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Combining Ability Analysis in Iron and Zinc Rich Rice Genotypes

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A B S T R A C T

In the present investigation, the magnitude of specific combining ability variances was higher than that of general combining ability for all the characters under study except spikelet fertility (%), kernel length, kernel length/breadth ratio and kernel elongation ratio indicating greater role of non- additive gene action in controlling most of the traits.

Introduction

The success of any breeding programme depends on selection of parents for hybridization and the choice of crosses to be advanced from the several crosses effected. This indicates that prior information on genetic background of the parents to be combined through crossing is very important. One of the techniques, widely used to extract information about the genetic system governing the inheritance of attributes, is the diallel analysis (Arunachalam, 1976). This design gives an idea about the relative magnitude of additive and non-additive components of heritable variance in expression of a trait. In case of diallel analysis developed by Griffing (1956) the additive and dominance components can be studied

precisely in the absence of epistasis. Super crosses and parents with high *SCA* effects and *GCA* effects can be picked up.

Materials and Methods

The present investigation was carried out at Regional Agricultural Research Station, Warangal, which is located at an altitude of 304 M above MSL, 17.97° N latitude and 79.60° E longitude in consecutive two seasons *viz. Kharif,* 2014, *Rabi*, 2014-15. *Kharif* (June – Dec) and *Rabi* (Nov – May) are the main crop seasons in this state can be called as rainy and post rainy seasons. The experimental material for heterosis and combining ability studies comprised of 10 genotypes *viz.,* MTU 1010, WGL-32100, Ramappa, RP-Bio-5478-270, RP-Bio-5478-166, RP-Bio-5478-176,

DRR Dhan-40, RP-Bio-5478-185, SM- 686, SM-787, their 45 F_1 hybrids generated from ten parents crossed (in diallel fashion without reciprocals during *kharif*, 2014) and two promising check varieties *viz.* BPT 5204 and Chittimuthyalu. The data obtained from F_1s and parents were analysed as per Method II (F_1s + parents) and Model – I (fixed effect) of Griffing (1956a) for combining ability. Analysis of variance for combining ability for yield, yield components (Table 1) indicated that general combining ability (*GCA*) mean squares were significant for all the characters. For specific combining ability (*SCA*), mean squares were significant for all the characters, except for spikelet fertility (%) and kernel breadth. In the present investigation, the magnitude of specific combining ability variances was higher than that of general combining ability for all the characters under study except spikelet fertility (%), kernel length, kernel length/breadth ratio and kernel elongation ratio indicating greater role of non-additive gene action in controlling most of the traits.

The specific combining ability effects, estimates of *gca* and *sca* variances and their ratios of 45 F_1 hybrids for yield and its components are presented in Table 2.

Results and Discussion

Overall results indicated that the grain yield per plant and its components except spikelet fertility percentage were chiefly governed by non-additive gene action, as the *SCA* variances were higher than the corresponding *GCA* variances. For days to 50% flowering and plant height, the crosses with significant negative *SCA* effects are desirable. Accordingly, the crosses showing high *SCA* effects with high *per se* performance in desirable negative side *viz.*, MTU 1010 x RP-Bio-5478-185 (high *GCA* x low *GCA*), WGL-32100 x Ramappa (low x high) for days to 50% flowering and the crosses, MTU 1010 x

Ramappa (high x low), RP-Bio-5478-270 x DRR Dhan-40 (low x high), RP-Bio-5478-176 x SM-787 (high x low), DRR Dhan-40 x RP-Bio-5478 -185 (high x medium) and DRR Dhan-40 x SM-787 (high x low) for plant height were highly useful for evolving genotypes with shorter duration and short stature. These crosses showing high x low or *vice versa* indicated the involvement of mostly additive x dominant interactions could be further exploited by identification of transgressive segregants in later generations or even through heterosis breeding too. These results are in accordance with findings of Verma and Srivasthava (2004) and Srijan *et al.,* (2016). In rice, the major yield deciding traits are number of productive tillers per plant, number of grains per panicle and 1000 grain weight. Five crosses in case of number of productive tillers per plant, nine for number of grains per panicle and only four for 1000 grain weight exhibited significant positive *SCA* effects in the present investigation. Among the 5 crosses with high *SCA* effects for productive tillers per plant, two *viz.*, RP-Bio-5478-270 x RP-Bio-5478 -185 (high x low) and DRR Dhan-40 x SM-686 (low x high) also exhibited better *per se* performance, whereas with respect to the remaining three crosses *viz.*, MTU 1010 x RP-Bio-5478-166 (low x high), MTU 1010 x RP-Bio-5478-176 (low x medium) and WGL-32100 x Ramappa (low x medium), the mean performance was poor.

