

## Gene action and combining ability studies in rice

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### ABSTRACT

Investigation was carried out to determine gene action and combining ability studies in rice. The material consisted of F<sub>1</sub> population of 30 crosses developed by crossing 10 genotypes with three testers. TDominance genetic variance were highly significant as compared to additive gene effects for total tillers plant<sup>-1</sup>, effective tillers plant<sup>-1</sup>, spikelets panicle<sup>-1</sup>, grains panicle<sup>-1</sup>, grain fertility, biological yield plant<sup>-1</sup>, harvest index, grain yield plant<sup>-1</sup>, 1000-grain weight and grain length and L:B ratio. The average degree of dominance was observed more than one for all the traits studied except plant height, panicle length, days to 50% flowering and days to maturity. The cross HPR 2639 x HPR 2143 is a good specific combination for grain yield plant<sup>-1</sup>, panicle length, spikelets panicle<sup>-1</sup>, grains panicle<sup>-1</sup>, biological yield plant<sup>-1</sup>, days to 50% flowering and plant height.

**Key words:** rice, gene action, general combining ability, specific combining ability, line x tester analysis

The nature and magnitude of gene action involved in expression of quantitative traits is important for successful development of crop varieties. The correct choice of parents for hybridization is crucial for development of cultivars. Combining ability analysis provides such information so as to frame the breeding programme effectively. This analysis helps in identification of parents with high general combining ability (*gca*) and parental combinations (cross) with high specific combining ability (*sca*). In order to combine desirable attributes alongwith high yield, the most appropriate approach is recombinant breeding. Breeding strategies based on selection of hybrids require expected level of specific combining ability (*sca*). Combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses for the exploitation of heterosis (Muhammad *et al.* 2007). The performance of parents may not necessarily reveal it to be a good or poor combiner. Therefore, gathering information on nature of gene effects and their expression in terms of combining ability is necessary.

The success of any breeding programme depends upon the knowledge of the nature and magnitude of genetic effects of different quantitative

traits. The common approach of selecting parents on the basis of *per se* performance, adaptation and diversity does not necessarily lead to the fruitful results. Therefore, the present study was taken up for selection of the best parents for hybridization based on the knowledge of combining ability of the parents.

The experimental materials used for the present investigation consisted of F<sub>1</sub> population of 30 crosses developed by crossing genotypes of rice *viz.*, HPR 2644, HPR 2604, HPR 2512, HPR 2555, HPR 2529, HPR 2373, HPU 741, HPR 2639, HPR 2589 and HPR 2653 with three diverse testers *viz.*, HPR 1068, HPR 1156 and HPR 2143. All the lines used as female parents were crossed to each of the testers by hand pollination using the standard procedure of emasculation in a line x tester mating design at RWRC Malan, during wet season, 2011. During wet season 2012 the F<sub>1</sub>'s (30) materials alongwith parental lines were evaluated in RBD with three replications at RWRC, Malan. In each replication entries (F<sub>1</sub>'s and parents) were grown in single row of 2m length with spacing of 20cm x 15cm transplanted as single seedling hill<sup>-1</sup>. The data was recorded on five random competitive plants in each replication for all the traits studied except days to 50% flowering and days to maturity which were recorded

on plot basis. The statistical analysis as per the design for analysis of variance as per Panse and Sukhatme (1985), Combining ability analysis was carried out following the method of Kempthorne (1957) and estimation of additive and dominance variance components, average degree of dominance was calculated as per line x tester mating design analysis.

Magnitude of  $\sigma^2A$  was found to be higher than that of  $\sigma^2D$  for plant height, panicle length and days to 50% flowering whereas magnitude of  $\sigma^2D$  was found to be higher than that of  $\sigma^2A$  for total tillers plant<sup>-1</sup>, effective tillers plant<sup>-1</sup>, spikelets panicle<sup>-1</sup>, grains panicle<sup>-1</sup>, grain fertility, biological yield plant<sup>-1</sup>, harvest index, grain yield plant<sup>-1</sup>, 1000-grain weight and grain length and L:B ratio and magnitude of  $\sigma^2D$  and  $\sigma^2A$  was found to be equal for days to maturity. For grain breadth only dominance variance was observed. Karthikeyan *et al.* (2009) found that the ratio between the estimates of additive and dominance variances indicated preponderance of non-additive gene action

**Table 1.** Estimates of additive and dominance variance, average degree of dominance for yield, physiological, phenological and grain quality traits

