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GENE ACTION AND HETEROSIS FOR YIELD AND ITS COMPONENT TRAITS IN RICE (*ORYZA SATIVA* L.) THROUGH LINE X TESTER ANALYSIS UNDER SALINE CONDITION

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Abstract

It is an important to know the degree of hybrid vigour for its commercial exploitation. Relative heterosis, heterobeltiosis and standard heterosis were studied in 21 hybrids in rice which made from seven lines and three testers followed L × T mating design. Out of twenty one hybrids L7 × T3 and L7 × T2 showed desirable heterosis for the grain yield and its component trails studied. Both additive and non-additive gene action were found to control the aspersion of all characters. The ratio of GCA -10 SCA variances exhibited grater relevance of non-additive gene action. In this case yield and its most of traits controlled predominantly by non-additive gene action and panicle length and kernel breath controlled by additive generation.

Key words: Gene action, Heterosis, heterobeltiosis, Rice

Introduction

Rice is an important cereal crop and staple food crop of India which occupies an area of 43.97 million ha which is the largest in the world, with an annual production of around 106.3 million - tonnes which is the second largest in the world after China. To meet the demands of increasing population and to maintain self-sufficiency, the present production levels need to be increased up to 120 million tons by 2020. The production of rice needs to be increased by almost 2 million tons every year. In order to keep pace with the growing population, the production and productivity of rice needs to be enhanced. It has been proved that use of Cytoplasmic Male Sterility (CMS) in developing rice hybrids increases grain yield by more than 20% relative to improved inbred rice varieties and also an insight knowledge of nature and relative magnitude of gene actions involved and combining ability of the parents used in hybridization in the genetic improvement of the crop is needed for a breeder to assess nicking ability in self-pollinated crops. Among large array of biometrical procedures for relative estimation of genetic components, line × tester by Kempthorne (1957) is an efficient procedures as it allows for inclusion of a large number of lines and provides reliable estimates of genetic components, estimates of heterosis and gene action governing a complex trait. Therefore, the present investigation was carried out with a view to understand the nature of gene action and heterosis for yield and its attributes in newly developed based heterotic rice hybrids through line × tester analysis.

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Materials and Methods

The present investigation was carried at Plant Breeding Farm, Faculty of Agriculture, Annamalai University during 2015 to 2016. The materials and methods pertaining to the study are detailed in this chapter. (Table 1) The experimental materials consisted of seven lines and three Testers.

Lines *viz.*

L1 (ITA132), L2 (0M1327-14), L3 (IR58190-40-3-1-2) L4 (BR802 -78-2-1-2), L5 (RP 1678-69-39-4), L6 (IR 60823-78-1 -2-3-1-2), L7 (IR 58125-96-2-3-3)

Testers

T1 (ADT36), T2 (ADT 45), T3 (Co 47)

The testers used in the study were all well adopted to this locality and their yield potential was up to the mark.

The seven lines and three testers were crossed in a Line × Tester manner resulting in twenty one hybrids. These genotypes and hybrids were grown in saline soil with electrical conductivity (EC) of 3.83 dsm^{-1}. The seeds of male and female parents were sown (two rows each) separately for effecting during 2016. The spacing adopted was 20 cm between rows and 15 cm plants in a row. Recommended cultural practices were followed. The panicles were covered with butter paper cover immediately after emergency from the boot leaf but before an thesis any spikelet,

In a crossing block, crosses were effected in Line x Tester fashion using the seven lines and three testers to get twenty one hybrids. The one third of the tip of the spikelets in the panicle of lines were clipped off using scissors during early morning hours (7-00 to 8.00 A.M) and the immature spikelets were removed. Then the panicle was covered with butter paper cover. At the time of anther dehiscence, panicle from desired male parent was collected and inserted through the top of the cover and brushed over the clipped off spikelets of line to effect pollination The crossed seeds of the twenty one hybrid combinations were collected and cleaned carefully. Twenty one hybrids and their ten parents were transplanted in rows with spacing of 20 cm between rows and 15 cm between plants in a row. In each cross, twenty plants were maintained. A randomized block design replicated three times. A recommended fertilizer schedule was followed along with the recommended cultural operations and plant protection measures. The observations were made on randomly selected ten plants for parents and hybrids for recording the following metric traits plant height. Number of productive tillers per plant, panicle length, number of filled grains/panicle, kernel length, kernel breath, kernel / B ratio, 100 grain weight and grain yield per plant. The combining ability variance analysis was based on method developed by Kempthorne (1957).

Results and Discussion

The heterosis per cent over mid, better and standard parent for different traits are furnished in table 5.

