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COMBINING ABILITY AND GENE ACTION FOR COOKING QUALITY TRAITS IN NUTRIENT RICH RICE (*Oryza sativa* L.) CROSSES

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ABSTRACT

The present study was conducted in two consecutive seasons (2014 and 2015) at Agriculture College, Warrangal (India) to assess the combining ability of hybrid rice (*Oryza sativa*) for various cooking quality parameters. The genotypes involved in the study comprised of 45 F_1 hybrids generated from 10 parents and two promising check varieties *viz.*, BPT 5204 and Chittimuthyalu. In present study, the magnitude of specific combining ability variances was found higher than general combining ability for all the quality characters studied, except for kernel length, kernel length/breadth ratio and kernel elongation ratio. This indicated the greater role of non-additive gene action in controlling most of these traits. The best specific crosses for cooking quality traits were WGL-32100 x RP-Bio-5478-185 (high x low), Ramappa x RP-Bio-5478-176 (high x low) and Ramappa x RP-Bio-5478 -185 (high x low) and interestingly these crosses involved parent Ramappa. These crosses were highly promising for cooking quality traits.

Keywords: Combining ability, cooking quality, gene action, rice

INTRODUCTION

The future of a rice variety majorly depends upon the cooking quality especially the volume expansion ratio, kernel elongation ratio and gelatinization temperature. The success of any breeding programme depends on the selection of parents for hybridization and the choice of crosses to be advanced from the several crosses affected. This indicates that prior information on genetic background of parents to be combined through crossing is very important. One of the techniques, widely used to extract information about genetic system governing the inheritance of attributes is diallel analysis (Arunachalam, 1976). This design gives idea about the relative magnitude of additive and non-additive components of heritable variance in the expression of a trait. In case of diallel analysis developed by Griffing (1956b), the additive and dominance components can be studied precisely in the absence of epistasis. Combining ability studies are meant to identify the superior parents with good combining ability which can be used to make a population with favourable and fixable genes for effective quality improvement. Combining ability analysis helps in the identification of parents with high general combining ability (*gca*) effects and cross combinations with high specific combining effects (*sca*) for commercial exploitation of heterosis and isolation of pure lines among the progenies of the heterotic hybrids.

In rice**,** the information on heterosis and gene action needs to be evaluated to develop quality hybrids. The suitable parents having favourable alleles on crossing produce heterotic hybrids in rice (Saikiran *et al.*, 2018). Rice hybrids developed with locally adaptable parents show better tolerance to biotic and abiotic stresses and fare well in the desired environmental conditions (Shobhana *et al.*, 2017). Therefore, the present study was aimed to assess the relative importance of general and specific combining abilities of nutrient-rich rice crosses.

MATERIALS AND METHODS

The present study was carried out at Regional Agricultural Research Station, Warangal, Telangana (India) which is located at an altitude of 304 m MSL, 17.97° N latitude and 79.60° E longitude. The study was conducted in consecutive two seasons *viz.*, *kharif* (June-Dec, 2014); *rabi* (Nov., 2014-May, 2015). The experimental material for heterosis and combining ability studies comprised of ten 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 and SM-787, their forty five 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 parents and checks were collected from IIRR-ICAR, Hyderabad (India) and Regional Agricultural Research Station, Warangal (PJTSAU). The entire experimental material consisted of ten parents and forty-five F_1s. The study was conducted in a randomized block design with 3 replications. All the necessary recommended package of practices was followed to raise the healthy crop. Five plants of each entry were tagged at random from each treatment and data were recorded with respect to rice cooking quality parameters *viz.*, hulling percentage, milling percentage, head rice recovery percentage, kernel length, kernel breadth, kernel length to breadth ratio, kernel elongation, volume expansion ratio and gelatinization temperature. The data obtained from F_1s and parents were analyzed for general and specific combining ability effects as per the method II (F_1s + parents) and model - I (fixed effect) of Griffing (1956a.b) for combining ability subjecting to Window stat.