Traits / Sources of variation	Mean sum of square		
	Additive Variance ( $\sigma^2A$ )	Dominance variance ( $\sigma^2D$ )	Average degree of dominance ( $\sigma^2D/\sigma^2A$ ) <sup>1/2</sup>
Yield traits & physiological traits			
Plant height	138.82	75.77	0.74
Total tillers plant <sup>-1</sup>	0.86	1.58	1.36
Effective tillers plant <sup>-1</sup>	0.76	1.91	1.58
Panicle length	1.81	0.87	0.70
Spikelets panicle <sup>-1</sup>	1417.11	1533.67	1.04
Grains panicle <sup>-1</sup>	977.41	1163.13	1.10
Grain fertility	20.38	73.30	1.90
Biological yield plant <sup>-1</sup>	106.85	185.11	1.32
Harvest index	22.05	27.26	1.11
Grain yield plant <sup>-1</sup>	17.89	52.81	1.72
Phenological traits			
Days to 50% flowering	7.55	2.77	0.61
Days to maturity	0.02	0.02	0.91
Grain quality traits			
1000-grain weight	0.18	1.87	1.26
Grain length [L]	0.05	0.08	1.31
Grain breadth [B]	0.01	0.01	1.21
L:B ratio	0.02	0.05	1.43

for the characters namely, plant height, no. of tillers plant<sup>-1</sup>, panicle length, grain weight panicle<sup>-1</sup> and grain yield plant<sup>-1</sup>. Shikari *et al.* (2009) also reported similar types of findings. The average degree of dominance was observed more than one for all the traits studied except plant height, panicle length, days to 50% flowering and days to maturity. In present estimation of general combining ability (*gca*) and specific combining ability (*sca*) for all the traits studied which showed that out of 10 lines HPR 2529 is good general combiner for panicle length, biological yield plant<sup>-1</sup>, grain yield plant<sup>-1</sup>, grain fertility, plant height and 1000-grain weight and the tester HPR 2143 is good general combiner for panicle length, spikelets panicle<sup>-1</sup>, harvest index, grain length and L:B ratio whereas, HPR 1156 for grains panicle<sup>-1</sup>, biological yield plant<sup>-1</sup>, grain yield plant<sup>-1</sup> and plant height. Among crosses HPR 2639 X HPR 2143 is good specific combination for grain yield plant<sup>-1</sup>, panicle length, spikelets panicle<sup>-1</sup>, grains panicle<sup>-1</sup>, biological yield plant<sup>-1</sup>, days to 50% flowering and plant height and the cross HPR 2653 x HPR 2143 is good specific combination for panicle length, grains panicle<sup>-1</sup>, biological yield plant<sup>-1</sup>, grain yield plant<sup>-1</sup>, total tillers plant<sup>-1</sup>, effective tillers plant<sup>-1</sup>, 1000-grain weight and grain breadth. Combining ability analysis helps in identifying potential parents either to be used in heterosis breeding or for isolation of transgressive segregants in the development of pure lines. The general and specific combining abilities were significant for all the characters, indicating the importance of both additive and non-additive genetic components. It was found that there was a predominance of the non-additive genetic components for expression of different traits. These results were in accordance with the findings of Muhammad *et al.*, 2007 and Hossain *et al.*, 2009, emphasized grain yield plant<sup>-1</sup> have high specific combining ability (*sca*) variance suggesting the predominance of non-additive genetic variance. The major role of non-additive gene effects in the manifestation of all the traits was confirmed by higher values of *sca* variance than for *gca* variance, the ratio of ( $\sigma^2gca/\sigma^2sca$ ) being less than one, and the degree of dominance being greater than one. These results indicate the preponderance of non-additive gene action in the expression of all the traits studied and suggest the feasibility of exploitation of non-additive genetic variation for traits through hybrid breeding. The importance of non-additive genes for expression of yield

and its components have also been previously reported (Dalvi and Patel 2009; Saidaiah *et al.* 2010 and Selvaraj *et al.* 2011). Further, for grain quality parameters higher estimates of *sca* variances than *gca* variances has also been revealed by Vanaja *et al.* (2003) and Thakare *et al.* (2010). Investigation of *gca* effects revealed that among lines and testers were good general combiners for grain yield and the other traits. Hence these good general combiners of males and females may be used in future for hybrid rice breeding programme.

The cross HPR 2639 x HPR 2143 is a good specific combination for grain yield plant<sup>-1</sup>, panicle length, spikelets panicle<sup>-1</sup>, grains panicle<sup>-1</sup>, biological yield plant<sup>-1</sup>, days to 50% flowering and plant height and the other cross combination is HPR 2529 X HPR 1156 showing high heterosis over standard check for grain yield plant<sup>-1</sup>, biological yield plant<sup>-1</sup>, grain fertility and plant height.

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