytoplasm 14 restorers and against GIG 1 cytoplasm 6 restorers were identified.

The restorers identified for the different CMS lines will help in developing hybrids with broad cytoplasmic base, enhanced heterosis and strengthen the future hybrid sunflower-breeding programme. The identified maintainers also will have greater application in developing new and superior hybrids, after converting them into CMS lines which are having superior agronomic background coupled with good combining ability. With the help of effective restorers identified in the present study for the alternate sources of cytoplasm, a significant improvement towards diversifying the parental base, especially with respect to the cytoplasm can be achieved, which may further lead to enhanced production and productivity of sunflower by breaking the yield stagnation.

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J. Oilseeds Res., **25**(2) : 183-185 (2008)

Short communication

Analysis of genetic variability, character association and path analysis in summer sesame, *Sesamum indicum* L.

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(Received: January, 2008; Revised: September, 2008; Accepted: October, 2008)

Abstract

Present studies revealed that based upon direct and indirect effects, number of capsules on main shoot as well as on *primary* and *secondary* branches for important traits for selection of high yielding sesame genotypes.

Keywords: Sesame, genetic variability, path analysis

Sesame, an ancient traditional oilseed crop of India is better known as "Queen of Oilseeds" by virtue of its quality oil. It is a seasonal and location bound crop hence, a particular variety does not perform uniformly in all locations and in all seasons. In Uttar Pradesh, it is predominantly cultivated in *kharif* season on area of about 1.03 lakh ha with a total production of 1.66 lakh tonnes. But its productivity is very poor 162 kg/ha as compared to national average 453 kg/ha which can be substantially enhanced by shifting the growing season in summer as witnessed in West Bengal. The major research breakthroughs that are considered possible by experts in coming decade is development of photoinsensitive varieties of sesame with low senescence. The present investigation was planned and implemented with a view to assess the quantum of 'variation and to elucidate the relative importance and association between seed yield and yield components so that systematic breeding efforts may be initiated to evolve high yielding summer sesame cultivars.

Forty two genotypes of sesame including 32 released varieties were sown on 21st February, 2006 in Randomised Block Design with two replications at Crop Research Farm, Nawabganj, C.S. Azad University of Agric. & Tech., Kanpur. The plot size was single row of 4m length and spaced at 30xl0 cm apart. Recommended agronomic practices were followed to raise the crop. Data were recorded on eight quantitative traits (Table 1) by randomly selecting five competitive plants/replication. Range, mean genotypic and phenotypic coefficient of variance and simple correlation coefficients were computed using standard statistical methods (Panse and Sukhatme, 1967) whereas, heritability in broad sense and genetic advance following Johnson *et al.* (1955). Path analysis was done following Dewey and Lu (1959).

Analysis of variance revealed highly significant differences *among genotypes for all the characters except primary and* secondary branches/plant as also reflected by high values of mean and range (Table 1). A close correspondence between the estimates of GCV and PCV was noted specially in case of plant height, days to maturity and seed yield/plot. Seed yield/plot and the characters related to number of capsules recorded high GCV and PCV estimates. Low estimates of GCV and PCV recorded for primary and secondary branches/plant culminated into low heritability and genetic advance. Estimates of heritability and genetic advance in combination are more important for selection than heritability alone. High heritability combined with high genetic advance observed for seed yield, capsules on primary branches, plant height and capsules on main stem and on secondary branches showed that these characters were controlled by additive *gene effects and phenotypic selection would be highly* effective. Similar results were reported earlier by Singh *et al.* (1997), Reddy *et al.* (2001), Krishnaiah *et al.* (2002) and Sudhakar *et al.* (2007). Days to maturity revealed high heritability and low genetic advance which might be due to predominance of non-additive gene action and/or less genetic variability for this trait in the present material.

Correlation studies provide better understanding of yield components which helps the plant breeder during selection. In general genotypic correlation coefficient was found higher than phenotypic correlation coefficient for most of the traits except plant height and capsules on secondary branches indicating strong inherent association between the traits and less influence of environmental factors. For plant height and capsules on secondary branches, environmental correlation coefficient was greater than both genotypic and phenotypic correlations suggesting that these two characters are showing high association due to favourable influence of particular environment which may change with the change in environment.

Seed yield/plot reflected high positive correlations with number of capsules on main stem as well as on primary branches (Table 2). These results are in consonance with those of Singh *et al.* (1997), Tomar *et al.* (1999), Ved Narain *et al.* (2004) and Sudhakar *et al.* (2007). Significant positive correlation was also observed between primary branches/plant with plant height, days to maturity, secondary branches/plant, capsules on primary branches and capsules on secondary branches; between secondary branches/plant with capsules on primary and secondary branches.

The path coefficient analysis estimated after deleting undesirable variable i.e., primary branches/plant revealed that number of capsules on main stem and number of capsules on primary branches/plant had positive direct effect coupled with positive correlation with seed yield (Table 3). Positive direct effect of capsules on secondary branches/plant and its negative correlation with seed yield suggested that restrictions like simultaneous selection model must be imposed to nullify its undesirable indirect effects (Singh and Kakar, 1997). Genotypic correlation coefficient of plant height with seed yield was almost equal to its direct effect both in direction and magnitude. Such correlation indicates true negative relationship and a direct selection through this trait will be effective.

Considering the direct and indirect effects along with character associations, the present studies suggest that numbers of capsules on the main stem as well as on primary and secondary branches are the important traits, to be considered for selecting high yielding sesame genotypes suitable for summer cultivation.

Table 1 Genetic parameters for seed yield and its components in summer sesame

Characters	Mean ±SEm	Range	GCV (%)	PCV (%)	H_{BS}(%)	GA*
Plant height (cm)	95.1 3.6	82.5-117.5	9.1	9.9	85.2	16.5
Days to maturity	115.4 2.1	107.5-122.5	3.4	3.8	76.3	7.0
Primary branches/plant	4.2 1.0	3.0-5.5	0.7	25.7	0.10	0.0
Secondary branches/plant	2.2 0.8	1.2-5.0	20.9	41.8	25.1	0.4
Capsules on main stem	23.2 2.5	5.0-38.0	28.3	30.4	86.8	12.6
Capsules on primary branches	3.1 3.9	21.5-66.5	25.8	27.4	88.6	21.6
Capsules on secondary branche	12.2 3.2	4.1-33.9	55.8	61.8	81.5	12.6
Seed yield/plot (g)	18.4 1.1	2.4-61.2	73.1	73.3	99.2	27.6

GCV = Genotypic coefficient of variance; PCV = Phenotypic coefficient of variation;
HBS = Heritability in broad sense; GA = Genetic advance
* = The selection differential (K) used was 2.06 at 5% selection intensity

Table 2 Genotypic correlation coefficient among eight characters in summer sesame

Characters	Days to maturity	Primary branches/plant	Secondary branches/plant	Capsules on main stem	Capsules on primary branches	Capsules on secondary branches	Seed yield/plot (g)
Plant height (cm)	0.12	3.05**	-0.54	0.10	-0.18	-0.35	-0.02
Days to maturity	1.00	5.14**	-0.04	-0.47	-0.27	0.01	-0.36
Primary branches/plant		1.00	2.45**	-3.21**	5.56**	4.29**	-4.31**
Secondary branches/plant			1.00	-0.54	0.78*	1.37**	-0.03
Capsules on main stem				1.00	0.19	0.29	0.52
Capsules on primary branches					1.00	0.44	0.19
Capsules on secondary branches						1.00	-0.01

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

Table 3 Direct (diagonal) and indirect effects of six characters on seed yield/plant in sesame at genotypic level

Characters	Plant height	Days to maturity	Secondary branches/plant	Capsule on main stem	Capsule on primary branches	Capsule on secondary branches	Genotypic correlation with seed yield
Plant height (cm)	-0.02	-0.016	0.025	0.050	-0.002	-0.065	-0.025
Days to maturity	-0.002	-0.132	0.002	-0.230	-0.003	0.001	-0.364
Secondary branches/plant	0.010	0.006	-0.047	-0.260	0.008	0.253	-0.030
Capsules on main stem	-0.002	0.063	0.025	0.485	0.002	-0.055	0.518
Capsules on primary branches	0.003	0.035	-0.036	0.097	0.010	0.082	0.191
Capsules on secondary branches	0.006	-0.001	-0.064	-0.143	0.004	0.0185	-0.012

Residual = 0.6987

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J. Oilseeds Res., **25**(2) : 186-187 (2008)

Short communication

G.Til 3 : A white and bold seeded sesame, *Sesamum indicum* L. variety for Saurashtra region of Gujarat

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(Received: October, 2007; Revised: September, 2008; Accepted: October, 2008)

Abstract

G.Til 3, a **white and bold seeded sesame variety was found suitable for cultivation in Saurashtra region of** *Gujarat.*

Keywords: Sesame, white and bold seeded

Sesame is the most ancient oilseed crop domesticated in India more than 5000 years ago (Duhoon *et al.*, 2000). It is a rich source of high quality edible oil and cake. The area under sesame cultivation in India is about 2.18 m.ha with the production of 0.73 m. tonnes. India is the world leader in terms of sesame production and export. A total of 39 varieties of sesame have been released for general cultivation in India.

Gujarat is the leading state among the sesame growing states in the country. Farmers of the state, particularly of Saurashtra region, prefer sesame to grow because of its drought tolerant nature compared to many other crops, fits well into various cropping sequences/systems and best suited with rainfall pattern of the region. Two white seeded sesame varieties, namely, G.Til 1 (1978) and G.Til 2 (1994) predominates in cultivation of sesame in the state. White seeded sesame has good export potential. Seeds of G.Til 2 are considered to be export quality and fetches premium price in the market. This article reports identification of a high yielding white and bold seeded sesame genotype, i.e., G. Til 3 (AT 93) that holds promise for rainfed production system. With a view to develop extra white bold seeded sesame varieties, breeding efforts were initiated at Agricultural Research Station, Amreli, Junagadh Agricultural University. A cross was attempted between G.Til 1 and AHT 85 in the year 1990 and segregating material was handled through pedigree method. As a result of these efforts, the culture, AT 93, was isolated and evaluated for its production potential in kharif seasons during 1997 to 2005 along with existing checks of sesame varieties in Randomized Block Design with four replications at different locations of the region (Table 1). The material was tested in PET (Preliminary Evaluation Trial), SSVT (Small Scale Varietal Trial) and LSVT (Large Scale Varietal Trial) consisting of 5.0 m length plot with variable row numbers, i.e., 3, 4 and 6, respectively. The spacing of 45 cm between the rows and 10 cm distance plant to plant was maintained. The agronomic package of practices recommended for the Saurashtra region was followed to reap the good yield.

The seed yield data recorded for this newly developed variety along with two checks *viz.*, G.Til 1 and G.Til 2 at six locations of Saurashtra region are presented in Table 1. The AT 93 recorded the mean seed yield (average of 28 trials) of 697 kg/ha as against 582 kg/ha of G.Til 1 and 618 kg/ha of G.Til 2 with an yield improvement of 19.8% and 12.8% over check variety G.Til 1 and G. Til 2, respectively.

Table 1 Mean performance of sesame genotype AT 93 (G.Til 3) in Saurashtra region

Location	No. of Trial	Year	Yield (kg/ha)			% increase over	
			AT 93	G.Til 1 ©	G.Til 2 ©	G.Til 1 ©	G.Til 2 ©
Amreli	8	1997-2005	879	679	749	29.4	17.4
Dhari	1	1997	747	774	768	-	-
N. Kandhasar	1	1998	477	477	498	-	-
Targhadia	6	1998-2005	770	634	703	21.5	9.5
Jamnagar	6	2000-2005	635	516	575	23.1	10.4
Junagadh	6	1998-2005	528	454	441	16.3	19.7
Average	28	1997-2005	697	582	618	19.8	12.8

C = Check

The morphological features of AT 93 and two check varieties are presented in Table 2. A perusal of this table indicated that long capsules in the culture AT 93 arises singly from leaf axils, whereas medium size capsules in both the check varieties arises more than one from leaf axils. On an average, primary branches/plant, productive capsules/plant and seeds/capsule are higher as compared to both the checks. Seed whiteness of AT 93 is similar to that of G.Til-2 but its seed size is more (1000 seed wt. = 3.23 g) than the seed size of G.Til-2 (1000 seed wt = 3.00 g). Whiteness and bold seed size of proposed variety may favour the production for export purposes.

AT 93 was also evaluated under field conditions for reaction to major pests and bacterial blight disease (Table 3). Disease score (on 0 -5 scale, 0 for resistance, 5 for most susceptible) of bacterial blight in AT 93 was comparable to both the checks, AT 93 recorded 0.3% infection for gallfly and free from mites as compared to maximum of 5.0% and 7.3%, respectively in check variety G.Til 2. Thus, AT 93 was found to be less susceptible to Gallfly and mites.

Looking to its consistence superior performance under rainfed conditions, the State Variety Release Committee has released this culture (AT 93) of sesame crop as G. Til 3 for commercial cultivation in Saurashtra region of the Gujarat State during August 2007. The Associate Research Scientist (Ag. Bot.), Agricultural Research Station, Amreli, Junagadh Agricultural University, maintains the breeder seed of G. Til 3. A large quantity of basic seed has been produced for sale. G. Til 3 has been registered (IC No. 545633) and preserved for long term storage.

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Table 2 Morphological description of AT 93 (G.Til 3) and checks

Descriptor	*Genotypes*		
	AT 93	GTil 1 (Check)	G.Til 2 (Check)
Branching pattern	Branching	Branching	Branching
Branching habit	Low branched	Low branched	Low branched
Stem hairiness	Glabrous	Glabrous	Hairy
Flower colour	Purplish white	Purplish white	Purplish white
Days to 50% flowering	39	41	39
Days to Maturity	85	87	85
Plant height (cm)	97	97	96
Primary branches/plant	3.02	2.76	2.91
Corolla hairiness	Sparsely hairy	Sparsely hairy	Sparsely hairy
Capsule/leaf axil	One	More than one	More than one
Capsule shape	Broad oblong	Narrow oblong	Narrow oblong
Capsule arrangement	Single opposite	Multi opposite	Multi opposite
Density of capsule hariness	Glabrous	Glabrous	Hairy
Capsule length	Long	Medium	Medium
Productive capsules/plant	60	55	57
Seeds/capsule	69	64	65
Seed colour	White	Creamy white	White
1000 seed weight (g)	3.23	3.13	3.00
Oil content (%)	46.2	47.4	46.0

Table 3 Comparison of AT 93 with two check varieties for infection of major pests (%) and bacterial blight

Entry	Per cent infection												Bacterial blight (Av. of 3 years)
	Gallfly				Mites				Leaf roller				
	2003	2004	2005	Av.	2003	2004	2005	Av.	2003	2004	2005	Av.	
AT 93	1	0	0	0.3	0	0	0	0.0	15	41	21	25.6	1.3
G.Til 1 ©	8	3	3	5.0	9	5	8	7.3	8	42	22	24.0	1.3
G.Til 2 ©	0	2	2	1.3	6	5	7	6.0	13	39	19	24.0	1.6

C = Check

J. Oilseeds Res., **25**(2) : **188-189 (2008)**

Short communication

Euclidean cluster analysis in late sown linseed, *Linum usitatissimum* L.

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(Received: November, 2007; Revised: July, 2008; Accepted: August, 2008)

Abstract

The studies on Euclidean cluster analysis in late sown linseed were carried out at Regional Research and Technology Transfer Sub-station of OUAT, Jashipur, Mayurbhag, Orissa. There were significant differences among linseed genotypes for eight traits. Efforts are on to breed linseed varieties with more capsules and primary branches based on the above situations.

Keywords: Linseed, capsules

Linseed (*Linum usitatissimum* L.) covers an area of 23.1 thousand ha with an annual production of 9.7 thousand tonnes in Orissa. The districts of Mayurbhanj and Keonjhar contribute about 54% to the total area. However, a significant number of farmers are forced to sow linseed *about one month late in this region due to excess moisture* in the field. Seed setting is highly affected due to higher temperature during later phase of growth. So, an experiment was laid out to study genetic diversity in late sown linseed. It would facilitate selection of genetically diverse parents for recombination breeding in late sown condition.

Twenty eight genotypes of diverse pedigree were grown in Randomized Complete Block Design with three replications at Jashipur Farm of OUAT. The crop was *sown one month late in November during rabi*, 2005-06 with a spacing of 25 x 5 cm. Five rows of 3 m length constituted a gross plot. Observations were recorded on eight quantitative characters (Table 2). Ten randomly selected competitive plants were used for recording observations. The non-hierarchical Euclidean cluster analysis was done to estimate the intra-and inter-cluster distances and to group the genotypes into different clusters (Spark, 1973).

The analysis of variance revealed highly significant differences among the genotypes for all the eight characters. Twenty eight genotypes were grouped into six clusters, i.e., cluster I (OL 93418-2, OL 92-4-3, Kiran, OL 7-7, OL 3-2, OL 92-16-3, OL 9349-2), cluster II (T 397, OML 3), cluster III (OL 3-1, OL 3-11, OL 92-4-2, OL 93418-1, OL 93421-1, OL 93414-3), cluster IV (OL 2-3, OL 2-3, OL 2-7), cluster V (OL 22-1, OL 19-6, OL 20-1, OL 18-4, OL 19-11, OL 92-2-2) and cluster VI (OL 2-5, OL 9344-1, OL 1-3, OL 4-1).

The clustering pattern revealed that the genotypes derived *from different parents were grouped into one cluster*..

Table 1 Estimates of average intra-and inter-cluster distances for six clusters involving 28 genotypes of linseed

Cluster No.	I	II	III	IV	V	VI
I	1.378					
II	3.119	0.964				
III	2.569	3.247	1.421			
IV	5.730	4.308	4.411	1.221		
V	3.434	3.884	2.565	4.926	1.649	
VI	4.870	4.433	3.047	4.101	2.318	1.600

Table 2 Intra-cluster means for eight characters of linseed

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/plant	No. of capsules/ plant	No. of seeds/ capsule	1000-seed weight (g)	Seed yield/ plant (g)
I	54.67*	106.38*	47.98	0.44*	17.28*	7.98	6.42	0.66*
II	60.17	107.67	46.75*	1.30	25.18	7.95	4.52*	0.70
III	56.44	110.89	54.53	0.93	24.86	8.34**	6.66	1.07
IV	66.78**	118.44**	65.17**	1.87**	28.10	7.59	5.46	0.73
V	54.83	108.67	50.61	1.56	28.15	7.29*	7.26**	1.15
VI	57.58	110.67	61.26	1.58	36.38**	7.41	6.69	1.36**

*, ** *Denote minimum and maximum figures, respectively.*

Again, the genotypes derived from same parents were distributed over different clusters, although cluster IV had genotypes of same parentage. This indicated that parentage and genetic diversity were not necessarily related. Such a situation might have occurred due to human selection pressure

The estimates of average intra-and inter-cluster distances are presented in Table 1. Cluster 5 showed maximum intra-cluster distance followed by cluster VI. Cluster II showed minimum distance. The highest inter-cluster distance existed between cluster IV and I followed by that between V and IV and VI and I. The inter-cluster distance was the lowest between cluster VI and V.

