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Genetic variability studies for yield and yield components in rice (*Oryza sativa* L.)

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Abstract

Rice is one of the globe's main cereal crops, feeding hundreds of individuals and serving as a staple food crop for more than two-thirds of India's population. Any crop improvement programme must depend on germplasm owned by numerous research organizations or institutes. To meet the demand, high yielding varieties with good quality traits must be created. The present investigation material consists of 57 rice germplasm accessions including seven checks has been planted in Randomized Block Design, within two replications. Analysis of Variance (ANOVA) indicates that there is a lot of variability within the genotypes. The higher percentage of the genotypic and phenotypic coefficient of variation were obtained for the number of unfilled grains per panicle, number of filled grains per panicle, biological yield, harvest index, the number of effective tillers per plant. The highest heritability found in plant height, the number of filled grains per panicle, biological yield, number of unfilled grains per panicle, 100 seed weight, spikelet fertility percent, panicle length, paddy length, days to 50% flowering, harvest index, suggesting that this features passed down from parents easily in hybridization programme.

Keywords: Morphological, hybridization, germplasm accessions, genetic variability, genotypes, phenotypes

Introduction

Plant genetic resources are the most important component of any breeding program because they serve as the raw material for them. Germplasm consists of tremendous genetic variability and serves as a store house of elite that can be future exploited for enriching the rice cultivars with potential genes of desirable traits. To separate one genotype from the other and to provide details on the degree of variability and other genetic parameters in terms of yield and other quality characters, germplasm collection and characterization are critical. Agro-morphological characterization provides the mark of identification and is an important tool for differentiating one genotype or variety from another. The germplasm of rice provides ample genetic diversity and treasury of useful genes. It is a rich reservoir of essential genes that can be used for crop enhancement by plant breeders (Yadav *et al.*, 2013) [9]. Any character's performance is determined by the type of variability found in the character's gene pool. As a result, a breeder's understanding of the level of diversity present in a crop species, gene pool is critical for launching a successful plant breeding program. Since a sound crop improvement programme depends on the magnitude of variability in the base population, genetic variability analyses are essential in the selection of parents for hybridization (Singh and Chaudhary, 1982). Any crop improvement programme must first evaluate and characterize a large number of native genotypes that are appropriate in one or more ways.

Methods and Materials

The present investigation was carried out *kharif* 2020 at Research Farm of Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh, India. The experimental materials comprised 57 lines of germplasm accessions of rice including 7 checks namely Dagad Deshi, RRF127, RRF140, DRR Dhan 42, MTU1010, Annada, and Swarna received from DBT Network Rice Project. The experiment material *i.e.*, 50 rice germplasm accession including seven checks were grown in a Randomized Block Design (RBD) with two replications. Row-to-row and plant-to-plant distances were 20 cm and 15 cm. The recommended agronomical practices were followed to raise good crop in the season. Observations were recorded on five randomly chosen plants of each accession for yield and yield contributing traits in rice.

Result and Discussions

The experimental material consists of 50 rice germplasm and 7 checks namely Dagad Deshi, RRF127, RRF140, DRR Dhan 42, MTU1010, Annada, and Swarna.

The experimental was carried out in Randomized Block Design with an objective of Genetic variability studies for yield and yield components in rice (*Oryza sativa* L.)

Analysis of variance

An analysis of variance for yield and yield attributing characteristics in 57 rice germplasm. The mean sum of

squared due to genotypes was highly significant (1% level of significance) for all 57 characters. This indicates that there is a lot of variability among the 57 rice genotypes for all of the traits. For quantitative traits, highest mean performance for plant height (163.9) followed by number of filled grains per panicle (123).

Table 1: Analysis of variation for yield and yield attributing character

S. No	Source of Variance	Mean Sum of Squares		
		Replication	Treatment	Error
	Degree of freedom	1	56	56
1	Days to 50% flowering	9.55	32.51**	3.92
2	Plant height (cm)	41.22	1328.32**	11.14
3	Panicle length (cm)	3.07	15.59**	1.14
4	No. Of effective tillers per plant	1.72	3.38**	0.86
5	No of filled grains per panicle	14.04	2870.46**	54.99
6	No. Of unfilled grains per panicle	18.56	764.59**	33.56
7	Spikelet fertility percent (%)	0.89	148.37**	8.63
8	100 seed weight(g)	0.01	0.37**	0.02
9	Grain yield per plant(g)	0.37	11.11**	4.74
10	Biological yield (g)	26.54	252.65**	8.57
11	Harvest Index (%)	66.49	322.64**	55.19
12	Paddy length (mm)	0.01	0.82**	0.07
13	Paddy breadth (mm)	0.02	0.13**	0.02
14	Paddy length breadth ratio	0.04	0.34**	0.05
15	Brown Rice length (mm)	0.15	0.45**	0.09
16	Brown Rice breadth (mm)	0.02	0.10**	0.03
17	Brown Rice length breadth ratio	0.04	0.30**	0.07

