Combining ability analysis for yield and contributing traits in short duration rice (*Oryza sativa* L.)

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ABSTRACT

The breeding value is an important genetic parameter determines utility of lines/genotypes to be used as parent in breeding program. This study was aimed at dissecting the breeding values (combining abilities) in 8 short duration rice lines for yield and 15 attributing traits. Altogether, 28 F_1s developed under half-diallel fashion along with eight parents were evaluated. The study revealed importance of both additive and non-additive gene effects in governing yield and yield components with preponderance of non-additive gene action for most of the yield components. Additive gene action was found important for 1000-grain weight. The parental genotype (NUD3) and (NDR 359) were found to be good general combiners. The hybrids namely NDR359/Sarjoo-52, NDR359/NUD2, NDR359/NDRK5088, NDR359/NDR1, NDR359/Nagina22, NDR359/NUD3, NDR359/CSR10, Sarjoo52/NDRK5088, Sarjoo52 X NDR 1, NUD 2/NDR1, NUD 2/NUD3, NDRK5088/Nagina22, NDRK5088/ NUD3, NDRK5088/CSR10, NUD 3/Nagina 22, Nagina 22/NUD3, NUD3/CSR 10 have shown significant favourable sca effect for yield and different yield components.

Key words: *Diallel analysis, breeding value, combining ability, gca effect, sca effect, additive gene action*

INTRODUCTION

Rice, a staple food crop which nourish over half of the global population is seems to be threatened adversely under shattering climatic scenario (Khus et al., 2005; Kumar et al., 2018; Rout et al. 2020). Rice researchers are increasingly challenged in the new century to meet the rapidly growing food demands of an ever-growing population. Its production is affected by many biotic and abiotic stresses across the ecologies throughout the world. Poor water management, increased competition for limited water resources, and the uncertain threats associated with global warming all highlight the looming water crisis that threatens agricultural productivity worldwide. The cultivation of short duration rice is very economical for farmers, but owing to very poor in yield potential and sustainability under extreme condition needs further research attention. In order to formulate efficient breeding strategies for improvement of yield, it is essential to characterise the nature and mode of gene action that determines the yield and its components. A sound breeding methodology rests on a proper understanding of the gene effects involved (Kumar et al., 2012).

The breeding value and combining ability studies of the parents and their crosses provide insights for the selection of compatible parents which prerequisite for any breeding program. Assessment of breeding values/ combining ability of the parents helps in its judicious utilization with precision and accuracy.

It unravels extent of genetics variances existing *viz.*, extent of additive and dominance variance insights hidden potential of genotypes to be utilized for further breeding invigoration with proper strategies. Its role is important to decide parents, crosses and adoption of appropriate breeding strategies to be followed to select desirable segregants (Salgotra et al., 2009; Srivastava et al., 2017). Therefore, the present investigation was undertaken to assess the breeding value and select right type of short duration genotype as parents in the hybridization programme and the appropriate breeding procedures to be followed for enhancement of genetic gain in short duration rice pool.

MATERIALS AND METHODS

The experimental material comprised of 8 short duration and popular rice varieties namely NDR359, Sarjoo-52, NUD2, NDRK5008, NDR1, Nagina 22, NUD3, CSR 10 were crossed in half diallel fashion during Kharif 2017. Total 28 crosses were evaluated along with parents (08) during Kh-2018 under randomised block design with three replications at Narendra Dev University of Agriculture and Technology, Ayodhya (Uttar Pradesh). The trial was transplanted with single seedling/hill in 20 cm x 15 cm spacing and in two 2 meter 2 long row under red-gravelly/ sandy (having pH 7.25) moderately fertile soil with low organic carbon (0.39%); available nitrogen (198.4 kg ha^{-1}); and medium in available phosphorus (15.7 kg ha^{-1}) and potassium (215.4 kg ha^{-1}). The fertilizer dose of 100 Kg N, 50 Kg P_2O_5 and 50 Kg K_2O per hectare as per recommendation was applied. Proper drainage facility was also provided in order to remove excess water during experimental period. Data were collected from 5 random but competitive plants, leaving border plant on each side of each genotype (Dhaliwal and Sharma, 1990). Observations were recorded on 16 characters viz., days to 50% flowering (DF), plant height (PH), flag leaf length (FL), flag leaf breadth (FB), panicle length (PL), number of panicles plant^{-1} (PN), grain number panicle^{-1} (GP), 1000-grain weight (TW), grain yield plant^{-1} (GY), biological yield plant-1 (BY), harvest index (HI), kernel length (KL), kernel breadth (KB), kernel L/B ratio (LBR), amylose content (AC) and alkali spreading value (AS). The combining ability analysis was carried out as per Griffing (1956), method-2 utilizing SPAR 2.0.