Inter-crossing of superior genotypes from distant clusters is expected to throw a wide spectrum of variability. In late sown condition, number of capsules and primary branches/plant are the most important selection criteria fro improvement of seed yield on the basis of GCV, H, GAM, correlation and direct and indirect effects (Naik and Satapathy, 2002). Cluster VI and IV have highest cluster means for number of capsules and primary branches, respectively (Table 2). Three genotypes (OL 9344-1, OL 1-3 and OL 4-1) were selected on the basis of number of capsules from cluster VI keeping the score of number of primary branches above the mean. Similarly, two genotypes (OL 2-3 and OL 2-4) were selected on the basis of primary branch number from cluster IV keeping the score of capsule number above the mean. The recombination breeding is going on to have varieties with higher number of capsules and primary branches for improving seed yield in late sown condition.

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J. Oilseeds Res., **25**(2) : 190-192 (2008)

Short communication

Genetic divergence in sesame, *Sesamum indicum* L.

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(Received: January, 2008; Revised: July, 2008; Accepted: August, 2008)

Abstract

Sixty genotypes of sesame, *Sesamum indicum* L. were assessed for genetic divergence with respect to seed yield and its components. Branches/plant contributed highest towards seed yield.

Keywords: Sesame, genetic divergence

Sixty genotypes of sesame were assessed for genetic divergence with respect to seed yield and other quantitative traits. The genotypes were grouped into eleven clusters. The cluster I having maximum number of genotypes (45) followed by cluster III (4) and IX (3), whereas, cluster II, IV, V, VI, VII, VIII, X and XI having one genotype each. The maximum inter-cluster distance was observed between cluster VIII and XI (11.04). Selection of the genotypes from these clusters for heterosis breeding may result into good recombinants. Among eleven characters studied for genetic divergence, branches/plant contributed maximum (24.41%) to the total divergence followed by plant height (18.98%), seed yield/plant (12.37%) and 1000-seed weight (11.41%).

The experiment comprising 60 genotypes having diverse origin was laid out in randomised block design with three replications at the Main Castor and Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar during *kharif*, 2005. Each plot consisted of single row of 5 mete length with a spacing of 45 x 30 cm. The data on ten randomly selected plants from each plot were recorded for eleven characters. The multivariate analysis was done as per Mahalanobis D^2 statistics (1936) as described by Rao (1952) and the genotypes were grouped into different clusters following Tocher's method described by Rao (1952).

The multivariate analysis giving the D^2 values between 60 genotypes revealed that all these genotypes could be grouped into 11 clusters (Table 1).

Table 1 **The distribution of 60 genotypes of sesame into different clusters on the basis of D^2 statistic**

Cluster No.	No. of genotypes	Name of genotypes in each cluster	Geographical area of distribution
I	45	ES 29, RMT 97, RT 328, RT 331, RT 340, OSSD 117, RT 338, EC 370773, RT 339, RT 329, ES 1-2-84, RMT 186, CST 783, RMT 261, RT 127, RMT 93, ES 351819, RT 46, HT 1, JTS 117, HT 6, SPRT 23, RMT 82, ES 55-3-84, RT 325, EC 351832, DORS 6B, ES 370937, RT 103, PKDS 37, EC 370929	Mandor (Rajasthan)
		AT 133, AT 102, AT 114, G.til 2, AT 130, AT 117, AT 77, AT 126, Mrug 1	Amreli (Gujarat)
		Pb. Til 1	Ludhiana (Punjab)
		G. til 1	Manund (Gujarat)
		TNAU 65	Tamil Nadu
		Tapi	Jalgaon (Maharashtra)
II	1	IS 352	Mandor (Rajasthan)
III	4	RT 334, OSSD 343, RT 305	Mandor (Rajasthan)
		C 1013	Andhra Pradesh
IV	1	AT 123	Amreli (Gujarat)
V	1	AT 113	Amreli (Gujarat)
VI	1	AT 124	Amreli (Gujarat)
VII	1	EC 362396	Mandor (Rajasthan)
VIII	1	ES 137	Mandor (Rajasthan)
IX	3	ES 99	Mandor (Rajasthan)
		G.til 10	Amreli (Gujarat)
		TMV 3	Vridhachalam (TN)
X	1	TNAU 63	Tamil Nadu
XI	1	PT 64	Patan (Gujarat)

Among these, cluster I consisted of 45 genotypes followed by cluster III (4), cluster IX (3) and cluster II, IV, V, VI, VII, VIII, X and XI with one genotypes each. Interestingly, the related genotypes of same state were distributed in different cluster. The results indicated that genetic divergence is not related to geographical diversity. This was in agreement with the earlier findings of Thangavelu and Rajasekaran (1983). Further, it suggested that selection pressure also played a greater role in determining the genetic closeness/divergence among the varieties. Similar conclusions were made by Bhatti (1970) who suggested that genetic drift and selection forces under diverse environments could cause even greater diversity than the geographical diversity.

The intercluster distances were greater than intracluster distances, revealing that considerable amount of genetic diversity existed among the genotypes studied (Table 2).

Table 2 Average intra (bold) and inter-cluster distance D ($D=\sqrt{D^2}$)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**4.83**	6.03	6.21	5.99	6.72	6.04	7.23	6.92	6.85	6.80	6.42
II		**0.00**	4.21	8.54	7.51	7.86	10.86	9.42	9.48	7.38	9.98
III			**4.81**	8.73	7.45	8.06	10.57	10.08	9.05	8.41	10.35
IV				**0.00**	5.11	3.53	3.93	5.56	5.26	6.17	8.86
V					**0.00**	4.48	7.97	8.78	5.76	7.79	10.35
VI						**0.00**	5.48	7.86	5.95	7.59	7.93
VII							**0.00**	6.27	5.72	7.61	8.70
VIII								**0.00**	6.89	6.28	11.04
IX									**5.13**	7.39	10.94
X										**0.00**	10.90
XI											**0.00**

Cluster IX showed maximum intracluster distances (5.13), intercluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to the clusters with maximum intercluster distances are genetically more divergent and hybridization between genotypes of divergent clusters are likely to produce wide variability with desirable segregants. The maximum intercluster distance was recorded between cluster VIII and XI (11.04), while, the distance was minimum between IV and VI (3.53). Hybridization between genotypes from distant clusters resulted in desirable recombinants.

Cluster VIII recorded highest mean for seed yield/plant, late maturity, length of main branch and 1000-seed weight (Table 3).

Table 3 Cluster mean and per cent contribution to total genetic divergence for different characters in sesame

Cluster No.	No. of genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Length of main branch (cm)	No. of branches/ plant	Capsule length (cm)	Capsules/ plant	Oil content (%)	Seeds/ capsule	1000-seed weight (g)	Seed yield/ plant (g)
I	45	44.8	95.3	89.6	58.1	2.7	2.6	44.4	48.5	56.5	3.2	5.1
II	1	43.0	95.7	67.7	47.1	2.3	2.6	40.4	48.0	60.7	3.0	4.9
III	4	41.3	92.3	72.2	50.1	2.5	2.5	40.5	48.3	51.6	3.3	4.1
IV	1	46.7	96.7	103.0	62.3	3.1	2.5	57.6	48.3	69.7	2.6	5.1
V	1	45.3	92.3	83.7	50.3	3.3	2.5	45.6	48.4	58.7	2.0	3.5
VI	1	48.3	96.0	91.0	50.2	2.7	2.5	39.7	48.2	71.3	2.5	3.5
VII	1	49.0	98.7	116.0	67.3	3.1	2.5	56.0	48.3	59.3	3.2	4.7
VIII	1	47.7	99.0	103.2	65.5	3.5	2.7	58.1	48.2	66.0	3.4	8.8
IX	1	46.7	96.7	96.4	56.3	3.7	2.6	49.0	48.4	49.1	3.0	5.0
X	1	45.3	96.0	91.8	52.9	2.9	2.9	66.5	48.5	50.3	3.1	6.7
XI	1	50.0	96.7	107.5	67.3	1.2	2.7	33.2	48.6	54.7	2.4	2.4
Per cent contribution to total genetic divergence		1.6	5.2	19.0	7.1	24.4	3.2	8.8	0.3	6.7	11.4	12.4

Cluster X recorded high mean seed yield and highest capsules/plant and their length. Cluster VII recorded highest plant height and length of main branch, whereas, cluster XI recorded highest oil content. Thus, the genotypes of outstanding mean performance from these clusters may be identified as potential parents and could be utilized in hybridization programme for developing high yielding varieties.

The maximum contribution towards genetic divergence is by branches/plant (24.41%) followed by plant height (18.98%), seed yield/plant (12.37%), 1000-seed weight (11.41%), capsules/plant (8.81%), length of main branch (7.06%) and seeds/capsule (6.72%). These characters should be given more emphasis for the purpose of further selection and choice of parents for hybridization. Similar results were also reported by Solanki and Gupta (2002), Raghuwanshi and Duhoon (2005) and Sudhakar *et al.* (2006).

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J. Oilseeds Res., **25**(2) : **193-196 (2008)**

Short communication

Combining ability studies for yield and its components in castor, *Ricinus communis* L.

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(Received: January, 2008; Revised: July, 2008; Accepted: October, 2008)

Abstract

The studies revealed that line DPC-9 and tester, RG-224 and RG-2779 were good general combiners for majority of yield component traits in castor.

Keywords: Castor, general combiner, tester

Castor, non-edible oilseed crop belongs to the family Euphorbiacea occupies a prime place in the country. The oil and its derivatives are being used in various industries as a lubricant, hydraulic fluids, printing inks, pharmaceutical, etc. The productivity of the crop in Andhra Pradesh is very low (404 kg/ha) due to the cultivation of age old varieties and non-adoption of improved crop production and protection technologies. Hence, there is an urgent need to develop high yielding varieties/hybrids with desirable agronomic traits and to achieve this, evaluation of germplasm lines, choosing best parents for crossing programme and identifying best hybrids is essential. The improvement in the seed yield depends on its component traits. For improving the yield potential of varieties and hybrids, the decision should be made on the choice of the right parents for hybridization. The knowledge of combining ability not only helps in the selection of parents for hybridization but also simultaneously illustrates the nature and magnitude of gene action governing the characters. Out of several methods, line x tester analysis helps in testing of large number of lines at a time. Therefore, the present study was planned to analyse the combining ability for yield and its components through line x tester mating design involving five lines and fifteen diverse males of castor.

The experimental material for this study comprised five elite lines and fifteen diverse testers chosen from the germplasm based on their desirable agronomic characters and wide genetic base. The resulting seventy five hybrids along with twenty parents were evaluated at College Farm, College of Agriculture, Rajendranagar, Hyderabad, during *rabi*, 2006-07. Recommended package of practices was followed with a spacing of 90 cm x 60 cm. Each plot consisted of three rows of five meter length. Observations were recorded on five randomly selected plants per plot for six characters *viz*., primary spike length (cm), effective spike length (cm), number of capsules/primary spike, 100 seed weight (g), seed yield/plant (g) and oil content (%). The data were further analyzed as per the method suggested by Kempthorne (1957).

The analysis of variance for combining ability revealed that both *gca* and *sca* variances were highly significant for all the characters studied indicating the importance of both additive and non-additive genetic variances in governing the inheritance of these traits. The estimates of general combining ability (GCA) and specific combining ability (SCA) variances, their ratios and gene action are presented in Table 1. General combining ability is genetically associated with additive gene action, while specific combining ability is due to dominance and epistasis. In present investigation, the perusal of results revealed that the variances due to GCA were higher in magnitude when compared with the variances due to SCA for the characters *viz*., number of capsules/primary spike and 100 seed weight which indicated the predominance of additive gene action, whereas non-additive gene action was predominant for the traits primary spike length, effective spike length, seed yield/plant and oil content as the SCA variances were higher than GCA variances. The estimates of gca effects revealed the line DPC-9 and testers RG-224, RG-2779 were found to be good general combiners for majority of the important yield components, i.e., seed yield, primary spike length, effective spike length and number of capsules/primary spike as they exhibited high means and recorded significant *gca* effects for these traits (Table 2). Favourable genes for oil content were predominantly contributed by RG-1471, DCS-9, RG-2724, RG-1471 and RG-224 by recording significant positive *gca* effects. On the contrary, RG-2374 was found to be poor combiner for important yield contributing characters by exhibiting negative values though it recorded significant positive *gca* effects for seed yield. It was observed that *per se* performance of parents for majority of the traits in general was related to their *gca* effects. Thus, if a trait is uni-directionally controlled by a set of alleles and additive effects are important, the choice of parents based on *per se* performance may be effective. As observed in present study similar findings were also reported by Mehta (2000), Tank *et al.* (2003) and Chandramohan *et al.* (2006).

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Table 1 Estimates of general and specific combining variances and proportionate gene action for six characters in castor

Character	$\sigma^2 gca$	$\sigma^2 sca$	$\sigma^2 gca/\sigma^2 sca$
Primary spike length	27.29	37.59	0.73
Effective spike length	32.51	47.92	0.68
Number of capsules/primary spike	43.84	34.96	1.25
100 seed weight	8.82	7.30	1.21
Seed yield/plant	733.12	1827.8	0.40
Oil content	0.54	1.29	0.42

Table 2 General combining ability (*gca*) effects of parents for six characters in castor

Parents	Primary spike length	Effective spike length	Number of capsules/ *primary spike*	100-seed weight	Seed yield/ plant	Oil content
Lines						
VP-1	7.89 **	8.05 **	4.15 **	0.32 *	11.10 **	-0.27 *
LRES-17	1.67 **	-0.12	-1.02	-0.10	16.62 **	-0.67 **
DPC-9	-2.98 **	0.82	2.63 **	3.54 **	10.42 **	0.31 *
Kranthi	-6.16 **	-7.10 **	-4.30 **	-2.19 **	-31.06 **	0.43 **
Kiran	-0.43	-1.64 **	-1.47 *	-1.57 **	-7.09 **	0.20
SE (g_i)	0.52	0.55	0.71	0.16	2.43	0.15
Testers						
48-1	1.15	2.04 *	2.88 *	2.88 *	24.52 **	0.46
Haritha	4.64 **	3.95 **	3.54 *	3.54 **	28.13 **	-2.47 **
DCS-9	-1.37	0.46	-3.08 *	-3.08 *	-2.08	1.77 **
DCS-5	-0.22	3.31 **	-0.13	-0.13	13.10 **	-0.06
RG-2724	-10.03 **	-10.92 **	-15.78 **	-15.78 **	-110.90 **	1.22 **
RG-178	-6.49 **	-10.65 **	-15.32 **	-15.32 **	-44.51 **	0.98
RG-1471	-10.21 **	-11.44 **	-16.40 **	-16.40 **	-9.01 *	2.00 **
RG-1468	3.53 **	2.02 *	0.34	0.34	-19.15 **	-1.96 **
RG-2374	-0.06	-1.23	-0.10	-0.10	13.72 **	0.29
RG-1713	1.08	-0.96	-0.25	-0.25	14.39 **	-2.35 **
RG-1719	-3.29 **	-2.81 **	-1.31	-1.31	16.01 **	-1.85 **
RG-224	10.49 **	14.15 **	30.40 **	30.40 **	80.50 **	1.06 **
RG-246	0.43	1.10	8.56 **	8.56 **	34.74 **	0.23
RG-2779	11.52 **	12.54 **	8.56 **	8.56 **	-28.08 **	0.15
RG-650	-1.17	-1.56	-1.91	-1.91	-11.39 **	0.52 *
SE (g_j)	0.90	0.96	1.40	1.23	4.22	0.26

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

The *sca* effects are of vital importance in heterosis breeding. For seed yield/plant, out of 26 crosses showing significant positive *sca* effects, 12 crosses had parents with high × high *gca* effects, 11 crosses had parents with high × low and 3 crosses had parents with low × low *gca* effects. The best hybrids on the basis of significant positive *sca* effects for seed yield/plant were LRES-17 × RG-1713, DPC-9 × RG-650, Kranthi × RG-246, VP-1 × RG-1719, DPC-9 × RG-178, Kiran × RG-2779, Kiran × RG-2374, DPC-9 × DCS-9, VP-1 × DCS-5 and Kranthi × RG-224. All of these hybrids recorded significant and desirable *sca* effects for one or more component traits of seed yield. In general, results revealed that as component traits of seed yield with significant and desirable effects increased, the value of *sca* effects for seed yield of hybrids also increased, e.g. the top ranking hybrid LRES-17 × RG-1713 recorded significant and desirable *sca* effects of all yield component traits. Similar findings were also reported by Mehta (2000) and Kanwal *et al.* (2006).

A comparison of five best cross combinations for various characters is presented in Table 3 The perusal of *sca* effects revealed that the *per se* performance of crosses had significant and positive correlation with *sca* effects for most of the traits studied. For seed yield/plant and other yield components the best performing hybrids were generally composed of good × good and good × poor combinations. The crosses with poor × poor combinations did not find place among the top performing hybrids for all the traits except oil content (the magnitude of *sca* effects were maximum in the better performing crosses, VP-1 × Haritha and LRES-17 × Haritha with low × low general combiners).

This indicated that one or both parents with good *gca* effects are desirable for producing high yielding early hybrids. Similar results were also reported by, Tank *et al.* (2003), Chandramohan *et al.* (2006), Kanwal *et al.* (2006) and Patel *et al.* (2007) who suggested that most of the superior combinations involved atleast one good general combiner and thus combining ability of parent might be considered as a reliable guide in the prediction of the yield potential of a cross. It also implies that there could be equal or proportionate distribution of favourable dominant genes among the parents which resulted in superior hybrids. This also emphasized the importance of judicious selection of parents for obtaining desirable hybrid combinations.