RESULTS AND DISCUSSION

The analysis of variance for combining ability for quality indicated that general combining ability (gca) mean squares were significant for all the characters (Table 1). For specific combining ability (sca), mean squares were significant for all the characters, except for kernel breadth (Table 2). The magnitude of sca variances was higher than that of gca for all the quality characters studied, except for kernel length, kernel length/breadth ratio and kernel elongation ratio indicating the greater role of non-additive gene

Table 1: Mean sum of squares for quality traits of 10 parents and 45 F_1 s of rice (combining ability analysis)

Source of variation	d.f.	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio (mm)	Volume expansion ratio	Kernel elongation ratio	Gelatinization temperature
Replications	2	1.13	0.21	0.23	0.04	0.03	0.03	0.02	0.003	0.55
Genotypes	54	8.48*	6.05**	26.41**	1.98**	0.04**	0.59**	2.49**	0.08**	11.73**
Parents	9	14.81**	17.03**	20.05**	2.28**	0.05*	0.76**	2.47**	0.09**	16.18**
Hybrids	44	7.25	3.90	28.23**	1.94**	0.04**	0.57**	2.54**	0.08**	10.96**
Parent vs. Hybrids	1	5.54*	1.48*	3.51*	0.70**	0.02	0.04	0.60**	0.01	5.77*
Error	108	5.74	3.52	5.13	0.03	0.02	0.02	0.03	0.005	1.77

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

Table 2: Gene action and proportions of gca and sca variances for grain quality traits in rice

Source of variation	d.f.	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio (mm)	Volume expansion ratio	Kernel elongation ratio	Gelatinization temperature
gca	9	5.31*	2.56*	21.99**	2.92**	0.03**	0.88**	3.06**	0.11**	12.86**
sca	45	2.33	1.90*	6.16**	0.20**	0.010	0.06**	0.38**	0.01**	2.12**
Error	108	1.91	1.17	1.71	0.01	0.007	0.009	0.010	0.002	0.59
σ^2 gca		0.284	0.116	1.69	0.242	0.002	0.073	0.254	0.010	1.023
σ^2 sca		0.416	0.732	4.456	0.195	0.003	0.054	0.376	0.009	1.530
σ^2 gca/ σ^2 sca		0.683	0.158	0.379	1.241	0.935	1.357	0.676	1.049	0.669

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

action in controlling most of the traits. The gca and sca effects of 45 F_1 hybrids for quality characters are presented in Tables 3 and 4. In present study, the milling traits *viz.*, hulling (%), milling (%) and head rice recovery were found under the influence of non-additive gene action as evident by high sca variance. These results are in conformity with Padmavathi *et al.* (2012) and Sahu Parmeshwar *et al.* (2017), for hulling, Sahu Parmeshwar *et al.* (2017) and Belhekar *et al.* (2017) for milling and Gonya Naik *et al.* (2011), Gnanamalar and Vivekanandan (2013a) and Belhekar *et al.* (2017) for head rice recovery.

The crosses, WGL-32100 x Ramappa (4.417) and RP-Bio-5478-270 x DRR Dhan-40 (3.733) were found associated with highly significant positive sca effects, whereas 4 crosses *viz.*, RP-Bio-5478-176 x DRR Dhan-40 (-5.574), Ramappa x RP-Bio-5478-270 (-4.296), NH-686 x NH-787 (-4.043) and RP-Bio-5478 -185 x NH-787 (-3.559) showed significant negative sca effects. Among the forty-five crosses studied, five crosses showed significant positive sca effects with a range of 0.233 (Ramappa x NH-787) to 0.498 (WGL-32100 x RP-Bio-5478-185). Five crosses showed significant negative sca effects for kernel L/B ratio trait. For volume expansion ratio character, only twenty crosses showed significant positive sca effects whereas seventeen crosses showed significant negative sca effects. The cross combination WGL-32100 x RP-Bio-5478 -185 (0.727) manifested highest positive and significant sca effects for volume expansion ratio followed by WGL-32100 x RP-Bio-5478-166 (0.677). The variation ranged from -1.024 (DRR Dhan-40 x NH-787) to 0.727 (WGL-32100 x RP-Bio-5478-185).

