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Assessment of genetic variability for grain yield and its components in fine rice (*Oryza sativa* L.)

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Abstract
The current field experiment was carried out during the *Kharif* 2021 at the Education and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Ratnagiri, with the goal of estimating the genetic variability for yield and yield-attributing character. Genotype differences were significant for each of the twenty-one traits being studied, according to the analysis of variance in the current experiment, which revealed that genotypes reported wide range of variation. A wide range of variation were observed in the characters like days to appearance of first flower, days to 50% flowering, plant height, number of filled spikelet per panicle, number of unfilled spikelet per panicle, total number spikelet per panicle. For the characteristics, tillers per plant, unfilled spikelet per panicle, straw yield per plant, iron, zinc, grain yield per plant and protein have higher phenotypic and genotypic coefficients of variation estimates were detected. This implies that the genotypes used in the study have a varied genetic background, and selection for these qualities may help the genetic improvement of crops. Number of tillers per plant, number of unfilled spikelet per panicle, straw yield per plant, grain breadth, test weight, l/b ratio, zinc, iron, protein, plant height, grain length, amylose, total number of spikelet per panicle, number of filled spikelet per panicle, spikelet fertility, grain yield per plant, panicle length, and days to 50% flowering all had high heritability estimates and high genetic advance estimates as a percentage of the mean. Based on the findings of the current study, it can be concluded that additive gene action predominates and that genotypes exhibit considerable genetic variability for all of the yield-related traits under consideration.

Keywords: Rice, genotypes, genetic variability, heritability, genetic advance, yield etc

Introduction
Rice (*Oryza sativa* L.) is one of the world's most important cereal crop, providing the major staple food for 50 per cent of the world population. It supplies two third of the calories for the two billion people of Asia and one third of calorie intake of nearly one billion people in Africa and Latin America. It belongs to family 'Pinaceae' and genus include 24 species out of which '*Oryza sativa*' and '*Oryza glaberrima*' are cultivated. *'Oryza sativa'* has three subspecies *viz*; India, Japonica and Jamaica. However, the chromosome number (2n=2x=24). It is self-pollinated and short-day plant.

Fine grain rice is categorized into two types medium slender (TW14-18gm) and short slender grain (TW10-14gm). They are known for their unique grain texture, palatability, fineness, cooking quality and taste. It is having highest preference among consumers for different preparations. The demand for fine grain rice in urban area is increasing day by day. Because of its premium grain quality and high demand, it fetches more price which help to farmer to increase their profit.

Genetic variation is one of the differences occurs among the individuals rice genotype due to differences in their genetic composition and the environment factors in which they were grow. The difference of the genetic variability having in the introduced rice genotype is much more essential to rice improvement programmed which must be exploited by the rice breeders for its yield improvement to achieve the demands of the rice producers.

It is vital to understand the genetic architecture of genotypes in order to develop effective breeding methods. It is critical to determine the relative amount of additive and non-additive genetic variations, heritability and genetic gain in relation to the breeder's target characteristics. To generate promising kinds, a systematic breeding programmed includes processes such as creating genetic heterogeneity, performing selection and utilizing selected genotypes.

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The wide range of genetic variability in segregating populations, which is dependent on genotype genetic variation, provides more selection opportunities. Estimates of GCV, PCV, heritability and genetic progress will be crucial in utilizing future rice improvement research estimates.

Material and Methods

The experiment was conducted in the Randomized Block Design (RBD) with two replications during *Kharif* 2021 at Educational and Research farm Department of Agricultural Botany, College of Agriculture, Dapoli. A plot measuring 3.0 x 0.6 m was maintained, with a row-to-row distance of 20 cm and a plant-to-plant distance of 15 cm. The following data were collected for each replication: Days to appearance of first flower, days to 50% flowering, days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), number of filled spikelet's per panicle, number of unfilled spikelet's per panicle, total number spikelet's per panicle, spikelet fertility (%), test weight (g), straw yield per plant (g), grain length (mm), grain breadth (mm), length / breadth ratio, harvest index (%) amylose (%), protein (%), zinc (ppm), iron (ppm), grain yield per plant (g).