Note:-**Significant at 1% level of probability

Genotypic and Phenotypic Coefficient of Variance: The RBD analysis offers details on variance, *i.e.* genotypic variance (GCV) and phenotypic variance (PCV). The phenotypic coefficient of variation (PCV) was higher in percentage than the equivalent genotypic coefficient of variation (GCV) for all of the quantitative features evaluated in the experiment, although there was strong consistency between GCV and PCV for all of the features. The existence of a large genotypic coefficient of variation suggests that the population has a lot of genetic variability. The characters viz.,

number of unfilled grains per panicle (43.17%), number of filled grains per panicle (30.50%), biological yield (27.69%), harvest index (26.09%), the number of effective tillers per plant (22.82%), 100 seed weight (20.87%) have high genotypic and phenotypic coefficient of variation that showed the presence of considerable amount of variability for these characters for all genotypes. Similar findings were reported by Limbani *et al.* (2017) [4], Prasad *et al.* (2017) [5] and Rashmi *et al.* (2017) [6], Iqbal *et al.* (2018) [2].

Table 1: Genetic parameters for various yield and yield related traits

Characters	Mean	Range		CV%	Coefficient of variation		h^2 (bs) (%)	GA	GA as % of mean
		Minimum	Maximum		GCV (%)	PCV (%)			
Days to 50% flowering	101.1	94.5	111.0	1.96	3.73	4.22	78.44	6.89	6.82
Plant height (cm)	163.9	88.5	190.5	2.03	15.65	15.79	98.33	52.42	31.98
Panicle length (cm)	26.7	19.5	32.4	4.00	10.06	10.82	86.38	5.14	19.26
No. Of effective tillers/Plant	4.9	3.0	10	18.90	22.82	29.63	59.32	1.77	36.22
No of filled grains/panicle	123.0	56.0	222.5	6.03	30.50	31.09	96.24	75.82	61.65
No. Of unfilled grains/ panicle	44.3	10.5	90.5	13.08	43.17	45.11	91.59	37.69	85.12
Spikelet fertility percent (%)	73.7	56.8	93.1	3.98	11.34	12.02	88.99	16.24	22.04
100 seed weight(g)	2.0	1.1	2.6	7.01	20.87	22.12	89.04	0.81	40.58
Grain yield/plant (g)	16.5	12.7	22.2	13.19	10.81	17.06	40.18	2.33	14.12
Biological yield/plant (g)	39.9	23.7	69.6	7.33	27.69	28.64	93.43	21.99	55.13
Harvest Index (%)	44.3	22.4	69.7	16.75	26.09	31.01	70.81	20.05	45.24
Paddy length (mm)	8.4	6.0	10.0	3.32	7.17	7.90	82.27	1.12	13.39
Paddy breadth (mm)	2.5	1.8	3.3	6.53	9.05	11.16	65.77	0.38	15.12
Paddy L/B ratio	3.4	2.6	4.4	7.17	11.13	13.36	69.44	0.64	19.12
Brown Rice length (mm)	6.2	4.5	7.2	4.97	6.77	8.40	64.92	0.69	11.24
Brown Rice breadth (mm)	2.1	1.7	2.8	8.75	8.40	12.13	47.95	0.25	11.98
Brown Rice L/B ratio	3.0	2.1	3.7	9.61	11.35	14.80	58.89	0.53	17.95

Heritability and Genetic Advance: Heritability means a measurement of that degree of phenotypic variation produced by the effect of gene action. Genetic advance is defined as an

increase in the average genotypic value of chosen plants overhead the hereditary population. The characters viz., plant height (98.33%), number of filled grains per panicle

(96.24%), biological yield (93.43%), 100 seed weight (89.04%), spikelet fertility percent (88.99%), and harvest index (70.81%) show high heritability coupled with high genetic advance. It indicates that heritability is due to additive gene action. The value with high heritability with moderate genetic advance were recorded for characters *i.e.*, panicle length (86.38%), paddy length (82.27%), paddy length breadth ratio (69.44%), paddy breadth (65.77%) and brown rice length (64.92%) suggesting control of expression by both additive and non-additive gene action in the development of the earlier features, heterosis breeding can be useful. Similar findings were also reported by Sharma and Bhuyan (2004) [7], Das *et al.* (2005) [1], Kumar *et al.* (2013) [3], Iqbal *et al.* (2018) [2].

Conclusion

The rice genotypes have a lot of variability, according to an analysis of variance. It demonstrated that each character had enough variation. The study PCV is higher than GCV. The high percentage of the genotypic coefficient of variation and phenotypic coefficient of variation was obtained for the number of filled grains per panicle and biological yield. The existence of a large genotypic coefficient of variation suggesting that the population has a lot of genetic variability and provides opportunities for genetic enhancement through trait selection. The high heritability found in plant height, the number of filled grains per panicle and biological yield suggesting that heritability is the heritable component, and it is a features passed down from parents to offspring. The largest genetic advance as percentage of mean was found for the number of filled grains per panicle, biological yield and harvest index suggesting that these traits are governed by additive gene effects, and that direct selection for these fixable features for the production of a beneficial rice plant.

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