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Assessment of genetic variability for yield and yield contributing traits in rice (*Oryza sativa* L.)

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Abstract

The present study was undertaken with 29 rice genotypes along with 3 checks to assess genetic factors such as (GCV) Genotypic coefficient of variation and (PCV) Phenotypic coefficient of variation, heritability and genetic advance (GA). The results showed significant variation across the genotypes, indicating that efficient selection is possible. All the traits showed high heritability. The estimates of genotypic coefficient of variation were lower than the corresponding phenotypic coefficient of variation, indicating that environmental factors influenced how the traits under study were expressed. The highest genetic advance as a percentage of the mean was seen in plant height, number of productive tillers per plant, number of grains per panicle, biological yield per plant, test weight, number of spikelets per panicle, and harvest index. High heritability coupled with high genetic advance as a percentage of the mean was recorded for plant height (91.80, 34.157), the number of productive tillers per plant (96.70, 35.196), the number of grains per panicle (97.10, 37.942), test weight (94.30, 26.284), biological yield per plant (95.80, 38.518), the number of spikelets per panicle (93.10, 31.631), and harvest index (95.20, 37.181) respectively indicating that selection for the improvement of these characters may be rewarding for further breeding programme.

Keywords: *Oryza sativa*, heritability, genetic variability and genetic advance

1. Introduction

Rice (*Oryza sativa* L.) is the most important cereal crop in the world. Rice belongs to the Gramineae family (Poaceae). *Oryza sativa* has a basic chromosome number (n) of 12 (2n = 24), and it originated in Southeast Asia. A staple cereal crop grown throughout the world, rice (*Oryza sativa* L.) provides more than half of the world's population with most of its carbohydrates (Williams *et al.* 2021) [21]. It has a significant nutritional and financial impact and provides most people with food and protein. It provides 160 million impoverished rural people with a means of subsistence and fulfils the caloric needs of 50% of the population (Santha *et al.* 2016) [18]. It is necessary to raise yield levels to fulfil the demands of a growing population. To increase productivity and create breeding programmes, variability must be created. In India, about 43.78 million hectares are used for the cultivation of rice, with a productivity of roughly 2705 kg/ha in 2019–2020 (Agriculture Statistics briefly, 2021) [1]. According to estimates, India's rice consumption will reach 185 million metric tonnes by 2030. National food security depends on increased and stable production of this food, which is the most important primary source of nutrition for over 65% of the total population. Shamim *et al.* (2012) [19] Before starting any programme for crop development and using the proper selection strategies, a critical analysis of genetic variability is required. An effective breeding programme requires an understanding of the genetic variability of the traits that contribute to yield, their relationships with one another, and their link to yield. Nayak *et al.* (2016) [12] Heritability assists plant breeders in predicting the characteristics of the upcoming generation, making suitable selections, and determining the extent of genetic improvement through selection. Tuhina-Khatun *et al.* (2015) [20]

2. Materials and Methods

2.1. Experiment site

The experiment was conducted at the Agriculture Research Farm Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Jalandhar (Punjab), during *kharif* season, 2022.

2.2 Experimental design

The research was conducted using a randomised block design (RBD) with three replications using 29 different rice genotypes with three checks. Twenty-five-day-old seedlings were transplanted to the main field with a spacing of 20 x 15 cm.

2.3 Experiment material

A fertiliser dose of 120:60:60 N:P:K kg/ha was applied. Standard agronomic procedures and scheduled plant protection measures were used.

Table 1: A list of the 32 rice genotypes used in this study.