Analysis was done on the average of all the plants for each characteristic under each replication (Panse and Sukhathme, 1967) [20]. Using the mean square values from the ANOVA table, the estimate of genotypic variance and phenotypic variance was calculated in accordance with the method recommended by Johnson *et al*. (1955) [12]. Based on the technique recommended by Burton *et al*., (1953) [6] the phenotypic and genotypic coefficients of variance were estimated. The approach outlined by Lush (1949) [16] was used to estimate heredity percent in a broad sense, while Robinson *et al.,* (1949) methods was used to classify features as having high, moderate, or low heritability. The Johnson *et al*., (1955) [12] technique was used to evaluate genetic advance, which was represented as a percentage of the mean according to the technique recommended by Johnson *et al*., (1955) [12] traits were categorised as having high, moderate, or low genetic advance.

Results and Discussion

The main requirement for a crop breeding programme is genetic variation. As a result, plant breeders are always looking for new strategies to explore and recombinase genetic material to gather or create variety. Before using diverse techniques, plant breeders should have a thorough understanding of the nature, expression, and extent of variability present in the population of crops. Therefore, assessing population variability becomes a prerequisite for each breeding effort.

The analysis of variance in the current experiment showed that genotypes reported a large range of variation and that genotype differences were significant for each of the twenty-one features under examination. Nevertheless, the level of variation varied depend greatly on the character in concern. Highly significant variations in treatment (genotypes) suggested that all of the features under examination had a considerable level of variability. The methods of selection to be used in each situation would rely on how well we understood the type and degree of variability. These findings were in conformity to those of Rukmini devi *et al.* (2016) [24], Rashmi *et al.* (2017) [22], Pratap *et al*. (2018) [21] and Bandi *et al.* (2018) [4]. The wide range of variation were observed for

the characters like days to appearance of first flower (87 to 105 days), days to 50% flowering (89 to 107 days), plant height (75 to 122 cm), number of filled spikelet per panicle (88 to 222), number of unfilled spikelet per panicle (13 to 71), total number spikelet per panicle (119 to 254). Mustafa and Elsheikh (2007) [19], Khaire *et al*. (2017) [13], Pratap *et al*. (2018) [21], Bhargavi *et al*. (2021) [5] and Chavan *et al*. (2022) [7] noted a similar range of variation in these traits.

Table 1: Analysis of variance for yield and yield attributing traits in rice

Sr. No.	Characters	Mean Sum of Squares		
		Replication (1)	Treatment (31**)	Error (31)
1	Days to appearance of first flower	1.891	25.564**	2.794
2	Days to 50% flowering	2.250	27.606**	2.315
3	Days to maturity	1.000	31.935**	2.839
4	Plant Height (cm)	5.581	296.845**	4.612
5	Number of tillers per plant	0.345	21.539**	0.856
6	Panicle length (cm)	3.422	11.468**	1.788
7	Number of filled spikelet per panicle	43.066	1329.955**	76.819
8	Number of unfilled spikelet per panicle	2.402	262.669**	12.324
9	Total number spikelet per panicle	65.813	1677.887**	90.207
10	Spikelet fertility (%)	0.021	65.08**	3.971
11	Test weight (g)	0.002	11.862**	0.072
12	Straw yield per plant (g)	5.881	51.631**	3.878
13	Grain Length (mm)	0.001	0.203**	0.005
14	Grain Breadth (mm)	0.001	0.14**	0.001
15	Length / Breadth ratio	0.000	0.28**	0.003
16	Harvest Index (%)	2.250	37.927**	17.243
17	Amylose (%)	0.092	4.467**	0.220
18	Protein (%)	0.236	3.32**	1.076
19	Zinc (ppm)	1.300	18.927**	1.739
20	Iron (ppm)	2.410	24.897**	3.049
21	Grain yield per plant (g)	1.891	18.015**	3.620

** = 1% significance

Three types of variability can be used to categorize each character's overall variability: phenotypic, genotypic, and environmental. This makes it easier to differentiate between the heritable and non-heritable characteristics in the study. Phenotypic variances were often greater than corresponding genotypic variances for a variety of characteristics. The estimated genetic parameters revealed that the phenotypic and genotypic variances varied to a significant degree. The characters total number of spikelet per panicle, number of filled spikelet per panicle, plant height, number of unfilled spikelet per panicle, spikelet fertility, and straw yield per plant give higher values for phenotypic variance than the corresponding genotypic variances among all thirty-two genotypes. Similar findings were observed by Sameera *et al*. (2015) [27], Khaire *et al*. (2017) [13].

