Original Research Article

Genetic Variability, Heritability and Genetic Advance in F_2 segregating population of cross RNR-15048 x Dokra-Dokriin rice (*Oryza sativa* L.)

ABSTRACT

The present experiment was conducted to study the variability, heritability and genetic advance in F_2 segregating population derived from the cross, RNR-15048 x Dokra-Dokri, evaluatedin augmented design with two checks at ICAR-IIRR, Hyderabad during the *Kharif*-2022. Analysis of variance revealed the presence of significant differences for all 11 traits examined, indicating the presence of genetic variation between the individuals studied. Higher values of PCV and GCV were observed for panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, and single plant yield. Least difference was observed between PCV and GCV value for almost all the traits indicating the least influence by the environment and possibility for genetic improvement of these traits through selection. The traits plant height, panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, spikelet fertility, thousand grain weight and single plant yield recorded high heritability (>60%) associated with high genetic advance as % of mean (>20) resulting in no environmental influence on the expression and selection for improvement of such characters could be worthwhile. High heritability coupled with moderate genetic advance as % of mean was observed for panicle length propounding non-additive gene action in their inheritance suggesting heterosis breeding could be useful for improving these traits. Overall high PCV and GCV coupled with high heritability and high genetic advance as % of mean was noticed for panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, and single plant yield suggesting significant amount of variability with predominance of additive type of gene action. Hence, direct phenotypic selection would be effective for improvement of these traits even in early generations.

Keywords: variability;F_2 segregating population; heritability; Additive gene action;genotype; phenotypic coefficient of variation (PCV); genotypic coefficient of variation (GCV).

1.INTRODUCTION

Rice (*Oryza sativa* L.) is a major staple food grain crop and carbohydrate-dietary source of more than 50 per cent of the world's population[1]. More than 90% of the world's rice is produced and consumed in Southeast Asia and tropical Latin America[2].Despite the fact that India generates 22% of the world's rice supply, population growth in India is expected to jeopardize food security by 2050 [3], putting pressure on future rice demand.The production per unit area needs to be increased from 2.4 tonnes per ha to3.4 tonnes per ha assuming the rice area under plough remains at same level [4],Although significant improvement in rice production and productivity, was achieved through green revolution, yieldplateau limited the further improvement sideways affected by various biotic and abiotic factors.Hence, guaranteeing food security in future is a big challenging task, particularly, for rice breeders in India as rice is pivotal for food and nutritional security in the country. Rice varieties with elevated productivity levels and flexible agronomic features are required forbreaking the existing yield threshold for which hybridization is one of the highly adapted and practically feasible solutionsfor creation of desired variability and achieving high productivity levels[5].

Heritability measures a character's transmissibility from one generation to another [8]. Put this line here. Presence of Genetic variation among grain yield and yield attributes is the basicrequisite to be considered during selection for the successful yield improvement through breeding. High segregation and recombination are observed in segregating populations which can be imposed for selection of superior progenies[6].Coefficient of variation is the measure of variability present in the traits of which Genotypic Coefficient of Variation (GCV) projects heritable variability and Phenotypic Coefficient of Variation (PCV) assesses the effect of environment on the genotype. Differences between PCV and GCV indicatesenvironmental effects on traits viz., small differences indicate low genetic difference, and large differences indicate high environmental effects. Hence small differences between GCV and PCV must be considered for yield improvement in further breeding programs [7]. Heritability measures a character's transmissibility from one generation to another [8]. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance are more precise in predicting the gain under selection[9]. The genetics of the traits can be better understood using third- and fourth-degree statistics i.e.,skewness and kurtosis in segregating generations [10]. Hence the present study was undertaken to determine variability, heritability, genetic advance as a percent of the mean in F_2segregating generation which could be useful in selection and further improvement.

2. MATERIALS AND METHODS

The experiment was carried out at Indian Council of Agricultural Research-Indian Institute of Rice Research (ICAR-IIRR), Rajendranagar, Hyderabad, during *kharif*2022. The experimental trial was laid out in ICAR-IIRR Rajendranagar Farm using Augmented Randomized Complete Block Design (ARCBD) consisting of 105 F_2 segregating population derived from cross RNR-15048 x Dokra-Dokri presented in Table1. The experimental area contains a total of five blocks. Prior determining individuals in each block,two checks were initially randomized. Each block was given a total of 24 entries, which included 22F_2'S and 2 checks.Twenty-five days old seedlings were transplanted in the main field with a spacing of 20 x 15 cm.All recommended cultural operations and plant protection measures were taken to ensure uniform and healthy crop stand. Eleven traits, namely, Plant Height (cm), Panicle length (PL) (cm), Total Number of Tillers per plant (TNT), No. of Productive Tillers per plant (NPT), Panicle weight (PW), No. of filled grains per panicle (NFG), No. of unfilled grains per panicle (NUFG), Total No. of grains per panicle (TGP), Spikelet fertility (SF) (%), 1000 grain weight (TGW)(gm), and Single plant yield (SPY) (gm) were recorded in every individual F_2 plant.

