

Analysis of Rice (*Oryza sativa* L.) Accessions Genetic Variability Related to Yield and Its Components

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Authors' contributions

This work was carried out in collaboration among all the authors. Authors ARK, SKS, Jayasudha and HSV designed the study and wrote the protocol. Author ARK, KSM and KM performed the statistical analysis and wrote the first draft of manuscript. Authors DKS, AS and PKM managed the further analyses of the study, improved and managed the literature searches the manuscript. All authors read and approved the final manuscript.

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ABSTRACT

This experiment was conducted to study the variability parameters of forty rice genotypes to evaluate genetic parameters i.e., Genotypic variability coefficient (GVC), Phenotypic variability coefficient (PVC), Heritability (H) and mean percent of Genetic advance (MGA) for nine different yield and yield-contributing traits at Agriculture Research Farm, Banaras Hindu University, Varanasi during *Kharif*-2018. The data were collected for nine yield and yield attributing traits subjected to alpha lattice design and analyzed in R-software. The PCV magnitude was found slightly higher than GCV indicating that this trait is less influenced by environmental factors. The highest GCV and PCV are found for yield (37.70 % to 38.27% respectively) followed by number of tillers per plant number of effective tillers per plant (GCV: 19.47%, PCV: 21.04%) and plant height (GCV: 14.99, PCV: 16.40). high heritability (>70%) coupled with high percent of mean genetic advance (MGA) (>20%) were recorded for days to fifty percent flowering, days to maturity, plant height, number of effective tillers, panicle length, spikelet fertility, test weight, grain yield per plant and harvest index indicating that the simple selection will be effective for this trait improvement.

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1. INTRODUCTION

Rice (*Oryza Sativa* L.) is a staple food crop for more than 2.7 billion people worldwide feeding half of the world's population [1,2] whereas, 90 % of rice is grown and consumed in Asia independently [3]. It is the second most important cereal in the world. With 60-70% calories rice is energy source for more than 2 billion people. Also, most farming communities depend on rice as the main livelihood source. This crop originated in South East Asia and discovered 24 species including two cultivated *Oryza sativa* L and *Oryza glaberrima* L. It is well found in different agro-ecological conditions with diverse adaptability. In Asia, *Oryza sativa* L. most preferred rice for cooking purposes. Increasing the yield of rice grains per unit area is essential for ensuring food security because of the shrinking amount of land available for farming and the rising world population, especially in growing Asia-Pacific nations like China and India (Yin et al. 2021). Rising temperature is one of the most important challenge in tropical climate [4].

Before beginning any breeding programme to accomplish the aim, it is crucial and a prerequisite to have knowledge of the genetic variability, heritability, and genetic progress of features under improvement is a major prerequisite for yield improvement programmes [5]. The main objective for this crop is genetic improvement in terms of grain yield and harvest index. But yield is a complex characteristic that is influenced by a number of morpho-physiological characteristics [6]. Variability study gives prerequisite vision for selection of better genotype over the existing cultivar in that locality for yield and its attributing traits. Although there is a large variation present in rice (*Oryza sativa*), highest yield is plateauing in very popular varieties. So, exposing present variation in rice to study yield and yield attributing traits helps researchers architecting new location specific as well as economic trait-specific varieties. The distinguished genotype can be further used as a donor for important traits or used as a recipient after vanishing the undesirable genes to breed a new variety. Morphological traits are governed by quantitative genes influenced by the environment. Grain yield in rice is highly influenced by a number of tillers, panicle length, grains per panicle and grain size, to conclude best output of data analysis through various important measures. Thus, understanding how

genes control yield and the qualities that contribute to it is crucial for developing an effective selection strategy for choosing a more desirable genotype. Heritability is a reliable indicator of how parents transmit their character to their offspring (Falconer, 1981). Heritability estimations assist plant breeders in choosing superior genotypes from a variety of genetic groups. However high genetic progress presence in a character is not requirement for high heritability (Johnson, et. al. 1955). Genetic gain measure under selection constitutes progress. Heritability in combination with high genetic advance helps in understanding how the environmental factors affect the genotype's expression and traits reliability. Additionally, the analysis of genetic heritability and genetic advance would offer reasonable estimations for choosing an appropriate breeding programme for this crop.

Hence, this experiment aimed at studying the important genetic variability of rice genotypes.

