COMBINING ABILITY FOR YIELD ATTRIBUTES IN GREENGRAM (*VIGNA RADIATA* L. WILCZEK)

R. NARASIMHULU*, N. V. NAIDU, K. H. P. REDDY AND G. MOHAN NAIDU
Department of Genetics and Plant Breeding,
S.V. Agricultural College, Tirupati - 517 502, A P
e-mail: narsi46@gmail.com

ABSTRACT
Five lines were crossed with four testers in Line × Tester fashion to estimate the combining ability for yield and yield attributing traits in greengram. Analysis of variance revealed significant differences among genotypes, crosses, lines, testers and line × tester interactions for most of the traits. Preponderance of non-additive gene effects was realized from higher values of specific combining ability compared to general combining ability and ratio of variances of SCA to GCA except for tolerance to MYMV. Parents *viz.*, MGG-351, WGG-42, LGG-460 and TM-96-2 were considered as superior parents as they recorded high *per se* performance with positive significant effects for seed yield per plant and other yield contributing traits. Cross combinations *viz.*, MGG-351 × PM-115, TM-96-2 × PM-112, MGG-295 × PM-110, TM-96-2 × WGG-37 WGG-42 × WGG-37 and WGG-42 × PM-110 were found to be good specific combinations for seed yield per plant and other desirable traits. These cross combinations could be utilized for further amelioration of seed yield in greengram.

INTRODUCTION

Greengram [*Vigna radiata* (L.) Wilczek], is an economically important short duration grain legume characterized by relatively more palatable, nutritive, cheap source of high quality and easily digestible protein, non-flatulent than other pulses and constitute an important source of cereal based diets in Asia (Kamleshwar *et al.*, 2014). In-spite of high demand, the yield of greengram worldwide is very low (384 kg/ha) and limited success has been achieved so far in augmenting its yield. To enhance the present yield levels, it is essential a systemic varietal improvement through hybridization and exploitation of generated variability through recombination breeding. To breed a genotype with high yielding potential, the information on the genetic mechanism controlling various traits in the material being handled, is a pre-requisite. The estimates of combining ability along with *per se* performance of genotypes in a crop improvement programme have a direct bearing upon the choice of breeding methodology to be followed and to identify the parent and crosses (Khattak *et al.*, 2004), which could be exploited for future breeding programme.

In literature, both additive and non-additive genetic systems, controlling seed yield and yield-relating traits in greengram, have been reported (Barad *et al.* (2008); Marappa (2008); Sathya and Jayamani (2011); Sujatha and Kajjidoni (2013) and Suresh (2014)). However, the major part of genetic variation for yield and its components was conditioned due to higher magnitude of non-additive genetic effects (Marappa (2008); Sathya and Jayamani (2011); Sujatha and Kajjidoni (2013) and Suresh (2014)). Seed yield and several yield-contributing characters lack stability due to strong environmental influence, suggesting the need for breeding for specific environment. Therefore, the present investigation was planned and executed to assess the nature of gene action involved and combining ability of parental genotypes for different characters utilizing Line × Tester mating design (Kempthorne, 1957) for evolving productive varieties in greengram.

MATERIALS AND METHODS

Five lines MGG-295, MGG-351, WGG-42, LGG-460 and TM-96-2 were crossed with four testers WGG-37, PM-112, PM-115 and PM-110 in Line × Tester fashion at the wetland farm of Sri Venkateswara Agricultural College, Tirupati, Andhra Pradesh, India to generate a total of 20 hybrids. All the genotypes (nine parents and 20 F_1's) were evaluated in Randomized Block Design with two replications during *kharif,* 2013. Each genotype was grown in two rows of three meters length with a spacing of 30cm between rows and 15cm between plants. Recommended agronomic and plant protection package of practices were followed to raise healthy crop. Data were recorded on five randomly selected competitive plants in each genotype and replication. Mean values on per plant basis were recorded for the characters *viz.*, plant height, number of branches/plant, clusters/plant, pods/cluster, pods/plant, seeds/pod, 100 seed weight, dry weight/plant, harvest index, tolerance to MYMV, seed yield/plant, total sugars (Dubois *et al.*, 1956) and the micro-kjeldah 'N' procedure was used for the determination of nitrogen and crude protein was estimated by multiplying the nitrogen content by a factor of 6.25. How-

ever, data on days to 50% flowering and days to maturity were recorded on plot basis. The mean data was analysed to compute combining ability effect and their variances according to Kempthorne (1957).