Plant height: Ten hybrids showed significantly positive heterosis over mid parent. The maximum relative heterosis was observed in L7 × T3 (7.99 percent). The hybrids L3 × T1 and L2 × T1 recorded significantly negative heterosis over better parent. The hybrids L7 × T3 (7.99 percent) L6 × T3 (6.96 percent) and L1 × T1, (6.79 percent) exhibited highest value of relative heterosis.

Number of productive tillers per plant: Significantly positive relative heterosis was observed in eighteen. out of twenty one hybrids and it ranged from -0.42 (L3 × T2) to 25.03 percent (L6 × T1). The heterosis over better parent was positive and significant in nine hybrids, which had a range of -11.15 (L2 × T3) to 18.99 percent (L7 × T1). Highest percentage of standard heterosis (26.22 percent) was observed in L7 × T3. Ten hybrids had significantly positive standard heterosis.

Panicle length: The hybrid L4 × T2 showed highest relative heterosis (51.74 percent). All hybrids displayed significantly positive relative heterosis. Fifteen out of twenty one hybrids had significantly positive heterobeltiosis, highest heterobeltiosis was observed in L7 × T2 (29.74 percent). All the hybrids showed significantly positive standard heterosis ranged from 35.39 (L5 × T3) to 19.12 percent (L6 × T1). Fifteen out of twenty one hybrid combinations revealed significant and positive heterosis under three categories of estimates.

Number of filled grains per panicle: The relative heterosis for this trait ranged between 6.87 (L1 × T3) and 15.74 percent (L6 × T1). All the hybrids recorded significantly positive relative heterosis, twenty out of twenty one hybrids had significantly positive heterobeltiosis. Highest heterobeltiosis was observed in L6 × T1 (15.22 percent). Maximum standard heterosis was found in L6 × T 3 (13.91 percent). All the hybrids showed significantly positive standard heterosis for filled grains per panicle.

Kernel length: The hybrid L7 × T3 showed highest relative heterosis (14.63 percent). Twenty out of twenty one hybrids displayed significant positive relative heterosis while twelve had significantly positive heterobeltiosis. Highest heterobeltiosis was observed in L7 × T3 (9.46 percent), maximum standard heterosis was found in L7 × T3 (21.84 percent). All the hybrids showed significantly positive standard heterosis for kernel length.

Kernel breadth: The hybrid L5 × T2 showed highest relative heterosis (49.25 percent). Sixteen out of twenty one hybrids displayed significant positive relative heterosis. Eight out of twenty one hybrids alone had significantly positive heterobeltiosis, highest heterobeltiosis was observed in L5 × T2 (30.44 percent). Except L3 × T2 all the hybrids showed significantly positive standard heterosis, maximum standard heterosis was found in L6 × T1 (37.70 percent).

Kernel L/B ratio: The hybrid L7 × T3 showed highest relative heterosis (13.96 percent). Eight out of twenty one hybrid combinations registered significantly positive relative heterosis. Highest heterobeltiosis was observed in L7 × T3 (8.26 percent). The combinations L3 × T3, L4 × T3, L7 × T1 and L7 × T3 alone exhibited

Table 1: Analysis of variance for nine characters

Source	df	Plant Height	No. of productive tillers per plant	Panicle length	No. of filled grains per panicle	Kernel length	Kernel Breadth	Kernel L /B ratio	100 grain weight	Grain yield per plant
Replication	2	9.8327	2.3862	9.4507	39.0363*	0.1864**	0.0122*	0.0161	0.0062	5.2079
Parents	9	84.4751**	11.7839**	27.9276**	40.1615**	0.1156**	0.1579**	0.2892**	0.0734**	20.7145**
Parents Vs. Hybrids	1	549.2969**	209.4111**	617.0986**	4285.4063**	3.1212**	1.1015**	0.1227**	0.1157**	81.1602**
Lines	6	9.0768	6.7720**	38.3332**	14.9427	0.0548**	0.1739**	0.3690**	0.0287**	0.6536
Testers	2	8.0599	7.9427**	9.8208	103.6563**	0.3232**	0.1029**	0.1576**	0.2354**	40.5737**
Lines x Testers	1	689.6953**	49.5376**	1.7075	64.4844**	0.0658*	0.1720**	0.0736**	0.0172	101.3613**
Hybrids	20	22.8758*	5.9070**	1.9064	17.5497	0.2908**	0.0621**	0.1808**	0.1577**	10.2842**
Error	60	8.9801	0.9822	4.9162	12.0208	0.0059	0.0025	0.0073	0.0043	3.8252

