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

Analysis of rice (*Oryza sativa* L.) accessions genetic variability related to yield and its components

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Abstract

This experiment was conducted to study the variability parameters of forty rice genotypes to evaluategenetic parameters viz., Genotypic variability coefficient ~~of variability~~(GVC~~V~~), Phenotypic variability coefficient ~~of variability~~(PVC~~V~~), Heritability (H) and mean percent of Genetic advance ~~percentof mean~~(MGA~~M~~) for eleven different yield and yield-contributing traits at Agriculture Research Farm, Banaras Hindu University, Varanasi during *Kharif*-2018. Thedatawere collected for nine yield and yield attributing traits ~~that were~~ subjected to alpha lattice designand analyzed in R-software. The PCV magnitude ~~of PCV~~ was found slightly higher than GCV indicating that ~~the~~ thistrait is less influencedby 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 percent of mean genetic advance ~~percent of mean~~ (MGA~~M~~) (>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 traitimprovement ~~for this trait~~.

Comment [a1]: What does it mean?

Comment [a2]: Give first its meaning before abbreviating!

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. With 60-70% calories~~It~~ riceis ~~the source of~~ energysource for more than 2 billion people~~ with 60-70% calories~~. Also, most farming communities depend on rice as the mainlivelihoodsource ~~of livelihood~~.~~The~~ Thiscrop originated in South East Asia and ~~has~~developped24 species includingtwo cultivated *Oryza sativa*L and *Oryzaglaberrim*L.It is well 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 variation in rice tostudy ~~for~~ yield and yield attributing traits helps researchers ~~to use that variability to~~ 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 ~~so,that~~ after vanishing the undesirablegenes to breed a new variety. Morphological traits are governedby 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 of data analysis ~~of data~~ through various importantmeasures ~~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 p~~ Howeverhigh genetic progress presence ~~of high genetic progress~~ in a character is not~~,however, a~~ requirement for high heritability (Johnson, et. al., 1955). ~~The measure of g~~Genetic gain measure under selection ~~is~~ constitutes~~genetic~~ progress. Heritability in combination with high genetic advance helps in identifying how the environmental factors affect the genotype's expression and ~~the~~ traitsreliability~~of traits~~.Hence,~~the current~~ this~~study~~ experiment~~is conducted~~ aimed~~to~~atstudying the important genetic variability of rice genotypes~~ for important genetic parameters~~.

Comment [a3]: Too old! Replace it by a new one!

Comment [a4]: It's not "understanding"?

Materials and Methods:

a) Rice genotypes and experimentaldesign ~~of experiment~~

The present experiment was conducted at Agricultural Research Farm, Banaras Hindu University, Varanasi, and Uttar Pradesh, India. ~~This experiment~~It~~consists~~consistedof 40 rice genotypes including two checks~~that~~cultivated ~~were examined in~~ followingalpha lattice design with three replications and 4 blocks with 15 × 20 cm spacing. These genotypes grains were sown in June 2018 and seedlings were 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.

Comment [a5]: Give precisions on fertilizers type, their doses and application periods. It is the same for protection measures! We don't know them!

Comment [a6]: Insert images of rice plants in experiment

b) Data collection

Data were collected for ninemorphological traits:~~(viz. Days~~ Timeto 50% flowering (~~DFF~~TFF), ~~Days to maturity~~Maturitytime(~~DM~~MT), Plant height (PH), Number of effective tillers (NET), Panicle length (PanLght), Spikelet ~~Fertility~~fertility(SF), test weight(TW), Grain yield per plant (GYPP), Harvest Index (HI)~~from each of the replication~~. ~~The traits, DFF~~ TFF and ~~DM~~MTwere recorded on ~~the~~ plot basis~~ whereas,for the remaining traits, the~~ while five plantswere randomly selected ~~plants~~ from each plot ~~were taken into consideration~~ for data~~the~~ collection ofremaining traits. Traits measures were calculated following formulae (……)

Comment [a7]: What does it mean? You'd rather write "grains weight"?

Comment [a8]: Give the source of these formulae

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 ($h^2 b$)=($\sigma^2 g/\sigma^2 p$) × 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)

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c) Statistical Analysis:

We used ~~T~~the Analysis of Variance (ANOVA) to compare the rice studied genotypes throught~~,~~Genotypicvariance (σ2g), phenotypic variance (σ2p), genotypic variation coefficient ~~of variation~~ (GVC~~V~~), phenotypic variation coefficient ~~variation~~ (PVC~~V~~), heritability in a broad sense (h2b), genetic advance (GA), genetic advance as percentage of means (GAM) was estimated in R ~~studio~~ software.……..