RESULTS AND DISCUSSION

Analysis of variance for combining ability (Table 1) showed highly significant differences among parents for all the characters except for number of seeds/pod, total sugars and seed yield/plant, indicating significant variation among parents used in this study. All the crosses showed significant differences for all the characters except for number of seeds/pod. Mean squares due to parents *vs* crosses were significantly different for all the characters except for 100 seed weight and seed protein, re-vealing good scope for manifestation of heterosis in all the characters studied. The effect of crosses was partitioned into lines, testers and their interactions. The variance due to lines showed highly significant differences for all the characters except for number of seeds/pod. The variance due to testers showed significant difference for 12 characters except for number of pods/cluster, seeds/pod and 100 seed weight. The variance due to interaction effect (Lines × Testers) showed significant difference for 13 characters except for plant height and number of seeds/pod indicating specific combining ability involvement in the expression of these traits and the importance of dominance or non-additive variances for majority of the characters. The importance of dominance variance for most of the traits was also reported by Bainade *et al.* (2014). The significant mean square of lines and testers indicated prevalence of additive variance for the yield and its components. Occurrence of both additive and non additive gene effects for yield and important yield component traits in greengram were reported from earlier studies by Anbumalarmathi *et al.* (2005), Marappa (2008), Barad *et al.* (2008), Sathya and Jayamani (2011), Sujatha and Kajjidoni (2013) and Suresh (2014).

Preponderance of non-additive gene effects in the manifestation of all the biometrical characters was observed by higher value of specific combining ability variance than the general combining ability variance. The ratio of variance due to general and specific combining ability ranged from 0.0119 to 0.6598 conforming the major role of non-additive gene action for all the traits under study except for tolerance to MYMV (Table 1). From the estimates of additive and dominance variance, it was observed that dominance variance was predominant for all the characters except for 100 seed weight and tolerance to MYMV indicating the major role of non-additive gene action and was highest for pods/plant followed by dry weight/plant and harvest index. The present results indicate the preponderance of non-additive gene action in the expression of most of the characters studied and scope for the exploitation of non-additive genetic variation for traits through heterotic breeding followed by selection at later generations. These results were in line with the findings of Sujatha and Kajjidoni (2013) and Suresh (2014).

The *gca* effects reflect performance of parental lines in combination with all other lines, so parents with highest *gca* effects should have greater impact on the trait improvement.

Table 1: ANOVA for combining ability in a Line × Tester analysis and estimation of genetic components for different quantitative traits in greengram

Source	df	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of clusters/plant	No. of pods/cluster	No. of pods/plant	No. of seeds/pod	100 seed weight (g)	Dry weight/plant (g)	Harvest index (%)	Seed protein (%)	Total sugars (%)	Tolerance to MYMV score (0-9 scale)	Seed yield/plant (g)
Replications	1	2.48	3.38	0.05	0.09	0.28	0.04	10.41	0.61	0.02	0.60	0.61	0.31	0.26	0.01	0.64
Treatments	28	7.45**	8.30**	47.93**	0.92**	7.08**	0.28**	126.20**	1.24**	0.81**	42.82**	29.43**	1.41**	0.47**	2.27**	12.13**
Parents	8	5.00**	8.25**	69.53**	0.82**	2.10**	0.15**	31.17**	0.86	0.84**	10.32**	16.30**	1.29**	0.26	3.45**	1.59
Crosses	19	8.39**	8.54**	39.45**	0.91**	9.47**	0.17**	154.10**	0.71	0.83**	55.33**	31.50**	1.12**	0.47**	1.85**	12.85**
Lines	4	25.98**	22.35**	128.39**	2.02**	24.92**	0.40**	400.11**	0.64	3.36**	111.67**	61.19**	1.21**	0.47**	8.32**	15.20**
Testers	3	3.80*	10.03**	27.08*	1.09**	5.66**	0.11	123.01**	1.25	0.09	94.11**	31.26**	1.08**	0.51**	0.25**	15.46**
Lines × Testers	12	3.68**	3.57**	12.89	0.49**	5.27**	0.11*	79.87**	0.59	0.17*	26.85**	21.66**	1.10**	0.47**	0.09*	11.42**
Parents vs Crosses	1	9.32**	4.10*	36.23*	1.90**	1.72**	3.34**	356.26**	14.43**	0.12	65.23**	95.31**	0.41	2.03**	0.81**	82.68**
Error	28	1.09	0.92	6.55	0.06	0.41	0.04	4.09	0.49	0.07	1.04	1.43	0.15	0.12	0.02	0.72
gca variance		0.21	0.22	1.16	0.02	0.18	0.00	3.25	0.01	0.03	1.25	0.43	0.00	0.00	0.08	0.06
sca variance		1.26	1.43	2.67	0.23	2.43	0.04	37.62	0.05	0.04	12.83	10.00	0.47	0.15	0.03	5.26
GCA/SCA		0.16	0.15	0.44	0.08	0.08	0.07	0.09	0.10	0.66	0.10	0.04	0.00	0.00	2.52	0.01
s²A		0.41	0.44	2.33	0.04	0.37	0.01	6.50	0.01	0.06	2.49	0.86	0.00	0.00	0.15	0.13
s²D		1.26	1.43	2.67	0.23	2.43	0.15	37.62	0.05	0.04	12.83	10.00	0.47	0.15	0.03	5.26
Ratio s²A:s²D		0.33	0.30	0.87	0.16	0.15	0.04	0.17	0.20	1.32	0.19	0.09	0.00	0.00	5.04	0.02