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

Table 2: Analysis of combing ability variance for nine characters

Variance	Plant Height	No. of productive tillers per plant	Panicle length	No. of filled grains per panicle	Kernel length	Kernel Breadth	Kernel L /B ratio	100 grain weight	Grain yield per plant
GCA	0.0986	0.0852	0.0209	-0.0309	0.0060	0.0013	0.0034	0.0040 .	-0.0142
SCA	3.3702	0.5516	-1.2705	2.2387	0.0154	0.0031	0.0146	0.0003	2.3343
GCA: SCA	0.02925	0.1544	-0.01645	-0.0138	0.3896	0.4193	0.2328	13.3333	-0.00608

significantly positive heterobeltiosis, while L2 × T1, L2 × T3 and L 4 × T1 showed non-significant positive heterosis over better parent. Maximum standard heterosis was found in L3 × T3 (11.21 percent). The hybrids L3 × T2 showed non-significant positive standard heterosis for kernel L/B ratio. The combination L1 × T1, L5 × T2, L6 × T1 and L7 × T2 alone revealed significant and negative heterosis under three categories of estimation.

100 grain weight: Nine out of twenty one combinations has positive and significant heterosis over mid-parent, which ranged between -6.75 (L1 × T2) and 11.84 percent (L6 × T3). The cross L6 × T1 (4.65 percent) alone had the significant positive heterobeltiosis. The heterobeltiosis varied from -11.18 (L1 × T1) to 4.65 percent (L6 × T1). Out of twenty one hybrids, fourteen hybrids showed significance for standard heterosis, seven were on positive side, which ranged from -8.10 (L4 × T1) to 14.90 percent (L1 × T3).

Grain yield per plant: The percentage of relative heterosis ranged from L6 × T3 (-6.24) to L3 × T1 (16.38). Significantly positive relative heterosis was observed in eight out of twenty one hybrids studied. Out of nine hybrids showed significant heterobeltiosis, only two were on positive side. The heterobeltiosis varied from -16.12 (L6 × T3) to 14.31 percent (L3 × T1). Only three hybrids showed significantly positive and nine hybrids showed non-significant positive standard heterosis. High heterotic ability over standard check was observed in L7 × T3 (12.07 percent) followed by L7 × T2 (8.96 percent).

The estimation of additive and dominance variance for each of nine characters are given in table-3. The magnitude of dominance variance was greater than additive variance for seven characters studied indicating the predominant role of dominant gene action in the expression of these characters. The additive variance was greater than dominance variance for two characters *viz.*, panicle length and 100 grain weight.

Contribution of lines, testers and their interactions for each of nine characters are furnished in table 4. The results indicated that the contribution of lines was much greater than the testers and their interactions for the following characters *viz.*, number of productive tillers per plant, kernel breadth and kernel L/B ratio, for the characters plant height, number of filled grains per panicle and grain yield per plant the contribution of interaction between the lines and testers was greater than the contribution of lines and testers. The contribution of testers was much greater than the lines and their interactions for the following characters *viz.* kernel length, 100 grain eight, and panicle length.

Table 3: Estimation additive and dominance variance of nine characters.

S. No.	Character	Additive Variance F = 1	Dominance Variance F = 1
1	Plant height	0.1971	3.3702
2	Number of productive		
	tillers per plant	0.1703	0.5516
3	Panicle length	0.0417	-1.2705
4	Number of filled grains		
	per panicle	-0.0618	2.2387
5	Kernel length	0.0119	0.0154
6	Kernel breadth	0.0026	0.0031
7	Kernel L/B ration	0,0068	0.0146
8	100 grain weight	•0.0079	0.0003
9	Grain yield per plant	-0.0283	2.3343

Table 4: Contribution of lines, tester and their interaction for nine characters.

S. No.	Characters	Contribution		
		Lines	Testers	Interaction (LxT)
1	Plan height	16.36	35.57	50.07
2	Number of productive			
	tillers per plant	47.57	25.65	26.78
3	Panicle length	18.83	46.40	34.77
4	Number of filled grains			
	per panicle	15.88	20.06	64.06
5	Kernel length	3.15	84.01	12.84
6	Kernel breadth	73.41	15.10	11.49
7	Kernel L/B ratio	66.84	16.20	16.96
8	100 grain weight	0.67	97.37	1.96
9	Grain yield per plant	35.65	1.17	63.17

A sound breeding methodology lies on the correct understanding of the inheritance of genes involved. Tai (1979) expressed that success of any plant breeding programme greatly depends on the knowledge of genetic architecture of population handled by the breeder. Line × Tester analysis is one of the important biometrical tools which provides information on the nature of gene action as either additive (or) non additive. Besides, it helps to assess the general combining ability of the parents. The general combining ability in respect of the characters is the manifestation of additive gene action and in such a case, crop improvement programme, selection followed by pedigree breeding is good. (Jayaprakash, 1992) where SCA variance was highly significant and found much greater than GCA variance, which suggested the preponderance of non-additive gene action suited for hybrid breeding.