Table 1. Details of the parents of the intra-specific cross studied in the present investigation

Parents	**Details**
RNR-15048	Short slender grain type with low glycemic index (51.72), good cooking quality,test weight of 12.9 g and resistant to blast developed from the cross between MTU1010 and JGL 3855.
Dokra-Dokri	Longest and boldest grain with 14 mm long, high in protein (6.06%) low in fiber with high test weight of 40.5 g.

2.1 Statistical analysis

The genetic variability parameters, namely, Genotypic and Phenotypic Coefficient of Variation were computed as outlined byBurton[11]while estimates of Heritability was calculated using the formula given byAllard[12]and genetic advance as percentage of mean was calculated by adopting the formula given byJohnson et al. [9] by using the R software version 1.4.1717.

3. RESULTS AND DISCUSSION

3.1 Mean performance

The F_2 data revealed that variance due to treatment (ignoring blocks) was highly significant for all the characters except total number of tillers per plant (TNT) and productive tillers (NPT)revealing that F_2 segregating populationunder study had enough variation showing the inherent genetic differences between the individuals given in Table-2. The Plant height had a range of variance 86.0 cm to 194.00 cm, with an average of 147.92 cmwhich is in agreement withGupta et al.[13]. The average panicle length in the F_2 population studied was noticed to be 28.29 cm, the lowest panicle length was 19.61 cm and the highest was 32.89 cm, similar results were observed byManojkumar et al. [14].Total number of tillers per plant ranged from 4.30 to 18.30 with an average of 9.01 whereas the average number of productive tillers per plant was 7.66, with a range of 4.00 to 14.50. The average spikelet fertility was 71.09 per cent, with the lowest spikelet fertility value being 32.02 per cent and the greatest spikelet fertility value being 96.77 per cent. The average TGW was 24.94 gm, with the lowest and the highest of 12.45 and 39.75 g respectively. Similar variation in F_2 were reported by Khandappagol et al. [15]. Single plant yield had a mean value of 27.19 g with minimum and maximum of 8.53 and 56.04 g respectively which is in agreement with the reports ofManojkumar et al.[14].

Table 2.Analysis of variance for 11 characters of F_2 segregating population.

Source	Treatment (ignoring Blocks)	Check	Test	Test vs. Check	Block (eliminating Treatments)	Std Error	Std. Deviation	CV	Residuals
Df	106	1	104	1	4				4
PH	927.99**	10497.60 **	844.03 **	89.97 ^{ns}	17.00 ^{ns}	2.87	29.66	3.1	21.10
PL	6.44 **	62.20 **	5.93**	3.18 **	1.39 *	0.25	2.55	1.26	0.13
TNT	6.25 ^{ns}	22.50 *	4.47 ^{ns}	174.86 **	2.65 ^{ns}	0.23	2.39	17.82	2.75
NPT	5.16 ^{ns}	25.60 *	3.30 ^{ns}	178.30 **	0.75 ^{ns}	0.19	1.99	17.08	1.85
PW	3.05 **	30.35 **	2.81 *	0.09 ^{ns}	0.23 ^{ns}	0.16	1.68	9.54	0.21
NFG	4175.13 **	41731.60 **	3716.55 **	14311.10 **	186.35 ^{ns}	6	62.04	6.26	119.35
NUFG	940.63 **	722.50 *	857.46 **	9808.63 **	76.15 ^{ns}	2.79	28.9	12.33	60.75
TGP	3939.68 **	53436.10 **	3497.56 **	423.97 *	42.10^{ns}	5.8	59.97	2.63	39.10
SF	205.29 **	4.44 ^{ns}	188.63 **	2138.70 **	15.54 ^{ns}	1.32	13.65	4.64	11.20
TGW	26.83 **	1863.22 **	9.31 **	12.75 **	0.56 ^{ns}	0.35	3.57	2.77	0.48
SPY	151.74 ***	19.91 ^{ns}	135.23 **	2000.30 **	8.97 ^{ns}	1.12	11.63	8.36	5.56

