HETEROSIS, COMBINING ABILITY, AND GENETIC RELATIONSHIP OF SELECTED PARENT LINES FOR HYBRID RICE DEVELOPMENT

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INTRODUCTION

Gathering information on nature of gene effects and their expression in terms of combining ability is necessary, since performance of parent alone is not sufficient to reveal it to be good or poor combiner (Pradhan et.al 2006).Evaluating the combining ability of parent line is exceptionally useful in a hybrid rice breeding program, especially when a large number of potential parental lines are available and most promising ones are to be identified on the basis of their ability to give superior hybrids.

OBJECTIVE

a) To determine the general and specific combining ability of the 14 parents for different quantitative characters and to measure the level of heterosis and identify the heterotic hybrids generated
b) To estimate kinship among parent lines using markers

METHODOLOGY

Yield trial and evaluation of entries were conducted at the experimental area of PhilRice, Central Experiment Station, Maligaya, Science City of Munoz, Nueva Ecija, Philippines from February 2015 to November 2015.

Table 1. Line x tester mating design used to developed test crosses

NO.	PARENTS	TESTERS (CMS)		
		1 IR68897A	2 IR73328A	3 IR80559A
1	Hanareumbyeo	PR47784H	PR47785H	PR47786H
2	Matatag 2-25kr-263-4-23R	PR47769H	PR35664H	PR47217H
3	Milyang23	PR47788H	PR47789H	PR47790H
4	PJ23R	PR36420H	PR33875H	PR47780H
5	PR31559-AR-32-4-3-2R	PR47793H	PR47794H	PR47795H
6	PR34142-5-1-3-2R	PR47767H	PR47768H	PR47216H
7	PR34302R	PR36020H	PR47770H	PR47771H
8	PR35749-HY-R	PR33876H	PR47777H	PR47778H
9	PR36246-HY-1-19-2-2R	PR39019H	PR47791H	PR47792H
10	PR36248-HY-2-5-1R	PR47774H	PR47775H	PR47776H
11	SRT-3R	IRRICA-001	PR47782H	IRRICA-002

(Male parents (Restorer lines))

A total of 33 hybrids (Table 1) were generated from the 3 CMS lines and 11 restorer lines. Genotyping of parents was also done at this stage Test entries also include M19 and PSB Rc 82 as check varieties

Fig. 1. Experimental setup for evaluation of entries
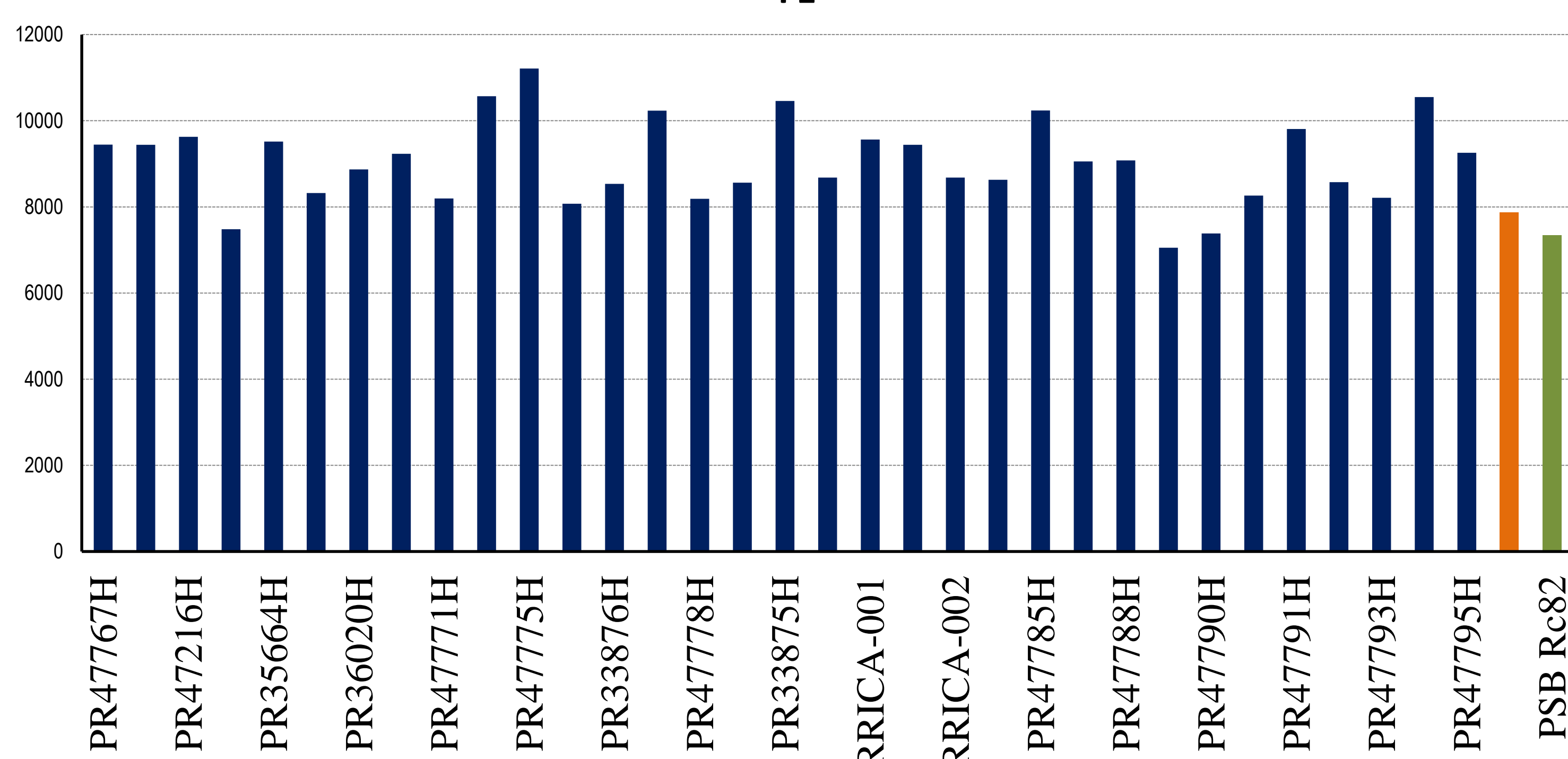
RESULTS