S.N.	Genotypes	Sources	S.N.	Genotypes	Sources
1	HUR-1304	BHU, Varanasi, Uttar Pradesh	17	URG-27	BHU, Varanasi, Uttar Pradesh
2	HUBR 2-1	BHU, Varanasi, Uttar Pradesh	18	URG-20	BHU, Varanasi, Uttar Pradesh
3	HUR-105	BHU, Varanasi, Uttar Pradesh	19	URG-34	BHU, Varanasi, Uttar Pradesh
4	HUR-4-3	BHU, Varanasi, Uttar Pradesh	20	URG-28	BHU, Varanasi, Uttar Pradesh
5	HUR-917	BHU, Varanasi, Uttar Pradesh	21	URG-19	BHU, Varanasi, Uttar Pradesh
6	URG-35	BHU, Varanasi, Uttar Pradesh	22	URG-49	BHU, Varanasi, Uttar Pradesh
7	URG-29	BHU, Varanasi, Uttar Pradesh	23	URG-36	BHU, Varanasi, Uttar Pradesh
8	URG-37	BHU, Varanasi, Uttar Pradesh	24	URG-30	BHU, Varanasi, Uttar Pradesh
9	URG-38	BHU, Varanasi, Uttar Pradesh	25	URG-22	BHU, Varanasi, Uttar Pradesh
10	URG-15	BHU, Varanasi, Uttar Pradesh	26	URG-1	BHU, Varanasi, Uttar Pradesh
11	URG-2	BHU, Varanasi, Uttar Pradesh	27	MTU-1061	BHU, Varanasi, Uttar Pradesh
12	URG-26	BHU, Varanasi, Uttar Pradesh	28	URG-14	BHU, Varanasi, Uttar Pradesh
13	URG-25	BHU, Varanasi, Uttar Pradesh	29	URG-10	BHU, Varanasi, Uttar Pradesh
14	URG-43	BHU, Varanasi, Uttar Pradesh	30	PR-126 Checks	PAU, Punjab
15	URG-46	BHU, Varanasi, Uttar Pradesh	31	PR-113 Checks	PAU, Punjab
16	URG-41	BHU, Varanasi, Uttar Pradesh	32	PR-121 Checks	PAU, Punjab

2.4 Data collection

Data were recorded on each replication, and five plants randomly selected were used for 12 quantitative traits: days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of productive tillers per plant, number of grains per panicle, number of spikelets per panicle, spikelet fertility, test weight (gm), biological yield per plant (gm), grain yield per plant (gm), and harvest index (%). The data from 32 rice genotypes was statistically analysed using R software.

2.5 Statistical analysis

The data collected on each character was subjected to the

following statistical analysis: ANOVA (analysis of variance). Panse and Sukhatme (1978) [15], Heritability in Broad Sense Burton and De Vane (1953) [3]; Genetic Advance Johnson *et al.* (1955) [7].

3. Results and Discussion

3.1 Genetic variability

3.2 Analysis of variance

Analysis of variance, the mean sum of squares (MSS) due to genotypes were highly significant for all the characters at 1% and 5% levels of significance, according to analysis of variance, and it was also revealed that there was enough genetic variability for all the traits (Table 2).

Table 2: Analysis of variance of 12 quantitative Traits.

Characters /Traits	Replication df=2	Genotype (df=31)	Error (df=62)
DFF	12.07	216.65**	21.15
DM	24.67	237.76**	13.40
PH	102.25	1084.35**	88.96
NTP	1.66	13.82**	0.45
PL	6.00	10.23**	3.11
NGP	13.17	1184.29**	34.75
TSW	3.44	27.10**	1.53
BYP	10.69	1191.14**	49.52
SF	1.33	30.39**	4.36
NSP	12.87	1116.29**	77.13
HI	1.02	112.60**	5.45
GYP	2.24	16.02*	6.25

Whereas, DFF: days to flowering, DM: days to maturity, PH: plant height (cm), NTP: number of productive tillers per plant, PL: panicle length, NGP: number of grains per panicle, TSW: test weight, BYP: biological yield per plant, SF: spikelet fertility, NSP: number of spikelets per panicle, HI: harvest index, GYP: grain yield per plant.

Table 3: Mean value for yield and yield contributing Traits.

