Study of Variability parameters in rice (*Oryza sativa* L.) genotypes for yield and its attributing traits.

Abstract

This experiment was conducted to study the variability parameters of forty rice genotypes to evaluate genetic parameters viz., Genotypic coefficient of variability (GCV), Phenotypic coefficient of variability (PCV), Heritability (H) and Genetic advance percent of mean (GAM) for eleven 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 that were subjected to alpha lattice design and analyzed in R-software. 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 high heritability (>70%) coupled with high genetic advance percent of mean (GAM) (>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 the simple selection will be effective for improvement for this trait.

Keywords: Genetic advance, Genetic variability, Heritability and Rice

Introduction:

Rice (*Oryza Sativa* L.) is a staple food crop for 2.7 billion people worldwide (Salim et al.) and 90% of rice was grown in Asia independently. It is the second most important cereal. It is the source of energy for more than 2 billion people with 60-70% calories. Also, most farming communities depend on rice as the main source of livelihood. The crop originated in South East Asia and has 24 species including two cultivated *Oryza sativa* and *Oryza glaberrim*. It is found well in different agro-ecological conditions with diverse adaptability. In Asia, *Oryza sativa* L. most are cultivable rice for cooking purposes.

Although there is a large variation present in rice (*Oryza sativa*), highest yield is plateauing in very popular varieties. So, exposing the variation present in rice to study for yield and yield attributing traits helps researchers to use that variability to architect 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 so, that 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, number of grains per panicle and grain size, to conclude best output analysis of data through various measures are important. 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. The presence of high genetic progress in a character is not, however, a requirement for high heritability (Johnson, et. al., 1955). The measure of genetic gain under selection is genetic progress. Heritability in combination with high genetic advance helps in identifying how the environmental factors affect the genotype's expression and the reliability

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of traits. Hence the current study is conducted to study the variability of genotypes for important genetic parameters.

Materials and Methods:

a) Rice genotypes and design of experiment

The present experiment was conducted at Agricultural Research Farm, Banaras Hindu University, Varanasi, and Uttar Pradesh, India. This experiment consists of 40 genotypes including two checks that were examined in alpha lattice design with three replications and 4 blocks with 15 × 20 cm spacing. The genotypes were sown in June 2018 and transplanted after twenty-five days in puddled soil. The recommended dose of fertilizer was applied. All plant protection measures were taken during the crop period.

b) Data collection

Data were collected for nine morphological traits (*viz*. Days to 50% flowering (DFF), Days to maturity (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) from each of the replication. The traits, DFF and DM were recorded on the plot basis whereas, for the remaining traits, the five randomly selected plants from each plot were taken into consideration for the collection of data.

c) Statistical Analysis:

The Analysis of Variance (ANOVA), Genotypic variance (σ2g), phenotypic variance (σ2p), genotypic coefficient of variation (GCV), phenotypic coefficient variation (PCV), heritability in a broad sense (h2b), genetic advance (GA), genetic advance as percentage of means (GAM) was estimated in R studio.

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

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

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

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

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

Genetic Advance (GA)=(k) × (σ_p) × ($h^2 b$)

Genetic Advance as a percentage of Mean (GAM)=(GA/X) × 100

Where, MSg=mean square of genotype, MSe=mean square of error, r=number of replication, σ2e=environmental variance, X=grand mean, k=intensity of selection at 5% (2.06)

Result and Discussion.

a) Mean performance and ANOVA:

The mean of all the forty genotypes for nine yield attributing traits were shown in table 1 and represented by box plot (Fig.1). The ANOVA results showed that the genotypes

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were genetically different since the mean sum of squares among all the genotypes for each character was very significant (Table 2). This suggested that a wide range of promising genotypes may be selected from the current gene pool.

b) Variability Parameter:

Variability study gives prerequisite vision for selection of better genotype over the existing cultivar in that locality for yield and its attributing traits (Table 3 and Fig 2). 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. 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. Similar results were obtained in rice by Kushwah *et al.,* (2021), Goswami, (2018) and Kishore *et al.,* (2015).

c) Heritability:

The 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. 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 magnitude of genetic improvement through selection. (Akinola *et al.* 2019) The phenotypic selection becomes more desirable when GCV is supplemented with heritability. (Burton and Davane, 1953). 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.,* (2014), Tadesse Girma *et al.,* (2018), Chavan *et al.,* (2019); Singh *et al.,* (2022) and Goswami, (2018).

d) 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 (Bornare *et al.,* 2014), 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). The presence of high heritability and genetic advance in most of the traits indicates the presence of additive gene action. So, these traits can be improved through direct selection. (Pratap *et al.,* 2014).