Figure 2. Yield advantage of hybrids over Mestiso 19 and PSB Rc82 (hybrid and inbred check varieties)

RESULTS AND DISCUSSION

For standard heterosis, 51% of the hybrids had yield advantage of at least 15 % over Mestiso 19 as the check. variety. Top three highest yield were obtained by PR47775H, PR47774H and PR47794H with grain yield of 11.4 t/ha, 10.6 t/ha, and 10.5 t/ha (Fig. 2). Based on the mid-parent heterosis, both positive and negative significant effect were shown in different traits . Significance of this component indicates unidirectional dominance, ie. none additive gene action.

Table 2. Estimates of GCA of parents for different agronomic characters

ENTRY NO.	PARENTS	Mat	Pl ht	Tiller No.	Pan. Length	Total No. of Grains	Spikelet Fert	1000 GW	Grain Yld
Lines									
1	Hanareumbyeo	0.61ns	-5.40**	1.15ns	-1.68**	-19.08*	-3.943ns	0.61ns	269.99ns
2	Matatag 2-25kr-263-4-23R	-0.27ns	-2.47**	-0.74ns	-0.38ns	-14.41ns	3.10ns	-0.33ns	-596.17ns
3	Milyang23	4.87**	-0.57**	-0.77ns	-0.01ns	14.25ns	-1.00ns	-2.31**	-1060.71ns
4	PJ23R	-1.12*	-1.18**	-0.27ns	-1.23**	-25.37**	2.54ns	1.91**	85.13ns
5	PR31559-AR-32-4-3-2R	-1.61**	1.65ns	-0.85ns	0.29ns	-1.75ns	0.98ns	0.73ns	303.4ns
6	PR34142-5-1-3-2R	-0.94*	0.63ns	0.36ns	-0.07ns	6.25ns	-0.40ns	-1.43**	467.98ns
7	PR34302R	0.94*	-0.38*	-0.07ns	1.21**	6.13ns	'-0.96ns	-1.10*	-271.2ns
8	PR35749-HY-R	-1.5**	0.13**	1.25ns	0.57ns	2.36ns	-0.84ns	-0.78ns	-52.45ns
9	PR36246-HY-1-19-2-2R	0.16ns	7.26**	-0.29ns	0.17ns	30.58**	-1.58ns	-0.88ns	-155.38ns
10	PR36248-HY-2-5-1R	-0.37ns	2.48**	-1.146ns	0.47ns	9.5ns	0.41ns	1.98**	797.09ns
11	SRT-3R	-0.38ns	0.24**	1.14ns	0.56ns	-8.63ns	1.89ns	1.78**	192.45ns
Testers									
1	IR68897A	-1.19*	-3.29*	0.35ns	-0.28ns	-7.29ns	0.71ns	0.11ns	-199.84ns
2	IR73328A	-0.13ns	2.72*	0.01ns	-0.17ns	5.75ns	0.46ns	0.34ns	756.98ns
3	IR80559a	1.31	0.82ns	-0.36ns	0.44ns	2.06ns	-1.13ns	-0.42ns	-488.33ns
	σ^2 gca	0.12	0.61	0.01	0.03	10.11	-0.3	-0.08	14811.69
	σ^2 sca	9.59	44.3	0.6	1.13	322.29	9.21	2.34	1334923

Estimates of variance for general combining ability (GCA) and specific combining ability (SCA) and their effects was computed using Line x Tester Analysis procedures. These led to generation of analysis of variance for line x tester analysis that included parents. Comparative estimates of GCA and SCA are shown in Table 3. The value of σ^2 gca was found to be lesser than value of σ^2 sca for different characters. This indicates that predominant roles of additive gene effects were established for different characters.