Table 3 Performance of five superior crosses for each of six characters in castor

Cross	*Per se* performance	*sca* effect	Parent 1		Parent 2	
			Per se performance	*gca* effect	*Per se* performance	*gca* effect
Primary spike length						
VP-1 × RG-2779	67.80	5.70 **	70.07	7.89 **	45.40	11.52 **
LRES-17 × RG-2779	67.67	11.79 **	52.33	1.67 **	45.40	11.52 **
VP-1 × RG-224	63.60	2.53	70.07	7.89 **	45.27	10.49 **
LRES-17 × RG-224	60.93	6.08 **	52.33	1.67 **	45.27	10.49 **
VP-1 × RG-2374	59.20	7.69 **	70.07	7.89 **	51.33	-0.06
Effective spike length						
VP-1 × RG-2779	62.13	6.56 **	63.27	8.05 **	42.00	12.54 **
VP-1 × RG-224	59.60	2.41	63.27	8.05 **	43.60	14.15 **
LRES-17 × RG-224	58.53	9.52 **	47.47	-0.12	43.60	14.15 **
LRES-17 × RG-2779	57.07	9.67 **	47.47	-0.12	42.00	12.54 **
VP-1 × DCS-5	50.27	4.42 *	63.27	8.05 **	28.47	3.31 **
Number of capsules per primary spike						
VP-1 × RG-224	88.60	6.22 *	60.33	4.15 **	75.40	30.40 **
Kranthi × RG-224	87.27	13.34 **	43.40	-4.30 **	75.40	30.40 **
LRES-17 × RG-224	85.53	8.32 **	44.00	-1.02	75.40	30.40 **
DPC-9 × RG-224	67.93	-12.92 **	58.27	2.63 **	75.40	30.40 **
VP-1 × Haritha	63.40	7.88 *	60.33	4.15 **	53.53	3.54 *
100 seed weight						
DPC-9 × RG-650	46.30	5.24 **	30.30	3.54 **	43.60	4.28 **
LRES-17 × RG-1471	45.10	4.08 **	28.20	-0.10	52.00	7.88 **
DPC-9 × RG-1471	44.50	-0.16	30.30	3.54 **	52.00	7.88 **
VP-1 × RG-1719	44.30	7.76 **	29.37	0.32 *	42.80	2.98 **
Kiran × RG-1471	41.77	2.23 **	23.80	-1.57 **	52.00	7.88 **
Seed yield per plant						
LRES-17 × RG-1713	325.47	84.25 **	168.51	16.62 **	204.69	14.39 **
VP-1 × RG-224	315.46	25.14 **	206.96	11.10 **	200.34	80.50 **
LRES-17 × RG-224	311.56	19.12 *	168.51	16.62 **	200.34	80.50 **
Kranthi × RG-224	302.78	43.13 **	205.19	-31.06 **	200.34	80.50 **
VP-1 × RG-1719	297.82	60.50 **	206.96	11.10 **	182.52	16.01 **
Oil content						
DPC-9 × RG-650	52.76	1.76 **	52.58	0.31 *	50.79	0.52 *
VP-1 × Haritha	52.64	1.24 *	48.65	-0.27 *	52.06	-2.47 **
DPC-9 × RG-246	52.62	1.65 **	52.58	0.31 *	50.77	0.23
LRES-17 × Haritha	52.57	1.26 *	47.83	-0.67 **	52.06	-2.47 **
VP-1 × RG-1471	52.39	1.86 **	48.65	-0.27 *	50.46	2.00 **

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

However, better performance of some hybrids with higher *sca* effects involving low × low general combiners, suggested the role of epistatic gene action (dominance × dominance) which may be due to genetic diversity in form of heterozygous loci. Similar results were also given by Dobariya *et al.* (1989) and Solanki and Joshi (2001) for oil content in castor and Pathak *et al.* (1989) for primary spike length and 100 seed weight.

A comparison of *per se* performance of the top five hybrids and their *sca* effects revealed that hybrids resulted from good × good general combiners ranked first with significant *sca* effects for all the traits, which indicated that additive gene action has contributed towards better expression of the traits. Looking to the magnitude of variances it was obvious that both types of gene actions governed characters under this investigation. Under such circumstances the parents with high *gca* effects and the cross combinations with high *sca* effects should be considered for the commercial exploitation of heterosis. The results are in accordance with the earlier reports of Kavani *et al.* (2001) and Kanwal *et al.* (2006).

For further work crosses with high *per se* performance, positive and significant *sca* effects and high heterosis for seed yield may be exploited for commercial cultivation by testing them over locations and years.

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J. Oilseeds Res., **25**(2) : **197-199 (2008)**

Short communication

Effect of Zn and Fe on yield of rainfed castor, *Ricinus communis* L.

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(Received: May, 2007; Revised: July, 2008; Accepted: August, 2008)

Abstract

The studies revealed that application of 12.5 kg $ZnSO_4$ + 25 kg $FeSO_4$/ha in castor as basal dose in conjunction with recommended NPK is recommended for higher productivity and benefits.

Keywords: Castor, $FeSO_4$, $ZnSO_4$, NPK

Castor (*Ricinus communis* L.) occupies an important place in the country's vegetable oil economy. During recent years, castor has emerged as a commercial crop with immense export potential earning valuable foreign exchange. India accounts for 54% of global castor area and 51% of the world castor production and ranks first in the area and production in the world. It ideally suits dry land farming in *kharif* and with limited irrigations in post-monsoon both in traditional and non-traditional areas. Castor is considered to be a good contingent crop in case of monsoon aberrations providing a cushion to resource-poor farmers of rainfed areas.

In Tamil Nadu, farmers raise local varieties of castor under rainfed condition as an intercrop with groundnut. The farmers seldom apply fertilizers and do not apply micronutrient fertilizers resulting in poor yields. In Tamil Nadu, the deficiencies of Zn and Fe have been reported to be 52 and 22 % of soils, respectively. The soil pH governs the solubility and consequently the availability of Zn and Fe to plants. The presence of $CaCO_3$ in soil also affects the availability of Fe through surface reaction by increasing the hydroxyl ion concentration. Fine textured soils retained major part of applied Fe in unavailable forms because of surface adsorption and only small fraction is made available. Kanwar (1976) reported that in soils with 2:1 type of clay minerals, Zn deficiency occurs due to entrapment of Zn in the inter-lattice wedge zones of clay structure when these zones expand due to hydration and contract upon drying.The micronutrients improve the chemical composition of seeds and general condition of plants. There is no information on the Zn and Fe nutrition of rainfed castor and the present investigation was therefore carried out to find out the micronutrient requirement of castor hybrid TMVCH1. A field trial was carried out in the farmer's field at Elachipalayam during *kharif* 2003 with seven treatments replicated thrice adopting Randomized Block Design with TMVCH1 castor. A uniform does of 12.5 tonnes of FYM /ha and 30:15:15 kg NPK/ha was applied to all the plots. Application of $ZnSO_4$ and $FeSO_4$ was done as basal dose as per the treatments. The soil was characterized by clay loam in texture, deficient in available Zn (0.7 ppm) and available Fe (3.2 ppm) and was alkaline (pH 8.2) and EC (0.3 dS/m). The treatments comprised T_1-12.5 kg $ZnSO_4$/ha; T_2-25.0 kg $ZnSO_4$/ha ; T_3-25.0 kg $FeSO_4$/ha; T_4-50.0 kg $FeSO_4$/ha; T_5-12.5 kg $ZnSO_4$ + 25.0 kg $FeSO_4$/ha; T_6-25.0 kg $ZnSO_4$ + 50 kg $FeSO_4$/ha and T_7-Control (Recommended N,P and K alone). At the time of harvest, the seed yield was recorded. Post harvest soil samples were collected and analyzed for available Zn and Fe and the data were subjected to statistical analysis (Panse and Sukhatme, 1978). The benefit cost ratio for different treatments was worked out considering gross returns and cost of cultivation .

Soil available Zn

Application of 25.0 kg $ZnSO_4$ + 50.0 kg $FeSO_4$/ha (T_6) registered the highest available Zn (1.60 ppm), while the control treatment (NPK alone) recorded the lowest available Zn(0.73 ppm) in the soil (Table 1). The soil Zn availability was maintained fairly at a higher level than NPK treatment and it continued to maintain the DTPA-Zn at a higher level. The availability of Zn has possibly increased partly due to the release of higher content of Zn (Kher, 1993) from $Zn_3(PO_4)_2\,4H_2O$ through dissolution of zinc phosphate as reported by Jurinak and Invouye (1962). Such increase in the concentration of any nutrient in soil solution on addition of adequate nutrients through fertilizer materials is in consonance with natural reaction of soil. This is because, soil acts as sink for such added material provided, there is no appreciable losses of added nutrients.

Soil available Fe

Application of 25.0 kg $ZnSO_4$ + 50.0 kg $FeSO_4$/ha showed the highest available Fe (4.27 ppm) followed by 12.5kg $ZnSO_4$ + 25.0 kg $FeSO_4$ (3.40 ppm) while the control treatment (NPK alone) recorded the lowest available Fe (2.33 ppm) in the soil samples (Table 1). The enhancement in DTPA-Fe due to the release of Fe from the native reserves in the presence of Zn (Gupta *et al.*, 1988). The enhanced Fe availability might be by the transformation of Fe in solid phase to soluble metal complexes (Nagendra Rao *et al.*, 1988) which are readily available by extractants such as DTPA, citric acid, etc.

Seed yield

Application of 12.5 kg $ZnSO_4$ + 25 kg $FeSO_4$ offered substantially higher castor seed yield (1545 kg/ha) closely followed by the application of 12.5 kg $ZnSO_4$ and 25.0 kg $FeSO_4$ (1482 kg/ha) while the control treatment recorded the lowest seed yield of 1290 kg/ha (Table 1). The application of $ZnSO_4$ and $FeSO_4$ along with NPK would have established balanced nutrient status during the active growth period supplying the Zn and Fe continuously in available form, thereby could have increased the plant growth and ultimately the crop yields. The same trend of results in castor was reported by AICORPO on Castor at S.K. Nagar centre (Anonymous, 2005). The seed yield increase over NPK due to application of $ZnSO_4$ @ 12.5 kg and 25.0 kg/ha was to the tune of 6.2 and 8.4 % respectively. With the application of $FeSO_4$ @ 12.5 and 25.0 kg/ha, the seed yield increase was 4.2 and 10.7%, respectively. The seed yield increase due to combined application of $ZnSO_4$ + $FeSO_4$ ranged from 15.0 to 19.8 % compared to the application of NPK alone. The yield response to Zn application was due to deficiency of Zn in the experimental soil (Sakal *et al.*, 1988).

The enhanced yield due to the Zn application could be due to the involvement of Zn in many metallo enzyme systems, regulatory functions and in auxin production. The other bio-parameters that could have helped in the increased yield were synthesis of carbohydrates and their translocation to the storage sinks because of better growth and more number of capsules/plant due to the application of $ZnSO_4$ which corroborates with the report of Suryanarayana Reddy *et al.*(1986) in Brinjal. Also the beneficial effect of applied Zn could be ascribed to the complementary effect of Zn on N. As N is believed to be the most important element, its increased availability by the indirect activation of Zn addition to soil might have accelerated the N absorption mechanism by the plant and subsequent bio-conversion of N into biomass generation. The favourable effect of Zn and Cu on fruit yield also could be attributed to their effect in maintaining an optimum balance of nutrients in the plant for better growth in Brinjal (Lindsay and Norwell, 1978; Dhakshinamoorthy and Krishnamoorthy, 1989). The favourable effect of n may be ascribed to its involvements in the synthesis of tryptophan, the precursor of indole acetic acid in plants, which is chiefly concerned with terminal growth of plants. Besides, it could have increased adenine dihydrogenase activity resulting in higher ATP production and reduction of glutamate dehydrogenase activity (Moore and Patrick, 1988).

Benefit Cost ratio

Pre-sowing application of 12.5 kg $ZnSO_4$ + 25.0 kg $FeSO_4$/ha as basal accrued the highest B:C ratio of 2.59, while the lowest B:C ratio of 2.38 was obtained by the application of 25.0 kg $ZnSO_4$/ha as basal. For the effective fertilizer management in castor and to realise the higher yield as well as B:C ratio, application of 12.5 kg $ZnSO_4$ + 25.0 kg $FeSO_4$/ha as basal in conjunction with recommended NPK is recommended. Though the higher levels of application of $ZnSO_4$ and $FeSO_4$ recorded 19.8 % of yield increase over NPK, it was found comparable with the application of 12.5 kg $ZnSO_4$ + 25.0 kg $FeSO_4$/ha as basal (15.0 % increase). However, the latter recorded the highest BC ratio of 2.59 among all the treatments. Hence in Zn and Fe deficient soils of Tamil Nadu, soil application of 12.5 kg $ZnSO_4$ and 25.0 kg $FeSO_4$/ha can enhance yields of castor under rainfed conditions.

Table 1 Effect of Zn and Fe nutrition on available Zn and Fe, castor seed yield and B:C ratio (2003-04)

Treatment	Available Zn (ppm)	Available Fe (ppm)	Seed yield (kg/ha)	*B:C ratio*	Per cent yield increase over NPK	Gross return (Rs/ha)	Cost of production (Rs/ha)
12.5 kg $ZnSO_4$/ha as basal	1.0	2.4	1370	2.47	6.2	21920	6313
25.0 kg $ZnSO_4$/ha as basal	1.3	2.6	1399	2.38	8.4	22384	6625
25.0 kg $FeSO_4$/ha as basal	0.8	2.7	1344	2.41	4.2	21504	6300
50.0 kg $FeSO_4$/ha as basal	0.6	3.0	1428	2.46	10.7	22848	6600
12.5 kg $ZnSO_4$ + 25.0 kg $FeSO_4$ as basal	1.2	3.4	1482	2.59	15.0	23712	6613
25.0 kg $ZnSO_4$ + 50 kg $FeSO_4$ as basal	1.6	4.3	1545	2.42	19.8	24720	7225
Control (Recommended N, P, K)	0.7	2.3	1290	-	-	20640	6000
CD (P=0.05)	0.3	0.6	48	-	-	-	-

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J. Oilseeds Res., **25**(2) : **200-202** (2008)

Short communication

Combining ability for yield and its components in castor, *Ricinus communis* L.

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(Received: March, 2007; Revised: July, 2008; Accepted: August, 2008)

Abstract

Combining ability for seed yield and its components in castor revealed that number of branches/plant and 100-seed weight, non-additive gene action was more important indicating hybrid breeding programme will be more useful for improving the seed yield.

Keywords: Castor, *Ricinus communis*, combining ability

The availability of pistillate lines in castor (*Ricinus communis* L.) has made it feasible it exploit heterosis in castor on commercial scale. A number of pistillate and staminate lines are now being used in the hybrid breeding programme of castor. Information on combining ability of pistillate lines and promising staminate lines would be useful to formulate crossing programme for development of new hybrid for commercial cultivation. Hence, a line x tester analysis was undertaken to obtain information on combining ability for yield, its attributes and other characters.

Six pistillate lines (VP 1, Geeta, JP 65, JP 83, SKP 42 and SKP 106) and five male parents (SKI 266, SKI 267, SKI 268, SKI 271 and SKI 280) selected based on their desirable agronomical characters were crossed in a line x tester mating design. Thirty hybrids along with eleven parents and four checks (GC 2, GCH 4, GCH 5 and GCH 6) were evaluated in Randomized Block Design with three replications at Main Castor-Mustard Research Station, Sardarkrushinagar during *kharif* 2002-03. Each plot comprised of 10 plants having inter and intra row spacing of 90 cm x 60 cm. Observations were recorded on five randomly selected plants for 10 characters *viz.*, days to 50% flowering, days to maturity, plant height up to main raceme, number of nodes upto main raceme, length of main raceme (cm), number of capsules on main raceme, number of effective branches/plant, seed yield/plant (g), 100-seed weight (g) and oil content (%). The data were statistically analysed to study combining ability according to the method suggested by Kempthorne (1957).

The variance due to parents was highly significant for all the characters, which indicate sufficient variability in the experimental material selected for the study. A comparison of parents vs hybrids (Table 1) revealed highly significant differences between parents and hybrids for all the characters except number of capsule on main raceme, indicating a substantial amount fo hybrid vigour in the crosses.

Table 1 Analysis of variance (mean square) for combining ability and estimates of components for different characters in castor

Source of variation	d.f.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of nodes upto main raceme	Length of main raceme (cm)	No. of capsules on main raceme	No. of effective branches/ plant	Seed yield/ plant (g)	100-seed weight (g)	Oil content (%)
Replications	2	2.008	24.447**	231.803**	0.755	360.520**	170.255	1.833**	109.423	0.023	0.182
Genotypes	40	89.827**	92.391**	604.156**	9.350*	184.340**	475.538**	4.967**	2115.084**	19.064**	1.581**
Parent	10	33.721**	122.158**	1006.148**	12.171**	288.979**	864.153**	4.448**	1337.855**	8.683**	4.250**
Female	5	22.322**	138.622**	1882.865**	12.185**	424.213**	1121.180**	9.244**	2224.989**	3.104**	6.586**
Male	4	38.933**	115.567**	75.073	8.009**	124.004**	377.391**	0.233	414.067**	9.999**	0.565
Female vs. Male	1	69.868**	66.198**	346.865*	28.747**	272.711**	1526.070**	1.327**	597.334**	31.317**	7.31**
Hybrids	29	70.632**	50.775**	467.449*	7.859**	3.395**	356.036**	118.786**	0.266	0.266	1711.948**
Parents vs. Hybrids	1	1207.54**	1001.561**	548.725**	24.371**	51.762**	54.938	1039.04**	13.025**	13.025**	2157.32**
Error	80	0.716	2.439	71.547	1.154	0.183	58.809	31.561	0.299	0.337	80.606
SEm±		0.488	0.902	4.884	0.620	3.244	4.428	0.247	5.183	0.316	0.335

* = Significance at P=0.05 levels; ** = Significance at P=0.01 levels

Mean square due to female were higher than those of male, suggesting greater diversity among the females for all the characters except days to 50% flowering and 10 seeds weight. However, males showed greater variation for days to 50% flowering and 100 seed weight. The variance components due to females (σ^2_f) were higher than those due to males (σ^2_m) for *all* the characters except number of capsules on main raceme and length of main raceme. The estimation of *sca* variance were considerably higher than *gca* variance (pooled) for days to 50% flowering, days to maturity, number of effective branches/plant, seed yield, 100-seed weight and oil content indicating preponderance of *non-additive gene* action in the inheritance of these traits. However, for plant height upto main raceme, number of nodes upto main raceme, number of capsules on main raceme and length of main raceme, *gca* variances were higher in magnitude than *sca* variances suggesting additive gene action for control of these traits. Lavanya and Chandramohan (2003), Solanki *et al.* (2004) and Tank *et al.* (2003) also observed non-additive gene action for seed yield and related traits.

Among the female, JP 65 and SKP 42 were the best general combiners for seed yield (Table 2). Female lines, VP 1, JP 65 and SKP 106 were good combiners for days to 50% flowering, days to maturity, plant height upto main raceme and number of nodes upto main raceme.