The genotypic and phenotypic coefficients of variation are used to quantify how much variation exists for a given feature in the population. It was found that the genotypic coefficients of variation for numerous individual traits were generally lower than the corresponding phenotypic coefficients of variation. But for several characters, the differences between GCV and PCV were less, indicating that they were less influenced by their surroundings. For the characters number of tillers per plant (39.55, 38.01), number of unfilled spikelet

per panicle (36.23, 34.57), straw yield per plant (29.35, 27.33), iron (25.37, 25.20), zinc (24.30, 24.05), grain yield per plant (22.90, 20.69) and protein (21.30, 20.71) higher PCV and GCV estimations were noticed. These findings matched those of studies conducted by Meena *et al*. (2018) [17], Mourya *et al*. (2018) [17], Saha *et al*. (2019) [25] this implies that the genotypes used for the study have a varied genetic background, and selection for these qualities may facilitate the genetic improvement of crops.

Heritability, which is the heritable component of phenotypic variation, is a great indicator of how characteristics are transmitted from one set of parents to their offspring (Falconer, 1960) [8]. The heritability estimates in the current study were high for each characteristic as per Robinson's (1949) [23] classification. The assessment depends on genetic advancement reported as a percentage of the mean, which is then used to compare traits. The heritability values for several yield and yield-attributing traits ranged from 37.5% to 99.29%. Heritability estimates were high for all of the traits that were examined. High estimates of broad sense heritability were found for the following traits: grain breadth (99.29%), test weight (98.80%), iron (98.68%), l/b ratio (98.16%), zinc (97.98%), plant height (96.94%), grain length (95.56%), protein (94.51%), number of tillers per plant (92.36%), number of unfilled spikelet's per panicle (91.04%), amylose (90.60%), total number spikelet's per panicle (89.80%), number of filled spikelet's per panicle (89.08%), spikelet fertility (88.49%), straw yield per plant (86.03%), days to 50% flowering (84.53%), days to maturity (83.67%), grain yield per plant (81.61%), days to appearance of first flower (80.30%), panicle length (73.02%). Low heritability estimate was observed in harvest index (37.50%). These results are according with the findings of Kurmanchali *et al*. (2019) [15], Meena *et al*. (2018) [17], Gokulkrishnan *et al*. (2014) [9], Islam *et al*. (2015) [11].

Table 2: Estimates of Components of variation for yield and yield attributing characters in rice.

Sr. No.	Characters	Phenotypic variance	Genotypic variance	Environmental variance
1	Days to appearance of first flower	14.18	11.39	2.79
2	Days to 50% flowering	14.96	12.65	2.31
3	Days to maturity	17.39	14.55	2.84
4	Plant Height (cm)	150.73	146.12	4.61
5	Number of tillers per plant	11.20	10.34	0.86
6	Panicle length (cm)	6.63	4.84	1.79
7	Number of filled spikelet per panicle	703.39	626.57	76.82
8	Number of unfilled spikelet per panicle	137.50	125.17	12.32
9	Total number spikelet per panicle	884.05	793.84	90.21
10	Spikelet fertility (%)	34.53	30.55	3.97
11	Test weight (g)	5.97	5.89	0.07
12	Grain yield per plant (g)	8.48	6.92	1.56
13	Straw yield per plant (g)	27.75	23.88	3.88
14	Grain Length (mm)	0.10	0.10	0.00
15	Grain Breadth (mm)	0.07	0.07	0.00
16	Length / Breadth ratio	0.14	0.14	0.00
17	Harvest Index (%)	27.58	10.34	17.24
18	Amylose (%)	2.34	2.12	0.22
19	Protein (%)	1.39	1.32	0.07
20	Zinc (ppm)	8.80	8.62	0.18
21	Iron (ppm)	14.32	14.14	0.19

Genetic advance denotes evolution through selection, while expression of genetic advance as a percentage of the mean aids in better understanding the effectiveness of selection in strengthening traits. The value of genetic advance ranged from 0.54 (grain breadth) to 55.00 (total number spikelet per panicle). High estimates of genetic advance were observed for the characters like total number spikelet per panicle (55.00%), number of filled spikelet per panicle (48.67), plant height (24.52), number of unfilled spikelet per panicle (21.99%), spikelet fertility (10.71%) and straw yield per plant (9.34%). Whereas low for iron (7.69%), days to maturity (7.19%), days to 50% flowering (6.73%), number of tillers per plant (6.37%), days to appearance of first flower (6.23%), zinc (5.99%), test weight (4.97%), grain yield per plant (4.90%), harvest index (4.06%), panicle length (3.87%), amylose (2.89%), protein (2.30), l/b ratio (0.76%), grain length (0.63%) and grain breadth (0.54%). Anjaneyulu *et al*. (2010) [3], Krishna *et al*. (2010) [14], Aditya *et al*. (2013) [1], Kurmanchali *et al*. (2019) [15] also recorded similar kind of results in rice.