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

Dhillon (1975) opined that combining ability provides useful information on the choice of parents in terms of expected performance of the hybrids and progenies. Singh and Harisingh (1985) and Tiwari *et al.* (1993) had also suggested that parents with high *gca* effects could produce transgressive segregants in F_2 or later generations. The close examination of the general combinability effects (Table 2) of the parents indicated that none of parents were found to be good combiner for all traits. Among the lines, TM-96-2 ranked as top by exhibiting significant *gca* effects for seven traits *viz.*, number of branches/plant, clusters/plant, pods/plant, dry weight/plant, tolerance to MYMV and seed yield/plant with earliness. This was followed by LGG-460 as a good combiner for seven traits *viz.*, number of branches/plant, clusters/plant, pods/cluster, pods/plant, harvest index, tolerance to MYMV and seed yield/plant with late maturity. The MGG-351 was also a good general combiner with good mean performance for five traits *viz.*, plant height, number of branches/plant, clusters/plant, pods/plant and dry weight/plant followed by MGG-295 for number of pods/cluster, seed protein and seed yield/plant; WGG-42 for test weight, harvest index, tolerance to MYMV and earliness were found as good general combiners.

The estimates of *gca* effects further revealed that the parental lines showing high *gca* effects for seed yield also exhibited high to average *gca* effects for one or other yield components. Similar results were reported by Sunil *et al.* (2010), Sathya and Jayamani (2011), Sujatha and Kajjidoni (2013) and Suresh (2014). These parents can be intensively used in the hybridization programme aimed at amelioration of seed yield.

Among the testers, WGG-37 was the best general combiner for most of the traits *viz.*, plant height, number of branches/plant, clusters/plant, pods/cluster, pods/plant, seeds/pod, dry weight/plant and seed yield/plant followed by PM-112 recorded significant *gca* effects for number of branches/plant, pods/plant, harvest index and seed yield/plant while PM-115 for seed protein and PM-110 for total sugars and tolerance to MYMV were found as good general combiners.

A perusal general combining ability effects revealed that the parents, TM-96-2, LGG-460, MGG-351, WGG-37 and PM-112 were the good general combiners for most of the traits while WGG-42 was the best combiner for earliness and short stature. Combination of *per se* performance and *gca* effects would result in the selection of potential parents with good reservoir of superior genes (Singh and Harisingh, 1985). Though the present investigation was evident that crosses involving MGG-351, LGG-460, TM-96-2 and WGG-42 as a parents would result in the identification of superior segregants with favorable genes for yield attributing characters as these parents had good *per se* performance and *gca* effects for most of the traits.

Specific combining ability estimates revealed a very wide range of variation for all the characters (Table 3). High *sca* effects mostly from the dominance and interaction effects existed between the hybridizing parents. In greengram owing to its autogamous genetic nature, *sca* effects are not readily useful. However, if *sca* is due to additive × additive gene action, it is fixable at later generations and superior transgressive segregants can be isolated from such crosses. In the present investigation, the cross MGG-351 × PM-115 recorded high

Table 2: General combining ability (gca) effects for different characters in Line × Tester analysis in F₁ generation.

Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of clusters/plant	No. of pods/cluster	No. of pods/plant	No. of seeds/pod	100 seed weight (g)	Dry weight/plant (g)	Harvest index (%)	Seed protein (%)	Total sugars (%)	Tolerance to MYMV score (1-9 scale)	Seed yield/plant (g)
Lines															
MGG-295	-0.08 ns	0.43 ns	1.13 ns	-0.12 ns	-0.02 ns	0.16 *	-0.07 ns	-0.37 ns	0.02 ns	0.75 ns	0.05 ns	0.31 *	-0.10 ns	1.30 **	0.70 *
MGG-351	1.30 **	0.68 *	4.84 **	0.26 **	0.94 **	-0.04 ns	4.50 **	-0.01 ns	-0.30 **	4.61 **	-4.34 **	0.08 ns	0.16 ns	0.89 **	0.20 ns
WGG-42	-2.33 **	-2.58 **	-6.13 **	-0.82 **	-3.05 **	-0.33 **	-12.12 **	0.39 ns	1.11 **	-5.64 **	2.58 **	-0.68 **	-0.38 *	-0.50 **	-2.43 **
LGG-460	2.17 **	1.92 **	-0.91 ns	0.28 **	0.93 **	0.25 **	5.12 **	0.13 ns	-0.49 **	-0.89 *	2.19 **	0.16 ns	0.20 ns	-0.78 **	0.70 *
TM-96-2	-1.08 *	-0.45 ns	1.07 ns	0.41 **	1.20 **	-0.03 ns	2.58 **	-0.13 ns	-0.34 **	1.18 **	-0.49 *	0.13 ns	0.12 ns	-0.91 **	0.82 *
SE (g)	0.38	0.30	0.97	0.07	0.23	0.07	0.76	0.25	0.10	0.38	0.46	0.14	0.14	0.05	0.34
Testers															
WGG-37	-0.10 ns	0.22 ns	2.45 *	0.28 **	0.65 **	0.14 *	3.15 **	0.50 *	-0.01 ns	3.62 **	-2.55 **	-0.26 ns	0.04 ns	0.09 ns	0.88 **
PM-112	-0.00 ns	0.13 ns	-0.69 ns	0.27 **	0.29 ns	-0.08 ns	2.30 **	-0.15 ns	0.05 ns	-0.01 ns	1.25 *	-0.14 ns	-0.28 *	0.17 **	0.80 *
PM-115	-0.70 ns	-1.38 **	-1.08 ns	-0.16 *	0.15 ns	0.03 ns	-0.89 ns	-0.03 ns	-0.13 ns	0.27 ns	0.18 ns	0.48 **	-0.04 ns	-0.06 ns	0.10 ns
PM-110	0.80 *	1.02 **	-0.68 ns	-0.38 **	-1.08 **	-0.08 ns	-4.57 **	-0.31 ns	0.09 ns	-3.88 **	1.12 **	-0.08 ns	0.27 *	-0.19 **	-1.79 **
SE (g)	0.34	0.27	0.87	0.06	0.20	0.06	0.68	0.22	0.09	0.35	0.41	0.12	0.13	0.05	0.30

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

Table 3: Specific combining ability (sca) effects of crosses for different characters in Line × Tester analysis in F₁ generation.