Plant height: The Line × Tester analysis showed predominance of non-additive gene action for plant height. The higher magnitude of s^2D variance than s^2A variance was observed by Janardhanam *et al.,* (2000) also indicated the role of non-additive gene action for plant height in rice.

Number of productive tillers per plant: The Line × Tester analysis revealed that this trait was governed predominantly by non-additive gene action which was revealed by the presence of high s^2D variance than s^2A variance. Similar high s^2D variance was noted by Devaraj and Nadarajan (1996) also reported non-additive gene action for this trait.

Panicle length: The Line × Tester analysis showed additive gene action although s^2A variance was higher than s^2D variance. This result was in agreement with the findings of Arutchenthil (1998).

Number of filled grains per panicle: The estimate of s^2D variance was high compared to s^2A displaying the predominance of non-additive gene action from Line x Tester analysis, such a high influence of SCA variance was observed by Ramalingam *et al.,* (1993) and Janardhanam *et al.,* (2000).

Kernel length: In Line × Tester analysis the variance due to s^2D was equal to s^2A variance. It indicated both additive and non-additive gene action predominance of non-additive gene action for this trait. Similar reports were given by Vivekanandan and Giridharan (1997) for this trait.

Kernel breadth: This trait was governed by both additive and non-additive gene action, which was revealed by the presence of a equal D and s^2A. Similar results were reported by Sarawagi *et al.,* (1991).

Kernel L/B ratio: The Line × Tester analysis revealed that the variance due to a^2D was more than the variance due to s^2A showed the predominance on non-additive gene action. Similarly Mohapatra and Mohanty (1985) also reported non-additive gene action for this trait.

100 grain weight: The Line × Tester analysis showed additive gene action since s^2A variance was higher than s^2D variance. In such situation pedigree breeding may be resorted population improvement. Similar trend was observed by Bobby and Nadarajan (1993).

Grain yield per plant: The combining ability analysis revealed the presence of more s^2D variance than s^2A variance, signifying the role of non-additive gene action for grain yield. Similar observations were made by Perraju and Sarma (1999) for this trait.

All the traits except panicle length and 100 grain weight, showed the predominance on non-additive gene

Table 5: Percentage of Heterosis for various yield and contributing traits

S. No	Hybrids	Plant height			Number of productive tillers per plant			Panicle length		
		(di)	(dii)	(diii)	(di)	(dii)	(diii)	(di)	(dii)	(diii)
1.	L1/T1	6.79**	0.74	2.64	11.49**	5.44	0.22	15.04*	4.65	28.12**
2.	L1/T2	1.87	-3.05	-3.05	9.76**	1.38	1.38	13.78*	3.35	26.54**
3.	L1/T3	3.22	-3.29	-0.03	15.14**	1.00	13.43**	10.84*	7.48	31.60**
4.	L2/T1	-1.91	-6.55**	-4.78	8.10*	2.32	-2.75	21.73**	15.77*	28.75**
5.	L2/T2	4.42*	0.37	0.37	16.86**	8.02	8.02	26.85**	20.45**	33.97**
6.	L2/T3	1.06	-4.37	-1.14	1.21	-11.15**	-0.22	14.11**	12.23	29.07**
7.	L3/T1	-3.36	-7.32**	-5.57*	8.44*	3.63	8.10	18.83**	13.09	25.59**
8.	L3/T2	4.34*	0.97	0.97	-0.42	-2.48	1.73	24.55**	18.35*	31.44**
9.	L3/T3	4.58*	0.40	2.96	4.91	1.18	13.63**'	15.58**	13.60	30.65**
10.	L4/T1	1.79	-4.61	-2.80	20.23**	12.48**	6.91	49.77**	25.83**	26.22**
11.	L4/T2	1.52	-4.02	-4.02	21.63**	11.17*	11.17*	51.74**	27.65**	27.65**
12.	L4/T3	4.92*	-2.34	0.96	11.00**	-3.58	8.28	44.66**	15.25*	32.54**
13.	L5/T1	3.58	-3.17	-1.34	16.35**	9.46*	4.04	26.72**	25.74**	28.12**
14.	L5/T2	4.87*	-1.11	- 1.11	12.01**	2.93	2.93	29.11**	27.91**	30.33**
15.	L5/T3	4.95*	-2.55	0.74	24.86**	9.01*	22.42**	24.84**	17.72*	35.39**
16.	L6/T1	5.39**	-0.39	1.50	25.03**	14.76**	9.08*	18.27**	17.81*	19.12*
17.	L6/T2	3.68	-1.13	- 1.13	24.11**	11.35*	11.35*	25.53**	24.84**	26.22**
18.	L6/T3	6.96**	0.41	3.80	22.45**	4.54	17.39**	24.12**	16.62**	34.12**
19.	L7/T1	1.68	-3.17	-1.34	22.21**	18.99**	13.10**	26.01**	24.65**	27.80**
20.	L7/T2	1.59	-2.39	-2.39	24.16**	17.98**	17.98**	31.36**	29.74**	33.02**
21.	L7/T3	7.99**	2.14	5.58*	24.75**	12.39**	26.22**	22.44**	15.80*	33.18**