Genetic advance as per cent of mean varied from 5.50 per cent for days to maturity to 75.24 per cent for number of tillers per plant. Highest values for genetic advance per cent of mean noted by number of tillers per plant (75.24%) followed by number of unfilled spikelet's per panicle (67.95%), straw yield per plant (52.02)%, iron (51.58%), zinc (49.04%), protein (41.48%), grain yield per plant (38.50%), number of filled spikelet's per panicle (36.03%), test weight (33.07%), total number spikelet's per panicle (32.85%), grain breadth (28.75%), length / breadth (25.49%), plant height (24.84%), panicle length (16.89%), spikelet fertility (13.28%), amylose (12.18%), grain length (11.46%), harvest index (9.68%), days to 50% flowering (6.82%), days to appearance of first flower (6.49%), days to maturity (5.50%). The results were in accordance with Sameera *et al*. (2016) [26], Gokulkrishnan *et al*. (2014) [9], Yadav *et al*. (2017) [28].

The most important selection criteria are heritability and genetic advance. In general, genetic advance and heritability estimates work better together than just heritability estimates to increase the genetic gain under selection. High heritability estimates and high genetic advance estimates as a percentage of the mean were documented for number of tillers per plant (92.36%, 75.24%), number of unfilled spikelet's per panicle

(91.04%, 67.95%), straw yield per plant (86.03%, 52.02%), grain breadth (99.29%, 28.75%), test weight (98.8%, 33.07%), l/b ratio (98.16%, 25.49%), zinc (97.98%, 49.04%), iron (98.68%, 51.58%), protein (94.51%, 41.48%), plant height (96.94%, 24.84%), grain length (95.56%, 11.46%), amylose (90.60%, 12.18%) total number spikelet's per panicle (89.80%, 32.85%), number of filled spikelet's per panicle (89.08%, 36.03), spikelet fertility (88.49%, 13.28%), grain yield per plant (81.61%, 38.50%), panicle length (73.02%, 16.89%), days to 50% flowering (84.53%, 6.82%), Similar kind of results were recorded by the Gokulkrishnan et al.

(2014) [9], Yadav et al. (2017) [28], Gour et al. (2017) [10], Sameera et al. (2016) [26].

High heritability estimates and low genetic advance as percent mean was detected in days to appearance of first flower (80.30%, 6.49%), days to maturity (83.67%, 5.50%), Low heritability estimates and low genetic advance as percent mean was recorded in harvest index (37.50%, 9.68%). These traits are affected by non-additive gene activity, so choosing them would not be beneficial for future crop development programmes. Similar findings were recorded by Sammera et al. (2016) [26], Ajmera et al. (2017) [2], Rashmi et al. (2017) [22].

Table 3: Estimates of coefficient of variation, heritability and genetic advance for yield and yield attributing characters in rice.