*Significant values are as follows: ns- Non-significant, * Significant at 5%, ** Significant at 1%; PH – Plant height (cm); PL – Panicle length (cm); TNT- Total number of tillers; NPT-Number of productive tillers; PW-Panicle weight (g); NFG-Number of filled grains; NUFG- No. of Unfilled grains; TGP- Total grains per panicle; SF – Spikelet fertility (%); TGW- Thousand grain weight (g) and SPY- Single plant yield (g).*

3.2 PCV and GCV

The development of a plant characteristic is greatly influenced by genetic variability and heritability. Prior knowledge of population variability estimates and the heritable elements of a trait are helpful tools in any breeding programme. It would be more challenging to enhance a character through selection unless a significant amount of the variation is heritable. Breeding would benefit from knowledge of the character's heritabilityapart from its phenotypic and genotypic coefficient of variation. In order to compare the variability seen across various traits, the coefficient of variation expressed at the phenotypic and genotypic levels was used.

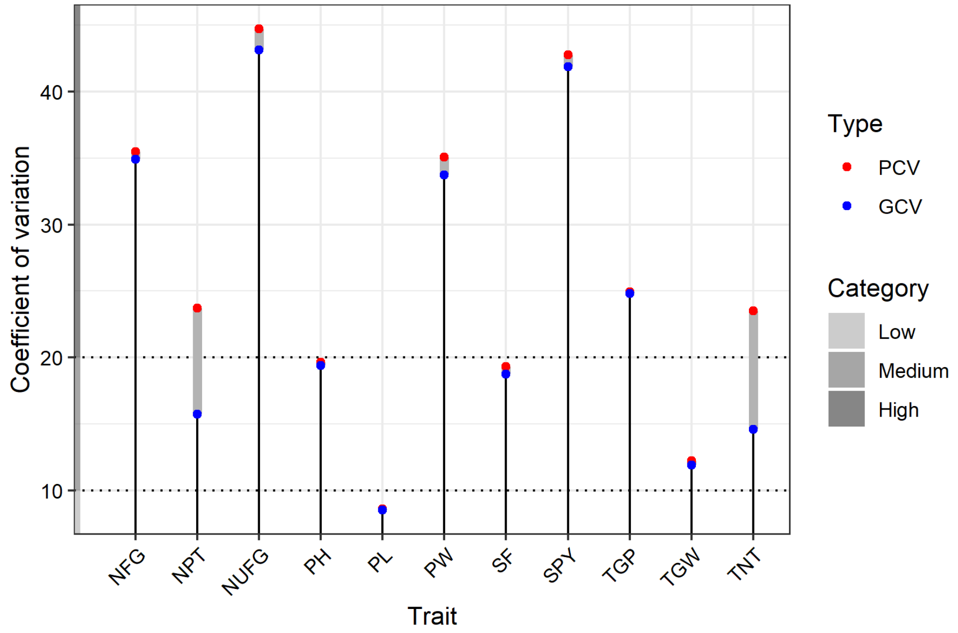
The results of genotypic (GCV) and phenotypic (PCV) coefficients of variation are presented in Table 3 and Fig. 1 that varied from high to moderate. For all traits higher PCV value was observed compared to GCV value, indicating the effect of environment. Greater difference between PCV and GCV values was recorded in Total number of tillers (TNT) followed by number of productive tillers (NPT) indicating higher influence of environment on these traits, resulting in low heritability values.However, panicle length, total grains per panicle, thousand grain weight recorded minimum variation between GCV and PCV values, indicating lesser influence of environment resulting in high heritability values (≥ 95 percent). Similar results were reported by Vijayakumariet al.[16] for panicle length and Gupta et al.[13] for thousand grain weight. Higher values of PCV and GCVwere observed for panicle weight(35.06,33.73) number of filled grains (35.50,34.92), number of unfilled grains(44.7343.12), total grains per panicle(24.93,24.79), and single plant yield(42.77,41.89). These results were consistent withDileep Kumaret al.[17],Sravaniet al.[18]for above traits;Borahet al.[19],Manojkumaret al.[14]for filled grains and total grains per panicle;Kujuret al. [20],Abdul Fiyaz et al.[21]for single plant yield. The higher values of PCV and GCV suggested the possibility of yield improvement through selection of these traits. High PCV but moderate GCV values were observed for total number of tillers (23.49,14.58) and number of productive tillers (23.72,15.73).Moderate values of PCV and GCV were observed for plant height (19.64,19.39), spikelet fertility (19.32,18.74) and TGW (12.23, 11.92). Similar results were observed by Sravaniet al.[18]for above three traits;vijayakumariet al.[16]for spikelet fertility;Abdul Fiyaz et al. [21]and Faysalet al.[22]for TGWsuggestinggreater influence of genetic factorson these traits and relatively less influence of the environment.Low values of PCV and GCV were observed for panicle length (8.61,8.52) similar findings were obtained byGnaneswariet al.[23];Yumkhaibamet al.[24].

