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Assessment of Genetic Variability Parameters for Yield and its Contributing Traits in Rice (*Oryza sativa* L.)

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ABSTRACT: The current study was undertaken to evaluate the genetic variability, heritability, and genetic advance as % of the mean for grain yield and its attributing traits in 42 rice genotypes. Analysis of variance revealed that the genotypes differed significantly for all the traits studied. For all of the traits, phenotypic coefficients of variation were higher than the genotypic coefficient of variation, indicating that the apparent variation is related to G × E interaction. The number of unfilled spikelets/panicles had the highest magnitude of the phenotypic coefficient of variation and genotypic coefficient of variation. The highest heritability (broad sense) was noted in this research in cooked rice length. The high heritability (%) combined with high genetic advance as % of mean was observed for plant height, flag leaf length, number of spikelets/panicle, number of filled spikelets/panicle, number of unfilled spikelets/panicle, 1000 seed weight, harvest index, biological yield and grain yield/plant, grain length, L: B ratio, brown rice length, milled rice length and cooked rice length.

Keywords: Rice, genetic variability, coefficient of variation, heritability, genetic advance as % of mean.

INTRODUCTION

The monocotyledonous angiosperm rice (*Oryza sativa* L.) is a member of the tribe Oryzeae, subfamily Bamboosoideae, and family Graminae. It is known as "Global Grain" because it provides around 20% of the world's calories and is the main source of food for more than 50% of the population. Unlike other cereals, rice is the only grain that is almost totally used as human food (Swaminathan, 1999). The global population of 7.7 billion will increase to 9.7 billion by 2050 (Anonymous (2018-19). Developing disease-resistant and high-yielding rice cultivars should receive special focus when it comes to improving rice yield. The current slowing trend in output and yield must be reversed to fulfil the rising demand. To optimize output and maintain the nation's food security and economic success, it is imperative to utilize the genetic resources and knowledge that are now accessible for rice.

An efficient breeding programme requires an understanding of the genetic variability of yield-contributing traits, how they interact, and how they relate to yield (Nayak *et al*., 2016). The comprehensive breeding programme includes actions like introducing genetic variability, engaging in the selection, and exploiting chosen genotypes to develop fruitful variations. A sensible evaluation of the genetic variability dimensions, particularly the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as % of the mean, is a core component of the grain yield and its contributing traits to play a rare vintage role in improving crop productivity as well as in developing breeding programmes. Genetic factors like genotypic coefficient of variation and phenotypic coefficient of variation evaluate the degree of environmental genotype modification as well as the genetic variability present in genetic resources. The heritability estimates give accurate information about a certain genetic trait that will be passed down through the generations and are an effective tool for breeders to choose parents for crop improvement and pick elite genotypes from a variety of genetic populations (Rashmi *et al*., 2017). Heritability estimations that are combined with genetic advance as % of mean are often more useful in detecting the gain amenable to selection. The current study was conducted within the framework of elucidating information on variability, heritability and genetic advance as % of the mean of yield and yield attributed attributes in prospective rice genotypes to support future breeding programmes for yield enhancement.

MATERIALS AND METHODS

The present investigation was carried out at the Research cum Instructional farm Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.). Quality parameters estimation was done at the crop quality laboratory (Dr. Richharia Research Laboratory). In *Kharif*, 2021, 42 aromatic and high-yielding rice genotypes were used including four checks: Chhattisgarh Devbhog, Chhattisgarh Sugandhit Bhog, Dubraj Sel.-1, Vishnubhog Sel.-1. The experiment was laid out in Randomized Complete Block Design with 2 replications. The observations were recorded for traits such as plant height, days of 50 % flowering, flag leaf length, days to maturity, effective tillers/plant, panicle length (cm), number of spikelets / panicle, number of filled spikelets/panicle, number of unfilled spikelets/panicle, spikelets fertility %, 1000 seed weight, harvest index, biological yield, grain yield / plant, grain length, grain breadth, L: B ratio, brown rice length, brown rice breadth, milled rice length, milled rice breadth, hulling (%), milling (%), HRR (%), cooked rice length, cooked rice breadth and amylose content (%). The observations were made on five competing plants from each genotype in each block that was randomly labeled. Finally, average values were calculated and statistical analysis was performed.

