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Short Communication

Analysis of combining ability status among parents and hybrids in rice (*Oryza sativa* L.)

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The development and use of hybrid rice varieties on commercial scale utilizing the cytoplasmic male sterility (CMS)-fertility restoration system has proved to be one of the milestones in the history of rice improvement. The hybrid rice technology, now in operation in nearly 20 countries, aims at further research and development efforts with respect to cytoplasmic diversification, and yield increment through higher exploitable heterosis levels. Combining ability test is one of the several biometrical models being routinely used to study the genetic basis of heterosis. With a few exceptions all the studies showed significant general combining ability (*gca*) and specific combining ability (*sca*) effects for yield and/or yield components indicating role of both additive and non-additive gene action. Relative proportion of *gca* and *sca* variances were found to vary in different studies. Reports on analysis of combining ability status of parents in relation to that of hybrids as well as frequency of crosses with performance exceeding that of better parent in relation to *gca* effect of parents are limited in literature. An attempt has been made here to analyze the results obtained through combining ability studies in relation to the performance of hybrids and to provide valid explanations for the same.

Thirty-five crosses generated in a Line × Tester (L × T) mating design with seven CMS lines and five pollen parents were evaluated along with parents in a randomized block design with two replications at IARI, New Delhi. Each replication consisted of two rows of each of the 47 entries with a row length of 3.5 m and spacing of 30 × 15 cm. In lieu of female lines (CMS), their respective maintainer lines were planted. The crop was raised under standard and uniform agronomic practices. Observations were recorded on randomly selected five plants from each replication for morphological and yield related traits. The mean values of each replication for the different characters recorded for hybrids and parents were subjected to statistical analysis and significance of variances due to different sources necessitated ANOVA for combining ability. The mean values recorded for hybrids were subjected to L × T analysis and the mean sum of squares along with variance of *gca* of the parents and *sca* of the hybrids were worked out on the standard procedure developed by Kempthorne [1]. The combining ability effects and their significance were estimated following standard statistical tools [2]. The distribution of crosses in relation to *gca* effect of parents and *sca* effect of crosses was worked out by taking into account the combining ability effects as significant positive (High), non-significant (Average) and significant negative (Low). For calculating the frequency of crosses with mean performance *per se* exceeding that of better parent, the *gca* effect of parents was classified into either positive (High) or negative (Low).

Analysis of combining ability for different characters (data not presented) revealed that the good general combiners identified among the parents for grain yield also exhibited significant positive *gca* effects for one or more of its components. Results were similar for *sca* effects also where crosses with significant *sca* effects for grain yield had significant *sca* effects for one or more yield components. Hence, it may be inferred that significant *gca* and *sca* effects for yield components generally result in significant combining ability effects for grain yield. However, in some of the crosses significant *sca* effects even for many yield components were not associated with significant *sca* effect for grain yield. Similarly, good general combiners for yield components among parents did not always exhibit high *gca* effect for grain yield. This could be due to yield component compensation and negative correlations, which arise in response to competition between developmentally flexible yield components [3] or component complementation between the two parents [4].

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Table 1. Distribution of crosses in relation to *gca* effect of parents and *sca* effect of crosses for yield and related traits

Character	*sca* of cross	*gca* of parents						Total no. of crosses
		H × H	H × A	A × A	H × L	A × L	L × L	
Grain yield/plant	+	0	0	3	0	0	0	3
	0	1	7	4	3	11	2	28
	-	0	0	3	0	1	0	4
Biological yield/plant	+	0	0	1	0	1	0	2
	0	0	6	9	1	10	2	28
	-	0	0	2	0	3	0	5
Harvest Index	+	0	0	2	0	1	0	3
	0	2	14	10	1	4	0	31
	-	0	0	0	0	1	0	1
1000-grain weight	+	2	3	1	1	5	2	14
	0	2	1	1	4	0	1	9
	-	1	3	1	3	3	1	12
Filled grains/main panicle	+	0	2	1	0	2	0	5
	0	0	6	11	1	5	1	24
	-	1	0	3	1	1	0	6
Total spikelets/main panicle	+	0	2	2	0	2	0	6
	0	0	4	9	2	5	2	22
	-	0	2	1	0	4	0	7
Fertility percentage	+	0	1	2	0	0	0	3
	0	0	12	10	0	7	0	29
	-	0	1	2	0	0	0	3
Panicle density	+	0	1	1	1	2	0	5
	0	0	7	15	0	3	0	25
	-	1	0	1	1	2	0	5
Panicle length	+	0	1	1	2	0	0	4
	0	6	4	5	4	7	1	27
	-	0	3	0	0	0	1	4
Productive tillers/plant	+	0	1	1	0	0	0	2
	0	1	9	10	3	7	1	31
	-	1	0	1	0	0	0	2