Table 3.Magnitude of variability, heritability, and genetic advance for different characters of F$_2$ segregating population during *kharif*, 2022.

Trait	Mean	Min	Max	GCV (%)	PCV (%)	h^2(%)	GA (%)	GAM (at 50%)	Skewness	Kurtosis
PH	147.92	86.00	194.00	19.39	19.64	97.50	58.44	39.51	-0.70 **	2.11 **
PL	28.29	19.61	32.89	8.52	8.61	97.86	4.92	17.38	-0.71 **	3.66 ^{ns}
TNT	9.01	4.30	18.30	14.58	23.49	38.55	1.68	18.68	0.64 **	4.22 *
NPT	7.66	4.00	14.50	15.73	23.72	44.00	1.65	21.53	0.73 **	3.92 ^{ns}
PW	4.78	1.23	9.21	33.73	35.06	92.58	3.20	66.96	-0.07 ^{ns}	2.46 ^{ns}
NFG	171.75	48.60	347.60	34.92	35.50	96.79	121.73	70.88	0.11 ^{ns}	2.62 ^{ns}
NUFG	65.46	6.80	159.80	43.12	44.73	92.92	56.13	85.74	0.51 *	3.13 ^{ns}
TGP	237.21	105.40	384.90	24.79	24.93	98.88	120.64	50.86	-0.04 ^{ns}	2.33 ^{ns}
SF	71.09	32.02	96.77	18.74	19.32	94.06	26.65	37.49	-0.58 *	2.90 ^{ns}
TGW	24.94	12.45	39.75	11.92	12.23	94.85	5.97	23.94	0.25 ^{ns}	5.91 **
SPY	27.19	8.53	56.04	41.89	42.77	95.89	23.00	84.62	0.64 **	2.81 ^{ns}

GCV - Genotypic coefficient of variation; PCV – Phenotypic coefficient of variation; h ^{2} *– Heritability; GA – Genetic advance; GAM- Genetic advance as percent of mean; PH – Plant height (cm); PL – Panicle length (cm); TNT- Total number of tillers; NPT-Number of productive tillers; PW-Panicle weight (g); NFG-Number of filled grains; NUFG- No. of Unfilled grains; TGP- Total grains per panicle; SF – Spikelet fertility (%); TGW- Thousand grain weight (g) and SPY- Single plant yield (g).*

Fig 1: Phenotypic and Genotypic coefficients of variation for different traits in F_2 Population of Rice



3.3Heritability (h^2), and Genetic Advance (GA)

The coefficient of variation doesn't offer the full scope of heritable variation. When selection parameters heritability in conjunction with genetic advance are followed greater degree of accuracy is possible that are more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance Johnson et al.[11].

The traitsplant height, panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, spikelet fertility, thousand grain weight and single plant yield recorded high heritability (>60%) associated with high genetic advance as % of mean (>20) presented in Table 3 and Fig. 2,3. Similar results were obtained byDileep Kumaret al.[17], Sravaniet al.[18],vijayakumariet al.[16]for above traits;Manojkumaret al.[14]for panicle length, number of filled grains per panicle, total grains per panicle and test weight;Gupta et al. [13]for plant height, single plant yield; AbdulFiyaz et al.[21]for total grains per panicle and test weight resulting in no environmental influence on the expression and selection for improvement of such characters could be worthwhile.High heritability coupled with moderate genetic advance as % of mean was observed for panicle length earlier reported byLakshmi et al. [25],Gupta et al.[13],Borahet al.[19]showing greater role of non-additive gene action in their inheritance suggesting heterosis breeding for improving these traits. Moderate heritability and genetic advance as % of mean was observed for total number of tillers per plant which is in conformity with the results ofSingh et al.[26].Moderate heritability associated with high genetic advance as % of mean was observed for number of productive tillers per plantindicating the presence of both additive and non-additive gene effects and considerable effect of the environment. Overall high GCV and PCV coupled with high heritability and high genetic advance as % of mean was recorded for panicle weight, number of filled grains, number of unfilled grains, total grains per panicle, and single plant yield. Similar findings were reported byShivani et al. [27], Bagudam et al. [28],Manojkumar et al.[14]for filled grains per panicle, total grains per panicle;Bhargava et al. [29]for total grains per panicle; suggesting significant amount of variability with predominance of additive type of gene action. Hence, direct phenotypic selection would be effective for improvement of these traits even in early generations.