With regard to grains per panicle, high *SCA* effects followed by high *per se* performance was registered in case of four crosses *viz.,* MTU 1010 x Ramappa (low x high), MTU 1010 x RP-Bio-5478-176 (low x low), WGL-32100 x Ramappa (high x high) and WGL-32100 x SM-686 (high x high) where as in rest of the crosses there is no reflection of high mean with high *SCA* especially in case of WGL-32100 x RP-Bio-5478-176 (high x low) and RP-Bio-5478-166 x DRR Dhan-40 (low x low).

Table.1 Analysis of variance (mean squares) for combining ability and proportions of *GCA* and *SCA* variances for grain yield and its components

Source of variation	d. f.	Days to 50% flowering	Plant height	Total no. of tillers/plant	No. of productive tillers/ plant	Panicle length	No. of grains/ panicle	Spikelet fertility	1000 grain weight	Grain yield/ plant
GCA	9	36.974**	825.843**	13.24**	6.18**	7.68**	2059.80**	28.33**	16.70**	48.59**
SCA	45	19.173**	260.980**	4.12**	3.00**	3.04**	452.91**	6.05	6.14**	7.20**
Error	108	1.65	11.11	0.70	0.60	0.64	49.64	4.35	0.50	1.10
σ^2 GCA		2.943	67.894	1.045	0.465	0.587	167.51	1.99	1.350	3.957
σ^2 sca		17.514	249.869	3.418	2.408	2.398	403.26	1.70	5.636	6.099
σ^2 GCA / σ^2 sca		0.168	0.272	0.306	0.193	0.245	0.415	1.175	0.240	0.649

Table.2 Mean sum of squares yield and yield components of ten parents and forty five F_1 s in rice (Combining ability analysis)

Source of variation	d.f.	Days to 50% flowering	Plant height	Total no. of tillers/plant	No. of productive tillers/ plant	Panicle length	No. of grains/panicle	Spikelet fertility	1000 grain weight	Grain yield/ plant
Replications	2	1.65	29.90	0.82	0.90	2.51	162.66	29.95	1.02	2.67
Genotypes	54	66.41**	1065.37**	16.93**	10.61**	11.45**	2162.17**	29.31**	23.71**	42.31**
Parents	9	78.88**	878.34**	11.25**	3.61*	16.76**	3465.35**	58.56**	17.53**	59.64**
Hybrids	44	62.30**	1127.59**	17.70**	12.10**	9.41**	1943.18**	23.75**	22.20**	37.35**
Parent Vs. Hybrids	1	135.33**	10.96*	34.02**	7.71*	53.50**	69.32*	10.83*	145.43**	104.59**
Error	108	4.97	33.33	2.11	1.80	2.33	148.93	13.07	21.51	3.32

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

Table.3 General combining ability (gca) effects of parents for yield and yield components in rice

Parents	Days to 50% flowering	Plant height	Total no. of tillers/plant	No. of productive tillers/ plant	Panicle length	No. of grains/panicle	Spikelet fertility	1000 grain weight	Grain yield/ plant
MTU 1010	1.267**	13.717**	-1.950**	-1.294**	-0.161	-5.799**	3.864**	-1.546 **	-2.733**
WGL-32100	-2.900**	-9.083**	-1.487**	-1.006**	-0.956**	15.851**	0.106	1.552**	2.722**
WGL-23985	0.767*	-6.515**	-0.008	0.189	-0.084	15.322**	-1.026	1.458**	2.066**
RP-Bio-5478-270	-0.539	-3.656**	0.818**	0.913**	-0.242	11.248 **	-0.627	0.666**	2.105**
RP-Bio-5478-166	1.794**	4.165**	1.359**	0.725**	-1.108**	-10.097**	-0.657	-0.764 **	-1.481**
RP-Bio-5478-176	2.211**	4.267**	0.305	0.171	-0.483*	-16.022**	-0.388	-1.488 **	-2.111**
DRR Dhan - 40	1.489**	11.670**	-0.177	0.031	0.801	-16.124**	-1.348*	-1.130 **	-1.355**
RP-Bio-5478 -185	-0.900*	0.597	-0.314	-0.460*	1.317**	-11.529 **	-1.114	-0.195	-1.383**
SM-686	-2.150**	-6.016**	0.977**	0.516*	0.961**	8.810**	0.086	0.713**	1.314**
SM-787	-1.039**	-9.236**	0.478*	0.215	-0.044	8.339**	1.104	0.736**	0.857**
SE (gi) ±	**0.798**	**2.065**	**0.520**	**0.480**	**0.498**	**4.365**	**1.293**	**0.441**	**0.652**