Table 3: General combining ability (*GCA*) effects of parents for quality traits in rice

Parents	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio (mm)	Volume expansion ratio	Kernel elongation ratio	Gelatinization temperature
MTU 1010	1.090**	0.768*	-2.716**	-0.011	0.037	-0.052*	-0.348**	-0.023*	-0.061
WGL-32100	-0.233	-0.372	1.123**	1.009**	-0.064**	0.628**	1.032**	0.133**	2.800**
WGL-23985	0.400	0.303	0.522	0.589**	0.051*	0.201**	0.565**	0.151**	-0.339
RP-Bio-5478-270	-0.275	-0.290	-0.471	0.401**	0.001	0.200**	0.497**	0.135**	-0.311
RP-Bio-5478-166	-0.314	-0.476	-0.913*	-0.362**	-0.117**	-0.037	-0.332**	-0.043**	-0.506*
RP-Bio-5478-176	-0.430	-0.063	1.703**	-0.346**	0.007	-0.190**	-0.216**	-0.106**	-1.061**
DRR Dhan-40	-1.018**	-0.523	-0.171	-0.340**	0.030	-0.216**	-0.379**	-0.070**	-0.339
RP-Bio-5478-185	1.070**	0.615*	-0.647	-0.322**	-0.023	-0.133**	-0.382**	-0.089**	-0.033
NH-686	-0.191	-0.242	1.774**	-0.357**	0.053*	-0.243**	-0.205**	-0.030**	0.133
NH-787	-0.098	0.279	-0.203	-0.260**	0.028	-0.158**	-0.233**	-0.059**	-0.283
SE (gi) ±	0.857	0.672	0.810	0.071	0.052	0.057	0.062	0.024	0.476

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

Table 4: Specific combining ability (s*ca*) effects of crosses for quality traits in rice