Fig 2. Heritability (h^2) for different traits in F_2 Population of Rice

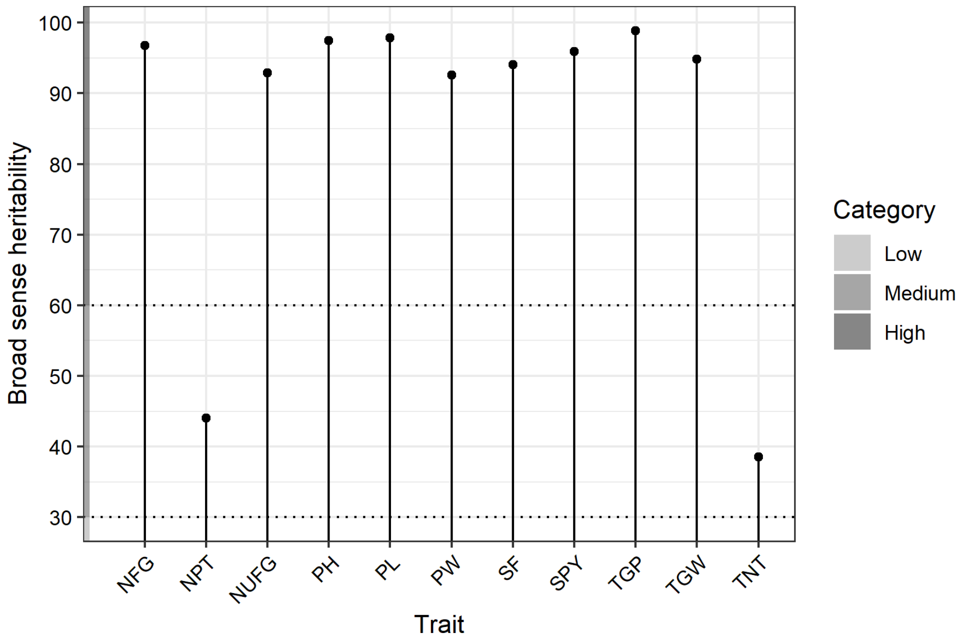
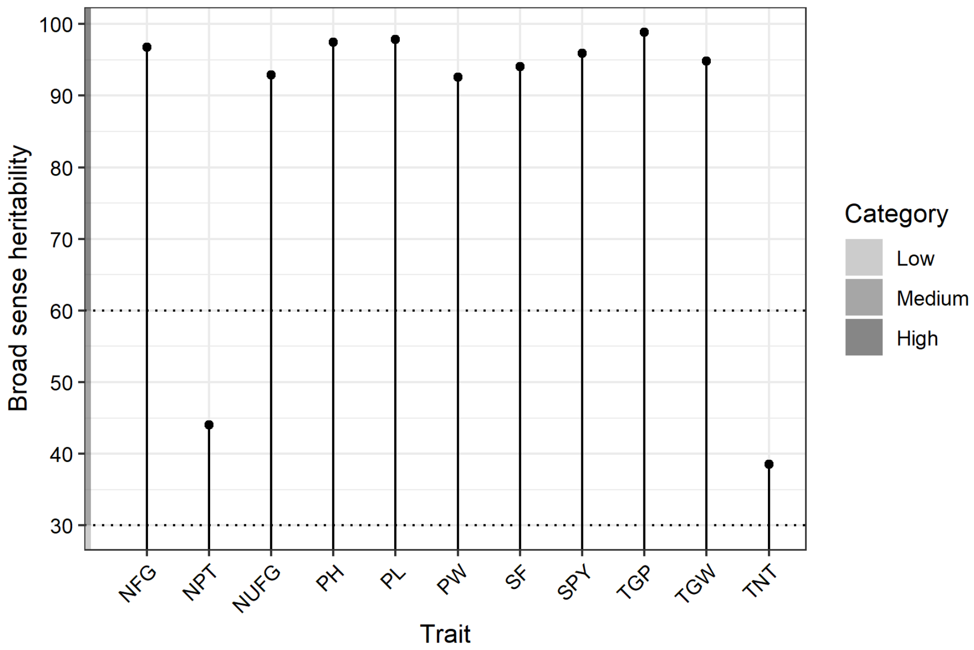


Fig 3. Genetic advance over mean for different traits in F_2 Population of Rice



4. CONCLUSION

The overall result showed the presence of adequate variability in the F_2 segregating population studied that could be effectively manipulated using appropriate breeding techniques and program to develop improved varieties. High GCV, PCV, heritability and genetic advance were observed in most of the traits, indicating the predominance of additive gene action and the possibility of direct phenotypic selection through these traits even in early generations.

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