Moreover, components of variation due to interaction of line x tester was found to be significant only to days to 85% maturity, plant height and spikelet fertility.
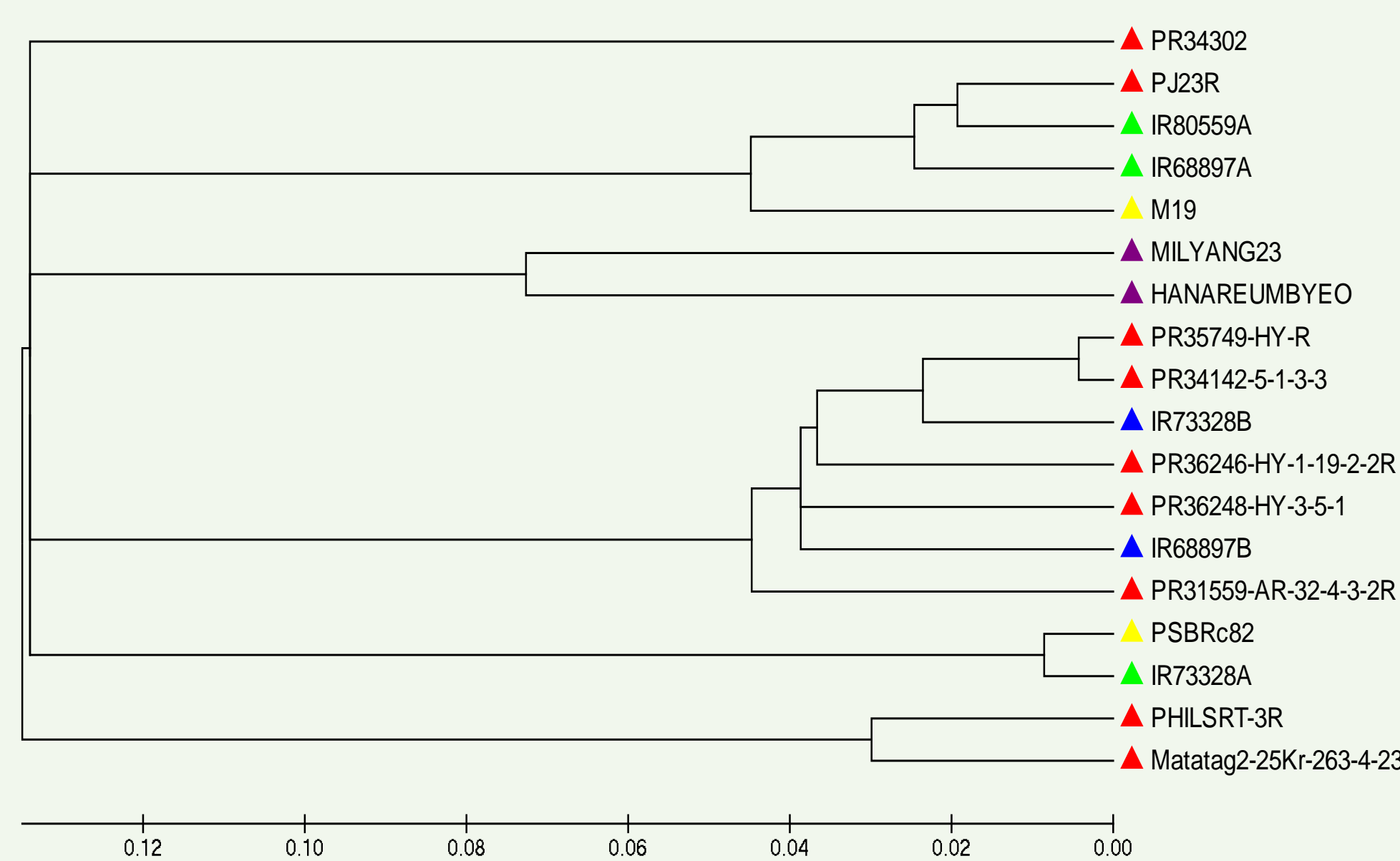
Based on the result, entries showed high consistency levels of genetic similarity.

Figure 3. Genetic structure of the entries based on Neighbor-joining method

CONCLUSION AND RECOMMENDATION

Significant positive and negative effects that can be obtained from line, tester and interaction of line x tester implies that there is wide variability of heritable traits among genotypes. Rice testcrosses derived from combinations of testers and lines used in this study using line × tester mating design had demonstrated desirably positive heterosis in traits that contributed to grain yield effects against mid-parental values. Aside from yield as a single trait itself, several yield components, with acceptable correlation coefficient values showed to have contributed fairly as well. Selections can be assembled from among parents used, to combine with new parent also, to produce new untested testcrosses with expected relatively high SCA effects; alternatively, lines with high GCA effects, but did not show to be good combiners can be endorsed to develop superior inbred rice lines. Relative to performance estimates using yield morpho-agronomic traits of the 33 crosses used in the study resulting high genetic similarity among parents may have mainly caused relatively lo heterosis levels of the testcrosses. This suggest the need to use more diverse parent lines.