Assessment of Genetic Variability and Transmissibility Index in Rice Genotypes (*Oryza sativa* L.)

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Original Research Article

ABSTRACT

Aim: To assess the Genetic Variability among the accession/ genotype and its contributing traits.
Methodology: A field experiment was conducted using 35 genotypes including 2 checks of rice during the season of *kharif,* 2017, at the Field Experimental Centre, Department of Genetics and Plant Breeding, SHUATS, Prayagraj, Uttar Pradesh to evaluate genetic variation and heritability of yield and related traits. The experiment was designed with a randomized block design (RBD) with three replications. Analysis of variance revealed significant difference among the genotypes for all traits indicating existence of genetic variability among the accessions.
Results: Highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for Spikelet's per panicle, tillers per hill, panicle per hill and grain filling. High heritability in broad sense was obtained for days to 50% flowering (99.6%), days to maturity (98.7%), test weight (97.9%), harvest index (96.9%) and grain yield per hill (96.6%) which is indicating the high heritable portion of variation. High to medium estimate of heritability in genetic advance were obtained for grain yield (38.51), spikelet's/ panicle (37.94), panicle/ hill (36.97) were

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indicating the roles of additive gene action and good scope of selection using their phenotype performance.

Interpretation: Considering, all of these characters, spikelet's per panicle, days to 50% flowering and days to maturity were important yield related traits and could be used for selection in future rice breeding programme.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is most widely cultivated cereal in the world, after wheat, and is a staple food for more than half of the world's population, especially in Asia. Rice is mainly cultivated by small farmers on areas of less than one hectare. Rice is vital for the nutrition of much of the population in Asia, as well as in Latin America and the Caribbean and in Africa; it is central to the food security of over half the world population [1]. Developing countries account for 95% of the total production, where as China and India alone contributing for nearly half of global output. Global rice production and trade in 2019-20 are forecasted to be decrease by 0.8% and 3.1% over previous year, respectively [2]. In 2019, global paddy production is estimated to be 516.8 million tonnes [3]. In India, overall paddy output is estimated at record 117.94 million tonnes of rice during 2019-20. It is 10.14 million tonnes higher than the five years' average production of 107.80 million tones [4]. The world population is expected to reach 8 billion by 2030 and necessitating a 50 % increase in rice production to meet the growing demand [5]. Rice productivity level is low compared to the productivity levels of many others countries in the world. It is grown in a diverse soil and climatic conditions, almost every state in the country however the major 5 states in rice production are West Bengal, Uttar Pradesh, Andhra Pradesh, Punjab and Tamil Nadu. Hybrid rice has higher yield potential over inbred varieties [6]. As a result, hybrid rice technology is projected to play an important role in increasing the rice production. Eastern India states attribute more than 80% of the total hybrid rice area. Grain quality characters are observed to play vital role for genetic divergence [7]. Besides from grain quality characters, agro-morphological characters like plant height, weight of panicle, 1000-seed weight, and panicle length also contribute towards genetic divergence [8]. Higher yield of hybrid rice is a complex result of genotype and environment interaction [9].

Genetic variability is a requirement for any crop improvement programme, the large spectrum genetic variability found in the gene pool consisting of indigenous and elite germplasm provides more opportunities for better selection. The plant breeder would benefit from knowing the nature and degree of genetic divergence in order to select the best parents for the breeding programme. Heritability used for measure the amount genetic improvement that will be passed to next generation [10]. Heritability combined with genetic advancement, and it will be more powerful in predicting genetic gain than heritability alone [11]. In addition, knowledge about the association of characters with themselves and grain yield is also important for direct and indirect selection of traits which contributes to yield [1]. Furthermore, understanding of the relationship between characteristics and grain yield is vital for direct and indirect selection of features that contribute to yield [1]. In view of this, hybrid and high yielding rice varieties has been taken as the components under the present study with the aim to identify the suitable phenotypic characters of high yielding rice genotypes.