2. MATERIALS AND METHODS

2.1 Rice Genotypes and Experimental Design

The present experiment was conducted at Agricultural Research Farm, Banaras Hindu University, Varanasi, and Uttar Pradesh, India. It consisted of 40 rice genotypes including two checks cultivated following alpha lattice design with three replications and 4 blocks with 15 x 20 cm spacing. These genotypes grains were sown in June 2018 and seedlings were transplanted after twenty-five days in puddled soil. The fertilizers, nitrogen (N), phosphorus (P) and potassium (K) were applied to the experimental plot as per the recommended doses per hectare (NPK ratio is 5:3:2). The standard agronomic practices were adopted for normal crop growth.

2.2 Data Collection

Data were collected for nine morphological traits: days to 50 % flowering (DFF), days to maturity time (DM), Plant height (PH), Number of effective tillers (NET), Panicle length (PanLght), Spikelet fertility (SF), test weight (TW), Grain yield per plant (GYPP), Harvest Index (HI). DFF and DM were recorded on plot basis while five plants were randomly selected from each plot for data collection of remaining traits.

2.3 Statistical Analysis

We used the Analysis of Variance (ANOVA) to compare the rice studied genotypes for the yield and yield attributes were done through F-test in R software. The phenotypic and genotypic variance components and coefficients of phenotypic and genotypic of variation to compare the variation among traits were calculated by the methods suggested by Lush (1940) and Chaudhary and Prasad (1968). Genotypic variation coefficient (GVC), phenotypic variation coefficient (PVC), heritability in a broad sense (h^2b), genetic advance (GA), genetic advance as percentage of means (GAM) was estimated in R software. Traits measures were calculated following formulae (Johnson HW, 1955) [7].

$$\text{Genotypic variance } (\sigma^2g) = (\text{MSg} - \text{MSe})/r$$

$$\text{Phenotypic Variance } (\sigma^2p) = \sigma^2g + (\sigma^2e)/r$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2g}}{X} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2p}}{X} \times 100$$

$$\text{Heritability } (h^2b) = (\sigma^2g/\sigma^2p) \times 100$$

$$\text{Genetic Advance (GA)} = (k) \times (\sigma_p) \times (h^2b)$$

$$\text{Genetic Advance as a percentage of Mean (GAM)} = (\text{GA}/X) \times 100$$

Where, MSg=mean square of genotype, MSe=mean square of error, r=number of replication, σ^2e =environmental variance, X=grand mean, k=intensity of selection at 5% (2.06)

3. RESULTS AND DISCUSSION

3.1 Mean Performance and ANOVA

Means of the forty genotypes for nine yield-attributing traits are shown in Table 1 and represented by box plot (Fig. 1).

The ANOVA results revealed that the mean sum of square due to studied accessions differed significantly for all the characters under study (Table 2). This implied the possibility of exploiting these genotypes in studying the inheritance of the traits and also their inclusion in breeding

programmes for achieving further improvement. Patel et al. (2014), Purusothoaman & Geetha [8], Nilanjaya et al. (2015), Rama Krishna Prasad et al. [9], Hrishikesh et al. (2019), S. K. Singh et al. [10], also observed sufficient variability.

3.2 Variability Parameters

According to Siva Subramanian and Menon (1973), GCV and PCV of more than 20% are considered as high, whereas values less than 10% are considered to be low and values between 10% and 20% are considered to be moderate. According to this, in the present results, most of the traits have high to intermediate GCV and PCV (Table 3 and Fig. 2). This indicated that these traits could be improved for breeding high-yielding rice varieties through selection and hybridization. The magnitude of PCV was found slightly higher than GCV indicating that the trait is less influenced by environmental factors. The highest GCV and PCV are found for yield (37.70 % to 38.27% respectively) followed by NET (GCV: 19.47%, PCV: 21.04%) and PH (GCV: 14.99, PCV: 16.40). The wide genetic base and adaptability is found better in this experiment. Hence direct selection for all characters in this experiment will be rewarding. Also, presence of sufficient variability in the characters studied offered possibilities to explore the material for further genetic improvement. Similar results were obtained in rice by Kushwah et al. [11], Goswami [12] and Kishore et al. [13].

Heritability: Variability parameters are unable to explain variability although these were supplemented by heritability which will give an idea about heritable portion of traits in terms of genotype rather than phenotype [1]. Hence, an adequate understanding of heritability assists plant breeders in predicting the nature of the successful generation, making an appropriate selection as well as assessing the genetic improvement level through selection [14]. The phenotypic selection becomes more desirable when GCV is supplemented with heritability [15]. All the traits under experimentation are categorized as highly heritable. (>70%). Here highest estimates of heritability (>70%) were found for: DFF (97.23%) followed by GYPP (97.03%), while the lowest heritability was described by HI (71.38%). The same result was obtained by Bornare et al. [16], Tadesse Girma et al. [17], Chavan et al. [18], Singh et al. [19] and Goswami, [12].