Genotypes	DFE	DM	PH	NTP	PL	NGP	TSW	BYP	SF	NSP	HI	GYP
HUR-1304	115.00	147.67	143.33	13.33	23.71	107.02	29.39	125.06	89.53	120.56	27.83	36.84
HUBR 2-1	115.00	148.00	84.37	13.27	23.44	114.08	23.16	108.59	82.43	139.76	30.01	32.89
HUR-105	110.00	143.00	87.03	10.27	21.51	76.08	21.93	83.19	84.34	90.29	36.56	29.79
HUR-4-3	100.00	134.33	102.32	9.60	22.25	79.22	21.84	70.32	82.45	96.03	43.81	30.33
HUR-917	100.33	132.67	96.46	10.20	22.39	86.68	25.31	95.66	83.37	105.29	35.39	34.70
URG-35	102.33	136.33	114.94	9.47	24.90	96.42	24.21	89.32	86.88	110.83	37.35	33.95
URG-29	103.67	136.67	89.42	9.00	26.34	74.08	24.81	74.79	85.94	86.63	45.08	34.49
URG-37	102.33	136.00	74.43	8.27	23.09	96.82	20.03	86.86	89.45	107.76	34.68	29.33
URG-38	107.67	140.33	86.85	15.00	23.95	132.82	23.35	131.59	91.02	145.43	24.94	33.23
URG-15	85.00	115.00	95.86	11.53	21.38	95.22	19.28	75.79	93.42	102.03	39.59	29.18
URG-2	98.67	133.33	111.80	16.60	27.85	150.35	22.07	148.32	92.30	162.36	21.73	32.37
URG-26	92.67	121.67	115.97	8.60	23.36	87.08	21.88	87.39	88.04	98.83	35.35	30.45
URG-25	96.00	127.33	135.81	12.87	27.42	108.28	21.45	126.39	86.00	126.03	23.72	29.18
URG-43	107.33	139.00	103.94	13.80	23.16	115.95	21.92	105.12	92.77	122.63	30.06	31.00
URG-46	110.00	142.00	116.07	14.27	24.18	133.42	20.19	106.19	89.98	134.76	28.49	29.56
URG-41	108.67	131.67	115.67	13.27	22.81	113.28	20.65	133.19	90.01	125.56	23.14	30.35
URG-27	97.67	129.33	118.21	14.53	20.65	104.15	24.16	111.06	91.61	113.43	29.81	33.61
URG-20	111.67	139.33	114.63	16.00	20.06	108.28	21.81	117.39	92.51	115.89	27.51	32.47
URG-34	102.67	136.33	97.24	11.73	25.65	116.75	22.29	108.26	89.20	131.43	29.73	32.31
URG-28	97.67	133.00	124.80	14.67	23.35	107.62	22.94	114.92	93.70	114.89	28.39	32.88
URG-19	96.67	127.33	90.47	11.73	23.62	88.88	19.85	90.92	92.19	96.69	31.92	27.80
URG-49	88.67	125.00	89.99	12.40	24.15	88.68	18.49	79.79	86.45	102.43	37.95	29.55
URG-36	96.67	129.00	155.20	11.93	24.00	93.08	22.49	83.46	87.40	107.89	39.13	32.97
URG-30	82.67	111.00	96.95	10.53	20.45	82.48	20.67	76.06	86.51	94.89	40.63	30.46
URG-22	94.00	126.00	84.53	10.87	22.53	97.15	20.98	96.66	89.37	109.16	31.97	30.43
URG-1	91.33	123.33	85.75	12.13	22.76	82.02	20.71	77.66	87.04	93.96	39.76	30.40
MTU-1061	95.67	127.00	99.31	11.40	22.38	120.68	23.28	113.12	90.44	129.49	28.99	33.17
URG-14	86.67	120.00	115.89	13.93	22.80	155.95	12.43	126.59	92.21	164.76	23.75	29.28
URG-10	97.00	129.33	135.01	14.27	25.17	106.28	21.69	107.26	91.03	116.69	29.11	30.92
PR-126 Checks	103.67	138.00	96.67	10.70	21.14	102.22	27.02	103.99	85.35	117.69	33.98	36.08
PR-113 Checks	106.67	140.33	95.33	12.13	22.39	115.75	28.10	99.46	89.15	129.76	35.17	36.29
PR-121 Checks	110.33	144.33	93.93	10.60	21.76	113.88	22.68	113.99	88.04	128.43	28.08	32.05
Mean	100.45	132.61	105.25	12.15	23.27	104.71	22.22	102.14	88.75	116.95	32.30	31.82
Min	82.67	111.00	74.43	8.27	20.06	74.08	12.43	70.32	82.43	86.63	21.73	27.80
Max	115.00	148.00	155.20	16.60	27.85	155.95	29.39	148.32	93.70	164.76	45.08	36.84
CV	4.57	2.76	8.96	5.53	7.58	5.63	5.58	6.89	2.35	7.51	7.23	7.86
CD 5%	7.50	5.97	15.39	1.09	2.88	9.62	2.02	11.48	3.40	14.33	3.81	4.08