Cross combinations	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches /plant	No. of clusters/ plant	No. of pods/ cluster	No. of pods/ plant	No. of seeds/ pod	100 seed weight (g)	Dry weight/ plant (g)	Harvest index (%)	Seed protein (%)	Total sugars (%)	Tolerance to MYMV score (1-9 scale)	Seed yield/ plant (g)
MGG-295 × WGG-37	-0.52 ns	0.28 ns	-0.70 ns	-0.21 ns	-1.69 **	-0.17 ns	-5.83 **	-0.51 ns	-0.08 ns	-2.10 *	-4.39 **	-0.89 **	-0.97 **	0.16 ns	-3.54 **
MGG-295 × PM-112	-0.13 ns	-0.63 ns	-0.95 ns	-0.09 ns	-0.48 ns	-0.11 ns	-2.28 ns	0.14 ns	-0.16 ns	2.23 **	-1.96 *	1.20 **	-0.01 ns	-0.12 ns	0.24 ns
MGG-295 × PM-115	1.08 ns	0.38 ns	-3.59 ns	-0.06 ns	0.17 ns	0.33 *	0.61 ns	0.42 ns	0.29 ns	-2.35 **	4.00 **	-0.93 **	0.61 *	0.00 ns	0.75 ns
MGG-295 × PM-110	-0.43 ns	-0.02 ns	5.24 *	0.36 *	2.00 **	-0.04 ns	7.49 **	-0.05 ns	-0.05 ns	2.21 *	2.35 *	0.62 *	0.37 ns	-0.06 ns	2.55 **
MGG-351 × WGG-37	1.60 *	1.52 *	-1.90 ns	0.36 *	-0.09 ns	-0.14 ns	-1.50 ns	-0.28 ns	0.05 ns	2.05 *	-3.83 **	-0.14 ns	0.60 *	0.27 *	-1.49 *
MGG-351 × PM-112	1.00 ns	0.63 ns	0.94 ns	-0.87 **	0.47 ns	0.10 ns	0.35 ns	-0.47 ns	0.14 ns	-4.82 **	3.63 **	-0.15 ns	0.10 ns	0.09 ns	-0.64 ns
MGG-351 × PM-115	-2.80 **	-2.88 **	2.53 ns	0.46 **	0.71 ns	0.09 ns	6.22 **	0.21 ns	0.17 ns	6.91 **	-1.65 ns	0.12 ns	-0.60 *	-0.10 ns	3.16 **
MGG-351 × PM-110	0.20 ns	0.73 ns	-1.57 ns	0.05 ns	-1.09 *	-0.06 ns	-5.08 **	0.54 ns	-0.36 ns	-4.15 **	1.85 ns	0.17 ns	-0.10 ns	-0.10 ns	-1.03 ns
WGG-42 × WGG-37	-1.27 ns	-1.22 ns	0.50 ns	-0.41 **	1.39 **	-0.22 ns	2.82 ns	-0.40 ns	-0.08 ns	-0.59 ns	3.77 **	-0.37 ns	-0.23 ns	-0.26 *	1.87 *
WGG-42 × PM-112	-0.37 ns	-0.12 ns	0.34 ns	-0.17 ns	-2.58 **	-0.08 ns	-9.73 **	0.54 ns	0.33 ns	-1.17 ns	-1.88 ns	0.12 ns	0.29 ns	-0.23 *	-1.96 **
WGG-42 × PM-115	0.83 ns	1.88 **	-0.63 ns	0.16 ns	-0.43 ns	0.22 ns	0.96 ns	-0.49 ns	-0.51 *	-1.94 *	-1.34 ns	0.59 *	-0.00 ns	0.18 ns	-1.75 *
WGG-42 × PM-110	0.83 ns	-0.52 ns	-0.20 ns	0.41 **	1.62 **	0.08 ns	5.94 **	0.35 ns	0.26 ns	3.70 **	-0.55 ns	-0.34 ns	-0.06 ns	-0.15 ns	1.84 *
LGG-460 × WGG-37	1.23 ns	0.78 ns	3.09 ns	0.24 ns	0.46 ns	0.23 ns	4.78 **	0.44 ns	-0.12 ns	1.41 ns	-0.02 ns	0.48 ns	0.19 ns	-0.06 ns	1.08 ns
LGG-460 × PM-112	0.13 ns	-0.62 ns	-1.28 ns	0.67 **	1.28 *	0.03 ns	5.57 **	-0.26 ns	-0.29 ns	0.39 ns	1.37 ns	-0.85 **	-0.29 ns	-0.14 ns	1.03 ns
LGG-460 × PM-115	-0.17 ns	0.38 ns	0.50 ns	-0.41 **	-1.39 **	-0.35 *	-7.05 **	-0.23 ns	0.26 ns	-2.75 **	-0.19 ns	0.18 ns	0.25 ns	-0.02 ns	-1.83 *
LGG-460 × PM-110	-1.17 ns	-0.52 ns	-2.32 ns	-0.49 **	-0.36 ns	0.09 ns	-3.30 *	0.05 ns	0.15 ns	0.96 ns	-0.16 ns	0.19 ns	-0.16 ns	0.22 ns	-0.28 ns
TM-96-2 × WGG-37	-1.02 ns	-1.35 *	-0.99 ns	0.01 ns	-0.08 ns	0.30 *	-0.28 ns	0.75 ns	0.23 ns	-0.77 ns	4.47 **	0.92 **	0.41 ns	-0.13 ns	2.08 **
TM-96-2 × PM-112	-0.62 ns	0.75 ns	0.95 ns	0.47 **	1.30 **	0.06 ns	6.09 **	0.05 ns	-0.02 ns	3.36 **	-1.17 ns	-0.31 ns	-0.09 ns	-0.01 ns	1.33 ns
TM-96-2 × PM-115	1.08 ns	0.25 ns	1.19 ns	-0.15 ns	0.95 ns	-0.29 *	-0.74 ns	0.08 ns	-0.21 ns	0.13 ns	-0.81 ns	0.04 ns	-0.26 ns	-0.09 ns	-0.32 ns
TM-96-2 × PM-110	0.58 ns	0.35 ns	-1.15 ns	-0.33 *	-2.17 **	-0.07 ns	-5.06 **	-0.89 ns	-0.00 ns	-2.72 *	-2.49 ns	-0.65 *	-0.05 ns	0.25 *	-3.08 **
SE (Sij)	0.76	0.60	1.94	0.13	0.46	0.13	1.52	0.50	0.20	0.77	0.91	0.28	0.28	0.11	0.67