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

Table.4 Specific combining ability (sca) effects of crosses for yield and yield components in rice

Cross	Days to 50% flowering	Plant height	Total no. of tillers/plant	No. of productive tillers/ plant	Panicle length	No. of grains/panicle	Spikelet fertility	1000 grain weight	Grain yield/ plant
MTU-1010 x WGL-32100	10.045**	-14.587**	-0.788	-1.028	-0.233	38.847**	6.973**	-5.293**	-0.750
MTU-1010 x Ramappa	-0.621	-16.205**	-0.607	0.111	-0.352	21.870**	4.636*	-2.949**	1.046
MTU-1010 x RP-Bio-5478-270	4.018**	25.458**	0.100	0.387	-1.214	-25.639**	-1.420	-4.157**	-6.912**
MTU-1010 x RP-Bio-5478-166	8.018**	25.729**	2.493**	2.375**	0.879	-6.801	-4.557*	-2.871**	-2.683**
MTU-1010 x RP-Bio-5478-176	2.934*	25.333**	2.081*	2.295**	1.480	23.260**	-2.146	-1.663*	0.237
MTU-1010 x DRR Dhan - 40	6.990**	13.560**	0.269	-0.291	0.753	-17.694**	-3.562	-0.361	-2.682**
MTU-1010 x RP-Bio-5478 -185	-3.955**	-3.034	-3.367**	-2.907**	0.274	-13.032	-5.953**	-1.899**	-1.651
MTU-1010 x SM-686	-3.038*	-3.924	-1.892*	-1.549*	-0.587	-3.862	0.443	1.942**	-0.818
MTU-1010 x SM-787	1.184	-3.044	-1.892*	-1.915*	-2.805**	12.037	-0.204	0.743	-1.651
WGL-32100 x Ramappa	-5.788**	-3.555	3.344**	2.956**	0.213	33.537**	-1.417	2.006**	2.748**
WGL-32100 x RP-Bio-5478-270	-1.482	-6.779*	0.458	-0.155	-0.222	-52.533**	-0.619	-2.882**	-4.765**
WGL-32100 x RP-Bio-5478-166	-0.816	9.765**	-1.986*	-1.047	0.414	-13.648*	-0.533	1.971**	-0.895
WGL-32100 x RP-Bio-5478-176	-1.899	-0.390	-2.382**	-3.494**	-0.811	33.487**	-0.548	0.509	0.241
WGL-32100 x DRR Dhan - 40	-2.843*	-15.983**	0.606	1.603*	-1.148	0.609	-1.991	2.604**	2.432*
WGL-32100 x RP-Bio-5478 -185	-3.788**	21.083**	-2.013*	-1.445*	-1.757*	-3.132	0.751	-0.227	2.706**

(Cont.)