Crosses	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio (mm)	Volume expansion ratio	Kernel elongation ratio	Gelatinization temperature
	1	2	3	4	5	6	7	8	9
MTU-1010 x WGL-32100	1.352	0.100	-0.179	-0.508**	0.180*	-0.540**	-0.240*	0.113**	-4.503**
MTU-1010 x Ramappa	1.065	1.759	1.555	0.146	-0.045	0.141	0.040	0.031	-0.364
MTU-1010 x RP-Bio-5478-270	-0.316	-1.252	-0.926	-1.040**	-0.127	-0.381**	-0.664**	-0.236**	-0.725
MTU-1010 x RP-Bio-5478-166	0.133	-0.912	-1.400	0.083	0.177*	-0.171	-0.352**	0.072	-0.530
MTU-1010 x RP-Bio-5478-176	-0.331	-0.105	-2.753*	-0.199	-0.041	-0.048	-0.475**	-0.042	0.359
MTU-1010 x DRR Dhan-40	-2.590 *	-2.382*	-1.849	-0.219*	-0.064	-0.029	-0.231*	-0.051	0.636
MTU-1010 x RP-Bio-5478-185	-1.188	-2.150*	-1.779	-0.494**	0.019	-0.272*	-0.339**	-0.099**	-1.003
MTU-1010 x NH-686	0.853	-1.073	-2.230	0.079	0.123	-0.092	-0.396**	-0.064	-0.503
MTU-1010 x NH-787	-0.556	-0.681	-1.744	-0.135	0.034	-0.107	-0.418**	-0.082*	-0.753
MTU-1010 x WGL-32100	1.352	0.100	-0.179	-0.508**	0.180*	-0.540**	-0.240*	0.113**	-4.503**
WGL-32100 x Ramappa	-2.078	-0.168	4.417**	-0.384**	-0.021	-0. 166	-0.420**	-0.104**	0.775
WGL-32100 x RP-Bio-5478-270	-1.850	0.748	0.816	-0.104	-0.133	0.182	-0.488**	-0.165**	1.747*
WGL-32100 x RP-Bio-5478-166	-0.724	-2.182*	-1.858	0.659**	-0.036	0.456**	0.677**	0.063	0.942
WGL-32100 x RP-Bio-5478-176	0.715	1.308	1.219	-0.026	0.166*	-0.275**	0.238*	0.069	-2.503**
WGL-32100 x DRR Dhan-40	0.287	0.458	-1.827	0.604**	0.007	0.275**	0.445**	-0.007	1.442*
WGL-32100 x RP-Bio-5478-185	-0.881	-1.060	1.472	0.893**	-0.010	0.498**	0.727**	0.145**	2.470**
WGL-32100 x NH- 686	0.836	-0.070	0.758	0.001	0.064	-0.145	0.550**	0.193**	1.636*
WGL-32100 x NH-787	1.627	1.579	0.831	0.581**	-0.091	0.413**	0.578**	0.026	1.386
Ramappa x RP-Bio-5478-270	0.354	1.107	-4.296**	-0.336**	0.065	-0.234**	-0.255**	0.004	-0.780
Ramappa x RP-Bio-5478-166	-1.344	0.240	-2.461*	-0.047	0.099	-0.127	0.330**	-0.051	-0.586
Ramappa x RP-Bio-5478-176	-0.278	-0.192	0.670	0.155	-0.029	0.142	0.448**	0.054	0.636
Ramappa x DRR Dhan-40	-1.136	-0.720	-0.846	0.498**	0.059	0.149	0.231*	0.135**	2.247**
Ramappa x RP-Bio-5478-185	-0.591	-0.901	-0.357	-0.090	0.008	-0.041	0.390**	0.141**	0.275
Ramappa x NH-686	0.663	0.433	2.033	0.345**	-0.025	0.222*	0.253**	-0.021	-0.225
Ramappa x NH-787	0.927	-0.135	3.216*	0.408**	-0.020	0.233**	0.208*	-0.025	0.859
RP-Bio-5478-270 x RP-Bio-5478-166	2.722*	1.873	-0.945	0.584**	0.107	0.161	0.299**	0.062	-0.947
RP-Bio-5478-270 x RP-Bio-5478-176	0.231	0.870	0.946	0.709**	0.102	0.210*	0.450**	0.038	0.609
RP-Bio-5478-270 x DRR Dhan-40	2.512*	0.406	3.733**	0.032	-0.047	0.077	0.223*	0.078	0.220
RP-Bio-5478-270 x RP-Bio-5478-185	-1.782	-1.556	0.449	0.601**	0.069	0.200*	0.576**	0.137**	0.247
RP-Bio-5478-270 x NH-686	0.982	-0.012	-1.925	0. 166	-0.067	0.167	0.512**	0.129**	0.747
RP-Bio-5478-270 x NH-787	-0.284	-0.056	2.302	0.605**	0.111	0.131	0.154	0.084*	-0.836

