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Assessment of variability and principal component analysis in rice (*Oryza sativa* L.)

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Abstract

The availability of genetic diversity for particular traits in populations is important for both development of crop improvement programmes and implementation of suitable selection methods. The current study is aimed at exploring the genetic variability present among 339 rice genotypes during *kharif*-2022 using augmented design. With the exception of chaffy grains/panicle, biomass yield/plant and seed yield/plant all the characters under study showed a minimal impact of the environment on the expression of the character with small differences between the GCV and PCV. High heritability and genetic advance were observed for all the characters except biomass yield/plant, chaffy grains/panicle and spikelet fertility suggesting presence of high variability among the genotypes and additive gene action. In PCA, the first six principal components (PC1 to PC6) with eigenvalues larger than 1 were found to account for 80.767% of the variation in all attributes analysed. Traits such as; flag leaf area, biomass yield/plant, total grains/panicle, filled grains/panicle, seed yield/plant, panicles/plant, and total tillers/plant were discovered to be important characters contributing to variability through the use of variable biplot analysis. Therefore, by using direct phenotypic selection, these traits can be improved and used in selection programmes.

Keywords: Variability, principal component analysis, rice, yield attributing traits

1. Introduction

Rice is the most versatile staple food for one-third of the world's population, and Asia produces approximately 90% of the world's rice (Hasan-Ud-Daula and Sarker). In the Asian diet, rice continues to be the main source of protein, fibre, and nutrients. It is essential to exploit genotypic diversity to increase rice production capacity. Any crop improvement programme must prioritise genetic richness in the germplasm since it is essential for integrating advantageous alleles and bringing about desired changes (Sharma *et al.*, 2021) [20]. It is crucial to understand the genetic variability of the species, the nature of trait relationships, and the role of different traits in improving yield through breeding (Ketema and Geleta, 2022) [11].

Yield is a complex character that is affected by the way that genes are organised, the environment in which it grows, and the degree and kind of genotypic variety. It is influenced directly or indirectly by other agronomic factors such as primary and secondary branches/panicle, panicle length, tillers/plant and filled grains/panicle (Beena *et al.*, 2021) [3]. In any crop improvement programme the first and foremost step is the evaluation and characterization of available germplasm for genetic variability and identification of diverse and productive genotypes from that accession. Understanding genetic variability can determine whether certain variances are heritable or not. The degree of heritable variation is significant since it helps to choose parents during crop improvement programme (Dutta *et al.*, 2013) [5]. However, heredity (Broad sense) may not be useful for selection based on phenotype because it is modified by the environment. In order to accurately forecast the genetic gain subject to selection, estimates of heritability combined with genetic advance are more accurate than estimates of heritability alone (Ogunbayo *et al.*, 2014) [18].

It is a common practice to diversify the parents to take advantage of the phenotypic diversity present in the germplasm to break through the yield plateau. It is usual practice to diversify the parents in order to take advantage of the variation present in germplasms and break through the yield plateau, which is frequently a sign of a reserved genetic foundation. Since variation in plants for yield and yield-related factors happens often, principal component analysis (PCA)

can be used to find patterns and reduce redundant in datasets. The primary advantage of PCA is that it allows you to measure the value of each dimension with respect to the variability of a dataset. In consideration of these facts, the current study was done to assess genetic variation and the level of variability present among genotypes of the 3k rice panel for yield and its attributing traits using heritability, genetic advance and PCA.

2. Materials and methods

The genotypes used in the present investigation comprised 339 lines (334 entries and 5 checks) of 3k-MCP (Mini Core Panel) of rice received from IRRI-SA Hub, ICRISAT Campus, Hyderabad, India. The experiment was carried out in *Kharif 2022* on the experimental field of ICAR-NRRI (National Rice Research Institute), Cuttack, using an augmented randomized block design in three blocks with five checks (Anjali, Vandana, IR64, MTU1010, Swarna, BPT5204). The checks were replicated three times. Three random plants per replication were selected to take the observations on plant height (PH) in cm, panicle length (PL) in cm, panicles per plant (PPP) in numbers, flag leaf length (FLL) in cm, flag leaf width (FLW) in cm, flag leaf area (FLA) in cm², total tillers per plant (TTP) in numbers, filled grains per panicle (FGP) in numbers, chaffy grains per panicle (CGP) in numbers, total grains per panicle (TGP) in numbers, spikelet fertility (SF) in %, biological yield per plant (BYP) in g, seed yield per plant (SYP) in g, harvest index (HI) in% and hundred seed weight (HSW) in g. Further, the number of days to 50% flowering was also recorded. Estimation of phenotypic and genotypic coefficients of variation, heritability, genetic advance and principal component analysis (PCA) was done using R studio software (version 4.2.2).