Cross	Days to 50% flowering	Plant height	Total no. of tillers/plant	No. of productive tillers/ plant	Panicle length	No. of grains/ panicle	Spikelet fertility	1000 grain weight	Grain yield/ plant
WGL-32100 x SM- 686	0.129	2.089	-0.454	0.196	1.928*	28.815**	0.388	0.888	3.389**
WGL-32100 xSM- 787	2.018	-3.641	0.495	0.380	-1.114	-21.043**	-2.020	-0.419	-1.364
Ramappa x RP-Bio-5478-270	2.518*	2.809	-3.688**	-2.930**	1.482	-25.453**	-1.200	-1.408*	-4.509**
Ramappa x RP-Bio-5478-166	2.851*	9.073**	-2.855**	-2.005**	3.562**	2.275	2.883	2.145**	2.114*
Ramappa x RP-Bio-5478-176	2.434*	-12.512**	2.473**	2.479**	-2.533**	-42.067**	-3.336	0.300	-1.212
Ramappa x DRR Dhan - 40	4.157**	23.108**	-2.546**	-2.714**	0.643	-5.498	1.128	0.515	-1.758
Ramappa x RP-Bio-5478 -185	3.545**	-5.722	1.091	1.360	-0.763	15.720*	2.383	0.897	0.846
Ramappa x SM-686	2.795*	0.634	0.083	0.128	-2.780**	-19.456**	0.880	-0.295	-2.898**
Ramappa x SM-787	4.351**	12.084**	1.133	0.932	-0.209	-6.361	-0.428	-1.991**	-0.037
RP-Bio-5478-270 x RP-Bio-5478-166	2.157	-22.637**	-2.241**	-1.133	-0.794	10.506	2.013	1.283	3.112**
RP-Bio-5478-270 x RP-Bio-5478-176	-2.260	-2.652	0.980	1.711*	-0.752	0.291	-1.385	-0.992	-0.028
RP-Bio-5478-270 x DRR Dhan - 40	-2.205	-26.949**	-1.252	-0.272	-2.239**	11.366	2.168	1.693*	2.559*
RP-Bio-5478-270 x RP-Bio-5478 -185	-3.149*	25.577**	5.381**	3.413**	-0.479	45.271**	1.224	2.318**	1.597
RP-Bio-5478-270 x SM-686	2.434*	-0.056	-0.223	0.077	1.201	14.435*	0.100	0.083	-0.657
RP-Bio-5478-270 x SM-787	-2.343	-10.063**	2.320**	1.878*	2.339**	-3.646	-1.247	0.667	3.010**

(Cont.)

Cross	Days to 50% flowering	Plant height	Total no. of tillers/plant	No. of productive tillers/ plant	Panicle length	No. of grains/ panicle	Spikelet fertility	1000 grain weight	Grain yield/ plant
RP-Bio-5478-166 x RP-Bio-5478-176	-1.927	-13.702**	0.946	-0.391	0.714	14.862*	-1.925	1.498*	0.738
RP-Bio-5478-166 x DRR Dhan - 40	3.129*	-16.871**	-0.329	-0.251	-3.220**	16.781*	-0.995	-2.044**	-0.034
RP-Bio-5478-166 x RP-Bio-5478 -185	-4.482**	-8.108*	0.161	0.467	-0.466	1.639	2.444	1.261	1.423
RP-Bio-5478-166 x SM- 686	-5.566**	-4.818	0.883	0.295	-2.983**	-20.923**	0.387	-6.007**	-2.581*
RP-Bio-5478-166 x SM-787	-3.677**	0.434	-1.174	-0.421	-0.518	-0.875	1.070	0.590	-1.530
RP-Bio-5478-176 x DRR Dhan - 40	-0.621	31.897**	0.998	0.303	2.692**	-5.888	2.436	-2.502**	0.799
RP-Bio-5478-176 x RP-Bio-5478 -185	-1.566	26.376**	-4.445**	-3.262**	0.009	-6.216	1.935	-0.134	0.756
RP-Bio-5478-176 x SM-686	0.018	-8.091*	-1.779*	-0.962	-1.362	-23.305**	0.628	-0.402	-2.611**
RP-Bio-5478-176 x SM-787	-3.760**	-10.731**	0.143	0.009	1.680*	-19.750**	-1.509	-2.162**	-0.464
DRR Dhan - 40 x RP-Bio-5478 -185	1.490	-15.330**	-0.297	-0.859	-2.621**	3.253	0.949	0.838	-0.773
DRR Dhan - 40 x SM-686	0.073	-5.260	1.736*	2.162**	-0.155	-0.253	-1.795	-1.487*	0.690
DRR Dhan - 40 x SM-787	-2.371	-20.518**	-2.065*	-2.074**	-0.301	7.085	0.871	-0.697	-0.419
RP-Bio-5478 -185 x SM-686	1.795	-8.198*	0.716	0.943	1.662*	-9.515	-1.322	-0.632	-2.566*
RP-Bio-5478 -185 x SM-787	6.351**	-6.048	0.105	-0.216	0.367	2.350	-2.840	-1.868**	-1.149
SM-686 x SM-787	1.934	8.932**	-0.352	0.275	-1.954*	-5.456	0.830	0.677	0.061
SE (Sij) ±	**2.391**	**6.188**	**1.560**	**1.438**	**1.494**	**13.080**	**3.876**	**1.321**	**1.954**