Conclusion:

The overall result showed the presence of adequate variability in the genotypes studied. This variation could be effectively manipulated using appropriate breeding

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techniques and programs to develop improved varieties. The high estimate of heritability and genetic advance were observed in most of the traits, indicating the predominance of additive gene action and the possibility of direct selection through these traits.

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Table 1: Mean performance of rice forty genotypes under study

SN	Name of 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

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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
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

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Table2: Analysis of variance for yield and its contributing traits forty rice genotypes under study.

SN	Trait	Replication	Genotypes	Residuals
		df=2	df=39	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

*,**

Table 3: Genetic parameters Mean, Range, Coefficient of variation, Heritability, GA and GAM

SN	Trait	Range		Mean	Coefficient of Variation			Heritabilty	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)

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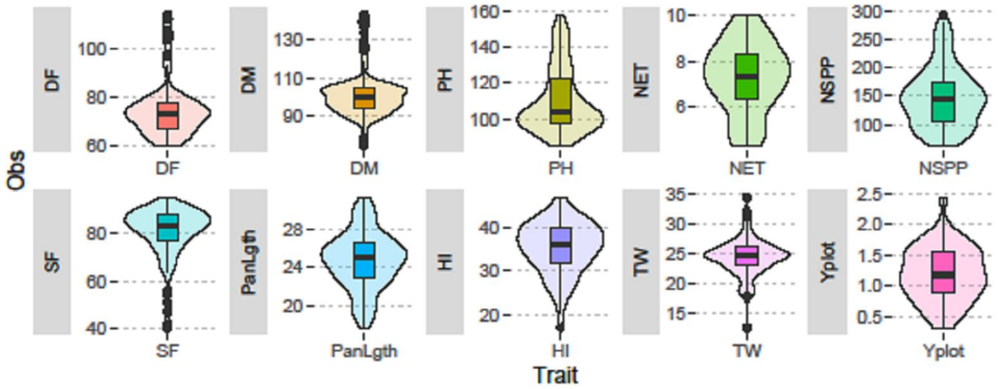

Fig 1: Box plot representing the performance of different traits under study.

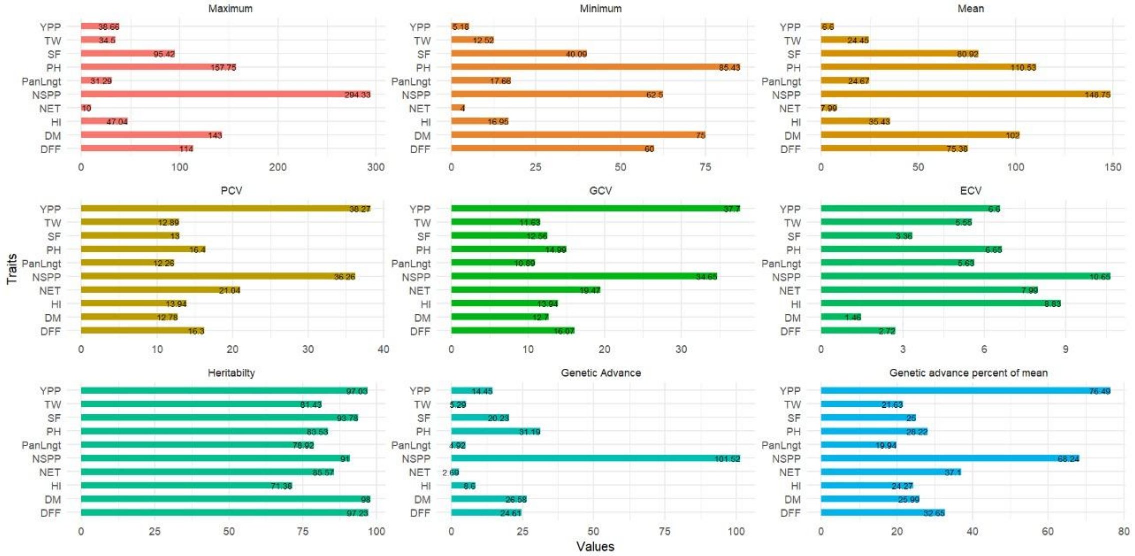

Fig 2. Graphical representation of variability parameters for the nine traits under study.

Acknowledgement:

The authors are highly thankful for the support given by the project "Harvest Plus-Develop High Zinc Rice for Eastern India", in Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi, Uttar Pradesh under Principal Investigation of Dr. S. K. Singh, funded by IFPRI (USA) and CIAT (Columbia) for providing the germplasm used in the present study, other facilities and financial support to get this work done.

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