The DFF varied from 82.67 to 115.00 days, with an overall mean value of 100.45. Days to maturity varied from 111.00 to 148.00 days, with an overall mean value of 132.61. Plant height varied from 74.43 to 155.20 days, with an overall mean value of 105.25. The NTP ranged from 8.27 to 16.60, with an overall mean value of 12.15. Panicle length varied from 20.06 cm to 27.85 cm, with an overall mean value of 23.27. The NGP observed ranges from 74.08 to 155.95, with an overall mean value of 104.71. The TSW observed ranged from 12.43 to 29.39 g, with an overall mean value of 22.22. The BYP per plant ranged from 70.32 to 148.32 g, with an overall mean value of 102.14. Spikelet fertility ranged from 82.43 to 93.70, with an overall mean value of 88.75. The NSP ranged from 86.63 to 164.76, with an overall mean value of 116.95. Harvest index varied from 21.73 to 45.08, with an overall mean value of 32.30. Grain yield per plant ranged from 27.80 to 36.84, with an overall mean value of 31.82.

3.3 Genetic variability

As a result, there is a lot of scope for effective selection. The results for yield and yield component characteristics in terms of mean, range, (GCV) genotypic coefficient of variation, and (PCV) phenotypic coefficient of variation, heritability, and genetic advance as a percentage of the mean Table 4. A perusal of these results revealed the maximum range of

variability for the trait NSP (86.63-164.76), while the minimum range (8.27-16.60) was recorded for NTP. For every trait in the current study, the phenotypic coefficient of variation exceeded the genotypic coefficient of variation. It implies that the observed variation is a result of both the genotypes and the appropriate influence of the environment. The GCV genotypic coefficient of variation and the PCV phenotypic coefficient of variation were estimated into three categories: low (below 10%), medium (10%–20%), and high (above 20%). In this study, the magnitudes of PCV and GCV were moderate for PH, NTP, NGP, TSW, BYP, NSP, and HI, indicating little scope for improvement of these traits through selection.

Similar results were reported by Lakshmi *et al.* (2022) [10] for PH, Deepthi *et al.* (2022) [6] for NTP, Khaire *et al.* (2022) [8] for TSW, Osman *et al.* (2020) [14] for BYP, Naik *et al.* (2022) [13] for NSP, and HI, Barhate *et al.* 2021 [5] for NGP. Low PCV and low GCV were observed for the following traits: DFF, DM, PL, SF, and GYP. Similar findings were found by Pushkarnath *et al.* (2022) [16] for DFF, DM, and PL; Khaire *et al.* (2017) [9] for SF; and Babu *et al.* (2012) [4] for GYP.

3.4 Heritability and Genetic Advance

Heritability estimates for the different traits studied ranged from PL 69.90 to 97.10 (NGP). All the traits under study have

high heritability estimates (> 60%). Similar findings were reported by Pushkarnath *et al.* (2022) ^[16] for NGP and PL, BYP, TSW, HI; Singhal *et al.* (2022) ^[17] for NTP, DFF and PH; Naik *et al.* (2022) ^[13] for DM; Nath and Kole (2021) ^[11] for SF; Lakshmi *et al.* (2022) ^[10] for NSP; Awad-Allah *et al.* 2022 ^[2] for GYP.