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Crosses	1	2	3	4	5	6	7	8	9
RP-Bio-5478-166 x RP-Bio-5478-176	1.526	0.720	1.708	-0.289**	-0.120	-0.010	0.605**	-0.085*	1.470*
RP-Bio-5478-166 x DRR Dhan-40	-2.505	-1.147	0.106	-0.015	0.057	-0.077	0.652**	-0.091*	1.414
RP-Bio-5478-166 x RP-Bio-5478-185	1.317	0.664	2.982*	-0.067	-0.043	0.000	-0.342**	0.042	0.109
RP-Bio-5478-166 x NH-686	1.295	1.688	-0.266	-0.275*	-0.056	-0.090	0.417**	0.010	-1.391
RP-Bio-5478-166 x NH-787	-1.115	0.497	-0.662	-0.312**	-0.138	-0.015	-0.401**	-0.101**	1.025
RP-Bio-5478-176 x DRR Dhan-40	2.014	0.743	-5.574**	0.096	-0.008	0.066	0.532**	0.069	0.303
RP-Bio-5478-176 x RP-Bio-5478-185	1.509	2.082*	2.359	0.051	0.035	-0.020	-0.452**	-0.136**	-0.003
RP-Bio-5478-176 x NH-686	0.200	-0.161	0.391	-0.233*	-0.088	-0.010	-1.009**	-0.074*	-1.169
RP-Bio-5478-176 x NH-787	0.210	1.501	-0.785	-0.110	0.217**	-0.276**	0.506**	0.111**	0.247
DRR Dhan-40 x RP-Bio-5478-185	-0.983	-0.709	1.460	-0.258*	0.079	-0.197*	-0.398**	0.062	-1.725*
DRR Dhan-40 x NH-686	1.985	0.365	0.226	-0.039	0.000	-0.007	0.498**	-0.124**	-0.891
DRR Dhan-40 x NH-787	-1.161	-0.773	3. 176*	-0.194	0.018	-0.109	-1.024**	0.049	-0.141
RP-Bio-5478-185 x NH-686	-1.036	0.107	2.341	-0.164	-0.101	0.036	-0.916**	-0.095*	1.136
RP-Bio-5478-185 x NH-787	2.991*	1.199	-3.559**	-0.332**	-0.182 *	0.037	0.485**	-0.079*	-0.114
NH-686 x NH-787	-1.688	-0.040	-4.043**	-0.043	-0.022	-0.006	-0.922**	-0.001	0.720
SE (Sij) ±	2.569	2.013	2.428	0.213	0.155	0.172	0.185	0.073	1.427

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

The kernel length, kernel length to breadth ratio and kernel elongation after cooking are important physical and cooking quality parameters in rice. For kernel length, kernel L/B ratio and kernel elongation, lower sca variance than gca variance was observed which indicated the importance of additive gene action in the inheritance of this trait. The additive gene action for these traits has been reported by Srijan *et al.* (2016) and Gaurav Dharwal *et al.* (2017) for elongation ratio (Sahuparmeshwar *et al.,* 2017). The cross combination WGL-32100 x NH-686 (0.193) manifested highest positive and significant sca effects for kernel elongation followed by WGL-32100 x RP-Bio-5478 -185(0.145). Out of the 24 crosses that exhibited positive sca effects, nine crosses were significant. Only seven crosses showed significant negative sca effects for kernel elongation ratio trait. The range was from -0.236 (MTU-1010 x RP-Bio-5478-270) to 0.193 (WGL-32100 x NH-686). The crosses WGL-32100 x RP-Bio-5478-185 (2.470) and Ramappa x DRR Dhan- 40 (2.247) showed significant positive sca effects and the crosses MTU-1010 x WGL-32100 (-4.503) and WGL-32100 x RP-Bio-5478-176 (-2.503) showed significant negative sca effects for gelatinization temperature trait.

Overall the result revealed the presence of both poor and good general combiners showing gca effects in desirable and undesirable side. In rice, the hulling, milling and head rice recovery percentages majorly represent the milling characters useful for selection of better parents. Significant sca effects were exhibited by 3 crosses for hulling, 5 crosses for head rice recovery, whereas only one cross showed significant *sca* effect for milling percentage. The best specific cross *viz.,* RP-Bio-5478-270 x DRR Dhan-40 registered significant sca effect for both hulling percentage and head rice recovery involved the parents with low x low gca effects, as such were considered useful for development of heterotic hybrids. With respect to head rice recovery, considered as the top most criteria by the millers and traders, two crosses *viz.,* WGL-32100 x Ramappa and Ramappa x NH-787 showed high *per se* performance and significant *sca* effects with high x medium and medium x low parents respectively, thus, a direct selection of superior plants in early segregating generations may not be much rewarding. Instead, recurrent selection and other population improvement methods could be advocated to achieve the targeted progress.