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

The high *SCA* observed in these 4 crosses is ascribed to prevalence of non-additive genetic effects and also interaction effects of dominant + and − alleles especially of additive x dominant or dominant x additive type. Therefore, these crosses could be better exploited by inter mating in early generations and postponing the selections to later generations (Table 4 and 5).

It is interesting to note that the promising crosses with high test weight (more than 20.00 g) also manifested high *SCA* effects which is an indicative of positive relation between these two estimates in case of 1000 grain weight. The best specific crosses identified for further improvement are WGL-32100 x Ramappa (high x high), WGL-32100 x DRR Dhan - 40 (high x low), Ramappa x RP-Bio-5478-166 (high x low), RP-Bio-5478-270 x RP-Bio-5478 -185 (high x low) and among these four, improvement for test weight could be quite easy and straight forward in case of a particular cross (WGL-32100 x Ramappa), in which the parents with high x high *GCA* effects were involved.

Only two crosses *viz*., MTU 1010 x WGL-32100 (high x medium) and MTU 1010 x Ramappa (high x low) have shown significant *SCA* effects for spikelet fertility.

Grain yield is the ultimate result, which is dependent on its components. Graffius (1959) suggested that there would be no separate gene system for yield *per se* and yield is an end product of multiplicative interaction between yield and its components. In the present study, significant *SCA* effects were registered by 8 crosses for grain yield per plant and the mean values were also high for 5 crosses. The top ranking cross WGL-32100 x Ramappa which expressed high *SCA* for grain yield also exhibited high *SCA* effects for other prime yield components *viz.,* 1000 grain weight, number of grains per panicle and

number of productive tillers per plant, whereas, in case of other crosses high *SCA* effect was observed for at least one component.

In 3 promising crosses *viz.,* WGL-32100 x Ramappa, WGL-32100 x SM-686, RP-Bio-5478-270 x SM-787, the corresponding *GCA* effects of the parents were of high x high nature. In rest of the crosses, the parents possessed either high x low or low x high *GCA* effects. The present study indicated that high mean performance is a good indicator of high *GCA* effects but not an indicator for high *SCA*. Hence, the *SCA* effects alone may not be an appropriate choice for deciding the breeding strategy wherein considerable importance has to be given for corresponding *GCA* of the parents apart from mean values of the parents and respective crosses too.

Accordingly, the crosses with good x good general combiners exhibiting high *SCA* effects can be utilized for improvement through single plant selection in segregating generations. In other crosses, having high *SCA* effects due to good x poor general combiners, the improvement would be possible through population improvement duly involving both additive and dominant gene actions. In case of the crosses showing high *SCA* effects with involvement of poor x poor general combiners, the heterosis breeding would be more appropriate.

Thinking in these lines, 3 crosses *viz.,* WGL-32100 x Ramappa, WGL-32100 x SM-686, RP-Bio-5478-270 x SM-787 which majorly involved additive gene action are recommended for grain yield improvement through direct selection. Whereas, for other promising crosses, WGL-32100 x DRR Dhan-40, Ramappa x RP-Bio-5478-166, RP-Bio-5478-270 x RP-Bio-5478-185 (for 1000 grain weight), MTU 1010 x RP-Bio-5478-176 (for number of grains per panicle) and RP-

Bio-5478-270 x RP-Bio-5478-185, DRR Dhan-40 x SM-686, MTU 1010 x RP-Bio-5478-166 (for number of productive tillers per plant), MTU 1010 x RP-Bio-5478-185, RP-Bio-5478-270 x DRR Dhan-40, RP-Bio-5478-176 x SM-787, DRR Dhan-40 x RP-Bio-5478-185 (for earliness), population improvement schemes like Bi parental mating and Recurrent selections to pool up the dominant desirable genes by breaking the linkages, if any, would be highly desirable. In future advanced generations such high x low combinations offer opportunity to practice selection on the transgressive segregants in the desired direction (Langham, 1961).

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