RESULTS AND DISCUSSION

Analysis of variance. The cornerstone of any plant breeding effort is genetic variability. In terms of grain output and quality, rice varieties vary greatly. The huge variation in genetic makeup accounts for the enormous variability in the combinations of numerous yield-related characteristics. The presence of genetic variability is necessary for ongoing progress since it allows breeders to create new types and hybrids. Analysis of variance was performed on the replication-wise mean data for the fourteen quantitative traits and thirteen-grain quality traits for yield and its contributing traits of 42 rice genotypes. The analysis of variance revealed a significant difference in all of the attributes shown in Table 2. The results are in close harmony with Sao *et al.* (2004), Babu *et al.* (2012); Islam *et al.* (2015); Khaire *et al.* (2017); Adhikari *et al.* (2018); Saha *et al.* (2019); Rathan *et al.* (2019); Bhor *et al*. (2020); Priyanka *et al.* (2020).

Genetic variability parameters. The assessment of heritable and non-heritable components in the total variability observed is indispensable in the adoption of a suitable breeding procedure. The heritable portion of the overall observed variation can be ascertained by studying the components of variation *viz*., range and mean performance, phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in a broad sense and genetic advance as % of mean was computed for yield contributing characters in Table 3. Number of spikelets/panicle (83.4 to 294.5), number of filled spikelets/panicle (43.4 to 241), plant height (71.86 to 178.31), days to maturity (107.5 to 148), and milled rice breadth showed the widest ranges of mean variation. Milled rice breadth (1.47 to 2.36) showed the narrowest range of mean variation.

Coefficient of variation. The phenotypic coefficients of variation and genotypic coefficients of variation were found to have a strong relationship for all characters examined. According to this study, estimations of the phenotypic coefficients of variation were higher than their respective genotypic coefficients of variation, implying that both environmental factors and genotypes participate in the apparent variation. According to a genetic study, the phenotypic coefficients of variation ranged from 52.52 % to 8.07 % ina number of unfilled spikelets/panicle and milled rice breadth respectively. The genotypic coefficients of variation ranged from 50.14 % to 7.02 % in a number of unfilled spikelets/panicle and milled rice breadth respectively. The number of unfilled spikelets/panicle (52.52 % and 50.14 %), harvest index (48.02 % and 45.77 %), grain yield / plant (43.78 % and 45.77 %), number of filled spikelets/panicle (33.3 and 29.73), biological yield (29.43 and 26.43), and number of spikelets/panicle (27.68 % and 23.33 %) are the characteristics with the highest PCV and GCV levels. Revealing that the genotype has enough variability and adopting individuals with these traits would assist in genetic advancement. The results are in agreement with Sao *et al.* (2004); Babu *et al.* (2012); Patel *et al.* (2014); Nayak *et al.* (2016); Khaire *et al.* (2017); Saha *et al.* (2019); Gupta *et al*. (2020); Noatia *et al.* (2021).

Heritability (Broad sense). To communicate the accuracy of phenotypic value, heritability estimates serve as a forecasting tool. The range of heritability varied from 99.24 % in cooked rice length to 38.78 % in panicle length. The highest heritability was noted in cooked rice length (99.24 %), followed by days to maturity (98.44 %), days to 50 % flowering(98.09 %), grain length (96.00 %), brown rice length (95.68 %), milled rice length (95.58 %), cooked rice breadth (94.18 %), L:B ratio (93.53 %), number of unfilled spikelets/panicle (91.15 %), harvest index (90.86 %), brown rice breadth (90.48 %), grain yield/plant (89.34 %), grain breadth (88.54 %), hulling % (88.23 %), milling % (84.00 %), plant height (81.17 %), biological yield (80.67 %), number of filled spikelets/panicle (79.71 %), flag leaf length (77.52 %), 1000 seed weight (76.18 %), milled rice breadth (75.51 %), number of spikelets/panicle (71.01 %). High heritability values indicate that phenotypic-based selection will be advantageous for these attributes. These results are in conformation with Islam *et al.* (2015); Khaire *et al.* (2017); Adhikari *et al.* (2018); Amudha and Ariharasutharsan (2020); Behera *et al*. (2020); Noatia *et al.* (2021).

Genetic advance as % of mean. High genetic advance as percentage of mean were found in characters like Number of unfilled spikelets/panicle(98.614 %), followed by harvest index (89.88 %), grain yield / plant (80.57 %), number of filled spikelets/panicle (54.69 %), biological yield (48.90 %), number of spikelets/panicle (40.49 %), 1000 seed weight (35.64 %), flag leaf length (35.56 %), L:B ratio (34.07 %), effective tillers / plant (32.05 %), milled rice length (31.15 %), brown rice length (29.10 %), grain length (28.51 %), plant height (27.63%), cooked rice length (25.76 %), HRR (21.22 %) and brown rice breadth (19.99 %). These findings are in accordance with those of Amudha and Ariharasutharsan (2020); Bhor *et al*. (2020); Kumar *et al*. (2020); Lipi *et al*. (2020); Mahamadali *et al*. (2020); Noatia *et al.* (2021); Priyanka *et al.* (2020).