In present study, out of 45 F_1 hybrids evaluated 10 crosses expressed good sca for kernel length and 5 crosses for kernel L/B ratio in desirable direction. Only one cross showed significant negative sca effect for kernel breadth. Four specific crosses *viz.,* WGL-32100 x DRR Dhan-40, WGL-32100 x RP-Bio-5478-185, WGL-32100 x NH-787 and Ramappa x NH-787 performed better in terms of sca for both the desirable traits (kernel length and kernel L/B ratio). However, the mean kernel length was in medium range *i.e.* 5.52 to 6.00 mm. It is interesting to note that high sca effects were not associated with high mean values for kernel length (6.00 mm). Top ranking crosses identified for improvement of both the traits (WGL-32100 x DRR Dhan-40, WGL-32100 x RP-Bio-5478-185, WGL-32100 x NH-787 and Ramappa x NH-787) and also other superior crosses (6 crosses for kernel length and 1 cross for kernel L/B ratio) which resulted exclusively from high x low gca combinations could be advanced postponing selections after some intermating in F_2 generation. In the study conducted by Adilakshmi and Upender (2014) also high magnitude of sca effects in several hybrids resulted from combination of high x low general combiners which may be due to dominant and recessive interactions and they were recommended for selection after inter-crossing among the promising genotypes in early generations.

The ultimate future of a variety majorly depends upon the cooking quality and among several cooking quality parameters volume expansion ratio, kernel elongation ratio and gelatinization temperature are of primary concern. Maximum number of hybrids (16) registered significant sca effects for volume expansion ratio in desirable direction; whereas only two hybrids were observed to have significant sca effects for gelatinization temperature. Four cross combinations *viz.,* WGL-32100 x RP-Bio-5478-185 (high x low general combing ability), Ramappa x RP-Bio-5478-185 (high x low general combing ability), RP-Bio-5478-270 x RP-Bio-5478-185 (high x low gcay) and RP-Bio-5478-270 x NH-686 (high x low gca) exhibited high sca effects for both volume expansion ratio and kernel elongation ratio as such were considered as best specific crosses for simultaneous improvement. Among the various superior crosses with significant *SCA* effects with respect to volume expansion ratio, five crosses *viz.,* WGL-32100 x RP-Bio-5478-185, WGL-32100 x NH-686, Ramappa x RP-Bio-5478-176, Ramappa x RP-Bio-5478-185 and Ramappa x NH-686 were classified as top ranking ones. In these crosses, Ramappa and WGL-32100 were one of the parents. The best specific crosses with high *per se* performance and significant sca effects for kernel elongation ratio (more than 1.81) were WGL-32100 x RP-Bio-5478-185 and Ramappa x RP-Bio-5478-185. In all the hybrids with significant sca effects, at least one parent with high gca was involved and other parent was the poor combiner. In such conditions, instead of direct selection adopting other strategies like population improvement and heterosis breeding would be more appropriate. Similar findings were reported by Gnanamalar and Vivekanandhan (2013).

The study revealed that the cross RP-Bio-5478-270 x DRR Dhan-40 was better hybrid for milling characters especially hulling and head rice recovery. In addition, two more crosses *viz.*, WGL-32100 x Ramappa (high x high) and Ramappa x NH-787 (high x low) were identified as best crosses for improvement of head rice recovery. For improvement of kernel length and kernel L/B ratio WGL-32100 x DRR Dhan-40 (high x low), WGL-32100 x RP-Bio-5478-185 (high x low) and WGL-32100 x NH-787 (high x low) were considered desirable. The best combiner was WGL-32100. The best specific crosses for cooking quality traits were WGL-32100 x RP-Bio-5478-185 (high x low), Ramappa x RP-Bio-5478-176 (high x low), and Ramappa x RP-Bio-5478-185 (high x low) and interestingly the crosses were highly promising with respect to cooking quality traits and these crosses involved parent Ramappa.

Conclusions: Among the parents WGL-32100 and Ramappa were graded as top ranking parents because high *SCA* effects, high *per se* performance in desirable direction was noticed in the crosses where these parents were included. In comparison to other trait, as per the study, development of hybrids was of high x high *GCA* types, whereas for other traits by parental mating or recurrent selection were considered as highly appropriate method to exploit both additive and non-additive type of gene actions.

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