RESULTS AND DISCUSSION

Analysis of variance

Parental lines compatibility is key to success of any breeding program, thus, imperative to be assessed for its judicious exploitation with precision and accuracy (Kumar et al., 2018). Rice which is directly linked to the dietary requirement and economy of most of the Asian countries is needs to be further invigorated for their productivity and production. Developing short duration and drought and salinity tolerant varieties (climate smart/resilient varieties) are very crucial to sustain this crop under current transitional climatic and demographic scenario. Keeping the views in consideration, this study was planned to assess parental lines combining ability (*gca* and *sca*) for their exploitation with great precision and accuracy. Persual of ANOVA for combining ability (Table 1) showed that mean square due to general combining ability (*gca*) was highly significant for all characters except KB. Mean squares due to specific combining ability (*sca*) were also significant for all the characters. This suggests the importance of both additive and non-additive gene effects in the materials under study. The study also showed that the magnitude of *gca* variances were greater than sca variances for DF, FB, GP, TW, GY, HI, KL, LBR, AC and AS, while for rest of the characters the magnitude of *sca* variance was greater. These traits (DF, FB, GP, TW, GY, HI, KL, LBR, AC and AS) are very important, and known to be major yield contributor is good indicator of success of transgressive breeding (Kumar et al., 2018). Whereas, characters shown greater degree of sca variance indicating prevalence of dominance gene action which is good for invigoration of hybrid breeding programme (Kumar et al., 2018). Hence any approach that facilitates simultaneous exploitation of additive and non-additive gene effects would be the most desirable for the improvement of these traits. The parental lines of this study are more suitable enhancing the genetic gain for yield and quality through transgressive approach.

The estimates of *sca* effect and *gca:sca* ratio (Table 2) indicates non-additive gene effect controlling all the characters except test weight (TW). Although the mean square for *gca* (additive genetic variance) was significant, the dominant component was preponderant for all the characters except for TW.

Table 1. Analysis of variance for general combining ability (*gca*) and specific combining ability (*sca*) for different characters.

Sl. no.	Source of Variation	d.f.	Mean sum of squares														
			DF	PH (cm)	FL (cm)	FB (cm)	PL (cm)	PN	GP	TW(g)	GY(g)	BY(g)	HI (%)	KL (mm)	KB (mm)	LBR (mm)	AC	AS
1.	GCA	7	110.064**	1045.61	21.040**	0.021**	2.421**	11.958***	1340.58***	13.256***	271.436***	884.070***	71.812**	0.295**	0.008	0.193	1.398**	0.395**
2.	SCA	28	28.007**	278.937***	22.018***	0.019***	3.043**	45.787**	576.320**	3.135*	194.321**	1183.24**	31.939***	0.238***	0.011**	0.131**	0.598***	0.142**
3.	Error	105	4.742	19.972	8.11	0.007	0.807	1.561	30.465	2.242	0.788	6.983	0.986	0.072	0.005	0.064	0.145	0.072
4.	GCA/ SCA		3.93	3.75	0.96	1.11	0.8	0.26	2.33	4.23	1.4	0.75	2.25	1.24	0.73	1.47	2.34	2.78

* and ** significant at 5 and 1 per cent probability levels, respectively.

Table 2. Estimates of components of genetic variance from 8 x 8 half diallel analysis using Griffing's Method-2.

Components of genetic variance	DF	PH (cm)	FL (cm)	FB (cm)	PL (cm)	PN	GP	TW (g)	GY (g)	BY (g)	HI (%)	KL (mm)	KB (mm)	LBR (mm)	AC	AS
Additive genetic variance	16.41	153.34	0.22	0.001	0.12	6.97	154.86	1.97	16.07	60.92	8.04	0.02	0.0006	0.012	0.17	0.05
Non-additive genetic variance	25.47	262.27	16.00	0.013	2.35	45.33	552.98	1.24	198.57	1189.73	31.09	0.17	0.007	0.073	0.46	0.083
Variance due to error	5.842	19.972	8.110	0.007	0.807	1.561	30.465	2.242	0.788	6.983	0.986	0.072	0.005	0.064	0.145	0.079
Ratio of additive to non-additive genetic variance	0.65	0.58	0.014	0.077	0.05	0.154	0.28	1.59	0.08	0.05	0.26	0.12	0.086	0.16	0.37	0.60

DF- Days to 50 % flowering, PH- Plant height, FL- Flag leaf length, FB- Flag leaf breadth, PL- Panicle length, PN- Number of panicles plant^{-1}, GP- Grain number panicle^{-1}, TW- 1000 grain weight, GY- Grain yield plant^{-1}, BY- Biological yield plant^{-1}, HI- Harvest index, KL- Kernel length, KB- Kernel breadth, LBR- Kernel L/B ratio, AC- Amylose content and AS- Alkali spreading value.