Comment [a9]: Give more information about ANOVA processing conditions and when you considered that compared means are different or not. In case of significant difference, what did you do to identify rice genotypes responsible of these differences? Give also information on R-software version

~~Genotypic variance (σ^2g)=(MSg-MSe)/r~~

~~Phenotypic Variance (σ^2p)=σ^2g+(σ^2e)/r~~

~~Genotypic coefficient of variation (GCV)== $\frac{\sqrt{\sigma^2 g}}{x}$ × 100~~

~~Phenotypic coefficient of variation (PCV)== $\frac{\sqrt{\sigma^2 p}}{x}$ × 100~~

~~Heritability (h^2b)=(σ^2g/σ^2p) × 100~~

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

~~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 m~~Means of ~~all~~ the forty genotypes for nine yield-attributing traits ~~were~~ areshown in table 1 and represented by box plot (Fig.1). The ANOVA results showed that ~~the~~ all ricegenotypes were genetically different since the mean sum of squares~~among all the genotypes~~from each over for ~~each~~everycharacter ~~was very significant~~ (Table 2).This suggested that a wide range of promising genotypes may be selected from the current gene pool.

Comment [a10]: ANOVA results are not compared through sum of square, but through F and P values!

Comment [a11]: That is a conclusion! So not indicated here! You should compare these 40 rice genotypes through analysed traits: plant high; precocity and late.....And you did not discuss your results!

b) Variability Parameters:

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% areconsidered 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).

Comment [a12]: You should first present your results before giving their meaning!

c) Heritability:

~~The v~~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~~ adequate understanding of heritability assists plant breeders in predicting the nature of the successful generation,

Comment [a13]: Affirmations or your results?

making an appropriate selection as well as assessing the ~~magnitude of~~ genetic improvement level 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).

Comment [a14]: Too old!

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~~ in most the traits indicates ~~the~~ presence of additive genes action. So, these traits can be improved through direct selection~~.~~(Pratap*et al.*, 2014).

Comment [a15]: You have to give the real meaning of these abreviations

Conclusion:

The overall result showed the presence of adequate variability trough ……in therice forty genotypes studied.~~ This variation could be effectively manipulatedusing appropriate breeding techniques and programs to develop improved varieties~~. Most of the traits showed ~~The~~ high estimate of heritability and genetic advance~~were observed in most of the traits~~, indicating the predominance of additive genes action and the possibility of direct selection throughthese traits.This variation could be effectively manipulatedusing appropriate breeding techniques and programs to develop improved varieties

Comment [a16]: Summarize concerned traits because it is too fuzzy!

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

Comment [a17]: Give these abbreviations meanings below this table and precise their units

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

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)

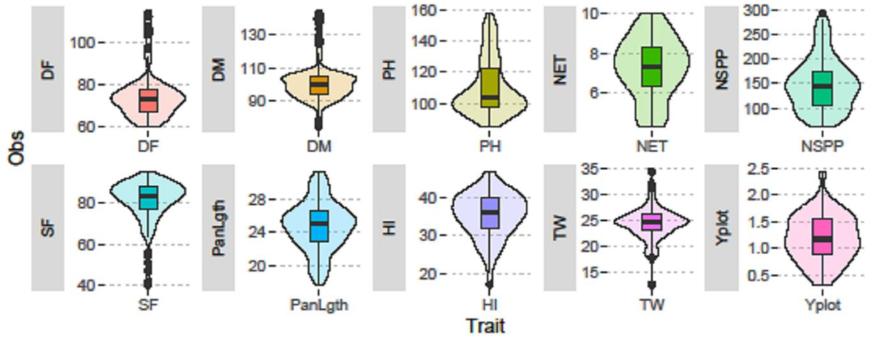

Fig 1: Box plot representing the performance of different traits under study.

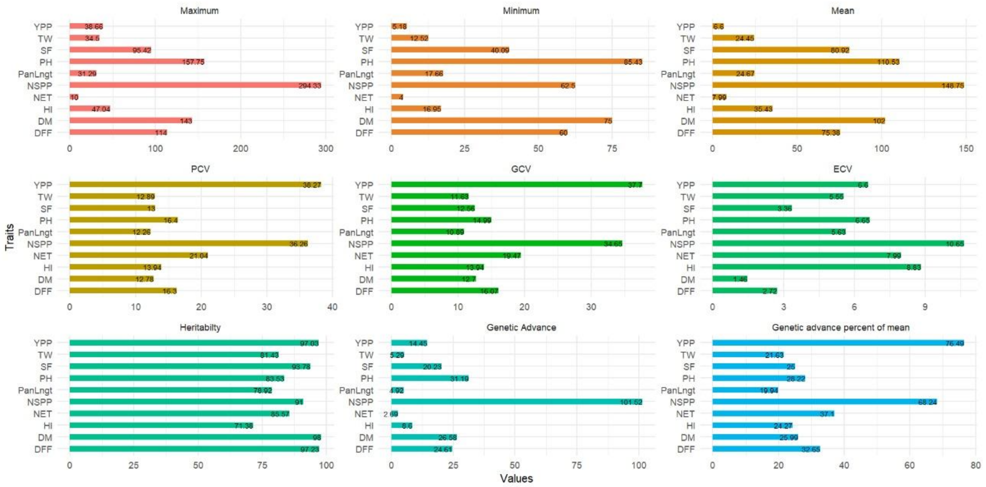

Fig 2. Graphical representation of variability parameters for the nine traits under study.

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