Table 1. Mean performance of rice forty genotypes under study

Sl. No.	Genotypes	DF	DM	PH	NET	SF	PanLgth	HI	TW	GYPP
1	HUR3022	84.67	99.87	66.94	34.73	64.44	28.55	34.44	22.82	18.24
2	HUR105	106.33	115.78	68.89	34.94	67.45	29.86	36.8	23.07	20.15
3	Karhani	79	100.3	71.79	31.39	58.36	21.98	31.64	21.18	11.75
4	BD105	74.33	93.18	71.64	35.68	66.41	27.74	33.54	17.69	9.64
5	URG-30	70.67	89.67	63.28	28.76	62.24	25.45	33.58	20.07	8.83
6	Dudhkandar	65.67	103.39	94.26	25.05	54.47	29.16	34.19	27.25	10
7	Sathi	69.67	99.64	87.32	27.09	50.13	21.47	29.99	18.2	4
8	URG-1	75.33	93.01	63.97	33.49	61.81	24.28	32.64	18.24	8.71
9	Sambhamahsuri	114.33	118.22	67.74	38.14	69.87	31.83	39.17	24.42	17.91
10	IR 91143-AC 290-1	80.33	98.62	64.81	33.81	66.25	26.95	32.91	18.87	8.21
11	URG-19	85.67	117.12	90.42	32.85	69.4	28.16	30.75	15.16	10.47
12	Swarna	121.67	141.21	68.41	31.17	55.09	30.17	34.25	24.72	16.56
13	URG-22	121.67	144.92	103.76	30.31	59.3	24.71	30.81	17.04	11.27
14	M-48	76	111	98.41	33.15	67.08	26.75	34.75	20.04	13.25
15	IR 82475-110-2-2-1-2	88.33	100.42	73.21	34.71	70.55	28.57	34.05	20.23	5.67
16	M-399	82.67	104.97	89.06	33.82	61	28.92	34.94	23.77	12.83
17	IR 91143-AC 293-1	80.33	93.89	67.76	33.74	65.4	26.3	31.3	23.17	13.24
18	URG-24	76.67	113.54	99.83	33.28	68.31	23.59	28.97	19.1	10.24
19	IR 85850-AC 157-1	83	97	63.96	32.47	60.67	18.53	23.47	17.33	4.67
20	IR 91143-AC 239-1	78.33	98.5	71.1	25.15	40.71	24.28	26.05	22.95	7.33
21	Nagina-22	74.33	102.66	88.73	31.53	58.18	22.97	27.14	18.82	6.67
22	IR64	79.67	95.84	67.08	31.92	61.5	25.34	27.22	20.89	7
23	BG-102	74.33	103.16	96.63	22.95	34.64	26.02	24.99	19.66	5.74
24	MTU1010	82.67	100.37	79.14	32.37	65.14	25.1	30.09	24.01	13.82
25	IR 95133:1-16-14-10-GBS-P6-1-5	84	105.33	75.06	32.95	62.72	33.53	39.07	24.53	15.2
26	IR15M1546	72.67	92.67	66.86	33.03	67.63	30.09	35.17	28.64	16.59
27	IR 95133:1-B-16-14-10-GBS-P5-1-3	81.67	102.56	70.94	33.98	65.96	31.75	34.01	24.99	16.74
28	IR15M1689	77.33	93.67	70.8	34.23	65.86	27.68	33.12	23.5	12.06
29	IR 95133:1-B-16-14-10-GBS-P5-2-3	87.33	105.78	70.44	30.9	65.19	30.86	34.09	21.64	11.83
30	IR 99642-57-1-1-1-B	85.67	107.22	83.61	34.57	67.17	31.21	34.6	23.37	18.27
31	DRR Dhan 48	88	102.11	67.59	34.89	67.83	31.29	34.51	29.71	25.59
32	HURZ-1	89.33	102.56	68.42	31.69	64.14	28.61	30.03	23.18	13.26