Table 2 Estimates of mean and general combining ability (*gca*) effects of the female parents for various characters in castor

Characters		VP 1	Geeta	JP-65	JP-83	SKP 42	SKP 106
Days to 50% flowering	$\bar{x}$	59.66	63.33	59.00	60.66	59.66	66.00
	gca	-2.589**	6.944**	-4.722**	1.811**	-0.322	-1.122**
Days to maturity	$\bar{x}$	124.0	122.00	114.00	127.00	111.66	128.00
	gca	-1.578**	3.489**	-3.244**	-0.111	1.622**	-0.178
Plant height (cm)	$\bar{x}$	25.53	93.35	46.87	64.92	40.87	31.40
	gca	-10.816**	19.384**	-11.869**	6.624**	0.478	-3.802
No. of nodes upto main raceme	$\bar{x}$	13.80	19.33	16.40	17.83	18.53	18.47
	gca	-1.524**	2.089**	-1.738**	0.476	0.529	0.169
Length of main raceme (cm)	$\bar{x}$	46.73	53.13	51.33	27.00	62.87	50.93
	gca	-0.831**	0.596**	-0.204	0.316**	-0.364**	0.489**
No. of capsules on main raceme	$\bar{x}$	60.07	91.15	64.13	37.83	86.33	66.33
	gca	-4.184*	7.149**	-2.224	0.109	3.576	-4.424*
No. of effective branches/plant	$\bar{x}$	1.27	6.00	4.00	1.60	2.66	2.47
	gca	-1.736	-0.589	-2.909*	-1.762	6.211**	0.784
Seed yield/plant (g)	$\bar{x}$	30.33	98.66	50.33	22.00	36.00	45.00
	gca	-0.980**	-0.013	1.473**	-0.647**	2.598**	-2.431**
100-seed weight (g)	$\bar{x}$	25.47	25.03	27.91	26.40	26.31	26.83
	gca	-0.130	0.092	-0.327*	0.082	-0.110	0.9393*
Oil content (%)	$\bar{x}$	49.26	48.69	47.52	45.28	48.86	48.77
	gca	-12.767**	19.233**	-8.500**	2.833	-3.300	2.500

In addition, Geeta, JP 83 and SKP 106 for length of main *raceme, Geeta for number of capsules on main raceme,* SKP 42 for number of effective branches/plant, SKP 106 for 100-seed weight and Geeta for oil content were found to be good general combiners. Among the males, SKI 267 and SKI 280 were best general combiners for the seed yield, SKI 280 for days to 50% flowering and days to maturity, SKI 267 for plant height upto main raceme and number of nodes upto main raceme, SKI 268 for length of main raceme, number of capsules on main raceme and number of effective branches/plant and SKI 280 for oil content (Table 3). The *sca* effects represent dominance and epistatic gene action and can be related to heterosis. The estimation of *sca* effect revealed than the best cross combiners were Geeta x SKI 266, Geeta x SKI 268, JP 65 *x SKI 268, JP 65 x SKI 271, JP 83 x SKI 266, JP 83 x SKI* 267, SKP 42 x SKI 271 and SKP 106 x SKI 280 for seed yield; VP 1 x SKI 267, Geeta x SKI 280, JP 65 x SKI 267, SKP 42 x SKI 266 and SKP 106 x SKI 268 for days to 50% flowering and days to maturity; Geeta x SKI 280 and SKP 106 x SKI 268 for plant height upto main raceme; JP 65 x SKI 271 for length of main raceme; SKP 42 x SKI 266 and SKP 106 x SKI 271 for number of capsules on main raceme; Geeta x SKI 268, JP 65 x SKI 266, JP 65 x SKI 268, JP 83 x SKI 266, JP 83 x SKI 280, SKP 42 x SKI 267, SKP 42 x SKI 271 and SKP 106 x SKI 280 for number of effective branches/plant; VP 1 x SKI 280, Geeta x SKI 266, JP 65 x SKI 268, JP 65 x SKI 271, JP 83 x SKI 267, JP 83 x SKI 271, SKP 42 x SKI 266 and SKP 106 x SKI 280 for 100-seed weight. The hybrid SKP 106 x SKI 280 with high positive *sca* effect for seed yield, number of effective branches/plant and 100-seed weight may be exploited through further breeding programme. The hybrid Geeta x *SKI 266, JP 83 x SKI 267, SKP 42 x SKI 271* and JP 65 x SKI 271 showed high *sca* effect for seed yield which can be also used for exploiting hybrid vigour in castor. The majority of crosses showed significant *sca* effect for all the characters except oil content involve at least one good general combiner suggesting additive x dominant type of gene action. The crosses JP 65 x SKI 268 and JP 65 x SKI 271 for yield; JP 65 x SKI 271 for length of main raceme; VP 1 x SKI 267 and JP 65 x SKI 266 for number of effective branches/plant; VP 1 x SKI 280, Geeta x SKI 2686 and SKP 106 x SKI 280 for 100-seed weight. Geeta x SKI 268 involve low x low combiner and produce high *sca* effect indicating epistatic gene action for this character which may be due to genetic diversity in the form of heterozygous loci for specific trait. Golakia *et al.* (2004), Lavanya and Chandramohan (2003) and Solanki and Joshi (2000) also observed low x low combiner produced high *sca* effect indicating epistatic gene action for this character. The results revealed that for seed yield and its major attributes *viz.*, number of effective branches/plant and 100-seed weight, non-additive gene action was more important indicating hybrid breeding programme will be more useful for improving the yield.

Table 3 Estimates of mean and general combining ability (*gca*) effects of the male parents for various characters in castor

Characters		SKI 266	SKI 267	SKI 268	SKI 271	SKI 280	σ^2*gca*	σ^2*sca*	σ^2*gca*/σ^2*sca*
Days to 50% flowering	$\bar{x}$	59.00	60.33	59.00	61.66	52.33	8.651**	10.680**	0.81
	gca	-0.211	-0.100	1.678**	0.956**	-2.32**			
Days to maturity	$\bar{x}$	120.33	119.33	118.00	125.33	108.33	4.589**	11.916**	0.385
	gca	-0.544	1.067**	-0.99**	2.844**	-2.38**			
Plant height (cm)	$\bar{x}$	61.33	51.93	61.20	59.27	51.27	63.47**	18.3108*	3.466
	gca	3.018	-4.12**	1.651	1.573	-2.127			
No. of nodes upto main raceme	$\bar{x}$	16.27	14.47	14.93	18.00	13.93	1.187**	0.1364	8.70
	gca	0.329	-1.22**	0.440*	0.729**	-0.282			
Length of main raceme (cm)	$\bar{x}$	45.27	38.47	52.53	42.13	36.07	0.2141	1.007**	0.213
	gca	-0.178*	-0.51**	0.256**	-0.067	0.500**			
No. of capsules on main raceme	$\bar{x}$	57.80	45.80	70.80	51.13	42.40	44.27**	41.96**	1.055
	gca	-1.342	-0.653	11.65**	2.091	-11.74**			
No. of effective branches/plant	$\bar{x}$	3.07	3.53	3.13	3.66	3.60	12.56**	12.354*	1.016
	gca	0.242	-0.391	6.687**	-1.902	-4.64**			
Seed yield/plant (g)	$\bar{x}$	65.00	45.00	54.33	43.66	70.00	105.295	526.66**	0.199
	gca	-1.59**	1.413**	-0.82**	1.228**	-0.239*			
100-seed weight (g)	$\bar{x}$	28.59	29.19	26.05	30.65	26.12	2.775**	3.639**	0.762
	gca	0.058	-0.015	0.111	-0.202	0.048			
Oil content (%)	$\bar{x}$	49.36	48.31	49.12	48.90	49.39	0.015**	0.078	0.198
	gca	-9.00**	-0.558	-0.722	-6.11**	16.39**			

* = Significant at P=0.05 level; ** = Significant at P=0.01 level

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J. Oilseeds Res., **25**(2) : **203-205 (2008)**

Short communication

Genetic analysis of quantitative traits in castor, *Ricinus communis* L.

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(Received: August, 2007; Revised: August, 2008; Accepted: September, 2008)

Abstract

The combining ability revealed that parents of castor *viz.*, SKI 205 and SPS-38-8 were good general combiners for yield and its components

Keywords: Variability, castor, combining ability

Castor, *Ricinus communis* is grown for industrial oil in Gujarat, Rajasthan and Maharashtra under irrigated condition (Damodaram and Hegde, 2002). Constant efforts to increase yield through hybridization and selection of the parents for heterotic breeding are important in crop improvement programmes. Hence, the information about combining ability is of immense help to the plant breeder in the choice of suitable parents. Hence, the combining ability of parents and nature of gene effects of yield and its components, was studied in castor using diallel analysis.

Ten diverse parental lines of castor *viz.*, SKI 205, SH 21, SKI 109, SKI 226, SPS 38-8, VI 9, SKI 291, SKI 294, SKI 299 and SKI 304 were crossed in 10 x 10 diallel fashion excluding reciprocals. The experimental material comprising 55 entries, which included 10 parental lines, 45 F_1s and a standard check (GCH 5) was evaluated for eleven different characters in Randomized Block Design with three replications at the Agronomy Instructional Farm, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar (Gujarat) during *kharif* 2005-2006. The plot size consisted of single row of parents and F_1s having 9.0 m length with inter and intra row spacing of 90 cm and 60 cm respectively allowing a total of 15 plants/row. Fertilizer, irrigation, plant protection and other cultural practices were adopted according to agronomical recommendations for raising the crop. Observations were recorded on five competitive plants selected randomly in each genotype in each replication for yield and its components traits. Data were subjected to standard statistical methods for analysis of variance. Combining ability analysis was computed as suggested by Jinks (1954), Griffing's (1956) Method-2, Model-I (fixed model).

It is revealed that mean squares due to general combining ability and specific combining ability were highly significant for all the characters (Table 1). The ratio of *gca* to *sca* genetic variance for various characters indicated that non-additive type of gene action was predominant in the expression of all the traits except for days to 50% flowering. The additive gene action played greater role in the inheritance of days to 50% flowering. These results are in accordance with the findings of Kanwal (2002) and Ramu *et al.* (2002) for seed yield/plant and other characters. The analysis of general combining ability effects of the parents (Table 2) revealed that none of the parents was good general combiner for all the characters. Five parental lines *viz.*, SKI 205, SPS-38-8, VI-9, SH 21 and SKI 226 exhibited good general combining ability effects for seed yield/plant and majority of its component traits. Among these, SKI 205 was the best general combiner as it possessed significant positive *gca* effects for seed yield/plant, days to 50% flowering, days to maturity of main spike, plant height, number of nodes up to main spike, number of capsules on main spike, number of effective branches/plant and harvest index in the desired direction but was poor general combiner for 100-seed weight and oil content. The second promising parent SPS 38-8 was superior as its genetic make up showed good general combining ability for seed yield as well as traits imparting earliness, effective length of main spike, number of capsules on main spike, 100-seed weight and average combiner for harvest index. Hence, it is worthwhile to use above parental lines in hybridization programme for the improvement in seed yield/plant in castor breeding.

Specific combining ability effects of crosses revealed that none of the crosses was consistently good for all the traits. However, as many as thirteen cross combinations exhibited significant and positive *sca* effects for seed yield/plant. These eight best specific combiners with their mean performance, *gca* effects of parents and their significant response to other traits are presented in Table 3. All these crosses showed significant positive response to two or more yield components indicating its direct effect for increasing seed yield/plant. The cross, SKI 205 x SH 21 with highest significant sca effects for seed yield/plant also recorded significant desirable *sca* effects for plant height number of effective branches/plant and harvest index. Another cross, SKI 294 x SKI 304 showed significant positive *sca* effects for seed yield/plant and dwarfness. The cross SKI 205 x SKI 226 recorded significant *sca* effects in desirable direction for seed yield/plant also possessed significant desirable sca effects for days to maturity of main spike, plant height, number of capsules on main spike and 100-seed weight.

The crosses with highest *sca* effects for seed yield/plant and other yield components were also good in *per se* performance (Table 3). These *per se* performance of a cross itself indicates its good *sca* effect. From this condition, it can be ascertained that additive and/or non-additive gene effects were involved in the expression of yield and other traits among top ranking crosses. A combination of the good general combiners was not necessarily the best cross combination for plant height, nor was a poor x poor cross always a poor combination. This indicated involvement of non-additive gene effects along with interallelic interaction in *sca*.

Table 1 Analysis of variance for combining ability, estimates of components of variance and their ratios for different characters in castor

Source of variation	d.f.	Days to 50% flowering	Days to maturity of main spike	Plant height (cm)	No. of nodes up to main spike	Effective length of main spike (cm)	No. of capsules on main spike	No. of effective branches/ plant	Seed yield/plant (g)	100-seed weight (g)	Harvest index (%)	Oil content (%)
GCA	9	192.56**	540.18**	492.76**	22.95**	156.77**	1361.18**	2.79**	53121.54**	30.34**	8.26**	1.53**
SCA	45	15.37**	70.48**	154.15**	3.08**	61.22**	681.76**	1.06**	32100.87**	7.18**	12.57**	1.20**
Error	108	1.43	4.18	1.32	0.28	7.70	14.23	0.07	662.11	0.05	0.36	0.40
$\hat{\sigma}^2_{gca}$		15.93	44.67	40.95	1.89	12.42	112.25	0.23	4371.62	2.52	0.66	0.10
$\hat{\sigma}^2_{sca}$		14.50	66.30	152.83	2.80	53.52	667.54	0.99	31438.77	7.12	12.21	0.80
$\hat{\sigma}^2_{gca} / \hat{\sigma}^2_{sca}$		1.09	0.67	0.27	0.67	0.23	0.17	0.23	0.14	0.35	0.05	0.12

* and ** significant at P=0.05 and 0.01 levels, respectively.

Table 2 Estimates of general combining ability effects of parents for eleven characters in castor

Parents	Days to 50 % flowering	Days to maturity of main spike	Plant height (cm)	No. of nodes up to main spike	Effective length of main spike (cm)	No. of capsules on main spike	No. of effective branches/ plant	Seed yield/ plant (g)	100-seed weight (g)	Harvest index (%)	Oil content (%)
SKI 205	-0.92**	-9.51**	-3.94**	-0.45**	-4.58**	8.48**	0.45**	131.18**	-0.01	0.34*	-0.26
SH 21	-4.27**	4.01**	2.38**	-0.40**	-3.76**	-3.82**	-0.17*	25.76**	1.25**	0.03	0.24
SKI 109	5.40**	5.80**	6.64**	1.52**	-0.06	-3.46**	0.71**	-28.70**	-0.07	-0.38*	0.25
SKI 226	1.55**	0.72	1.57**	-0.31*	0.74	-6.54**	-0.01	14.73*	-0.19**	1.36**	0.81**
SPS-38-8	-4.50**	5.02**	13.93**	3.26**	8.53**	22.90**	-0.68**	58.39**	3.07**	0.12	-0.01
VI-9	3.94**	-0.88	-1.84**	-0.83**	0.20	10.36**	-0.30**	42.43**	0.15*	0.84**	-0.45**
SKI 291	-4.15**	-0.43	-6.59**	-1.28**	0.99	-3.11**	-0.21**	-72.89**	-2.09**	-0.45**	-0.09
SKI 294	-3.98**	-10.87**	-6.27**	-1.09**	1.43	-4.08**	-0.34**	-76.54**	1.26**	-1.77**	-0.09
SKI 299	4.14**	10.19**	-1.42**	-0.45**	-1.58*	-8.58**	0.77**	-54.13**	-1.89**	-0.12	-0.28
SKI 304	2.79**	-4.04**	-4.46**	0.06	-1.91*	-12.17**	-0.21**	-40.21**	-1.49**	0.04	-0.12
SEm.±	0.33	0.56	0.31	0.15	0.76	1.03	0.07	7.05	0.06	0.17	0.17

* and ** significant at P=0.05 and 0.01 levels, respectively.

The cross SKI 205 x SH 21 with good x average general combiners registered the highest sca effects for seed yield/plant but with respect to per se performance, it stood sixth. This indicated that the parents with higher *gca* effects are desirable for a cross having high *sca* effects for realization of maximum heterosis. The present study indicated that there was no correspondence between high ranking *sca* effects and the *per se* performance of the crosses for most of the traits. It can be concluded from this trend in the present population that, the high magnitude of *sca* effects alone are not sufficient for good performance of a cross. At least one parent should be good general combiner along with high degree of *sca* effects for better performance of a cross. The presence of predominantly large amount of non-additive gene action indicated the necessity for maintenance of heterozygosity in the population. Breeding methods such as biparental mating followed by reciprocal recurrent selection may increase frequency of genetic recombination and hasten the rate of genetic improvement for seed yield/plant and other yield components. The characters like days to 50% flowering predominantly governed by additive gene action can be improved profitably following pedigree method of breeding in the population under study. The two parental lines *viz.*, SKI 205 and SPS-38-8 were good general combiners for seed yield/plant and its component traits, hence, identified as promising lines for their exploitation in practical plant breeding. Two crosses *viz.*, SKI 205 x SKI 226 and SKI 294 x SKI 304 can be exploited in practical plant breeding for selection of better transgressive segregants.