The genetic advance as percent of the mean revealed high values (>20%) for PH, NTP, NGP, TSW, NSP, HI, and BYP. The utilization of these traits and the passing of these traits from parent to offspring imply that the maximum genetic gain is possible. Similar findings were reported earlier by Singhal *et al.* (2022) ^[17] for PH, NTP, and TW; Pushkarnath *et al.* (2022) ^[16] for BYP, HI and NSP; Lakshmi *et al.* (2022) ^[10] for NGP. Moderate genetic advance as a percentage of the (10–20%) mean was recorded for DFF, DM, and PL. It indicates partial genetic gain by selection. Similar results were reported by Pushkarnath *et al.* (2022) ^[16] for DFF and PL and Naik *et al.* (2022) ^[13] for DM. whereas low genetic advance as a percentage mean was observed by SF and GYP. Similar findings were reported by Awad-Allah *et al.* (2022) ^[2] and Babu *et al.* (2012) ^[4] for GYP.

High heritability coupled with high genetic advance as a percentage of the mean was recorded for PH (91.80, 34.157),

NTP (96.70, 35.196), NGP (97.10, 37.942), TW (94.30, 26.284), BYP (95.80, 38.518), NSP (93.10, 31.631), and HI (95.20, 37.181), indicating that the heritability observed was due to the additive gene effect and therefore selection would be effective in improving these traits. Similar findings were reported by Singhal *et al.* (2022) ^[17] for PH, NTP, and TW; Lakshmi *et al.* (2022) ^[10] for NGP; Pushkarnath *et al.* (2022) ^[16] for BYP, HI and NSP. But DFF (90.20, 15.727), DM (94.40, 13.050), and PL (69.60, 11.379) had observed high heritability combined with moderate genetic advance as a percentage of the mean, showing the importance of additive and non-additive gene effects for the characters.

Similar results were reported by Pushkarnath *et al.* (2022) ^[16] for DFF and PL and Naik *et al.* (2022) ^[13] for DM. High heritability with low GA was observed in SF and GYP. Similar results were reported by Awad-Allah *et al.* (2022) ^[2] for SF and Babu *et al.* (2012) ^[4] for GYP. In the current study, high heritability, and high genetic advance as percent of the mean were shown for PH, NTP, NGP, NSP, BYP, TSW, and HI, indicating the predominance of an additive gene action and, consequently, the potential for the trait to be improved through selection.

Table 4: Genetic parameter study for yield and yield contributing Traits.

Characters/ Traits	PCV	GCV	H ₂ (bs) (%)	GA	GA (5%)
DFF	8.460	8.037	90.20	15.797	15.727
DM	6.713	6.521	94.40	17.306	13.050
PH	18.063	17.306	91.80	35.952	34.157
NTP	17.664	17.372	96.70	4.277	35.196
PL	7.939	6.622	69.60	2.648	11.379
NGP	18.975	18.695	97.10	39.728	37.942
NSP	16.495	15.915	93.10	36.991	31.631
BYP	19.509	19.099	95.80	39.341	38.518
SF	3.586	3.319	85.60	5.613	6.325
TSW	13.526	13.137	94.30	5.840	26.284
HI	18.968	18.503	95.20	12.010	37.181
GYP	7.262	5.669	80.90	2.901	9.117

Whereas, PCV: Phenotypic Coefficient of variation; GCV: Genotypic Coefficient of variation; GA: Genetic advance; H(bs): Heritability (broad sense).

Conclusions

The results of each trait had sufficient variability. Most of the traits had high heritability and genetic advance estimates, which suggested additive gene action was predominating and that direct selection might be occurring via these traits. High heritability coupled with high genetic advance as a percentage of the mean was recorded for plant height, number of productive tillers per plant, number of grains per panicle, test weight, biological yield per plant, number of spikelets per plant, and harvest index, indicating that the heritability observed was due to the additive gene effect and therefore selection would be effective in improving these traits.

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