2. MATERIALS AND METHODS

2.1 Experimental Design and Trial Management

A total 35 genotypes along with two check varieties were used in study. Genotypes were collected from Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj and ICAR-Indian Institute of Rice Research, Hyderabad as represented in Table 1. These 35 genotypes were sown during *kharif* 2017 in randomized block design with three replications and each genotype were sown in rows spaced 20cm apart and within the rows plant to plant distance was kept 15cm. The recommended dose of fertilizers @ 120: 60: 40 N: P: K kg per ha was applied. The half dose of nitrogen was applied as basal dose and full dose of P_2O_5 and K_2O applied at the time of transplanting. The rest of the nitrogen was top dressed in two split doses at the time of

maximum tillering stage i.e. 25 days after the transplanting and between panicle initiation and boot leaf stage i.e. 53 days after transplanting. Observation were recorded on randomly five selected plants from each replication *viz.,* days to 50% flowering, plant height (cm), flag leaf length (cm), flag leaf width (cm), number of tiller per plant, number of panicles per plant, panicle length (cm), number of spikelet's per Panicle, biological yield per plant (g), days to maturity, harvest index (%), test weight (g), grain yield per plant (g).

2.2 Statistical Analysis

Statistical analyses were done using the Statistical IndoStat Software, the variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme [12] PCV and GCV were calculated by the formula given by Burton [13], heritability in broad sense (h^2) by Burton and De Vane [14] and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson et al.*,* [15].

3. RESULTS AND DISCUSSION

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. Analysis of variances revealed that the mean sum of squares due to genotypes showed highly significant for all the 13 quantitative characters. Significant genetic variation in various component characters exhibited by the genotypes indicated these characters might be effective. The results from analysis of variance

among 35 rice (*Oryza sativa* L.) genotypes for 13 quantitative characters are presented in Table 2. In other words the performance of the genotypes with respect to these characters was statistically different indicating sample scope for selection of different characters for rice improvement. These findings were in accordance with the findings of Panigrahi et al.*,* [16] Bornare et al., [17] and Christian et al., [18].

Estimates of genotypic ($\sigma^2 g$) and phenotypic variance ($\sigma^2 p$) were obtained for different characters and are presented in Table 3. A close perusal estimates of variance revealed that phenotypic variance was higher than the genotypic variance among all the component characters. Hence genotypic and phenotypic variances both are more significant to study the association between Grain yield and its component characters. A wide range of genotypic and phenotypic variance was observed for the characters like number of spikelet's per panicle (1260.01 and 1499.26), plant height (106.39 and 120.67), days to maturity (92.57 and 93.77), days to 50% flowering (92.04 and 92.39), biological yield per hill (55.47 and 96.10), grain yield per hill (34.80 and 36.04), harvest index (21.17 and 21.84), flag leaf length (15.28 and 20.18), number of tiller per hill (11.03 and 14.16), test weight (10.27 and 10.49), whereas, number of panicle per hill (9.15 and 10.66) and panicle length (4.75 and 5.77) showed narrow range of variance. The least genotypic and phenotypic variance was observed in flag leaf width (0.03 and 0.04).

Table 1. List of 35 rice genotypes used in present study

Sl.No.	Name of Entry	Sl.No.	Name of Entry
1	MLT-3501	18	MLT-3521
2	MLT-3502	19	IRRI-25
3	MLT-3503	20	IRRI-17
4	MLT-3504	21	IRRI-4
5	MLT-3505	22	HHZ 3-SAL6-Y1-Y1
6	MLT-3506	23	IR-11A 257
7	MLT-3507	24	IR-10N 276
8	MLT-3508	25	HHZ 4 SAL12- LI1-LI1
9	MLT-3509	26	PR-133
10	MLT-3510	27	IR-11N 187
11	MLT-3511	28	IR-118 304
12	MLT-3512	29	SHIATS DHAN-1
13	MLT-3514	30	SHIATS DHAN -2
14	MLT-3515	31	SHIATS DHAN-3
15	MLT-3516	32	SHIATS DHAN-4
16	MLT-3518	33	SHIATS DHAN-5
17	MLT-3520	34	MTU-1001 (CHECK)
		35	PHB-71(HYBRID CHECK)