Table 3 **Best three crosses showing significant desirable *sca* effects along with *gca* of their parents and *per se* performance for different characters in castor**

Characters	Crosses	sca effects	gca of the parents	Per se performance	Rank on the basis of mean value
Seed yield/plant (g)	SKI 205 x SH 21	519.04**	G x A	553.51	6
	SKI 294 x SKI 304	373.50**	P x A	630.10	2
	SKI 205 x SKI 226	305.34**	A x P	824.61	1
Days to 50 % flowering	SKI 291 x SKI 299	-8.58**	G x P	52.67	44
Days to Maturity of main spike	SKI 291 x SKI 299	-22.02**	A x P	103.73	37
	SKI 294 x SKI 299	-18.97**	G x P	96.33	44
	SKI 109 x SKI 294	-10.92*	P x G	100.00	42
Plant height (cm)	SKI 291 x SKI 304	-19.14**	G x G	43.07	45
	SKI 205 x SH 21	-14.69**	G x P	57.00	41
	SKI 226 x SKI 294	-13.48**	P x G	55.07	44
No. of nodes up to main spike	*SKI 205 x SPS-38-8*	-4.55**	G x P	15.32	30
	SKI 109 x SKI 299	-2.45**	P x G	15.66	26
	SKI 226 x SKI 299	-2.28**	G x G	14.00	43
Effective length of main spike (cm)	SPS-38-8 x SKI 294	23.20**	G x A	82.44	1
	SKI 226 x SPS-38-8	12.64**	A x G	69.65	2
	SKI 226 x VI 9	*11.10***	*A x A*	*62.87*	*4*
No. of capsules on main spike	SPS-38-8 x SKI 291	68.28**	G x P	178.20	1
	SPS-38-8 x SKI 294	51.83**	G x P	160.77	2
	SKI 294 x SKI 299	40.87**	P x P	118.33	8
No. of effective branches/plant	SPS-38-8 x SKI 291	2.55**	P x P	5.94	5
	SKI 205 x SH 21	1.44**	G x P	6.00	3
	SKI 291 x SKI 294	1.39**	P x P	5.12	9
100- seed weight (g)	SH 21 x SPS-38-8	6.07**	G x G	36.46	1
	VI 9 x SKI 304	3.53**	G x P	31.44	10
	SPS-38-8 x SKI 291	2.91**	G x P	32.99	6
Harvest index (%)	SKI 205 x SH 21	11.05**	G x A	41.13	12
	SKI 291 x SKI 304	6.80**	P x A	46.10	3
	SKI 109 x SKI 304	4.43**	P x A	43.80	5
Oil content (%)	VI 9 x SKI 304	2.09**	P x A	51.15	4
	SPS-38-8 x SKI 299	1.42*	A x A	50.26	16
	SH 21 x SKI 109	1.32*	A x A	51.44	2

G = Good; A = Average; P = Poor *gca* effects; *, ** significant at 5% and **1%** levels, respe**ctively.**

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J. Oilseeds Res., **25**(2) : **206-209** (2008)

Short communication

Response of castor to different spacing and fertilizer levels under dryland conditions

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(Received: March, 2007; Revised: October, 2008; Accepted: October, 2008)

Abstract

The studies on the effect of spacing and fertilizer on the productivity of castor were carried out at Solapur. It was observed that castor hybrid DCH-32 planted at 60 x 45 cm with the application of 25:12:5 kg (N:P_2O_5:K)/ha in Inceptisols for dryland conditions and water scarcity zones of Maharashtra were found better for higher and economic cultivation of castor.

Keywords: Castor, Inceptisols, irrigation

Castor cultivation and multiple uses of its seed and oil are well established in India. Castor (*Ricinus communis* L.) plays an important role in country's non-edible vegetable oil economy. Castor oil is mainly used in the manufacture of the wide range of ever expanding industrial products such as nylon fibres, jet-engine lubricants, hydraulic fluids, cosmetics, pharmaceuticals, cake is used to control nematodes in the gardens and meal is extensively used as manure. With the exception of Gujarat and Rajasthan, the general productivity of rainfed castor in rest of the country ranges from 275 to 1600 kg/ha. *A multitude of factors* such as its cultivation on sub-marginal and marginal lands, uncertainty of rainfall and its erratic distribution, delayed sowings; poor management of crop with little or no inputs, use of poor quality seed, imbalance fertilizer management and improper maintenance of plant population are responsible for low yields under rainfed situations. In view of this, the field experiment was conducted to assess the response of castor genotypes to various spacing and fertilizers under dryland condition. The field experiment was conducted during monsoon season of 1999 to 2004 at the research farm of All India Co-ordinated Research Project for Dryland Agriculture, Solapur, on medium deep soil (Inceptisols). The soils were low in available nitrogen (122 kg/ha), medium in available phosphorus (13 kg/ha) and high *in available potash contents (460 kg/ha). The* experiment was laid out in Split-Split Plot Design with three replications. The main plot treatments comprised of three spatial configurations *viz.*, 60 x 45 cm, 90 x 30 cm and paired planting at 60-120 x 30 cm. The three fertilizer levels *viz.*, 0:0, 25:12.5 and 50:25 N: P_2O_5 kg/ha was given as sub-plot treatments. The fertilizer was applied by hand drilling (Moghada) at the depth of 5 cm while, two castor genotypes *viz.*, VI-9 and DCH-32 were tried as sub-sub plot treatments. The bean yield was computed on the basis of plot-wise yields. The fertilizer dose was applied as per the treatments. The recommended cultural practices and plant protection measures were adopted as per the need of the crop.

Rainfall received during the experimental years was deficit than normal and it was ranged from -11.0 to -51.5 %. Year 2003 was the most drought year.

Rainfall (mm) received during the experimental years

Season	1999	2000	2001	2002	2003	2004
Kharif (MW 23-37)	316.4(25)	439.4(29)	198.5(15)	472.0(35)	222.0(13)	404.9(26)
Rabi (MW 38-08)	100.0(7)	113.2(11)	346.7(16)	98.5(8)	74.0(7)	81.7(9)
Annual	511.5(40)	630.6(46)	600.2(37)	644.5(49)	351.1(25)	638.1(43)
(Surplus/ Deficit)%	-29.0	-13.0	-17.0	-11.0	-51.5	-11.5
Normal	723.4 (46)					

Effect of spacing: *Castor crop planted at 60 x 45 cm* spacing produced significantly higher bean yield of 1088 and 1698 kg/ha during the years 2002 and 2004, while during the years 1999, 2000 and in pooled means, it was not influenced significantly due to various spacing.

Economic analysis revealed that castor planted at 60 x 45 cm spacing recorded highest net returns (Rs.12311/ha) with B:C ratio of 2.18 and Sustainable value index 0.56 The same treatment also recorded highest SYI 0.53 and moisture use efficiency 2.83 kg/ha/mm (Table 4 and 5).

Weiss (2002) reported that for castor grown in the 750-900 mm rainfall range, 100 cm row width with 30 cm spacing between the plants is standard. Hanumanta Rao *et al.* (2000) reported spacing of 90x30 cm for early and medium duration castor variety/hybrid in rainfed areas.

Effect of fertilizer levels: Pooled results revealed that application of 50:25 N:P_2O_5 kg/ha produced significantly higher castor bean yield (1169 kg/ha) over control but it was at par with 25:12.5 N:P_2O_5 kg/ha (1095 kg/ha) (Table 1). Economic analysis revealed that fertilizer level of 50:25 N:P_2O_5 kg/ha to castor recorded the highest net returns (Rs.12002/ha) with B:C ratio of 2.04 and SYI 0.54. The same treatment also recorded highest SYI 0.51 and moisture use efficiency 2.90 kg/ha/mm (Table 4 and 5). Weiss (2000) reported that 1700 kg/ha castor seed yield removes the nutrients equivalent to 50 kg N, 20 kg P and 16 kg K, ignoring that contained in the plants themselves. Reddy *et al.* (2004) reported that application of 60:40:30 N: P_2O_5:K_2O kg/ha gave highest yield of castor.

Effect of genotypes: The castor hybrid DCH-32 produced significantly higher bean yield over all the years of experimentation (1198 kg/ha) while, the straw yield of castor showed reverse trend. Economic analysis revealed that the DCH-32 gave the highest net returns (Rs.12072/ha) with B:C ratio of 2.05 and SVI 0.56. The DCH-32 also recorded highest SYI 0.54 and moisture use efficiency 3.10 kg/ha/mm (Table 4 and 5). Raghavaiah *et al.* (2003) reported that DCH-32 produced higher yield in farmers' field conditions. Reddy *et al.* (2004) reported that castor hybrid DCH-32 produced significantly higher bean yield over DCS-9 and PCS-4 and superior performance of DCH-32 was attributed to lengthy spikes more number of capsules and higher test weight of seed.

Interaction effects

Genotypes x Fertilizer levels: During the years 2000 and 2001, the castor hybrid fertilized with 50:25 N:P_2O_5 kg/ha produced significantly higher castor bean yields of 1756 and 779 kg/ha, respectively, as compared to rest of the treatment combinations (Table 2).

Spatial configurations x Fertilizer levels: During the year 2001, spacing of 90x90 cm in association with 50:25 N: P_2O_5 produced significantly higher castor bean yield of 655 kg/ha (Table 3).

Genotypes x Spatial configurations: During 2001-02, castor DCH-32 when planted in paired row geometry i.e., 60-120x30 cm produced significantly higher bean yield of 782 kg/ha (Table 3).

Thus, the castor hybrid DCH-32 planted at 60 cm x 45 cm spacing with application of 25 kg N + 12.5 kg P_2O_5/ha fertilizer dose in Inceptisols found better under dryland conditions of the scarcity zone of Maharashtra State.

Table 1 Bean yield (kg/ha) of castor as influenced by various spatial configurations, fertilizer levels and genotypes (Pooled mean)

	Treatment	1999-00	2000-01	2001-02	2002-03	2004-05	Mean
			A) Main plots : Spatial configurations				
S_1	60x45cm	1047	1493	522	1088	1698	1136
S_2	90x30 cm	999	1399	604	1009	1514	1078
S_3	60-120x30cm	1127	1298	588	938	1390	1048
	SEm±	92.2	48.2	4.2	9.6	35.1	36.2
	CD (P=0.05)	N.S.	N.S.	16.7	37.7	138.0	N.S.
			B) Sub-plots : fertilizer levels (N:P_2O_5 kg/ha)				
F_0	0:0	985	1224	516	805	1445	998
F_1	25:12.5	1052	1476	566	1006	1529	1095
F_2	50:25	1136	1491	632	1224	1628	1169
	SEm±	35.5	36.7	6.7	19.7	35.1	30.12
	CD (P=0.05)	N.S.	114	20.3	60.8	108.3	87.8
			C) Sub-sub plots : Genotypes				
V_1	VI-9	922	1228	430	954	1456	977
V_2	DCH-32	1193	1565	711	1069	1612	1198
	SEm±	38.9	33.1	5.1	19.0	27.3	18.6
	CD (P=0.05)	115.0	98.2	15.2	56.4	81.1	53.3
			D) Interactions				
			1) Spatial configurations x fertilizer levels				
	CD (P=0.05)	N.S.	N.S.	Sig.	N.S.	N.S.	N.S.
			2) Fertilizer levels x Genotypes				
	CD (P=0.05)	N.S.	Sig.	Sig.	N.S.	N.S.	N.S.
			3) Spatial configurations x Genotypes				
	CD (P=0.05)	N.S.	N.S.	Sig.	N.S.	N.S.	N.S.
			4) Spatial configurations x fertilizer levels x Genotypes				
	CD (P=0.05)	N.S.	N.S.	N.S.	N.S.	N.S.	N.S.
	CV (%)	7.5	8.6	6.7	10.2	9.2	16.8

Table 2 Bean yield (kg/ha) of castor as influenced by interaction effect due to fertilizer levels x genotypes

Fertilizer level	2000-01		2001-02	
	VI-9	DCH-32	VI-9	DCH-32
F_0:0:0	1149	1298	377	655
F_1 :25:12.5	1310	1642	428	704
F_2:50:25	1226	1756*	485	779
SEm ±	32		18.1	
CD (P=0.05)	109		60.2	

Table 3 **Bean yield (kg/ha) of castor as influenced by interaction effect due to spacing x fertilizer levels and spatial configurations x genotypes**

Spatial configurations	2001-02 Fertilizer levels			2001-02 Varieties	
	F_0:0:0	F_1 :25:12.5	F_2:50:25	VI-9	DCH-32
S_1:60x45cm	450	494	622	398	646
S_2:90x30 cm	553	606	652	498	710
S_3:60-120x30cm	545	597	623	394	782
SEm ±		10.26		8.86	
CD (P=0.05)		33.11		26.30	

Table 4 Economics of castor as influenced by spacing, fertilizer levels and genotypes

Treatment	Yield (kg/ha)		Gross returns (Rs/ha)	Cost of cultivation (Rs/ha)	Net returns (Rs/ha)	B:C ratio
	Bean	Stalk				
A) Main plots – Spatial configurations						
S_1 60x45cm	1136	4569	22738	10427	12311	2.18
S_2 90x30 cm	1078	4420	21606	10247	11359	2.11
S_3 60-120x30cm	1048	4504	21147	10247	10900	2.06
SEm±	36.2	158.4	658.2	-	-	-
CD (P=0.05)	N.S.	N.S.	N.S.	-	-	-
B) Sub-plots – fertilizer levels (N:P_2O_5 kg ha^{-1})						
F_0 0:0	998	4008	19984	10550	9430	1.89
F_1 25:12.5	1095	4589	22000	11027	10973	2.00
F_2 50:25	1169	4896	23507	11505	12002	2.04
SEm±	30.12	19305	573.0	-	-	-
CD (P=0.05)	87.8	399.4	1672.6	-	-	-
C) Sub-sub plots – Genotypes						
V_1 VI-9	977	4909	20052	10337	9715	1.94
V_2 DCH-32	1198	4086	23609	11537	12072	2.05
SEm±	18.6	232.8	390.3	-	-	-
CD (P=0.05)	53.3	472.2	1119.6	-	-	-
D) Interactions						
1) Spatial configurations x fertilizer levels						
CD (P=0.05)	N.S	N.S.	N.S.			-
2) Fertilizer levels x Genotypes						
CD (P=0.05)	N.S	N.S.	N.S.			-
3) Spatial configurations x Genotypes						
CD (P=0.05)	N.S	N.S.	N.S.			-
4) Spatial configurations x fertilizer levels x Genotypes						
CD (P=0.05)	N.S	N.S.	N.S.	-	-	-

Table 5 **Consumptive use, moisture use efficiency and sustainability of castor as influenced by spatial configurations, fertilizer levels and genotypes (pooled mean)**

Treatment	Bean yield (kg/ha)	Consumptive use (mm)	MUE (Kg/ha mm)	Sustainable yield index (SYI)		Sustainable value index (SVI)
				Bean	Straw	
A) Main plots : *Spatial configurations*						
S_1 60x45cm	1136	401	2.83	0.53	0.46	0.56
S_2 90x30 cm	1078	400	2.70	0.49	0.40	0.52
S_3 60-120x30cm	1048	399	2.63	0.50	0.45	0.45
B) Sub-plots – fertilizer levels (N:P_2O_5 kg/ha)						
F_0 0:0	998	394	2.53	0.47	0.40	0.47
F_1 25:12.5	1095	402	2.72	0.49	0.45	0.51
F_2 50:25	1169	403	2.90	0.51	0.45	0.54
C) Sub-sub plots – Genotypes						
V_1 VI-9	977	414	2.36	0.43	0.39	0.45
V_2 DCH-32	1198	386	3.10	0.54	0.49	0.56

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J. Oilseeds Res., **25**(2) : 210-211 (2008)

Short communication

Delineation of effects of production factors on castor, *Ricinus communis* L. productivity in Rajasthan

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(Received: August, 2008; Revised: October, 2008; Accepted: November, 2008)

Abstract

The studies suggested that non-adoption of weeding, fertilizer and plant protection from whole package of castor crop resulted in less net returns.

Keywords: Castor, package of practices, input

Castor (*Ricinus communis* L.) is mainly valued for important bio-degradable industrial oil which is used for deriving products like dyes, detergents, plastics, printing ink, patent leather, ointment, polishes, paints, lubricants and hydraulic fluids. India meets >70% of world's requirement of castor oil and earned foreign exchange of Rs. 1000 crore through export of castor oil during 2006-07. The productivity of castor grown in 6.28 lakh ha area in the country is 1213 kg/ha (Anonymous, 2007). Non-adoption of full package due to high cost of cultivation (Rs. 18,000 to 20,000/ha) is a reason for poor productivity of castor grown on low fertile light soils of Rajasthan. Under such circumstances, prioritization of the components of whole package according to their contribution to seed yield is warranted. Under scarce resource condition, farmers can give maximum emphasis to those particular inputs which contributes maximum towards yield. Research work on these aspects in castor is meagre and hence this trial was conducted.

The field experiment was conducted at Agricultural Research Station, Mandore, Jodhpur during 2004-05, 2005-06 and 2007-08. The soil of the site was loamy sand having pH 8.1 with low available nitrogen (145 kg/ha), medium available phosphorus (30 kg/ha), potassium (394 kg/ha) and sulphur (13 ppm). Eight treatment combinations {T_1 = Full package (recommended dose of fertilizers: 80 kg N + 50 kg P_2O_5 + 20 kg S/ha; plant protection measures: seed treatment with Apron SD @ 6g/kg seed + spray of Endosulphan 1.0 l/ha after 2nd picking and 3 weedings at 20, 40 and 60 DAS), T_2 = T_1- fertilizers, T_3 = T_1 - plant protection measures, T_4 = T_1 - weeding, T_5 = T_1 - fertilizers + plant protection measures, T_6 = T_1 - fertilizers + weeding, T_7 = T_1 - plant protection measures + weeding, T_8 = T_1 - fertilizers + plant protection measures + weeding} were tried in Randomized Block Design with 3 replications. The net plot size was 4.8 m x 6.0 m. Crop was sown in the 2nd fortnight of July every season at 120 cm row and 60 cm plant spacing. Seeds of castor hybrid 'RHC-1 @ 8 kg/ha was sown 3-4 cm deep through dibbling. Half the nitrogen (40 kg/ha), full phosphorus (50 kg/ha) and sulphur (20 kg/ha through gypsum) as per treatment were applied as basal dose in the first week of July every season. Remaining half dose of nitrogen (40 kg/ha) was top dressed in two equal splits at 35 and 90 DAS. The crop was initially raised as rainfed, but after withdrawal of rain, it was irrigated 8 times at 18-20 days interval. The total rainfall received during the season 2004-05, 05-06 and 07-08 was 114, 227 and 163 mm, respectively. Harvesting of spikes was done in 6 pickings at monthly interval starting from 90 DAS.

Adoption of full package (weeding, fertilizers and plant protection measures) produced significantly higher seed yield of 2667 kg/ha. This increase in yield was due to production of more spikes/plant (16), higher seed weight (26 g/100 seed) and full plant stand (13,500/ha). Among the individual production factors, non adoption of weeding (T_4) reduced yield considerably by 1558 kg/ha. The final plant stand measured 90 DAS was also reduced significantly due to non adoption of weeding (T_4). Withdrawal of weeding (T_4) allowed the weeds to grow for full crop pendancy, which completely smothered the crop plants resulting in poor stand (8,400 plants/ha) and consequently low yield. Length of primary raceme and spikes/plant were reduced significantly in all treatments (T_4, T_5, T_7 and T_8) where weeding was not done. Presence of weeds in the crop plants increased plant height of castor however it was significant in T_7 only. Severe competition with weeds produced castor plants with shorter raceme, lower number of spikes and suppressed plant stand which ultimately reflected in poor seed yield. Poor plant stand also allowed second flush of weeds in crop during rabi season because there was no smothering effect of crop on new emerging *rabi* weeds. Weed species, *Amaranthus viridis* and *Celosia argentia* in *kharif* and *Chenopodium album* and *Chenopodium murale* in *rabi* dominated the un weeded plots. Hence weeding emerged as the most important component of crop production under the agro climatic conditions of western Rajasthan. At S K Nagar (Gujarat), non adoption of weeding suppressed castor seed yield significantly by 2169 kg/ha followed closely by non adoption of fertilizer inputs (1322 kg/ha) thus proving their importance in castor production (Anonymous, 2007).