S. No	Hybrids	Number of filled grains per panicle			Kernel length			Kernel breadth		
		(di)	(dii)	(diii)	(di)	(dii)	(diii)	(di)	(dii)	(diii)
1.	L1/T1	11.21**	9.32**	8.68**	3.44*	3.01	5.51**	7.14**	-1.70	16.53**
2.	L1/T2	10.72**	10.40**	10.40**	6.96**	6.13**	7.80**	12.66**	12.10**	12.10**
3.	L1/T3	6.87**	4.07*	9.19**	5.37**	0.76	12.16**	9.66**	0.00	20.16**
4.	L2/T1	13.52**	12.49**	10.02**	4.09**	3.78*	6.29**	-2.37	-5.27*	12.30**
5.	L2/T2	10.33**	9.11**	9.11**	7.67**	6.71**	8.65**	4.86**	-0.54	10.89**
6.	L2/T3	6.97**	3.34	8.43**	6.84**	2.28	13.85**	4.09*	0.34	20.56**
7.	L3/T1	8.80**	6.70**	6.59**	3.44*	2.99	6.41**	0.74	-7.31**	9.88**
8.	L3/T2	11.37**	11.31**	11.31**	6.40**	4.68*	8.17**	5.05**	4.84	4.84
9.	L3/T3	9.60**	6.98**	12.24**	10.54**	6.58**	18.63**	4.77**	-4.19*	15.12**
10.	L4/T1	12.54**	11.19**	9.42**	6.29**	4.73*	7.26**	0.70	-2.04	16.13**
11.	L4/T2	7.70**	6.84**	6.84**	7.52**	7.20**	7.20**	10.84**	4.86*	17.54**
12.	L4/T3	8.07**	4.72*	9.87**	9.91**	4.02*	15.79**	5.38**	1.85	22.38**
13.	L5/T1	11.26**	9.93**	8.15**	4,58**	3.22	8.53**	32.22**	7.82**	27.82**
14.	L5/T2	12.80**	11,89**	11.89**	4.10**	1.55	6.78**	49.25**	30.44**	30.44**
15.	L5/T3	7.84**	4.48*	9.62**	9.84**	6.79**	18.87**	37.13**	11.24**	33.67**
16.	L6/T1	15.74**	15.22**	10.65**	1.22	-0.74	5.75**	24.18**	16.16**	37.70**
17.	L6/T2	11.16**	8.48**	8.48**	2.87*	-0.28	6.23**	16.87**	15.04**	18.75**
18.	L6/T3	13.85**	8.57**	13.91**	11.64**	9.24**	21.60**	20.94**	12.42**	35.08**
19.	L7/T1	11.51**	11.42**	7.17**	4,60**	4.02*	6.53**	-1.52	-2.18	17.54**
20.	L7/T2	11.05**	8.94**	8.94**	3.70**	3.05	4.36*	7.33**	-1.68	18.15**
21.	L7/T3	10.52**	5.92**	11.13**	14.63**	9.46**	21.84**	1.68	1.68	22.18**

Table 5 Contnued .....