Heritability coupled with genetic advance as percent of mean. Determining the gene activity involved in character expression depends critically on estimates of heritability and genetic progress expressed as a percent mean. Breeders should use caution when making choices depending on heritability since it can disclose both additive and non-additive gene effects. It is better to have high heritability and a high genetic advance as a percentage of the mean, which shows that heritability is most likely caused by an additive gene effect and is least impacted by the environment. Relying solely on these traits will be advantageous for speedy grain yield development in advanced rice breeding lines due to their high transmissibility and variability. The high heritability (%) combined with high genetic advance as percent of mean was observed for plant height followed by flag leaf length, number of spikelets per panicle, number of filled spikelets/panicle, number of unfilled spikelets/panicle, 1000 seed weight, harvest index, biological yield, grain yield / plant, grain length, L: B ratio, brown rice length, milled rice length and cooked rice length. These results Sao *et al.* (2004); Babu *et al.* (2012); Patel *et al.* (2014); Nayak *et al.* (2016); Rahangdale *et al.* (2019); Bhor *et al*. (2020); Devi *et al.* (2020); Kumar *et al*. (2020); Lipi *et al*. (2020); Noatia *et al.* (2021).

Table 1: List of the rice genotypes used in the study as experimental materials.

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	R 2307-43-3-1-38-1	22.	R 2419-523-1-314-1
2.	R 2315-49-1-42-1	23.	R 2451-671-1-335-1
3.	R 2315-49-2-43-1	24.	R 2422-776-1-359-1
4.	R 2322-58-1-52-1	25.	R 2433-976-1-428-1
5.	R 2377-70-2-61-1	26.	R 2447-1027-1-456-1
6.	R 2358-101-81-1	27.	R 2449-1032-1-462-1
7.	R 2358-103-1-82-1	28.	R 2449-1037-1-463-1
8.	R 2358-103-2-83-1	29.	CG Devbhog (Check)
9.	R 2358-109-1-86-1	30.	CG Sugandhit Bhog (Check)
10.	R 2370-112-2-90-1	31.	Dubraj Sel.-1 (Check)
11.	R 2370-115-1-93-1	32.	Vishnubhog Sel.-1 (Check)
12.	R 2400-161-2-132-1	33.	R2369-483-1-259-1
13.	R 2409-259-1-205-1	34.	R2369-475-1-251-1
14.	R 2409-266-2-207-1	35.	R2282-552-1-309-1
15.	R 1771-311-1-223-1	36.	Banspatri
16.	R 1771-315-1-224-1	37.	Maharaji
17.	R 2412-329-1-231-1	38.	JDP 2520-2-4-1
18.	R 2412-338-1-236-1	39.	R 2443-1839-1-1008-1
19.	R 2418-423-1-258-1	40.	Lokti Machi
20.	R 2418-471-1-294-1	41.	Kadamphool
21.	R 2419-522-1-313-1	42.	Antarved

Table 2: Analysis of variance (ANOVA) for different characters in rice.

Sr. No.	Characters	Source of variance		
		Replication	Treatment	Error
		d.f.(1)	d.f.(41)	d.f.(41)
1.	Days of 50 % flowering	0.964	173.27**	1.672
2.	Days to maturity	0.583	248.42**	1.949
3.	Plant height (cm)	52.583	859.83**	89.381
4.	Flag leaf length (cm)	17.545	214.61**	27.173
5.	Effective tillers / plant	3.772	5.689**	1.275
6.	Panicle length (cm)	9.67	13.72**	6.055
7.	Number of spikelets/panicle	664.2	4651.145**	788.631
8.	Number of filled spikelets/panicle	27.2	3923.008**	442.829
9.	Number of unfilled spikelets/panicle	189	1219.993**	56.461
10.	Spikelets fertility %	173.09	175.572**	57.193
11.	1000 seed weight (g)	11.52	31.821**	4.302
12.	Biological yield (g)	34.458	243.615**	26.065
13.	Harvest Index (%)	39.786	746.692**	35.757
14.	Grain yield / plant (g)	16.01	82.627**	4.652
15.	Grain Length (mm)	0.05	2.44**	0.05
16.	Grain Breadth (mm)	0.01	0.1**	0.006
17.	L:B ratio	0.01	0.68**	0.023
18.	Brown Rice Length(mm)	0.05	1.34**	0.03
19.	Brown Rice Breadth(mm)	0.02	0.09**	0.005
20.	Milled Rice Length(mm)	0.02	1.48**	0.033
21.	Milled Rice Breadth(mm)	0.01	0.05**	0.007
22.	Hulling (%)	14.28	89.85**	5.622
23.	Milling (%)	22.58	79.3**	6.894
24.	Head Rice Recovery (%)	116.88	129.7**	35.387
25.	Cooked Rice Length (mm)	0.02	2.21**	0.008
26.	Cooked Rice Breadth (mm)	0.01	0.15**	0.004
27.	Amylose Content (%)	0.09	9.97**	2.328

****:** Significant level at 0.01 %, ***:** Significant level at 0.05 %

Table 3: Genetic variability parameters of yield and yield contribution characters.