Withdrawal of fertilizers from full package (T_2) reduced the yield leve! by 676 kg/ha whereas, non-adoption of plant protection measures (T_3) from full package reduced the yield by 343 kg/ha only. No fertilization to castor grown on loamy sand soil which is poor in available nitrogen and medium in phosphorus and sulphur directly affected the plant growth and there by the seed yield. This indicates that fertilizer is the next most important practice after weeding to enhance productivity of castor under irrigated crop culture. Due to lesser incidence of pest and diseases in treatment whole package - plant protection measures (T_3) reduction in seed yield was less. Withdrawal of fertilizer and weeding from whole package (T_6) induced substantial decline in seed yield (1780 kg/ha) in comparison with removal of fertilizer and plant protection measures from total package, T_5 (753 kg/ha), highlighting the importance of weeding and fertilizer management in castor. The oil per cent of castor seed measured from the primary spike yield was not influenced by withdrawal of different components of production from whole package.

Economic analysis revealed that adoption of total package accrued greater monetary benefits (net return and B:C ratio of Rs. 25,926/ha and 2.31 respectively). Non-adoption of weeding, fertilizer and plant protection measures in the whole package reduced the net return by Rs. 23,691/ha, Rs. 9,288/ha and Rs. 4,485/ha, respectively. This indicates that non adoption of weeding and fertilizer either alone or in conjunction depressed net return to greater extent. Non adoption of plant protection, weeding and fertilizer made this crop non remunerative (Rs. - 256/ha).

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Table 1 **Growth, yield attributes, seed yield, oil and monetary returns as influenced by different components of production system in irrigated castor 9Mean of 2004-05, 2005-06 and 2007-08)**

Treatment	Final Plant stand ('000/ha)	Plant height up to primary raceme (cm)	Nodes up to primary raceme	100 seed weight (g)	Length of primary raceme (cm)	Spikes /plant	Oil (%)	Seed yield (kg/ha)	Net return (Rs/ha)	B:C ratio
T_1 : Full package	13.5	57	16	26	45	16	50.1	2667	25,926	2.31
T_2 : T_1- Reco. dose of ferti. (RDF)	13.2	61	13	24	42	12	49.4	1991	16,638	1.93
T_3 : T_1- Plant protection (PP)	13.1	62	16	26	46	15	50.1	2324	21,441	2.12
T_4 : T_1- weeding	8.4	67	14	24	35	8	48.7	1109	2,235	1.13
T_5 :T_1- RDF+ PP	13.3	62	13	25	42	12	49.4	1914	16,184	1.94
T_6 : T_1- RDF + weeding	8.6	69	14	23	32	7	48.9	887	236	1.02
T_7 : T_1- PP+ weeding	8.1	70	14	24	35	9	48.3	960	573	1.04
T_8 : T_1- RDF + PP + weeding	8.8	67	13	23	31	8	49.3	834	(-) 256	0.98
SEm ±	0.9	4.2	0.7	0.7	2.6	1.1	0.9	71.5	-	-
CD (P=0.05)	2.6	12.6	2.3	2.0	7.9	3.2	NS	204	-	-

J. Oilseeds Res., **25**(2) : 212-213 (2008)

Short communication

Response of niger, *Guizotia abyssinica* C. to sowing time and fertility levels

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(Received: January, 2008; Revised: October, 2008; Accepted: November, 2008)

Abstract

Effect of sowing time and fertilization was seen on niger at Marathwada Agricultural University, Parbhani. Niger sown in first fortnight of July and supplied with 30:60 NP kg/ha recorded the highest productivity.

Keywords: Niger, *Guizotia abyssinica*, sowing time

Niger (*Guizotia abyssinica* C.) is an important oilseed crop grown in tropical and subtropical countries like India, Ethiopia, East Africa, West Indies and Zimbabwe. However, India and Ethiopia are two major niger growing countries in the world. In India, niger is grown on area of 4.2 lakh ha with a production of 1.12 lakh tonnes with average yield of 252 kg/ha (Anonymous, 2005). Niger is grown during *kharif* under rainfed condition on variety of soils. In addition to culinary use of seed and oil, it is also used as spice in chutney, pickles, ketchup, etc. In Maharashtra region, there is great scope for boosting the yields of niger with sowing of crop at appropriate time and supplied with optimum fertilizer level, particularly nitrogen and phosphorus as crop is grown under marginal condition of cultivation.

A field experiment was conducted during *kharif* season of 2006-07 in Split Plot Design with three replications. The soil was clay in texture, low in available nitrogen (170 kg/ha) and phosphorus (11.8 kg/ha) and slightly alkaline in reaction (pH 7.95). The crop was sown with hand line sowing at a spacing of 45 cm row to row distance in a plot size of 4.5 m x 4.5 m. Newly released genotype from MAU, Parbhani, PNS-6 was used. Sixteen treatment combinations comprised four main plot treatments of sowing times (D_1 - On set of monsoon; D_2 - 15 days after D_1; D_3 - 30 days after D_1 and D_4 - 45 days after D_1) and four fertility levels as sub-plot treatments (no fertilizer, 10:20 NP kg/ha, 20 : 40 NP kg/ha and 30:60 NP kg/ha).

Table 1 Yield and yield attributes of niger as influenced by various treatments

Treatment	Capsules/ plant	No. of seeds/ plant	Test weight (g)	Seed yield (kg/ha)	Straw yield (kg/ha)
Sowing time					
D_1 : 28th June	34.58	995.42	4.16	636	4795
D_2 : 12th July	36.73	1003.10	4.18	640	4816
D_3 : 28th July	31.86	976.11	4.02	528	4451
D_4 : 12th August	27.90	949.20	3.96	442	4214
SEm±	0.12	6.65	0.01	1.7	57.5
CD (P=0.05)	0.35	19.38	0.03	5.1	167.6
Mean	**32.76**	**980.95**	**4.08**	**561**	**4569**
Fertility levels					
F_0 : No fertilizer	30.31	494.09	3.91	485	3841
F_2 : 10:20 NP kg/ha	32.95	979.26	4.03	562	4424
F_3 : 20:40 NP kg/ha	34.37	989.68	4.17	586	4812
F_4 : 30:60 NP kg/ha	34.45	1000.50	4.25	607	5200
SEm±	0.36	6.68	0.03	3.5	124
CD (P=0.05)	1.06	25.29	0.09	10.3	362
Mean	**33.02**	**865.88**	**4.09**	**560**	**4569**

Effect of sowing time on yield attributing characters like number of capsules/plant, number of seeds/plant and test weight were highest and significantly superior with D_2 - 2nd week of July as compared to all other sowing dates though on par with D_1 - 4th week of June (Table 1). Yield data showed that the seed yield (640.3 kg/ha) and straw yield (4816.8 kg/ha) were also significantly higher with D_2 - 2nd week of July sowing as compared to all other sowing except it was on par with D_1 - 4th week of June. Patil (1979) observed that the seed and straw yield of niger was on par with sowing dates upto 1st July and significantly lowered with delay in sowing after 1st July at Igatpuri (MS).

Yield contributing characters *viz.*, capsules/plant, seed number/plant and test weight were significantly higher with highest fertilizer dose 30:60 NP kg/ha as compared to all other lower fertility levels except on par with application of 20:40 kg NP/ha. Seed yield and straw yield (522.1 kg/ha) recorded with highest level of fertility (30:60 NP kg/ha) were significantly higher as compared to all other lower fertility levels except this with fertility level 20:40 NP kg/ha (Table 1). Khot *et al.*(1990) reported that the highest yield of niger (392 kg/ha) was recorded with application of 30:60:20 NPK kg/ha, which was on par with 20:40:20 NPK kg/ha and significantly higher over other lower levels and control. The interaction effect was not evident. Dhange *et al.* (2008) reported that increase in seed yield of niger was with application of 60 kg P_2O_5/ha and it was on par with 40 kg P_2O_5/ha. Singh and Verma (1975) stated that application of 40 kg P_2O_5/ha gave significantly higher seed yield of 16.9 and 12% over control and 20 kg P_2O_5/ha. Paikaray *et al.* (1997) stated that application of N at 40 kg/ha significantly increased the grain yield by 60%. Trivedi and Ahlawat (1991) from Navsari observed that niger seed yield was maximum with 40 kg/ha as compared to 20 kg and no P application.

Above investigation clearly shows that the niger crop sown upto 1st fortnight of July and supplied with 30:60 NP kg/ha recorded the highest productivity.

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J. Oilseeds Res., **25**(2) : 214-215 (2008)

Short communication

Efficacy of fungal bio-pesticide, *Verticilium lecanii* in combination with botanical spreaders to *Lipaphis erysimi* (Kalt.) on mustard

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(Received: November, 2007; Revised: February, 2008; Accepted: July, 2008)

Abstract

Studies revealed that neem oil and sunflower oil increased the effectiveness of *Verticillium lecanii* against mustard aphid, *Lipaphis erysimi* (Kalt.)

Keywords: *Verticillium lecanii, Lipaphis erysimi,* effectiveness

Mustard is an important *rabi* oilseed crop which is heavily infested by mustard aphid, *Lipaphis erysimi* (Kalt.) resulting in 65.5 to 95.7% losses in seed yield. Several bio-control agents have been tried against this pest to bring down the pesticidal applications, and *Verticillium lecanii* (Zimmerman) has been reported effective (Rana and Singh, 2002). Certain botanical spreaders were used to increase the persistence of the fungus, *V. lecanii* under environmental conditions and thereby to improve its efficacy. The efficacy of *V. lecanii* in combination with plant products like rapeseed oil and neem oil have earlier been investigated (Meyer *et al.*, 2002). According to Visalakshy *et al.* (2005), sunflower oil and neem oil enhanced the mycelial growth of *V. lecanii* on potato dextrose agar media. In the present experiment, different botanical spreaders were mixed with *V. lecanii* sprays and evaluated their effect on virulence of *V. lecanii* against *L. erysimi* in mustard crop. Field-cum-laboratory experiment was laid out in Completely Randomized Block Design with seven treatments replicated four times during the *rabi* season of 2005-06, at Junagadh Agricultural University, Junagadh. The *V. lecanii* alone and in combination with five different botanical spreaders were tested. The *V. lecanii* (VERTICEL) preparation, a wet dispersible powder supplied by Excel Industries Ltd, Mumbai. The spore counts of 1×10^8 cfu/g material for *V. lecanii* were studied. The suspension of *V. lecanii* along with different spreaders was sprayed on mustard plants with the help of a knapsack sprayer. Soap @ 5 g/l was mixed to obtain an oil diluted suspension. The care was taken to obtain the uniform coverage of spray solution in the respective plots. After 24 hours of treatment, the treated leaves were collected from the respective plots and provided to the one day starved third instar nymphs of *L. erysimi*. The initial culture was maintained by collecting the nymphs of *L. erysimi* from the untreated mustard field located at the College Farm, University Campus, Junagadh. The field-collected nymphs were brought to laboratory and kept in Petri dishes (10 × 2 cm diameter). Fresh mustard leaves were provided as food for them, everyday morning till the emergence of adult. The cotton plug soaked in water was attached to the cut end of the leaf petiole, to avoid desiccation of leaves. For transferring the aphids to new leaves they were slightly disturbed initially by touching with camel hairbrush so as to withdraw their mouthparts from the leaf tissue, after that aphids were transferred to fresh leaves with help of a wet camel hairbrush and then they were used for laboratory studies. These laboratory-reared nymphs were allowed to feed on the treated leaves for 24 h and then transferred into other Petri dishes provided with fresh untreated food. Twenty- five nymphs/treatment in each replication were studied. All the tests were carried out in the laboratory at 26 + 2°C and 70 to 80% relative humidity. Mortality counts were recorded at 1, 3, 5, 7 and 10 days after treatment. Nymphs were considered as dead, if they did not respond to the stimulation by touch with camel hairbrush. The data in percentage were transformed into arcsine percentage before analysis. Natural mortality was corrected as per (Abbott, 1925).

The results showed that *V. lecanii* combined with neem oil was significantly effective treatment with highest nymphal mortality after 10 days of treatment (Table 1). The treatments of *V. lecanii* combined with sunflower oil, mustard oil, cottonseed oil and groundnut oil were found at par with each other for increase of aphids mortality, respectively. The results obtained from the present findings are in contrast with Erkilic (1992) who reported that there was no significant difference in mortality following treatment with water and oil-based formulations of *V. lecanii* against *M. persicae*. The productivity and entomocidal activity of *V. lecanii* were found to increase when lactic acid and its salts were added to nutrient media together with surface-active agents (Zukauskiene and Sirvinskas, 1993). Glycerol and cutinol proved better in promoting the virulence of *V. lecanii* (Williams *et al.*, 2000). However, the present findings are concurrence with the observations of Meyer *et al.* (2002) who reported that the addition of rape seed oil 100% and neem oil 2000 ppm to the suspension of *V. lecanii* enhanced the number of spores on *Franklinella occidentalis*. Similarly, sunflower oil and neem oil significantly enhanced the mycelia growth of *V. lecanii* (Visalakshy *et al.*, 2005).

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Thus, it can be concluded that Neem oil and Sunflower oil were found the most potential to enhance the effectiveness of *V. lecanii* against *L. erysimi* in mustard crop.

Table 1 Mortality in third instar nymphs of *L. erysimi* due to *V. lecanii* combined with botanical spreaders

Treatment	Nymphal mortality (%)				
	1 DAS	3 DAS	5 DAS	7 DAS	10 DAS
V. lecanii (4.0 g/l alone)	22.9 *	29.3	33.0	38.0	41.0
	(15.1)	(23.9)	(29.7)	(37.9)	(43.0)
V. lecanii (4.0 g/l) + Mustard oil (0.1 %)	28.3	34.6	38.2	41.2	43.0
	(22.4)	(32.2)	(38.2)	(43.4)	(46.5)
V. lecanii (4.0 g/l) + Groundnut oil (0.1 %)	24.6	32.0	35.7	39.3	41.6
	(17.3)	(28.1)	(34.1)	(40.1)	(44.2)
V. lecanii (4.0 g/l) + Sunflower oil (0.1 %)	31.6	35.9	41.3	44.4	49.0
	(27.5)	(34.3)	(43.6)	(48.9)	(57.0)
V. lecanii (4.0 g/l) + Cottonseed oil (0.1 %)	28.9	35.3	40.7	41.2	43.0
	(23.4)	(33.3)	(42.5)	(43.3)	(46.4)
V. lecanii (4.0 g/l) + Neem oil (0.1 %)	32.9	37.1	42.6	45.7	50.4
	(29.5)	(36.5)	(45.7)	(51.1)	(59.3)
Untreated control	5.7	5.7	5.7	5.7	5.7
	(0.0)	(0.0)	(0.0)	(0.0)	(0.0)
S.Em.±	0.8	1.0	0.9	0.9	0.7
CD (P=0.0 5)	2.5	2.9	2.7	2.8	2.0
C.V. (%)	6.7	6.5	5.7	5.2	3.5

* Angular transformed values, Figures in parenthesis are per cent mortality; DAS = Days after spraying

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J. Oilseeds Res., **25**(2) : 216-217 (2008)

Short communication

Study on castor, *Ricinus communis* L. production in relation to limiting production factors in North Gujarat

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(Received: August, 2008; Revised: October, 2008; Accepted: November, 2008)

Abstract

Studies on full package of practices for gainful cultivation of castor revealed that it is highly remunerative. Application of fertilizer was the most critical input for castor followed by weeding and plant protection measures.

Keywords: Package of practices, fertilizer, castor

In North Gujarat irrigated castor is an important industrial and commercial crop playing a significant role in the economic status of farmers. Different factors (Fertilizer, plant protection and weeding) contribute towards the establishment and growth of castor crop and ultimately the final yield of castor. But, relative contribution of these factors has not been quantified in castor under North Gujarat agro-climatic conditions. Hence, the study was made to study the influence of different input factors alone or in combination on the productivity of irrigated castor.

Field experiments were conducted during three *kharif* seasons of 2004-05 through 2007-08 at Main Castor-Mustard Research Station, S.D. Agricultural University, Sardarkrushinagar. The soil of the experimental plot was loamy sand with pH 8.0. It has an initial fertility status of 214 kg/ha available nitrogen, 50 kg/ha available P_2O_5 and 190 kg/ha available K_2O. The experiment was laid out in Randomized Block Design with eight treatments replicated three times using castor hybrid GCH-7. The treatments consisted of full package, and deletion of one or more of inputs like, fertilizer, plant protection and weeding (Table 1). The rainfall received during 2004, 2005, 2006 and 2007 was 381.3, 586.8, 1096.7 and 697.6 mm, respectively.

Table 1 Seed yield of castor as influenced by different production factors

Tr. No.	Treatments	Seed yield of castor (kg/ha)				Pooled
		2004 -05	2005-06	2006-07	2007-08	
1	Full package	4104	3199	3259	4179	3685
2	FP- Fertilizer (F)	2076	2423	2427	2856	2446
3	FP – Plant protection (PP)	3348	2544	3056	3532	3120
4	FP- Weeding (W)	3263	2461	2759	2009	2623
5	FP – (F + PP)	2903	1940	2170	2755	2442
6	FP – (F + W)	2779	1880	1812	2054	2131
7	FP – (PP + W)	3116	2420	2561	2508	2651
8	FP – (F + PP + W)	2404	1600	1797	1874	1896
S. Em. ±		338	149	193	232	165
C. D. (P=0.05)		1024	453	588	705	486

It was found that adoption of full package of practices resulted in the maximum seed yield during all the years of experimentation as well as in pooled data (Table 1). Studies conducted at Bawal, Kanpur, Mandor and Yethapur on optimization of castor production under resource constraints also indicated the need for adoption of full package of practices to obtain the highest yield of castor (Anonymous, 2008). The whole package oriented demonstration conducted in different states during 1995-96 have also conclusively proved the superiority of the improved technology over the prevailing farmers' practices (Reddy *et al.*, 1997). Similar findings were also documented by Patel *et al.* (2003) and Deshmukh *et al.* (2003). During the first year, yield of castor was reduced significantly in absence of fertilizer, where as other production factors like plant production and weeding reduced the yield of castor, but did not cross the level of significance. During fourth year, weeding played significant role in reduction of castor yield. Significantly lower seed yield of castor was recorded when weeding operation was deleted as compared to full package followed by fertilizer application. The pooled effect of production constraints on crop yield was found in the order of fertilizer (33.62 %) > weeding (28.82 %) > plant protection (15.33 %). On an average full package of practices resulted in achieving highest yield of 3685 kg/ha which was declined to 2446, 3120 and 2623 kg/ha without fertilizer, plant protection and weeding, respectively. The combinations of different resource constraints further reduced the yield of castor. On an average significantly the lower seed yield (1896 kg/ha) was produced when it was grown without fertilizers, weeding and plant production. The combine contribution of all these inputs in castor production was 48.5% in comparison with full package of practices.