Table 2. Analysis of variance for 13 characters in 35 rice genotypes during *Kharif*, 2017

Source of variation	d.f.	Mean Sum of Squares												
		DF	PH	FLL	FLW	T/H	P/H	PL	S/P	DM	BY	HI	TW	GY/H
Replication	2	0.3627	32.63	12.19	0.01	0.8	3.98	0.41	11.73	0.82	33.31	0.2	0.04	0.0002
Treatment	34	276.48**	333.45**	50.75**	0.12**	36.24**	28.96**	15.28**	4019.28**	278.92**	207.05**	64.18**	31.05**	105.63**
Error	68	0.35	14.27	4.89	0.006	3.12	1.5	1.02	239.25	1.2	40.63	0.67	0.21	1.24

* Significant at 5% and ** Significant at 1 % level of significance respectively d.f. degree of freedom, DF Days to 50% Flowering, PH Plant Height, FLL Flag Leaf Length, FLW Flag Leaf Width, T/H Tillers per, hill, P/H Panicles per hill, PL panicle Length, S/P Spikelets per Panicle, DM Days to Maturity, BY Biological Yield, HI Harvest index, TW Test Weight and GY/H Grain Yield per hill

Table 3. Genetic parameters for 13 quantitative characters in 35 rice genotypes

S. No.	Characters	$\sigma^2 g$	$\sigma^2 p$	Coefficient of variation		h^2	GA	GA as % of mean
				GCV	PCV			
1	Days to 50% Flowering	92.04	92.39	9.33	9.35	99.6	19.72	19.18
2	Plant Height	106.39	120.67	9.46	10.07	88.2	19.95	18.29
3	Flag Leaf Length	15.28	20.18	10.7	12.29	75.7	7.01	19.18
4	Flag Leaf Width	0.03	0.04	13.59	14.72	85.2	0.37	25.85
5	Tillers/ hill	11.03	14.16	19.37	21.4	77.9	6.04	13.35
6	Panicles/ hill	9.15	10.66	18.89	20.91	85.8	5.77	36.97
7	Panicle Length	4.75	5.77	8.22	9.06	82.3	4.07	15.36
8	Spikelet's/ Panicle	1260	1499.3	24.09	25.1	84	67.03	37.94
9	Days to Maturity	92.57	93.77	7.24	7.29	98.7	19.69	14.82
10	Biological Yield/ hill	55.47	96.1	11.69	11.75	57.7	11.65	15.17
11	Test Weight	10.27	10.49	15.49	15.66	97.9	6.53	31.57
12	Harvest Index	21.17	21.84	11.45	11.63	96.9	9.33	23.23
13	Grain Yield/ hill	34.8	36.04	19.02	19.36	96.6	11.94	38.51