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S. No	Hybrids	Kernel L/B ratio			100 grain weight			Grain yield per plant		
		(di)	(dii)	(diii)	(di)	(dii)	(diii)	(di)	(dii)	(diii)
1.	L1 T1	-4.19*	-11.80**	-9.51**	-4.03*	-11.18**	-6.54**	7.22*	4.80	-0.27
2.	L1 T2	-5.04**	-6.24**	-3.80	-6.75**	-9.07**	-4.31*	4.89	0.09	0.09
3.	L1 T3	-2.83	-7.80**	-5.41*	6.03**	3.05	14.90**	-2.80	-12.85**	-0.18
4.	L2 T1	6.60**	3.73	-5.41*	1.19	-2.95	-5.36*	5.13	4.32	-0.73
5.	L2 T2	2.62	-1.90	-1.90	-2.18	-3.40	-3.40	-5.99	-8.96*	-8.96*
6.	L2 T3	3.11	2.61	-5.51*	8.69**	1.88	13.59**	-2.37	-11.25**	1.65
7.	L3 T1	1.90	-6.66**	-3.20	1.17	-4.06	-4.18*	16.38**	14.31**	8.78*
8.	L3 T2	1.23	-0.58	3.10	-6.47**	-6.54**	-6.54**	6.86**	2.47	2.47
9.	L3 T3	13.60**	7.24**	11.21**	8.10**	2.46	14.25**	-1.82	-11.57**	1.28
10.	L4 T1	5.55**	4.18	-7.71**	-1.61	-5.51*	-8.10**	8.18*	7.30	2.10
11.	L4 T2	-3.29	-8.81**	-8.81**	-1.52	-2.88	-2.88	0.14	2.74	2.74
12.	L4 T3	7.15**	5.11*	-3.20	9.46**	2.46	14.25**	-5.49	-14.13**	-1.65
13.	L5 T1	4.70*	-1.74	-15.22**	4.23*	0.68	-3.27	-1.22	-2.59	-7.31
14.	L5 T2	-6.89**	-18.22**	-18.22**	0.80	-1.18	-1.18	10.64**	6.49	6.49
15.	L5 T3	5.97**	-3.48	-11.11**	9.82**	2.23	13.99**	-2.16	-11.57**	1.28
16.	L6 T1	-8.97**	-11.14**	-23.32**	6.52**	4.65*	-2.88	9.36**	6.63	1.46
17.	L6 T2	-1.76	-10.51**	-10.51**	-0.47	-4.05	-4.05	1.97	-2.93	-2.93
18.	L6 T3	3.27	-2.28	-10.01**	11.84**	2.46	14.25**	-6.24	-16.12**	-3.93
19.	L7 T1	6.98**	4.87*	-9.51**	0.35	-4.61*	-5.23*	4.09	2.79	-2.19
20.	L7 T2	3.45*	-11.71**	-11.71**	-0.98	-1.31	-1.31	13.04**	8.96*	8.96*
21.	L7 T3	13.96**	8.26**	-0.30	7.50**	1.64	13.33**	8.11*	-2.15	12.07**

* - Significant at 5% level di – Relative heterosis,dii – Heterobeltiosis, diii – Standard heterosis **-Significant at 1% level

action and therefore heterosis breeding may be useful to improve yield.

As a whole, predominance of unfixable non-additive gene action was observed for all the traits except panicle length and 100 grain weight, therefore improvement of these traits appeared to be difficult as simple pedigree breeding will not be able to fix the superior lines in the early segregating generations. Since some of the traits are controlled by both additive and dominance variance, one (or) two cycles of recurrent selection followed by pedigree breeding will be effective and useful for the improvement of these traits. Further, these traits can also be improved by adoption of bi-parental mating in F2 among selected segregants and followed by selection procedure such as diallel selection mating Dhaliwal and Sharma (1990) also reported that non-additive gene effects were predominant for yield and its components.

A good hybrid should manifest high amount of heterosis for commercial exploitation. The hybrid performance is assessed normally in terms of percent increase over mid-parent, better parent, and standard variety. 'Such information helps in the evaluation of hybrids. Relative heterosis is of limited importance because it is only the deviation of Fi from mid parental value (Grakh and Chaudhary, 1985). Heterobelotiosis is a measure of hybrid vigour over the better parent. Bobby and Nadarajan (1994) stressed the need for computing standard heterosis for commercial exploitation of hybrid vigour.

In this study, none of the hybrids recorded significantly negative heterotic effect for plant height in all three types, while L3 × T1 alone recorded significantly negative heterosis over better and standard parents and L2 × T1 showed significantly negative heterosis over better parent. Which indicated that these crosses were the best for dwarfness. Pandey and Kaushik (1999) observed similar high negative heterobeltiosis for plant height. Both positive and negative heterosis for all the three types was noted by Janardhanam *et al.,* (2001).

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For number of productive tillers per plant, out of

twenty one hybrids studied, seven had superior performance in all three categories of which maximum heterosis was observed in L4 × T2, L5 × T3, L7 × T2 and L7 × T3. High heterosis over better and standard parent for this trait was observed by Annadurai and Nadarajan (2001) observed high heterosis in all three categories.

In this study, fifteen combinations out of twenty one hybrids had significantly positive heterosis in all three types for panicle length. The combinations L1 with testers T1, T2 and T3, L2 × T3, L3 × T1 and L3 × T3 showed significant heterosis over mid and standard parents. Similar findings were reported by Suresh *et al.,* (1999).