Economics of various treatments worked out on the basis of pooled data (Table 2) indicated that among the various treatments, full package accrued the highest net returns of Rs. 71325/ha with the highest of B:C ratio 4.42. It was followed by full package without plant protection and weeding. Non adoption of fertilizer, plant protection and weeding recorded the lowest net returns (Rs. 33640/ha) and B:C ratio (3.44).

From the above results it is concluded that adoption of full package of practices gave the highest seed yield and proved more remunerative in terms of net return and benefit cost ratio. Among the various production constraints, application of fertilizer was found most crucial followed by weeding and plant protection.

Table 2 Economics of different production factors in the castor production (mean of four years)

Tr. No.	Treatments	Seed yield (kg/ha)	Gross returns (Rs/ha)	Cost of cultivation (Rs/ha)	Net returns (Rs/ha)	BCR	Contribution (%)
1	Full package	3685	92125	20840	71285	4.42	100.00
2	FP- Fertilizer	2446	61150	18610	42540	3.29	33.62
3	FP – Plant protection	3120	78000	19840	58160	3.93	15.33
4	FP- Weeding	2623	65575	17440	48135	3.76	28.82
5	FP – (F + PP)	2442	61050	17610	43440	3.47	33.73
6	FP – (F + W)	2131	53275	16310	36965	3.27	42.17
7	FP – (PP + W)	2651	66275	16440	49835	4.03	28.06
8	FP – (F + PP + W)	1896	474000	13760	33640	3.44	48.55

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J. Oilseeds Res., **25**(2) : 218-219 (2008)

Short communication

Genetic analysis of budfly resistance and yield components in linseed, *Linum usitatissimum* L.

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(Received: August, 2007; Revised: October, 2008; Accepted: October, 2008)

Abstract

Nine elite parents *viz.*, NL-115, NL-142, NL-151, NL-119, NL-126, Kiran, R-552, Padmini and Shekar were crossed with two parents, JRF-5 and Neelum during 2003. Simple recurrent selection should be utilized to capitalize the additive genetic variation for budfly resistance.

Keywords: Linseed, budfly, recurrent selection

Linseed crop suffers from several diseases and insect pest in India (Gill, 1987). The significant yield losses occurs in linseed due to budfly, alternative blight, powdery mildew and rust. The extent of losses by budfly (*Dasyneura lini*) is ranged from 20 to 97% and 60% due to alternaria blight and powdery mildew (Srivastava *et al.*, 1997). There is a need to develop resistant varieties to budfly, Alternaria blight and powdery mildew to stabilize the yield potential of crop. Therefore, the present investigation was undertaken to study the genetics of budfly resistance and important economic traits through simplified triple test cross analysis of Jinks *et al.* (1969).

Nine elite (female) parents *viz.*, NL-115, NL-142, NL-151, NL-119, NL-126, Kiran, R-552, Padmini and Shekar were crossed with 2 (male) parents *viz.*, JRF-5 (resistant to budfly) and Neelum (susceptible to budfly)during *rabi* 2003. The Eighteen crosses along with parents were grown in a single block where ten plants of each genotype were individually randomized as per the methodology suggested by Mather and Jinks (1982) during *rabi* 2004. Data were recorded on all plants for plant height (cm), days to maturity, number of capsules/plant, number of branches/plant, seed yield/plant (g) and budfly percentage. *The detection and estimation of additive (D), dominance* (H_1) and epistatic components of genetic variation were carried out according to Jinks *et al.* (1969). The epistasis was significant for all characters i.e., budfly incidence (%), plant height, days to maturity, number of capsules/plant, number of branches/plant and seed yield/plant (Table 1). Epistasis for yield and its components has been reported in linseed by Rao and Singh (1985 a, b), Tak and Gupta (1989). This indicated that epistasis played an important role in the control of these characters hence, this component of genetic variation should not be ignored while deciding breeding plants. Therefore the assumption of absence of epistasis may not be realistic for one or more characters. Estimates of individual line (P_i) contribution to the epistatic comparison for $L_{1i} + L_{2i} - P_i$ for different characters (Table 2) indicated that the parent Padmini showed maximum epistatic contribution for budfly percentage and NL-151 for plant height and number of capsules/plant. Parents NL-115, NL-126 and Kiran showed maximum epistatic contribution for seed yield/plant, number of branches/plant and days to maturity respectively. In the development of pureline cultivars, the masking effects of epistasis are of no consequence, if selection is delayed until virtual homozygosity is attained, since only additive types of epistasis are present in purelines (Cokerham, 1961).

Table 1 Test of epistasis for different characters

Source of variation	Degrees of freedom	Mean squares					
		Plan height (cm)	Days to maturity	No. of capsule/ plant	No. of branches/ plant	Seed yield/ plant (g)	Budfly (%)
Epistasis $\bar{L}_{1i} + \bar{L}_{2i} - \bar{P}_{i}$	8	30.61**	44.20**	4899.93**	1.81*	3.57**	26.83*
Within family	98+	5.63	5.46	928.28	0.75	0.96	12.81

*, ** Significant at 5% and 1% level, respectively; + = The degree of freedom are less than expected due to the loss of plants

Estimation of additive and dominance components: The additive (D) and dominance (H_1) components of genetic variation were estimated in the presence of epistasis. Analysis of variance for sums and difference for different characters (Table 2) indicated that the mean squares due to sums ($L_{1i} + L_{2i}$) were significant for all characters under study. The mean squares due to differences ($L_{1i} + L_{2i}$) were significant for days to maturity, number of branches/plant and seed yield/plant while it was non significant for plant height, number of capsules/plant and budfly.

Table 2 Analysis of variance for the sums and differences for different characters

Source of variation	Degrees of freedom	Mean squares					
		Plan height (cm)	*Days to maturity*	*No. of capsule/ plant*	*No. of branches/ plant*	*Seed yield/ plant (g)*	*Budfly (%)*
Sums							
$\overline{L}_{1i} + \overline{L}_{2i}$	8	59.45**	95.24**	5346.68**	5.82**	3.11**	33.66**
Differences							
$\overline{L}_{1i} + \overline{L}_{2i}$	8	7.82	37.78**	1620.08	2.29**	2.70*	13.17
Within family	67	5.74	5.58	978.97	0.60	1.09	10.64
Components of genetic variation							
D		107.44	179.32	8735.44	10.44	4.04	46.04
H_1		NS	64.40	NS	3.40	3.22	NS
F		-7.12	42.28	-277.36	-0.76	-0.42	1.13
$r^{S/D}$		0.17	-0.35	0.05	0.10	0.07	-0.05
$\sqrt{H_1/D}$		-	0.60	-	0.57	0.89	-

*,** Significant at 5% and 1% level, respectively, NS = Non-significant

Estimation of additive, dominance component and degree of dominance revealed that all characters showed partial dominance (>1). The low degree of dominance for these characters indicated a considerably higher role played by the additive gene effects in the control of these characters than the dominance gene effects. Similar findings were reported by Rao and Singh (1985 a, b). The estimates of F is non-significant for all characters under study indicated that there is a dominance contribution to variation but the dominance is ambidirectional. Therefore, simple recurrent selection should be utilized to capitalize the additive genetic variation for budfly resistance.

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J. Oilseeds Res., **25**(2) : **220-222 (2008)**

Short communication

Differential feeding of mustard saw fly, *Athalia lugens proxima* Klug. on *Brassica* species and Indian mustard varieties

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(Received: August, 2008; Revised: October, 2008; Accepted: November, 2008)

Abstract

The highest feeding index for grubs of *Athalia lugens proxima* Klug. at 6:18 (Light: Dark) and at 9:15 (Light: Dark) condition, was recorded on *B. alba* while lowest preferred species was *Crambe abyssinica* with lowest feeding index, respectively against standard plant *B. campestris*. Among Indian mustard varieties the feeding index was lower for all varieties over standard Pusa Bold except Varuna at 6:18 (Light: Dark). It is also evident that duration of light hours influenced the feeding efficacy of grubs of *A. proxima* on same host.

Keywords: Feeding index, Indian mustard, sawfly

The mustard saw fly *Athalia lugens proxima* Klug. (Hymenoptera: Tenthredinidae) is a serious crop pest of rapeseed-mustard crops in India (Butani and Jotwani, 1984). Reduction in seed yield due to saw fly may go up to 100 % (Sachan, 1990). Earlier Shukla (1985) reported upto 68% avoidable losses due to this pest. Selection of a particular plant species by an insects is mainly govern by physical and/or chemical attributed of plant concerned (Kogan, 1982). Therefore the present study was undertaken to locate sources of resistance against saw fly in *Brassica* species.

The mustard saw fly was reared on fresh tender leaves of Indian mustard (*B. juncea* var. Varuna) in the laboratory at 20±1°C and 75±5% R.H. Third instar larvae of *A. proxima* were feed individually on eight different *Brassica* species and thirteen varieties of Indian mustard (Table 1 and 3) at 20±1°C and 75±5% R.H. with 6:18 (Light: Dark) and 9:15 (Light: Dark) in B.O.D. incubator. Feeding/consumption rate/grub was assessed with the help of graph paper at the intervals of 24 hrs. The preference index for each treatment was calculated as par Kogan and Goeden (1970).

Feeding index © for grubs of *A. proxima* after eight days was highest on *B. alba* followed by *B. juncea* > *Eruca sativa* > *B. nigra* > *B. napus* and lowest on *B. carinata* and *Crambe abyssinica* at 6:18 (Light: Dark). Whereas the feeding index was highest on *B. alba* followed by *B. juncea* > *B. carinata* > *B. napus* > *B. nigra* > *Eruca sativa* > *Crambe abyssinica* against standard, *B. campestris* at 9:15 (Light: Dark).The only *B. alba* (1.02) showed the marginally higher feeding index © over the standard species at 9:15 (Light: Dark). During eight day of feeding the highest preference index was recorded on 6th day *viz.*, 1.45, 1.29, 1.28, 1.15, 1.15, 0.82 for *Eruca sativa*, *B. juncea*, *B. alba*, *B. nigra*, *B. napus*, and *Crambe abyssinica*, respectively at 6:18 (Light: Dark) while at 9:15 (Light: Dark) highest feeding index © was observed on 5 th day *viz.*,1.83, 1.05, 0.50, 0.48, 0.32, 0.23 for *B. alba*, *B. juncea*, *Eruca sativa*, *B. carinata*, *B. napus*, and *Crambe abyssinica*, respectively against standard species at 9:15 (Light: Dark). Among different crucifers plants, *B. campestris* var. sarson were most preferred for feeding of grubs of *A. proxima* (Singh and Sachan, 1998).

The higher feeding index © 1.49 for *B. alba*, 1.45 for *Eruca sativa*, 1.15 for *B. napus*, 1.33 for *B. juncea*, 1.15 for *B. nigra* was noticed on 7th day, 6th day, 6th day, 8th day, respectively at 6:18 (Light: Dark) remaining species were less preferred whereas at 9:15 (Light: Dark) the highest feeding index © was recorded as 1.83 for *B. alba* on 5th day and 1.05 for *B. juncea* remaining species were less preferred over standard species *B. campestris*. Feeding index © of *Athalia proxima* was higher at 6:18 hrs (Light: Dark) than at 9:15 hrs (Light: Dark). Sehgal *et al.* (1975) reported a higher feeding index for the plants, *B. chinensis*, *B. juncea*, *B. napus*, *B. oleracea* var. capitata and *R. sativus* over the standard plant *toria*.

The feeding index © for grubs of *A. proxima* was lower for all varieties over standard Pusa Bold except Varuna at 6:18 (Light: Dark) (Table 3 and 4). The feeding index © was higher on Varuna followed by Kranti > Kiran E > Ashirvad > Krishma > Basanti > Rohini > Vardan > Kanti > Kiran B > PRKS-22 > Pusa Krisma at 6:18 (Light: Dark) while at 9:15 (Light: Dark) the order was Rohini > Kranti > Basanti > Pusa Krisma > Krishma > Kiran E > Varuna > Ashirvad > Vardan > Kiran B > PRKS-22 and Kanti against standard Pusa Bold (1.00).

Therefore, it is concluded that *B. alba* were preferred most close to standard, *B. campestris* and among Indian mustard varieties, Varuna and Rohini were preferred most close to standard, Pusa Bold. It is also evident that increase/decrease in the duration of light hours decrease/increase the feeding efficacy of grubs of *A. proxima* and increase/decrease value of feeding index © was recorded on same host plant when decrease/increase the duration of light hours. This study showed the higher feeding index © for grubs of *A. proxima* recorded at 6:18 (Light: Dark) than at 9:15 (Light: Dark) conditions.

Table 1 Differential feeding of *A. proxima* grubs on *Brassica* species at 6:18 (Light : Dark)

Test plants	Feeding index ©								
	1 day	2 day	3 day	4 day	5 day	6 day	7 day	8 day	Mean
B. alba cv. PSB-I	0.60	0.64	0.79	0.85	0.81	1.28	1.49	1.20	0.96
Eruca sativa cv. T-27	0.59	0.66	0.56	0.58	0.91	1.45	0.89	0.79	0.80
B. campestris cv. BSH-I	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
B. napus cv. sheetal	0.50	0.85	0.24	0.23	0.85	1.15	0.59	0.47	0.61
B. carinata cv. CCN-06-1	0.84	0.98	0.49	0.48	0.00	0.00	0.33	0.27	0.42
B. juncea cv. varuna	0.59	0.58	0.31	0.32	1.05	1.29	1.02	1.33	0.81
B. nigra cv. PBR-I	0.55	0.64	0.39	0.33	1.03	1.15	0.58	0.83	0.69
Crambe abyssinica cv. CA01	0.21	0.23	0.02	0.01	0.89	0.82	0.67	0.49	0.42
SEm ±	0.19	0.20	0.22	0.23	0.33	0.33	0.44	0.34	
C D (P=0.05)	0.58	0.61	0.65	0.69	0.98	0.99	1.32	1.03	
C V (%)	55.14	50.13	79.25	84.12	70.30	56.45	92.49	74.25	

Table 2 Differential feeding of *A. proxima* grubs on *Brassica* species at 9:15 (Light : Dark)

Test plants	*Feeding index ©*								
	1 day	2 day	3 day	4 day	5 day	6 day	7 day	8 day	Mean
B. alba cv. PSB-I	0.26	0.57	0.93	0.69	1.83	1.50	1.07	1.31	1.02
Eruca sativa cv. T-27	0.81	0.51	0.36	0.22	0.50	0.32	0.40	0.24	0.42
B. campestris cv. BSH-I	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
B. napus cv. sheetal	0.88	0.44	0.82	0.62	0.32	0.16	0.18	0.20	0.45
B. carinata cv. CCN-06-1	0.85	0.73	0.71	0.38	0.48	0.19	0.51	0.62	0.56
B. juncea cv. varuna	0.32	0.34	0.77	0.46	1.05	0.61	0.77	0.76	0.64
B. nigra cv. PBR-I	0.55	0.35	0.52	0.32	0.00	0.00	0.81	0.98	0.44
Crambe abyssinica cv. CA01	0.32	0.21	0.41	0.39	0.23	0.27	0.49	0.43	0.34
SEm ±	0.18	0.24	0.28	0.24	0.35	0.17	0.36	0.38	
C D (P=0.05)	0.53	0.68	0.82	0.73	1.04	0.50	1.07	1.15	
C V (%)	46.47	71.03	62.13	75.12	83.88	58.93	86.34	92.89	

Table 3 Differential feeding of *A. proxima* grubs on Indian mustard varieties at 6:18 (Light : Dark)

Test plants	*Feeding index ©*								
	1 day	*2 day*	*3 day*	*4 day*	*5 day*	*6 day*	*7 day*	*8 day*	*Mean*
Krishma	1.06	1.00	1.24	1.23	0.63	0.63	0.77	0.44	0.88
Basanti	0.80	1.23	1.32	1.23	0.56	0.84	0.84	0.00	0.85
Kranti	0.95	0.47	1.78	0.70	0.95	1.20	0.89	0.51	0.93
Ashirvad	0.71	1.06	1.32	1.26	0.80	1.10	0.85	0.00	0.89
Kiran E	1.01	1.00	1.24	1.15	0.58	0.91	0.88	0.44	0.90
Rohini	0.66	0.57	0.76	0.88	0.68	1.07	0.96	0.51	0.76
Varuna	0.79	1.05	1.51	1.58	1.27	1.29	0.98	0.00	1.06
Kiran B	0.32	0.67	0.74	0.68	0.52	0.77	1.14	0.44	0.66
Vardan	0.80	0.75	0.92	0.85	0.70	0.99	0.92	0.00	0.74
Pusa Krishma	0.50	0.59	0.34	0.26	0.16	0.33	0.84	0.00	0.38
Pusa Bold	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
PRKS-22	0.48	0.62	0.65	0.68	0.73	0.89	0.79	0.00	0.61
Kanti	0.80	0.82	1.36	1.20	0.47	0.60	0.53	0.00	0.72
SEm ±	0.25	0.23	0.26	0.27	0.25	0.26	0.19	0.29	
C D (P=0.05)	0.73	0.67	0.75	0.79	0.73	0.75	0.55	0.85	
C V (%)	57.09	47.99	44.24	48.32	62.57	49.61	37.20	196.6	

Table 4 Differential feeding of *A. proxima* grubs on Indian mustard varieties at 9:15 (Light : Dark)

Test plants	*Feeding index ©*								
	1 day	2 day	3 day	4 day	5 day	6 day	7 day	8 day	Mean
Krishma	0.85	0.63	0.33	0.36	0.76	0.95	0.80	0.33	0.63
Basanti	0.57	0.57	0.51	0.50	1.19	1.20	0.74	0.44	0.72
Kranti	1.08	1.06	0.48	0.51	0.61	1.36	0.89	0.00	0.75
Ashirvad	0.13	0.09	0.38	0.37	0.63	1.40	0.82	0.53	0.54
Kiran E	*0.81*	*0.82*	*0.17*	*0.17*	*0.67*	1.23	*0.57*	0.33	0.60
Rohini	0.87	0.85	0.53	0.50	0.88	1.41	0.82	0.94	0.85
Varuna	0.06	0.60	0.13	0.13	1.33	1.62	0.56	0.00	0.55
Kiran B	0.45	0.44	0.06	0.05	0.49	1.11	0.80	0.78	0.52
Vardan	0.40	0.41	0.29	0.24	0.68	1.27	0.95	0.00	0.53
Pusa Krishma	0.79	0.74	0.41	0.43	0.97	0.33	0.89	0.78	0.67
Pusa Bold	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
PRKS-22	0.25	0.30	0.11	0.08	0.85	1.29	0.79	0.00	0.46
Kanti	0.24	0.27	0.09	0.09	0.57	0.60	0.79	0.44	0.39
SEm ±	0.19	0.18	0.18	0.18	0.32	0.22	0.25	0.33	
C D (P=0.05)	0.58	0.52	0.52	0.53	0.94	0.63	0.72	0.97	
C V (%)	54.84	51.53	90.26	92.25	68.69	32.78	53.74	134.4	

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J. Oilseeds Res., **25**(2) : 223-225 (2008)

Short communication

Sclerotinia rot tolerance in oilseed *Brassica*

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(Received: September, 2007; Revised: July, 2008; Accepted: August, 2008)

Abstract

Out of 91 accessions of *Brassica* spp. (Australia, China and Indian origin), the *Brassica juncea* line, JO 009, JN 031, JN 033 of Australia origin were found tolerant to *Sclerotinia sclerotorium* (Lib.) De Bary infection at seedling stage. Genotype RQ 011 was tolerant at seedling and silique formation stages. Few lines of Indian origin were also mentioned as tolerant to disease.