| Sr. No.	Characters	Mean	Range	PCV (%)	GCV (%)	h²b	GA	GAM
1	Days to appearance of first flower	96	87-105	3.92	3.51	80.30	6.23	6.49
2	Days to 50% flowering	98	89-107	3.92	3.60	84.53	6.73	6.82
3	Days to maturity	128	119-139	3.25	2.97	83.67	7.19	5.50
4	Plant Height (cm)	98	75-122	12.44	12.25	96.94	24.52	24.84
5	Number of tillers per plant	8.46	4.75-17.30	39.55	38.01	92.36	6.37	75.24
6	Panicle length (cm)	22.93	28.50	11.23	9.59	73.02	3.87	16.89
7	Number of filled spikelet per panicle	135	88-222	19.63	18.53	89.08	48.67	36.03
8	Number of unfilled spikelet per panicle	32	13-71	36.23	34.57	91.04	21.99	67.95
9	Total number spikelet per panicle	167	119-254	17.76	16.83	89.80	55.00	32.85
10	Spikelet fertility (%)	80.65	68.30-90.36	7.29	6.85	88.49	10.71	13.28
11	Test weight (g)	15.03	10.38-20.63	16.25	16.15	98.80	4.97	33.07
12	Grain yield per plant (g)	12.71	8.50-21.30	22.90	20.69	81.61	4.90	38.50
13	Straw yield per plant (g)	17.94	12.10-32.80	29.35	27.23	86.03	9.34	52.02
14	Grain Length (mm)	5.53	4.54-6.26	5.82	5.69	95.56	0.63	11.46
15	Grain Breadth (mm)	1.88	1.51-2.73	14.05	14.00	99.29	0.54	28.75
16	Length / Breadth ratio	2.98	1.88-3.62	12.61	12.49	98.16	0.76	25.49
17	Harvest Index (%)	41.91	33.29-51.98	12.53	7.67	37.50	4.06	9.68
18	Amylose (%)	23.44	20.38-24.84	6.53	6.21	90.60	2.86	12.18
19	Protein (%)	5.55	3.60-8.36	21.30	20.71	94.51	2.30	41.48
20	Zinc (ppm)	12.20	6.46-18.32	24.30	24.05	97.98	5.99	49.04
21	Iron (ppm)	14.91	8.51-20.68	25.37	25.20	98.68	7.69	51.58
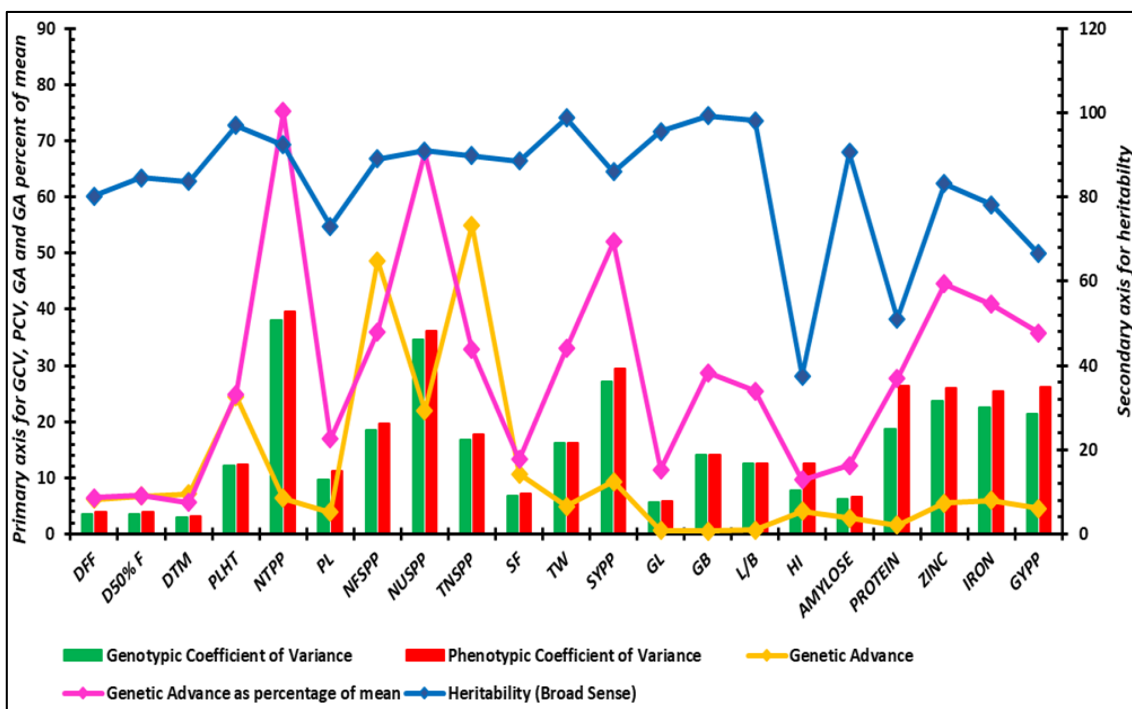
Fig 1: Shows a graphical representation of genotypic and phenotypic coefficient of variation, heritability and genetic advance as a percentage of the mean.

Conclusion
Based on the results of the current investigation, it is observed that the genotypes showed significant genetic variability for all the characters under study linked to the yield, most of the

characteristics showed high estimates of heritability and genetic advance, demonstrating the dominance of additive gene action. This suggests that there is plenty of scope for choosing promising genotypes to increase productivity. Using the right breeding methods and programmers, this variability might be successfully managed to create better kinds.

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