These results, that existence of both additive and non-additive gene effects with prevalent of non-additive gene action for yield and contributing traits are fully corroborated with the study of researchers like Peng and Virmani (1990), Manuel and Prasad (1992), Sharma et al. (1996), Ganesan et al. (1997), Vanaja et al. (2003), Behera et al. (2016), Behera et al. (2017), Srivastava et al. (2017) and Kumar et al. (2018).

General combining ability effects

Additive component of genetic variance is useful for maximizing genetic gain through transgressive approach. In this study, the genotype NUD 3 was found to be a good general combiner for yield and quality related traits like DF, PH, FL, PL, GP, GY, BY, HI, KL, KB and AC (Table 3) hence, very useful for inbred line development. Besides, others lines like NDR 359 which is good general combiner for PH, FB, GP, GY, BY and HI; Sarjoo-52 for PN; NDRK 5088 for DF, PH, FB, PL, GP, GY, BY, KL, AC and AS; NDR 1 for PN, GP, GY, BY and AS; Nagina 22 for PH and TW and CSR 10 for DF, PH, FL, GP, GY, HI, KL, LBR and AS were also very useful to be parent in transgressive rice breeding program for yield, quality and sustainability traits.

Specific combining ability

Specific combining ability in plants is driven by dominant genetic variances are very useful for exploiting in hybrid rice breeding program. In this study, altogether seventeen F_1's NDR359/Sarjoo52, NDR359/NUD2, NDR359/NDRK5088, NDR359/NDR1, NDR359/Nagina 22, NDR359/NUD3, NDR359/CSR10, Sarjoo52/NDRK5088, Sarjoo52 X NDR 1, NUD 2/NDR1, NUD 2/NUD3, NDRK5088/Nagina 22, NDRK5088/NUD3, NDRK5088/CSR10, NUD3/Nagina22, Nagina22/NUD3, NUD3/CSR10 exhibited significant *sca* effects for GY (Supplimentary Table 1). Amongst, all have at least one parent with positive gca effect, while 7 hybrids have both parents with positive gca effect (Table 3). The hybrid NUD 3/Nagina 22 showed significant favourable *sca* effects for eight yield components (Table 4). The hybrids NDR359/NUD3, NDRK5008/Nagina22 and NDRK5008/NUD3 showed significant favourable *sca* effects for seven yield components; NDR359/NDRK5088, NDR359/Nagina22, Sarjoo52/ NDR1, NUD2/NDR1, NUD2/NUD3, NDR1/CSR10 and NUD3/CSR10 for six yield

Table 3. Estimate of general combining ability (*gca*) effect of parents for various characters.

Sl. no.	Components of genetic variance	DF	PH (cm)	FL (cm)	FB (cm)	PL (cm)	PN	GP	TW (g)	GY (g)	BY (g)	HI (%)	KL (mm)	KB (mm)	LBR (mm)	AC	AS
1	NDR359	-0.925	-3.873*	1.34	0.076**	-0.099	-0.088	11.684**	0.705	7.151**	10.884**	2.984**	0.05	-0.021	0.073	-0.21	-0.08
2	Sarjoo 52	4.575**	18.188**	-1.14	-0.028	-0.394	1.997**	-21.45**	-0.38	-7.874**	-12.511**	-4.235**	-0.12	0.034	-0.144*	0.10	-0.16*
3	NUD2	5.125**	11.148**	-1.565	-0.026	-0.519	-1.527**	-9.494**	-.947*	-6.619**	-12.011**	-2.519**	-0.37**	0.014	-0.269**	-0.21	-0.26**
4	NDRK5088	-2.725**	-3.233*	-0.908	0.050*	0.531*	-0.961*	6.498**	0.14	1.361**	9.089**	-1.260**	0.185*	0.004	0.099	0.49**	0.26**
5	NDR 1	0.025	2.588*	-0.941	-0.043	0.451	0.903*	4.664*	-1.535**	1.566**	5.984**	0.032	0.01	-0.001	0.017	0.16	0.18**
6	Nagina 22	0.275	-6.312**	-0.831	-0.066*	-0.52*	-0.551	-7.155**	2.317**	-2.504**	-5.061**	-0.474	-0.075	-0.05*	0.057	0.18	-0.05
7	NUD3	-1.825*	-5.013**	1.966**	-0.001	0.771*	0.266	11.626**	-0.127	4.931**	7.039**	2.169**	0.160*	0.044*	0.005	0.25*	-0.14
8	CSR 10	-4.525**	-13.492**	2.076**	0.037	-0.224	-0.039	3.630*	-0.175	1.986**	-3.411**	3.304**	0.160*	-0.026	0.163*	-0.76**	0.23*
	SE (gi)	0.715	1.32	0.84	0.02	0.27	0.37	1.63	0.44	0.26	0.78	0.29	0.08	0.02	0.07	0.11	0.08
	S E (gt-gj)	1.08	2	1.27	0.04	0.4	0.59	2.47	0.67	0.4	1.18	0.44	0.12	0.03	0.11	0.17	0.12