+, 0, - : Significant positive, Non-significant and Significant negative *sca* H : Positive *gca*; A : Non-significant *gca*; L : Negative *gca*

The distribution of crosses in relation to *gca* effects of parents (Table 1) showed that almost all types of *sca* effects were obtained from any kind of combination of *gca* effects and hence, performance of hybrids was independent of that of parents. Similar results were reported in some of the earlier studies also [5, 6]. Significantly positive *sca* effects for a particular trait were noticed even in average × average, average × low or low × low *gca* parental combinations. For example, three crosses that had significant positive *sca* for grain yield were obtained from average × average combinations while average × average and average × low combinations also resulted in four hybrids with significant negative *sca*. Rest 28 crosses with non-significant *sca* had all possible combinations of *gca*. Except 1000-grain weight, for none of the traits high × high *gca* combinations resulted in high *sca* status. The high × high combination resulted in significant negative *sca* for filled grains, panicle density and productive tillers/plant while for 1000-grain weight this combination exhibited all possible *sca* status. The manifestation of high, low or non-significant *sca* effects by any sort of combination among the parents might be due to differential expression of component traits in specific residual genetic backgrounds. As the yield components are correlated either positively or negatively, it is usual to find for a particular parent, *gca* in the desirable direction for some traits and in the undesirable direction for others. Therefore, establishing the status of a parent with respect to *gca* over a number of component characters assumes importance.

Analysis of frequency of crosses with mean value exceeding that of better parent (pollen parent) in relation to *gca* effect of parents (Table 2) indicated that for grain yield, high × high and high × low parental combinations appear in equal frequencies. However, for other yield related traits like 1000-grain weight, filled grain number, panicle density, productive tillers etc. the high × low combinations appeared in higher frequency. In general the order was, high × low > high × high > low × low. The superiority of high × low cross may be due to the fact that such a cross can result in strong transgressive segregants for the desired traits, due to segregation of genes with strong potentials and their specific buffers [7]. Also, irrespective of residual

Table 2. Frequency of crosses with mean value exceeding that of better parent (pollen parent) in relation to *gca* effect of parents for different characters

Character	*gca* of parents		
	H × H	H × L	L × L
Grain yield/plant	0.44	0.44	0.12
Biological yield/plant	0.37	0.48	0.15
Harvest Index	0.25	0.44	0.31
1000-grain weight	0.22	0.44	0.34
Fertility percentage	0.50	0.50	0.00
Total spikelets/main panicle	0.27	0.52	0.21
Filled grains/main panicle	0.29	0.54	0.17
Unfilled spikelets/main panicle	0.17	0.49	0.34
Panicle density	0.31	0.54	0.15
Panicle length	0.31	0.45	0.24
Productive tillers/plant	0.33	0.67	0.00
Plant height	0.18	0.45	0.37
Days to maturity	0.33	0.42	0.25
Days to 50% flowering	0.36	0.46	0.18

Figures represent the frequency of crosses found in each group

genetic background, high genes express nearly same phenotypes when they are homozygous or heterozygous. But low genes can express their potential only in a homozygous residual genetic background. Thus, high × high or low × low crosses usually result in situations resembling essentially their parents whereas high × low crosses produce heterozygous genotypes, which express high effects and consequently are superior to both the parents. In the light of results obtained, it appears that the best approach in rice would be to start with high × low type of crosses followed by high × high crosses. The necessity to evaluate the parents for their nicking ability do not cease as grouping of parental lines into high, average or low helps in selecting the parents, and analysis of status of combining ability of parents in relation to hybrids may provide insight into level of expression of a particular trait in a specific genetic background.

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