Except L2 × T3 for mid-parental heterosis all the remaining combinations had significantly positive heterosis for number of filled grains per panicle in all the three types of heterosis. Similar results were found by Annadurai and Nadarajan (2001).

Out of twenty one hybrids, twelve combinations recorded significantly positive heterosis over mid, better and standard parent for kernel length. Maurya and Singh (1978). Observed significantly positive heterosis for kernel length on three bases.

For kernel breadth, out of twenty one hybrids studied, two had significantly negative heterosis in all three categories. The hybrids L2 × T1 and L3 × T3 showed significant and negative heterosis over better parent and it was desirable. However, Reddy and Nerkar (1992) observed positive heterosis for kernel breadth in all three categories.

The combination L3 × T3 alone in all three types of estimation recorded significantly positive heterosis for kernel L/B ratio. Eight crosses *viz.*, L1 with testers T1, T2 and T3, L4 × T2, L5 × T2, L6 × T1, L6 × T2 and L7 × T2 showed significantly negative values for all the three types of heterosis. The hybrids L4 × T3, L7 × T1 and L7 × T3 showed significantly positive heterosis over mid parent and better parent. Vivekanandan and Giridharan (1995c) observed negative heterosis in all three types of heterosis for kernel L/B ratio.

Heterosis was not much pronounced for 100 grain weight, but the hybrids L1 × T3, L2 × T3, L3 × T3, L4 × T3, L5 × T3, L6 × T3 and L7 × T3 showed better heterotic expression for heterosis. Similar results observed by Annadurai and Nadarajan (2001). Vivekandan *et al.,* (1992) showed positive expression over mid and better parent for 100 grain weight. Out of twenty one hybrids only two L3 × T1 and L7 × T2 recorded significantly positive heterosis over mid, better and standard parent for grain yield per plant, the hybrids L1 × T1, L3 × T1, L3 × T2, L4 × T1, L5 × T2, L6 × T1, L7 × T2 and L7 × T3 showed significantly positive heterosis over mid parent. Annadurai and Nadarajan (2001) observed high positive heterosis for grain yield per plant on three types of heterosis. Nguygen Thi Lang and Buichi Buu (1993) obtained high positive relative heterosis.

Swaminathan *et al.,* (1972) stressed the need for calculating standard heterosis, for commercial exploitation of hybrid vigour. The hybrid which likely to be released to commercial scale should surpass the yield level of locally cultivated superior variety or hybrid. Hence, in practical breeding programme, standard heterosis would alone be taken into consideration for selection of hybrids rather than mid and better parental heterosis.

Devaraj and Nadarajan (1996) opinioned that of the three types of heterosis the standard heterosis is especially important because the hybrid to be released is expected to outperform the existing superior local variety on hybrids. In the present study, the hybrid L3 × T1 showed shortened in plant height. Ten hybrids for number of productive tillers per plant, all the hybrids for panicle length, number of filled grain per panicle and kernel length, except L3 × T2, all hybrids for kernel breadth. The hybrids L3 × T2 and L3 × T3 for kernel L/B ratio.

Seven crosses *viz.*, L1 × T3, L2 × T3, L3 × T3, L4 × T3, L5 × T3, L6 × T3 and L7 × T3 for 100 grain weight and three hybrids *viz.*, (L3 × T1, L7 × T2 and L7 × T3) for grain yield per plant registered higher heterotic value over standard variety.

To sum up the above results, the hybrids L7 × T3, L5 × T3, and L6 × T3 recorded superior heterotic expression for six traits among that L7 × T3 alone recorded superior heterotic expression for number of productive tillers per plant, panicle length, number of filled grains per panicle, kernel length and 100 grain weight along with grain yield over standard parent. Hence selection pressure on these characters will certainly help to obtain high yielding. They were followed by the combinations L3 × T3 and L4 × T2 for five traits, L3 × T2, L6 × T1, L6 × T2 and L4 × T3 for four traits, L1 × T2, L2 × T1, L4 × T1, L5 × T2, for four traits out of nine traits studied.

Conclusion

The traits grain yield per plant and plant height contributed maximum to the genetic diversity. Distribution of barnyard millet in to various clusters indicated the presence of considerable genetic diversity for most of the traits among the genotypes. The clusters XI and I were the distant clusters and clusters V and VI were the least divergent clusters. The clusters XIII and XII

possessed the high mean values for many of the traits studied. With respect to grain yield per plant the clusters XI, XIII and V appeared to be the superior clusters. As per the D^2 statistic and principal component analysis, the accessions of cluster XI (BAR 242, BAR 351and BAR 353) and cluster I (BAR 183, BAR 223, BAR 228) can be exploited as diverse parents in crossing programme for development of hybrids and good recombinants for grain yield per plant. It could generate good amount genetic variability in barnyard millet genotypes under the sodic soil condition.