$\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance, h^2 = Heritability. GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation GA= Genetic advance
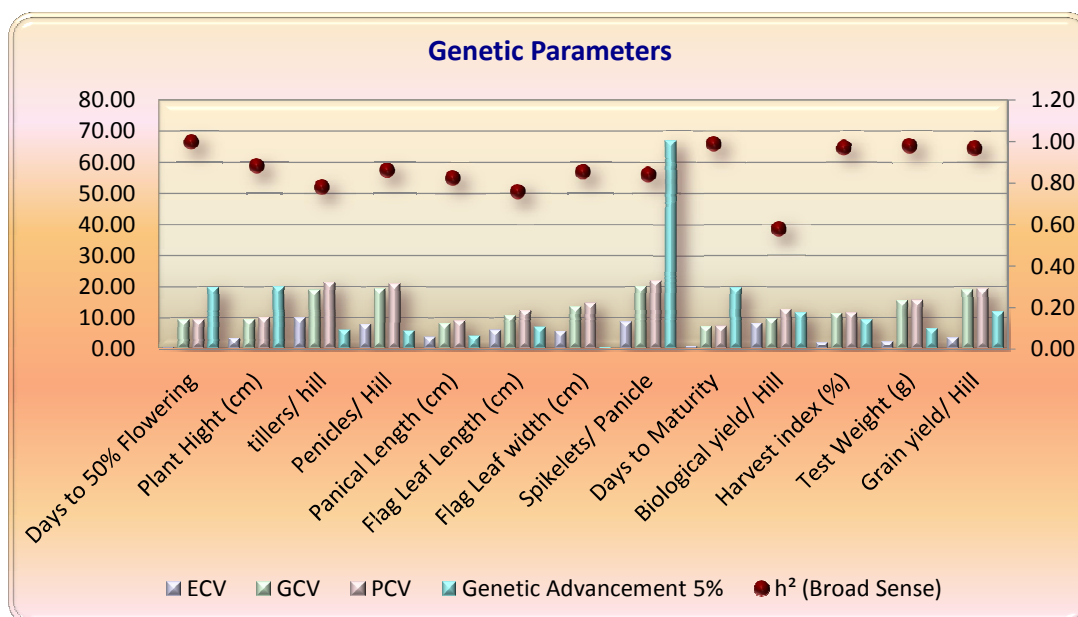
Fig. 1. Histogram depicting Environmental coefficient of variation, genotypic coefficient of variation, phenotypic coefficient of variation, Genetic advance and Heritability for 13 quantitative characters of rice genotypes

In crop of rice, the phenotypic variance was higher than the genotypic variance for yield and all yield attributing characters which indicates there is influence of environmental factors on these traits. Similar findings were reported by Gangashetty et al., [19], for grain yield per plant, plant height, number of spikelet's per panicles and biological yield.

The studies on phenotypic coefficient of variance and genotypic coefficient of variance indicates that the presence of high amount of variation and role of the environment on the expression of these traits. A wide range of phenotypic coefficient of variance (PCV) was observed for different traits. The wide range of PCV was observed for the character ranging from 7.29 to 25.1 for days to maturity. Higher PCV was recorded for spikelet's per panicle (25.10), followed by number of tillers per hill (21.40), panicle per hill (20.91). Moderate estimates of PCV were recorded for grain yield per hill (19.36), test weight (15.66), flag leaf width (14.72), biological yield per hill (11.75) and harvest index (11. 63). Lowest PCV was recorded for days to maturity (7.29) followed by panicle length (9.06), days to 50% flowering (9.35), and plant height (10.07). Similar findings were reported by Singh et al. [20] for grain yield per hill and spikelet's in rice.

A genotypic coefficient of variance (GCV) was observed for different traits. The wide range of GCV was observed for the character ranging from 7.24 to 24.9 for days to maturity. Higher GCV was recorded for spikelet's per panicle (24.09), followed by panicle per hill (18.89), grain yield per hill (19.02), and tillers per hill (19.37). Moderate estimates of genotypic coefficient of variance were recorded for test weight (15.49), flag leaf width (13.59) and harvest index (11.45). Lowest GCV was recorded for days to maturity (7.24) followed by days to 50% flowering (9.33), plant height (9.46), biological yield per hill (11.69),flag leaf length (10.70).Similar findings were reported by Kumar [21], and Singh et al., [20,22], for grain yield per plant and spikelets per plant [23].

There was a good corresponding between genotypic and phenotypic coefficient of variance for all the quantitative characters studied. The magnitude of phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV) for all the quantitative characters.