Sl. No.	Genotypes	DF	DM	PH	NET	SF	PanLgth	HI	TW	GYPP
33	DRR Dhan 45	88.33	107.56	74.18	28.96	56.69	28.02	33.89	24.84	16.3
34	IR15M1633	80.33	99.78	76.3	28.84	50.83	28.42	32.54	27.48	13.17
35	BRRIdhan 72	100.67	115.11	74.83	32.59	66.63	32.26	33.59	26.93	18.48
36	IR 95133:1-B-16-14-GBS-P1-2-2	86.67	105.11	71.99	32.31	66.59	30.85	31.99	24.34	14.39
37	IR 95133:1-B-16-14-GBS-P1-2-3	86.33	110.56	73.68	31.58	66.49	33.54	30.01	24.62	14.83
38	BRRIdhan 64	86.67	110.11	81.15	35.98	68.71	28.56	32.54	25.56	19.94
39	IR15M1537	81	97.11	70	31.09	59.16	28.73	32.25	25.84	15.41
40	HURZ-3	84.67	101.89	68.83	27.4	58.47	27.82	33.79	22.57	10.94

(DFF: days to 50 % flowering, DM: days to maturity time, PH: Plant height, NET: Number of effective tillers, PanLght: Panicle length, SF:Spikelet fertility, TW: test weight, GYPP: Grain yield per plant, HI: Harvest Index)

Table 2. Analysis of variance for yield and its contributing traits forty rice genotypes under study

SN	Trait	Replication df=2	Genotypes df=39	Residuals df=78
1	DFF	3.81	444.9**	4.23
2	DM	15.83	508.51*	2.24
3	PH	41.36	877.81**	54.13
4	NET	0.33	6.35**	0.33
5	PanLngt	1.79	23.62**	1.93
6	SF	6.84	317.5*	7.40
7	TW	0.79	26.15**	1.84
8	YPP	0.018	0.61**	0.0061
9	HI	104.50	83.07**	9.795

*, **: Significant at 5%, and 1% respectively

(DFF: days to 50 % flowering, DM: days to maturity time, PH: Plant height, NET: Number of effective tillers, PanLght: Panicle length, SF:Spikelet fertility, TW: test weight, GYPP: Grain yield per plant, HI: Harvest Index)

Table 3. Genetic parameters mean, range, coefficient of variation, heritability, GA and GAM

Sl. No.	Trait	Range		Mean	Coefficient of Variation			Heritability	Genetic Advance	Genetic advance percent of mean
		Max	Min		PCV	GCV	ECV			
1	DFF	114	60	75.38	16.3	16.07	2.72	97.23	24.61	32.65
2	DM	143	75	102	12.78	12.7	1.46	98	26.58	25.99
3	PH	157.75	85.43	110.53	16.4	14.99	6.65	83.53	31.19	28.22
4	NET	10	4	7.99	21.04	19.47	7.99	85.57	2.69	37.1
5	PanLngt	31.29	17.66	24.67	12.26	10.89	5.63	78.92	4.92	19.94
6	SF	95.42	40.09	80.92	13	12.56	3.36	93.78	20.23	25
7	TW	34.5	12.52	24.45	12.89	11.63	5.55	81.43	5.29	21.63
8	HI	47.04	16.95	35.43	13.94	13.94	8.83	71.38	8.6	24.27
9	NSPP	294.33	62.50	148.75	36.26	34.65	10.65	0.91	101.52	68.24
10	YPP	38.66	5.18	6.6	38.27	37.7	6.6	97.03	14.45	76.49

(DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, NET: Number of effective tillers, PanLnght: Panicle length, SF: Spikelet Fertility, TW: test weight, YPP: rain yield per plot, HI: Harvest Index)