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

sca effects for number of branches/plant, pods/plant, dry weight/plant and seed yield/plant with early maturity, while the crosses WGG-42 × PM-110 and TM-96-2 × PM-112 showed significant *sca* effects for four traits *viz.,* number of branches/plant, clusters/plant, pods/plant and dry weight/plant followed by MGG-295 × PM-110 for number of clusters/plant, pods/plant, seed protein and seed yield/plant. The cross TM-96-2 × WGG-37 for harvest index, seed protein and seed yield/plant found to be superior while WGG-42 × WGG-37 showed significant *sca* effects for number of clusters/plant, harvest index, tolerance to MYMV and seed yield/plant. These crosses could be exploited effectively through heterosis breeding programme for getting desirable recombinants from the segregating population.

In majority of the crosses and for most of the traits, high *sca* was either due to high × low or low × high or low × low combining parents, which further substantiate the operation of non-additive gene action. An ideal combination involves high magnitude of *sca,* high *gca* in both or at least in one of the parent. These include TM-96-2 × WGG-37 for seed yield/plant; LGG-460 × WGG-37 for number of pods/plant; MGG-351 × WGG-37 for number of branches/plant and dry weight/plant; LGG-460 × PM-112 and TM-96-2 × PM-112 for number of branches/plant and pods/plant. High *sca* effects in these crosses are readily fixable as its superior performance is due to interaction of desirable high *gca* effects of both the parental genotypes involved in the cross combinations. It is also evident that cross combinations, which expressed high *sca* effects for seed yield/plant, have invariable positive *sca* effects for one or more yield related traits also. Grafius (1959) has already suggested that there may not be separate gene(s) for yield *per se* and yield being end product of multiple gene interactions among various yield components.

Further it revealed the potentiality of the parents with low *gca* effects in expressing high *sca* in cross combinations, wherein the parental combinations provide the environment for the full expression of the genes controlling the trait. Though the parents themselves would not express any superiority for that trait, accumulation of favourable genes may be the cause of parents with poor *gca* giving rise to hybrids with high *sca* effects. Gupta (1981) also observed that *gca* of the parents in general had no bearing on the *sca* effects of the hybrid *i.e.* the crosses involving parents with high *gca* recorded poor *sca* effects, while the parents with poor *gca* effects exhibited high *sca* effects. Therefore, it may not always be necessary to attempt crosses between high × high *gca* parents. Crosses with average or low *gca* parents can also manifest high *sca* effects, in suitable cross combinations, which is attributable to interaction effects.

In the present study it is noted that additive and non-additive gene actions are found important in the evolution of high yielding genotypes and improvement can be expected by delaying the selection to later generations, when the dominance and epistatic gene interactions disappear, restoring to intermating of segregants followed by recurrent selection. The conventional breeding methods such as bi-parental mating or diallel selective mating, there after followed by pedigree method of selection is appropriate for improvement of productivity.

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APPLICATION FORM

NATIONAL ENVIRONMENTALISTS ASSOCIATION (N.E.A.)

To,
The Secretary,
National Environmentalists Association,
D-13, H.H.Colony,
Ranchi - 834 002, Jharkhand, India

Sir,
I wish to become an Annual / Life member and Fellow* of the association and will abide by the rules and regulations of the association

Name _____

Mailing Address _____

_____

Official Address _____

_____

E-mail _____ Ph. No._____(R)_____(O)

Date of Birth _____ Mobile No. _____

Qualification _____

Field of specialization & research _____

Extension work (if done) _____

_____

Please find enclosed a D/D of Rs.. No. .... Dated .... as an *Annual / Life membership fee.*

*Attach **Bio-data and some recent publications along with the application form when applying for the Fellowship of the association.**

Correspondance for membership and/ or Fellowship should be done on the following address :

SECRETARY,
National Environmentalists Association,
D-13, H.H.Colony,
Ranchi - 834002
Jharkhand, India
E-mails :   m_psinha@yahoo.com   Cell : 9431360645
            dr.mp.sinha@gmail.com   Ph. : 0651-2244071