The genotypic coefficient of variance is most important and useful in the measurement of range and genetic variability for a specific character; it also provides a means to compare the genetic variability for the quantitative traits. In

the present investigation, the highest genotypic coefficient of variation accompanied with higher phenotypic coefficient of variation for number of spikelet's per panicle, tillers per hill, panicle per hill, grain yield per hill suggest enough genetic variability present among 35 rice genotypes. These findings are similar with the findings of Devi et al., [24], Dhurai et al., [25], Dwivedi et al., [26], Idris et al. [27], Guru et al., [28], Iqbal et al., [29], Islam et al., [8], Jambhulka et al., [30] and Kalpana et al., [9].

Heritability in broad sense according to Lush [31], is the ratio of total genotypic variance to phenotypic variance expressed in percentage. The estimates of heritability are more advantageous when expressed in terms of genetic advance. Johnson et al., [15] suggested that without genetic advance the estimates of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability. The estimates of heritability ranged from 57.7 % (Biological yield per hill) to 99.6% (Days to 50% flowering). High heritability (> 80%) was observed for days to 50% flowering (99.6%), Days to Maturity (98.7%), test weight (97.9%), harvest index (96.9%), Grain yield per hill(96.6%), Plant height (88.2%), Panicles per hill (85.8%), Flag leaf width (85.2%), spikelet's per panicle (84.0%), and panicle length (82.3%). Moderate heritability from 50 to 80 % was observed for biological yield (57.7%), flag leaf length (75.7%), and tillers per hill (77.9%).

Here, the genetic advance as percent mean ranged from 13.35 to 38.51. High genetic advance as percent mean was observed for grain yield per hill (38.51) followed by spikelet's per panicle (37.94), panicles per plant (36.97), and test weight (31.57).

In the present study, traits like days to 50% flowering, days to maturity, test weight, harvest index, grain yield per hill, plant height, panicles per hill, flag leaf width, spikelet's per panicle and panicle length depicted high estimates of heritability in broad sense. Therefore, selection from these traits will be worthful for further rice improvement programme. These results are in consistence with the findings of Borbara et al., [32], Yadav [33], Panwar [34], Karim et al., [35] and Fiyaz et al., [36].

In the present study, high estimates of heritability coupled with moderate to low values of genetic advance as percent mean was observed for

days to 50 % flowering (99.6 and 19.72), spikelets per panicle (84 and 67.03), grain yield per hill (96 and 11.94), tillers per plant (77.9 and 6.04), and panicles per plant (85.8 and 5.77) respectively suggesting that there was preponderance of additive gene action for the expression of these characters. Hence, selection of these characters can bring enhancement in rice production and productivity. Above results, in respect to heritability and genetic advance are similar in the agreement with the earlier reports on rice by Ketan et al., [37], Kishore [38], Konate et al., [39], Kumar et al., [40], Mamata et al., [41], Tomar et al., [42] and Maurya et al.,[43].

4. CONCLUSION

Based on the findings of the present investigation, it could be concluded that sufficient genetic variation existed in the present set of materials and the varieties could be used in future breeding programmes for improvements in this crop. Further, the elite rice IR-11N 187, IR-11A 257, SHIATS DHAN-2 and SHIATS DHAN-1 and the hybrids MLT-3502, MLT-3505 and MLT 3503 being stable for most of the yield attributing traits and good for grain yield could be recommended to farmers for cultivation after further testing and evaluation. Analysis of variance indicated highly significant difference among the genotypes for all the traits. This indicates that there is an adequate scope for selection of promising lines from the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environment influence affecting the phenotypes. Wide range of phenotypic (VP or $\sigma^2 p$) and genotypic variance (VG or $\sigma^2 g$) were observed in the experimental material for all the traits studied. The highest variability (Vp and Vg) was recorded for number of spikelet's per panicle (1499.26 and 1260.01) followed by plant height (120.67 and 106.39). An estimate of GCV and PCV revealed that phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters, which indicate the presence of environmental effect on the expression of character studied. Higher difference between GCV and PCV were depicted for tillers per hill, biological yield per hill, panicles per hill, and flag leaf length, respectively. High heritability coupled with high genetic advance in the present set of genotypes and elite rice that was indicating predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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