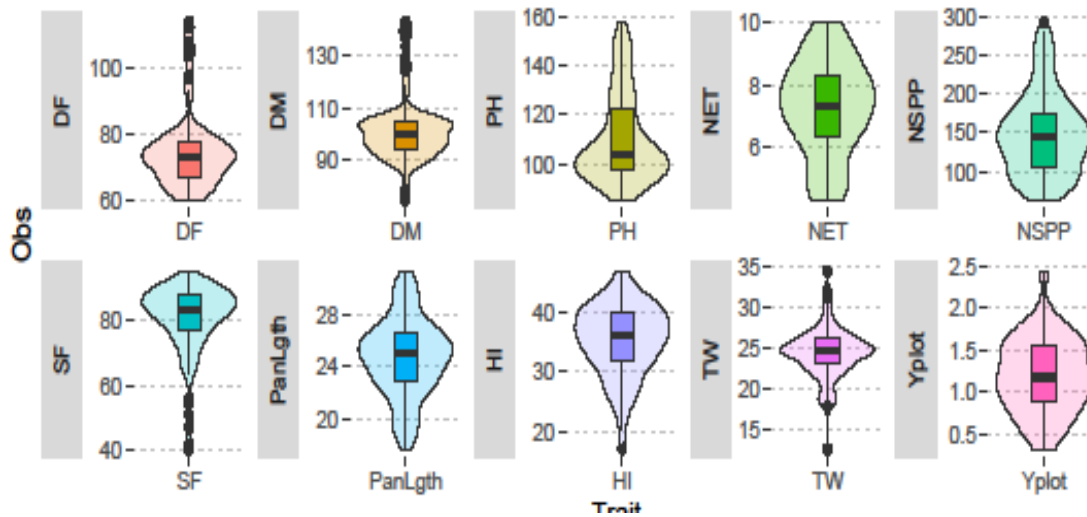


Fig. 1. Box plot representing the performance of different traits under study
 (DFF: days to 50 % flowering, DM: days to maturity time, PH: Plant height, NET: Number of effective tillers, PanLgth: Panicle length, SF: Spikelet fertility, TW: test weight, GYPP: Grain yield per plant, HI: Harvest Index)

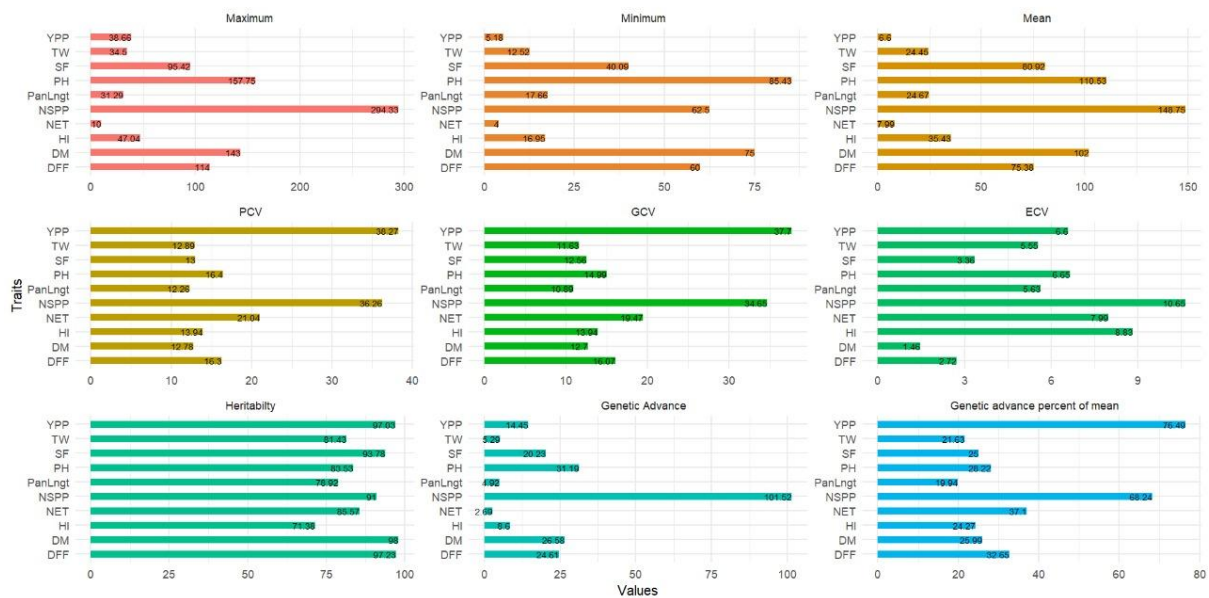


Fig. 2. Graphical representation of variability parameters for the nine traits under study

Genetic advance: Genetic improvement i.e. genetic gain can be predicted by heritability along with genetic advance and helps in the selection of the best individual [16], In the present experiment, the high heritability (>70%) coupled with high genetic advance per cent of mean (GAM) (>20%) were recorded for DFF (H:97.23, GAM: 32.65), DM (H:98.00, GAM: 25.99), PH (H:83.53, GAM: 28.22), NET (H:85.57, GAM:37.10), PanLnght (H:78.92, GAM:19.94), SF (H:93.78, GAM:25.00), TW (H:81.43, GAM:21.63), GYPP (H:97.03,

GAM:76.49) and HI (H:71.38, GAM: 24.27). Similar results were reported by Devi et al. [1], Asante et al. [15], Adjah et al. [20]. The high heritability and genetic advance in most the traits indicates presence of additive genes action. So, these traits can be improved through direct selection (Pratap et al. 2014).

4. CONCLUSION

The overall result showed the presence of adequate variability for all the traits. Most of the

traits showed high estimate of heritability and genetic advance, indicating the predominance of additive genes action and the possibility of direct selection through these traits. This variation could be effectively manipulated using appropriate breeding techniques and programs to develop improved varieties.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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