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TRIPLE TEST CROSS ANALYSIS IN RICE

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ABSTRACT

The triple test cross analysis carried ~~out in rice for nine characters revealed the presence of~~ epistasis for most of the characters except seed weight per panicle. In the absence of epistasis, additive components (variance for sums) were significant for all the traits while the dominance components (variance for differences) were significant only for six characters. The estimates of additive (D) and dominance (H) components were highly significant for most of the traits, although, the D component was higher than H.

Key words: Additive, dominance, epistasis, rice, triple test cross.

In any attempt to obtain efficient estimates of the additive, dominance and environmental components of variation for a metrical trait from second degree statistics, three difficulties inevitably arise. First, it is assumed that nonallelic interactions are absent although these analyses rarely provide a valid test of this assumption. Second, estimates of dominance components invariably have much larger standard errors than the corresponding additive components. Third, additive and dominance components are differentially affected by linkage and correlated gene distributions in the parents and are only comparable in the unlikely event of population sample being in linkage equilibrium. To overcome these difficulties, a design which is a simple extension of design III of Comstock and Robinson [1] has been proposed by Kearsey and Jinks [2]. This design, known as 'triple test cross', provides not only an efficient estimates of dominance but also an unambigous test for epistasis. In the present study, triple test cross analysis has been carried out for nine characters using ten F_1 ratooned rice hybrids and their parents.

MATERIALS AND METHODS

Ten F_1 hybrids and their parents comprising five stabilised lines, viz., Intan x Gowri, VMH x IR 36, Jaya x Halubbalu, Jaya x Mahsuri and MH x Prakash and two leading varieties, Jaya and Mahsuri (all in ratoon generation) were evaluated in RBD with three replications. Five plants were randomly tagged from each treatment in each replication and scored for nine quantitative characters. The method proposed by Jinks and Perkins [3] was applied to detect epistasis and to test and estimate the additive and dominance components of genetic variance.

RESULTS AND DISCUSSION

Analysis of variance to detect epistasis for nine characters (Table 1) indicated that all the traits except seed weight/panicle showed significant epistasis. Analysis of variance to detect additive and dominance components is also presented in Table 1. In the absence of epistasis, analysis of variance for sums and differences provides direct tests of significance for the additive (significance of sums) and dominance components (significance of differences). The sums were highly significant for all the characters, while the differences were highly significant for five characters and moderately significant for one character. The estimates of σ^2_m were highly significant for six characters and nonsignificant for remaining three characters. The estimates of σ^2_{ml} were significant only for plant height and number of seeds/panicle.

The estimates of additive (D) and dominance (H)components are presented in Table 2. The D component was highly significant for eight characters and moderately significant for

Table 1. Mean sum of squares for detecting type of gene action for nine characters in F_1 ratoon generation of rice

Source	d.f.	Plant height	Panicle length	Productive tillers per plant	Seeds per panicle	Seed wt. per panicle	Seed wt. per plant	Grain elongation after cooking	1000-seed weight	Straw. wt. per plant
$\bar{L}_1 + \bar{L}_2 - 2\bar{P}$	4	115.97**	25.98**	171.20**	1824.56**	0.23	33.12**	0.01*	2.08**	80.08**
Analysis of variance for sums and differences in respect of nine characters in rice										
Sums	4	1393.57**	14.80**	325.35**	3065.84**	0.63**	141.93**	0.03**	31.86**	214.40**
Differences	4	20.22**	7.28**	14.87**	85.36**	0.25	13.64**	0.00	0.36*	0.42
Error		0.15	0.11	1.71	59.16	0.03	5.57	0.00	0.00	2.26
σ^2_m		232.23**	2.45	53.94**	501.11**	0.10	22.72**	0.00	5.30**	35.35**
σ^2_{ml}		3.345*	1.195	2.19	4.36	0.03	1.35	0.00	0.60	-0.30

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

Table 2. Estimates of genetic parameters, dominance ratios and correlation coefficients of sums and differences in respect of nine characters in F_1 ratoon generation of rice

Parameter	Plant height	Panicle length	Productive tillers per plant	Seeds per panicle	Seed wt. per panicle	Seed wt. per plant	Grain elongation after cooking	1000-seed weight	Straw wt. per plant
D	928.92^{**}	9.8^{**}	215.76^{**}	2004.45^{**}	0.404^{**}	90.90^{**}	0.022^{*}	21.23^{**}	141.42^{**}
H_1	13.38^{**}	4.78^{**}	8.77^{**}	17.46^{*}	0.148^{*}	5.38^{**}	0.0019^{*}	0.2438^{*}	-1.225
F	258.28^{**}	114.20^{**}	247.44^{**}	3470.4^{**}	-5.039^{**}	-103.89^{**}	-0.1003^{**}	17.928^{**}	-39.71^{**}
E_2	0.15	0.11	1.71	59.16	0.03	5.57	0.0000	0.003	2.26
$(H/D)^{1/2}$	0.12	0.698	0.2016	0.093	0.6062	0.2432	0.3005	0.1072	-0.01
Sum/diff	-0.076	0.55	-0.099	-0.339	-0.673^{**}	-0.118	-0.500^{**}	0.26	0.207

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

grain elongation after cooking. On the other hand, the H component was significant for all the characters except straw weight/plant. The $(H/D)^{1/2}$ estimate was less than unity for all the characters except panicle length and seed weight/panicle, indicating the high magnitude of D component as compared to H component. Correlation coefficient of sums and differences was negative and highly significant in respect of seed weight/panicle and grain elongation after cooking while it was positive and highly significant for panicle length.

The results of the present study, thus, revealed the presence of epistasis for all characters except seed weight/panicle. The estimate of D component is independent of dominance but will be biased by the presence of epistasis. Nevertheless, it is still likely to provide the best source for prediction of variance of the recombinant inbred populations [4].

As both additive and dominance gene effects were significant for all the characters, simple selection procedures in the immediate progenies will not help much in achieving improvement in these characters. The results presented here indicate that the epistatic component plays an important role in governing all the characters except seed weight/panicle. Therefore, epistasis cannot be ignored. The D components were highly significant for all characters, indicating the operation of exploitable additive gene action in later generations. The presence of epistasis for all the traits can be exploited by recurrent selection techniques [5].

Since the present study has been conducted at one location for only one year, the estimates of additive and dominance components are confounded with environmental effects (location, year, etc.). The characters which showed absence of epistasis may give evidence of epistasis under other environmental conditions. Similarly, the characters which showed presence of significant epistasis may not do so if tested in other environments. Therefore, more elaborate experiments conducted at different locations for more than one year will give a clear picture about the genetic architecture of these characters and help in developing more efficient breeding procedures.

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