Keywords: *Sclerotinia*, Indian mustard

Sclerotinia sclerotorium (Lib) De Bary infects more than 400 plant species including cultivated crops and oilseed *Brassica* and causes Sclerotinia-rot (Boland and Halls, 1994). This ascomycete can cause systemic and aerial infection by myceliogenic and carpogenic germination of sclerotia surviving in soil. Being ubiquitous necrotroph, it is severely affecting cultivation of oilseed *Brassica* grown in different countries. The primary method of managing it with non-host crop and fungicide application may not achieve an economic benefit. If genetic resistance to Sclerotinia-rot is available, reliance on fungicide would lessen and cultivation of oilseed *Brassica* crops would become more profitable. Hence, evaluation of *Brassica* spp. for resistance is important. An efficient and reliable screening method would allow large scale evaluation of germplasm. Methods that have been used to identify the resistant sources under screen house condition, include soil and stem inoculation at seedling and siliquae initiation stage, respectively.

A diverse range of 91 accessions of *Brassica* spp. of Australian, Chinese and Indian origin were used in this study varying in growth habit and seed qualities. Five seedlings were maintained in 12 cm diameter pots and allow to grow in natural environment (2-25°C) even during screening period. Inoculum (Hisar isolate) was raised by using boiled and sterilized wheat grains. Fifteen days old culture having mycelia and sclerotia were inoculated by placing near collar region of 45 days old seedling of each plant of every genotype and replicated five times. Disease incidence was calculated on the basis of seedling collapsed. Genotype contracted less than 25% disease was categorized as tolerant, whereas genotype having 25-50% disease incidence as susceptible and >50% as highly susceptible. Stem inoculation method was adopted as described by Zhao *et al.* (2004) with some modifications. The fifth leaf of 90 days old plant of each cultivar was severed near petiole junction using sterilized razor blade and inoculated by placing mycelia and sclerotia raised on boiled and sterilized wheat grains covered with cellotape. Disease incidence was calculated on average of stem rotted and also measured on the basis of stem break and irreversible wilting occurred. Days to wilting/stem break were calculated from symptom appearance to irreversible wilting and stem break (Zhao *et al.*, 2004).

In soil inoculation method, water soaked lesion appeared within 4-6 days after inoculation near collar region and collapsed within 15 days. None of the genotypes was observed free from incidence of *Sclerotinia*-rot. Among *Brassica juncea* lines JO 009 (18.2%), JN 031 (23.8%) and JN 033 (25.0%) of Australian origin were observed as tolerant whereas none of the Indian and Chinese lines of *B. juncea* expressed tolerance. In *Brassica napus* AG outback (15.8%), rainbow (20.0%), RQ 011 (18.2%) and RQ 001-02 M2 (22.7%) of Australian origin, Neelam (25.0%) and GSL-1 (22.7%) of Indian origin and YU-178 (25.0%) (Zhao *et al.*, 2004) of Chinese origin were observed as tolerant. Seedling stage inoculation was carried out at this stage since systemic infection takes place by prevailing environmental condition for myceliogenic germination of sclerotia and ultimately resulting into Sclerotinia stem rot of *Brassica juncea* in/under Indian field condition. If the plant/genotype gets escaped by systematic infection even than it can get infected at lateral stage i.e., blooming/siliquae initiation stage. Therefore, stem inoculation was conducted, water soaked lesion symptom appeared within 4-7 days

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depending upon genotype, rate of disease progress also varied among genotype. Using stem inoculation near petiole junction revealed that the genotypes RQ 011 (25.0), RR 001 (25.0), M 616 (25.0) (Zhao *et al.*, 2004) of *B. juncea* of Australian origin expressed tolerance as the stem cracked within 15 days and such genotypes can also be protected by adopting curative chemical means to check the progress of disease. None of Indian and Chinese origin line was observed as tolerant. Screening through stem inoculation was observed to be a promising method for screening of germplasm under screen house natural environmental condition for large collections.

Table 1 Screening of *Brassica* spp. germplasm accessions/varieties of Indian, Chinese and Australian origin against *Sclerotinia* rot caused by *Sclerotinia sclerotorium*

Accession No.	Name of accession	Soil inoculation PDI*	Stem inoculation PDI*	Days to stem breaking
Australian *B. napus* accessions				
EC 552585	Lanthen	40.0	43.3	13.2
EC 552586	AG outback	15.8	35.0	14.0
EC 552587	Trigold	36.8	40.0	13.5
EC 552588	Monty	57.1	51.0	12.4
EC 552589	Rainbow	20.0	40.0	13.5
EC 552590	Rivette	38.1	45.0	13.0
EC 552591	RQ 011	18.2	25.0	11.3
EC 552592	Tranby	42.9	37.3	13.8
EC 552593	RR 002	50.0	33.3	14.2
EC 552594	AV Sapphire	33.3	NG	NG
EC 552595	BST 702M2	63.2	29.3	14.6
EC 552596	RQ 001-02M2	22.7	40.0	13.5
EC 552597	RR 013	47.4	29.3	14.6
EC 552598	RR 009	95.6	36.6	13.7
EC 552599	Surpass 400	40.0	41.3	13.4
EC 552600	RR 005	80.0	51.3	12.4
EC 552601	Scar	68.4	30.0	14.5
EC 552602	Mystic	59.1	31.3	14.4
EC 552603	RR 001	54.5	25.0	15.0
EC 552604	Carlton	81.8	32.6	14.3
EC 552605	Skipton	57.9	40.0	13.5
EC 552606	Trilogy	80.0	30.0	9.4
EC 552607	AG Spectrum	47.4	85.0	9.0
EC 552608	TQ 0055-02W2	73.7	85.0	9.0
EC 552609	Purler	75.0	43.3	13.3
Australian accessions *B. juncea*				
EC 552573	JN 004	47.6	43	13.3
EC 552574	JN 010	80.9	43	13.2
EC 552575	JN 028	52.4	49	12.7
EC 552576	JN 031	23.8	45	13.0
EC 552577	JN 032	28.6	96	8.0
EC 552578	JN 033	25.0	55	12.0
EC 552579	JM 016	48.3	25	15.0
EC 552580	JM 018	61.9	35	14.0
EC 552581	JO 006	38.1	70	10.6
EC 552582	JO 009	18.2	85	9.0
EC 552583	JR 042	45.5	56	12.3
EC 552584	JR 049	76.2	55	12.0
Chinese accessions *B. juncea*				
EC 564640				
EC 564641				
EC 564642	CBJ 003	80.9	70	10.6
EC 564643	CBJ 004	95.0	50	12.5
EC 564644	TABP	66.7	55	12.0
EC 564645	MPJR	96.2	35	14.0
EC 564646	NINYOU-4	NG		
EC 564647	XINYOU-5	NG		
EC 564648	XINYOU-8	95.4	30	14.5
EC 564649	XINYOU-9	52.4	65	11.0
Indian *B. napus* accessions				
Neelam		25.0	65.3	11.0
GSL-1		22.7	90.0	8.5
GSL-2		50.0	85.0	9.0
Chinese *B. napus* accessions				
EC 557008		76.2	65.3	13.4
EC 557009		55.0	58.6	11.0
EC 557010		81.8	40.0	10.7
EC 557011		61.9	68.6	13.5
EC 557012		68.2	66.6	10.7
EC 557013		95.0	53.3	10.9
EC 557014		57.1	77.3	12.2
EC 557015		61.9	55.0	9.8
EC 557016		86.4	59.6	8.0
EC 557017		50.0	77.3	11.6
EC 557018		66.6	50.0	9.8
EC 557019		63.6	55.0	12.5
EC 557020		52.3	50.0	12.0
EC 557021		52.3	61.3	12.5
EC 557022		25.0	80.0	11.4
EC 557023		54.5	83.3	9.5
EC 557024		80.9	50.0	9.3
EC 557025		52.3	NG	12.5
EC 557026		95.0	73.3	NG
EC 557027		95.4	45.0	10.2
Indian accessions *B. juncea*				
Varuna		80.9	43.3	13.2
Seeta		95.2	43.3	13.2
Sanjukta-Asesh		76.2	40.0	13.5
RH-30		96.2	35.0	14.0
RL 1359		80.0	50.0	12.6
Prakash		63.2	27.3	14.8
RH 781		47.4	33.3	14.2
PBR 97		76.2	35.0	14.0
RH 819		52.4	28.6	14.7
Durgamani		61.9	33.3	14.2
Sej-2		95.8	35.0	14.0
RH 8113		50.0	50.0	12.5
Kranti		42.9	35.0	14.0
PCR 7 (Rajat)		33.3	50.0	12.0
Vardan		83.3	35.0	14.0
RH 8812		80.9	30.0	14.5
GM 1		80.0	25.0	15.0
Vaibhav		71.4	43.3	13.2
PBR 91		57.1	26.6	14.9
Rohini		38.1	32.6	14.3
RLM 619		33.3	28.3	14.7
CD (P=0.05)		7.12	6.58	0.39

NG = Not germinated; PDI = Per cent disease incidence

Differences in level of susceptibility do help in identification of genotype with tolerance to *Sclerotinia*-rot. Similarly, Singh and Tripathi (1994), Pathak *et al.* (2002), Steward Wade (2003), Zhao *et al.* (2004) and Bradley *et al.* (2006) used petiole inoculation, detached leaf assay, oxalic acid and soil inoculation for screening of different germplasm of *Brassica* species. The differences observed in the level of susceptibility under lab or green house screening method could accurately be confirmed in the field. Therefore, it is advocated to confirm the level of tolerance under sick fields having assured inoculum in rhizosphere. None of the oilseed *Brassica* germplasm lines/accessions exhibited complete resistance to *Sclerotinia*-rot. The genotypes of *B. juncea* namely, JO 009, JN 031 and JN 033 of Australian origin were observed tolerant whereas, none of the Indian and Chinese lines was observed tolerant at seedling stage. In *B. napus*, AG outback, Rainbow, RQ 011 and RQ 011-02M2 of Australian origin, Neelam and GSL 1 of Indian origin and YU 178 of Chinese origin were tolerant at seedling stage. Interestingly, the genotype RQ 011 was observed tolerant at both seedlings and at siliquae formation stage. Based upon the available level of tolerance, it is advocated that the identified genotypes could be utilized to further enhance the level of resistance/tolerance rather than as donor parents for incorporating resistance against *Sclerotinia*-rot.

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J. Oilseeds Res., **25**(2) : **226-227** (**2008**)

Short communication

Linolenic acid heredity in *Linum usitatissimum*

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(Received: May, 2007; Revised: June, 2008; Accepted: July, 2008)

Abstract

Parental material with low linolenic acid i.e., ED 1747 was crossed reciprocally with high linolenic line LC 2063 as well as fiber flax genotypes, Somme, Bethune and Flander at PAU, Ludhiana. The studies suggested that segregating progenies in 3 out of 4 F_2 crosses releaved enhanced values for linoleic acid. In the cross 1747 x Bethune, where segregants had as high as 55% oleic acid, showing the presence of genetic modulating desaturation for oleic to linolenic acid in Bethune, which may prove rewarding to develop edible grade linseed with high oleic acid content.

Keywords: Linseed, linoleic acid, oleic acid

Oil quality in linseed, *Linum usitassimum* has traditionally been determined by linolenic acid content. High linolenic acid is important due to widespread usage of linseed oil as an industrial drying oil. With the availability of cheaper synthetic additives its usage as an industrial oil is now declining. Further, higher level of linolenic acid in the oil makes it unsuitable for human consumption because of rancidity and flavour reversion associated with auto oxidation of this fatty acid (Graef *et al.*, 1988; Saeldi and Rowland, 1977). Induced mutagenesis have helped elimination of this fatty acid from the oil (Rowland and Bhatty, 1990). Genetic determination of genes governing the fatty acid desaturation steps, between oleoyl CoA to linolenic acid have been the subject of past attention. Higher level of linolenic acid was attributed to alleles at two loci which act in additive manner (Green, 1986; Rowland, 1991). The genes encoding microsomal desaturases capable of desaturating linoleic acid have been identified as *LuFAD*3A and *LuFAD*3B. Both these genes carry point mutations that produce stop codons (Verinten *et al.*, 2005). In this communication we describe our attempts to assess the linolenic acid heredity in Indian linseed and fiber flax genotypes in crosses with a low (<2%) linolenic mutants.

Parental material for the experiment comprised low linolenic acid strain, ED 1747. This was crossed reciprocally with high linolenic acid genotype LC 2063 as well as fiber flax genotypes Somme, Bethune and Flander. For understanding the inheritance of the trait, F_1, F_2 and backcross generations were studied. Backcross generations could be developed from only two crosses. Fatty acid composition of the plants was determined by gas liquid chromatography (Appelqvist, 1968), using standard methods for transesterification developed at the lipid chemical laboratory, SvalOf, Sweden. Pooled samples of 15 self-seeds obtained from parents or individual seeds in segregating (F_2/BC) generations were analysed to decipher the fatty acid composition.

Distribution of mean linolenic acid levels in parents is presented in Table 1. Linolenic acid levels in F_1 were intermediate to the parental values and there were no significant differences in F_1 and F_2 means for all the four crosses which indicated the absence of dominance (Table 1). There were no reciprocal differences as was evident from similar F_1 values in reciprocal combinations. Continuous variation and class overlap (Table 3) for linolenic acid values in F_2 and backcross generations did not permit the formation of discrete classes and fitting the data into classical Mendelian segregation ratios. Therefore, only two classes, one with high linolenic acid (>5%) and the other low in linolenic acid (<5%) were considered for the genetic analysis. The proportion of individuals in 0-5% class of the total seeds analysed in four crosses *viz.*, ED 1747 x LC 2063, ED 1747 x Somme, ED 1747 x Bethune and ED 1747 x Flander was 0.08, 0.04, 0.03 and 0.05, respectively, which were nearly equal to the expected proportion of 0.06%, if the hypothesis of the two gene control with additive gene effect was considered. On the basis of these observations, the F_2 segregation ratios were tested against theoretical expectation of 15:1 (Table 2). The segregations revealed a perfect fit with the hypothesis that two genes showing no dominance and acting in additive manner govern the linolenic acid heredity in the crosses studied. Analysis of the backcross generations in two crosses (Table 4) further supported the inferences drawn from F_2 generations as these fitted perfectly with the expected BC_1 segregation ratio (3:1). The digenic additive nature of the genes controlling linolenic acid content was demonstrated previously in the Canadian fiber flax genotypes (Rowland, 1991). Based on the current segregation data and past publication, the genotype of high linolenic acid strains, LC 2063, Somme, Bethune and Flanders was postulated to be $L_1L_1L_2L_2$. The low linolenic acid genotype (ED 1747) thus possessed the genetic constitution $l_1l_1l_2l_2$. It has been a universal observation that reduction in the linolenic acid content in linseed is associated with a concomitant increase in linolenic acid content, but no significant increase in the oleic acid content. This was attributed to very strong desaturation activity in the linseed fat biosynthetic pathway. That this character is highly conserved in nature was apparent from inability of the linseed breeders across the world to increase oleic acid content despite repeated mutagenesis in the past.

In the present studies also the segregating progenies in three out of the four F_2 crosses evaluated revealed enhanced values for linoleic acid. The sole exception was the cross ED 1747 x Bethune, where segregants with as high as 55% oleic acid could be recorded. This might suggest the presence of genetic factors modulating desaturation from oleic to linolenic acid in Bethune. Further selection in this cross combination could prove rewarding to develop edible grade linseed with high oleic acid content.

Table 1 **Fatty acid profile of some linseed genotypes used in genetic investigation**

Genotype	Palmitic	Stearic	Oleic	Linoleic	Linolenic
ED 1747	6.9	3.4	18.1	70.6	0.9
LC 2063	6.9	5.1	26.7	11.7	48.9
Somme	5.8	4.1	28.1	15.7	45.3
Flander	6.9	4.1	31.0	18.4	38.6
Bethune	5.9	2.9	28.9	15.1	45.5

Table 2 **Mean linolenic acid content (%) in F_1 and F_2 generations of linseed crosses**

Combination	F_1	F_2
ED 1747 x LC 2063	21	23
ED 1747 x Somme	23	21
ED 1747 x Bethune	24	20
ED 1747 x Flander	20	19
Overall mean	20	20.7

Table 3 **Segregation for linolenic acid content in F_2 generations of various cross combinations**

Combination	Sample size	Linolenic acid (%)				χ^2 (15:1)
		<5	5-25	25-50	>50	
ED 1747 x LC 2063	176	15	54	104	3	1.55
ED 1747 x Somme	*92*	*4*	*32*	*56*	*1*	*0.56*
ED 1747 x Bethune	73	2	55	16	0	1.57
ED 1747 x Flander	234	12	93	127	2	0.43
Overall mean	575	-	-	-	-	0.27

Table 4 **Segregation for linolenic acid content in test cross (BC_1) generation of two linseed crosses**

Combination	Linolenic acid (%)				χ^2 (15:1)
	<5	5-25	25-50	>50	
(LC 2063 x ED 1747) x ED 1747	14	2	52	5	1.32
(Somme x ED 1747) x ED 1747	10	3	32	-	0.57
Overall χ^2	-	-	-	-	1.69

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GUIDELINES TO THE CONTRIBUTORS

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