* and ** Significant at 5 and 1 per cent probability levels, respectively. DF- Days to 50 % flowering,PH- Plant height, FL– Flag leaf length, FB- Flag leaf breadth, PL– Panicle length, PN- Number of panicles plant-1, GP- Grain number panicle-1, TW- 1000 grain weight, GY- Grain yield weight, GY- Grain yield plant-1, BY- Biological yield plant-1, HI- Harvest index, KL- Kernel length, KB- Kernel breadth, LBR- Kernel L/B ratio, AC- Amylose content and AS- Alkali spreading value.

components; Sarjoo52/NUD3, NDR359/Sarjoo52, NDR359/CSR10 and NDRK5008/CSR 10 for five yield components.

The crosses NDR359/NDRK5088, NDR359/NDR1, NDR359/NUD3 NDR359/CSR10, NDRK5008/NUD3, NDRK5008/CSR10 and NUD3/CSR 10 for GY showing high *sca* effects were in the category of high x high general combiner cross combinations. This is attributable to additive and/or additive x additive type of gene effects which are fixable in nature (Singh et al., 1971; Verma et al., 2018; Kumar et al., 2018; Behera et al. 2018). Therefore, there is high probability of obtaining good transgressive segregants in the progeny of these crosses for improvement of these traits. On the other hand, two crosses-NDR359/Sarjoo52 and NDR359/NUD2 has displayed high *sca* effects for GY had common female parent with significant gca while male parent with non-significant gca respectively. The case of high *sca* between high x poor combiners could produce good segregants only if the additive genetic effects are present in the good general combiners and complimentary epistatic effects in the poor combiners and they act in the same direction to maximise desirable plant attributes (Singh and Chaudhary, 1992; Srivastava et al., 2017 & 2018; Kumar et al., 2019).

The non-significant *sca* effect was exhibited by the cross Sarjoo52 x NDR1 for GY. According to Devraj and Nadarajan (1996) these are expected to produce desirable recombinants in advance generation of inbreeding. The cross Sarjoo 52/NUD 2 showed high sca effect for DF and PH while parents were poor x poor general combiners. This is believed to be due to epistatic gene action (Kumar et al., 2019). In other hybrids also, all kinds of parental combinations like high x high, high x low, medium x medium and medium x low were found. These types of interactions attributed to either additive x additive and additive x dominance genetic interactions were also reported by Dhaliwal and Sharma (1990), Katre and Jambhale (1996), Ramalingam et al. (1997), Vanaja et al. (2003) and Kumar et al. 2018. It was suggested that the superiority of these crosses may be due to complimentary and duplicate type of gene interactions. Therefore, these crosses are expected to produce desirable segregants and could be exploited successfully in enhancement of genetic gain for important traits in varietal improvement programme.

The present study reveals importance of both additive and non-additive gene effects in governing yield and yield attributes with preponderance of non-additive gene action. In this situation, where both non-additive and additive components were important for the expression of characters, especially when the former component is preponderant, simple pedigree method of selection would be ineffective for its improvement (Jensen, 1970; Kumar et al., 2019). Population improvement programme like reciprocal recurrent selection which may allow to accumulate the fixable gene effects as well as to maintain considerable variability and heterozygosity for exploiting non-fixable gene effects will prove to be the most effective method (Joshi, 1979; Srivastava et al., 2017; Kumar et al., 2019). However, rice is the highly self-pollinated crop, one pollination event only produces one seed, hence, this selection procedure not workable.

CONCLUSION

Thus the present study concludes that possible choice is the use of biparental mating among selected crosses or use of selection procedure such as diallel selective mating to exploit both the additive and non-additive genetic components for further breeding invigoration in rice. The parent NUD3 and NDRK 5088 could be utilised in hybridization programme to harness heterosis in short duration pool because of its good general combining ability for yield and its components. Hybrids namely NDR359/ Sarjoo 52, NDR359/NUD2, NDR359/NDRK5088, NDR359/NDR1, NDR359/ Nagina 22, NDR359/NUD3, NDR359/CSR10, Sarjoo52/ NDRk5088, Sarjoo52/ NDR 1, NUD 2/ NDR1, NUD 2/NUD3, NDRK5088/ Nagina 22, NDRK5088/NUD3, NDRK5088/CSR 10, NUD 3/ Nagina 22, Nagina 22/NUD3, NUD3/CSR 10 could be utilised for development of high yielding short duration hybrids. Besides, parental lines involved in the study also harbours several resilient traits, hence, those might be useful for development of climate resilient rice varieties which is most researchable issue arises owing to climate change.

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N.B.: This article has supplementary material which is available on demand from coressponding author.