Characters	Mean	Range		CV (%)		h^2(bs) %	GA%	GAM%
		Min.	Max.	PCV	GCV			
Days of 50 % flowering	105	83	118	8.92	8.83	98.09	18.90	18.02
Days to maturity (days)	133	108	148	8.39	8.33	98.44	22.69	17.02
Plant height (cm)	131.84	71.86	178.31	16.52	14.89	81.17	36.43	27.63
Flag leaf length (cm)	49.38	24.81	71.71	22.27	19.60	77.52	17.56	35.56
Effective tillers / plant	7.60	4	11.4	24.55	19.54	63.38	2.44	32.05
Panicle length (cm)	24.30	16.21	31.17	12.94	8.06	38.78	2.51	10.34
Number of spikelets/panicle	188.40	83.4	294.5	27.68	23.33	71.01	76.28	40.49
Number of filled spikelets/panicle	140.30	43.3	241	33.30	29.73	79.71	76.72	54.69
Number of unfilled spikelets/panicle	48.11	15.1	138.3	52.52	50.14	91.15	47.44	98.61
Spikelets fertility %	75.18	54.55	89.82	14.35	10.23	50.86	11.30	15.04
1000 seed weight (g)	18.71	9.81	29.31	22.71	19.82	76.18	6.67	35.64
Biological yield	39.46	11.4	59.8	29.43	26.43	80.67	19.30	48.90
Harvest Index (%)	41.19	11.89	115.93	48.02	45.77	90.86	37.02	89.88
Grain yield / plant (g)	15.09	3.28	29.78	43.78	41.38	89.34	12.16	80.57
Grain Length (mm)	7.74	5.34	9.89	14.42	14.13	96	2.21	28.51
Grain Breadth (mm)	2.34	1.89	3.1	9.83	9.25	88.54	0.42	17.93
L:B ratio	3.35	2.27	4.5	17.68	17.10	93.53	1.14	34.07
Brown Rice Length (mm)	5.61	4.05	7.68	14.77	14.44	95.68	1.63	29.10
Brown Rice Breadth (mm)	2.03	1.68	2.94	10.72	10.20	90.48	0.41	19.99
Milled Rice Length (mm)	5.49	3.8	7.12	15.82	15.47	95.58	1.71	31.15
Milled Rice Breadth (mm)	2.04	1.47	2.36	8.07	7.02	75.51	0.26	12.56
Hulling (%)	66.18	41.48	76.19	10.44	9.81	88.23	12.56	18.98
Milling (%)	59.61	36.9	69.88	11.01	10.09	84.00	11.36	19.06
HRR (%)	50.40	25.62	63.78	18.03	13.63	57.14	10.69	21.22
Cooked Rice Length (mm)	8.36	5.86	10.49	12.60	12.55	99.24	2.15	25.76
Cooked Rice Breadth (mm)	2.95	2	3.54	9.37	9.09	94.18	0.54	18.18
Amylose Content (%)	17.92	14.34	23.16	13.84	10.91	62.13	3.17	17.72

CONCLUSION

Analysis of variance revealed that the genotypes differed significantly for all the traits studied. The highest magnitude PCV and GCV were observed for a number of unfilled spikelets/panicles indicating that selection will benefit genetic improvement. The high heritability (%) combined with high genetic advance as % of mean indicates it is most likely due to an additive gene effect. As a result, selecting advanced rice breeding lines based on these characteristics will be useful for increasing grain yield quickly.Top 10 promising rice genotypes based on grain yield / plant performance R 2412-338-1-236-1, R 2358-109-1-86-1, R 2370-115-1-93-1, R 2370-112-2-90-1, R 2409-266-2-207-1, R 2447-1027-1-456-1, R 2358-101-81-1, R 2377-70-2-61-1, R 2358-103-2-83-1, R 2449-1032-1-462-1. These can be incorporated in future rice hybridization programmes and can be released as new high-yielding varieties after thorough testing.

FUTURE SCOPE

Throughout the research work, the top promising rice genotypes based on grain yield/plant performance are suggested to be used for incorporation in the future rice hybridization programme and can be released as new high yielding varieties after thorough testing.

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Conflict of Interest. None.

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