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References

Annadurai, A. and N. Nadrajan (2001). Heterosis for yield and its component traits in rice. *Madras Agric. J.,* **87:** 184-186.

Arutchenthil, P. (1998). Line × Tester analysis in rice (*Oryza sativa* L.) Utilizing male sterile lines. M.Sc. (Ag.) Thesis, Annamalai Univ., Chidambaram.

Bobby, T.P.M. and N. Nadarajan (1994). Heterosis and combining ability studies in rice hybrids involving CMS lines. *Oryza*, **31:** 5-8.

Devaraj, M. and N. Nadarajan (1996). Gene action for seven biometrical traits in rice. *Ann. Agric. Res.,* **16(3):** 360-361.

Dhaliwal, T.S. and H.L. Sharma (1990). Combining ability and material effects for agronomic and grain characters in rice. *Oryza*, **27:** 133128.

Hossain, K., A. Aktar, H. Begum, A. Ansari and M.M. Rahman (2009). L×T analysis for yield and its related trains in rice. *Bangladesh J. Pl. Breed. Genet.*, **22(2):** 01-06.

Grakh, S.S. and M.S. Chaudhary (1985). Heeterosis for early maturing and high yield in Gossypium arboretum. *Indian J. Agric. Sci.*, **55:** 10-13.

Janardhanam, V., N. Nadarajan, S.K. Ganesh, S. Jebaraj and K. Chozhan (2000). Combining ability studies for yield and its components in rice (*Oryza saliva* L.). *Madras Agric. J.,* **86:** 542-544.

Janardhanam, V., N. Nadarajan, S.K. Ganesh and S. Jebaraj (2001). Studies on heterosis in rice (*Oryza sativa* L.). *Madras Agric. J.,* **88(10-12):** 721-723.

Jayaprakash, P. (1992). Evaluation of breeding value of some parents and crosses in sesame (*Sesamum indicum* L.) M.Sc. (Ag.) Thesis, Annamalai Univ., Annamalainagar.

Kempthorne, O. An Introduction to Genetic Statistics. John Wiley and Sons Inc., New York, London.

Mohaptra, K.C. and H.K. Mohanty (1985). Inheritance of some quantitative characters including heterosis in rice by combining ability analysis. In: Rice Genetics: 579-591. IRRI, Manila, Philippines.

Nguyen Thi Lang and But Chi Buu (1993). Combining ability and heterosis for some physiological traits in rice. *IRRN.*, **18:** 7-8.

Pandey, D.P. and R.K. Kaushik (1999). Heterosis in rice crosses involving V20V CMS lines under mid hill conditions of H.P. *Crop Res.*, (Hisar), **18(2):** 234-239.

Perraju, P. and N.P. Sarma (1999). Combining ability studies in rice. *Oryza*, **36(3):** 248-249.

Rashid, M., A.A. Cheema and M. Asraf (2007). L× T analysis in 13 Basmatirice, *Pak. J. Bot*, **36(6):** 2035-2042.

Ramalingam, J., P. Vivekanandan and C. Vanniarajan (1993b). Combining ability analysis in low land early rice. *Crop. Res.*, **6:** 228-233.

Reddy, C.D.R. and Y.S. Nerkar (1992). Quantitative inheritance of panicle traits in indica rice. *Crop Res.*, **4:** 173-175.

Sarawagi, A.K., M.N. Srivastava and B.P. Chowdhary (1991). Partial diallel cross analysis of yield and its related characters in rice (*Oryza sativa* L.) under irrigated and rainfed situations. *Indian J. Genet*, **51(1):** 30-36.

Suresh, S., K.S. Paramasivam and N. Muppidathi (1999). Study of heterosis for yield components in rice. *Madras Agric. J.,* **86(7-9):** 520-522.

Tai, G.C.C. (1979). An internal estimation of expected response to selection. *Theor. Appl. Genet.*, **54:** 273-275.

Vishwakarma, D.N., D.M. Maurya, S.K. Mishra, G.P. Verma and Rakesh Kumar (1998). Heterosis studies in rice using CMS system. *Ann. Agric. Res.*, **19(4):** 370-374.

Vivekanandan, P. and S. Giridharan (1995c). Heterosis for kernel characters in rice. *IRRN.*, **20(1):** 7.

Vivekanandan, P. and S. Giridharan (1997). Combining ability for grain traits in rice. *Madras Agric. J.,* **84(3):** 129-132.

Yadav, L.S., D.M. Maurya, S.P. Giri and S.B. Singh (1999). Combining ability analysis for yield components in hybrids rice. *Oryza*, **36(3):** 208-210.