3. Results and Discussion

3.1 Genotypic and phenotypic coefficient of variation

The genetic variability present in a population is utilised by crop improvement programmes. Genetic variation within the population and/or between the genotypes under selection determines how effectively a crop will respond to selection. In the current study, the genotypic coefficient of variation (GCV) ranged from 9.97% for spikelet fertility to 38.19% for seed yield per plant, while the phenotypic coefficient of variation (PCV) ranged from 12.18% in spikelet fertility to 55.04% for chaffy grains/panicle (Table-1). Sivasubramanian and Menon (1973) [22] defined PCV and GCV values as high if they are greater than 20%, low if they are less than 10%, and moderate if they are between 10% and 20%. Both GCV and PCV were high for panicles/plant, flag leaf area, filled grains/panicle, chaffy grains/panicle, total grains/panicle, biomass yield/plant, seed yield/plant, harvest index and hundred seed weight. High values of PCV and GCV indicate the existence of substantial variability for any character and selection might be effective based on the same character. Similar results of high GCV and PCV have been reported by Abebe *et al.* (2017) [1] for grain yield and unfilled grains/panicle, Ajmera *et al.* (2017) [2], Behera *et al.* (2018) [4] and Nath and Kole (2021) [17] for seed yield/plant. In the current study, PCV was higher than GCV for all the traits under observation and it was earlier observed by Tuhina-Khatun *et al.* (2015) [23], Longjam and Singh (2019) [26] and Patel *et al.* (2021) [19] in rice. In any trait, the magnitude of the differences between GCV and PCV indicates how much the

environment has influenced that trait; large differences indicate a great deal of environmental influence, whereas small differences indicate a lot of genetic influence. Because of the minor variations between the PCV and GCV for all traits except chaffy grains/panicle, biomass yield/plant, and seed yield/plant, the study discovered less environmental influence on the phenotypic expression of all of these traits. It also means that selecting individuals based on these traits for prospective crossover programmes will be successful (Tuhina-Khatun *et al.*, 2015) [23].

Table 1: Genetic parameters for yield and attributing traits of 339 genotypes of 3k rice panel

Trait	GCV	PCV	Hbs	GA	GAM
DFF	13.32	13.58	96.22	26.55	26.96
PH	17.93	18.07	98.47	43.07	36.71
PL	12.13	12.62	92.33	5.37	24.05
PPP	29.06	33.38	75.83	4.73	52.21
FLL	16.84	18.31	84.64	9.40	31.96
FLW	13.50	17.19	61.66	0.30	21.87
FLA	24.05	28.77	69.86	11.81	41.47
TTP	27.78	33.17	70.12	4.96	47.99
FGP	32.84	36.35	81.60	49.63	61.20
CGP	37.06	55.04	45.33	10.18	51.47
TGP	28.70	32.63	77.35	52.53	52.07
SF	9.97	12.18	66.93	13.47	16.82
BYP	29.77	44.97	43.82	30.83	40.65
SPY	38.19	49.02	60.72	10.57	61.40
HI	33.41	38.96	73.56	14.23	59.12
HSW	20.34	22.18	84.12	0.89	38.49

(GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; Hbs: Heritability (broad sense) in %; GA: Genetic advance; GAM: Genetic advance as % of mean)

3.2 Heritability and genetic advance

A character could be enhanced through selection more easily if there was a substantial heritable component. It is possible to determine the relative contributions of genetic and non-genetic variables to the overall variance of phenotypic traits within a population by conducting a heritability analysis. Selection for such a trait may be easier due to a large additive effect since any quantitative trait with a very high heritability estimate suggests that environmental effects contribute to phenotypes in a relatively small proportion (Vaghela *et al.*, 2009) [24]. Estimated values of heritability in the broad sense (Hbs) for various features ranged from 43.82% for biomass yield/plant to 98.47% for plant height. A trait's heritability can be classified as high (> 60%), moderate (31-60%), or low (0-30%), according to Johnson *et al.* (1955) [8]. Except for chaffy grains/panicle and biomass yield/plant, all of the evaluated traits had high heritability estimates. Similar findings are seen in the works of Longjam and Singh (2019) [26] for days to 50% flowering, plant height, length of leaf, spikelet fertility and test weight and Patel *et al.* (2021) [19] for plant height, effective tillers, spikelet fertility and seed yield/plant. Heritability has an impact on genetic gain under selection. Genetic advance (GA) under selection, is the enhancement of characteristics genotypic values for the new population as compared to the base population during a single cycle of selection at a specific level of selection intensity (Wolie *et al.*, 2013) [25]. In this study, spikelet fertility had the lowest genetic advance as % of mean (GAM) of 16.82%, whereas seed yield per plant had the highest GAM of 61.40%. Johnson *et al.* (1955) [8] defined GAM values as high when they are

greater than 20%, low when they are less than 10%, and moderate when they are between 10% and 20%. In the current study, high GAM values were expressed by all the traits under observations except spikelet fertility. In the works of Abebe *et al.* (2017) ^[1] for unfilled grains/panicle and grain yield/plant and Longjam and Singh (2019) ^[26] for total tillers/plant, and grain yield/plant, high GA were reported.

To increase selection effectiveness, it is necessary to combine heritability with genetic advance (Johnson *et al.*, 1955) ^[8]. Heritability and genetic advance (as % of mean) provide an indication of the level of improvement that can be achieved by phenotypic selection (Lalitha *et al.*, 2019) ^[14]. High heritability and high GAM indicate that additive gene action predominates in the expression of traits like seed yield per plant, harvest index, hundred seed weight, total tillers/ plant, panicle length, plant height, panicle numbers/plant, flag leaf length, flag leaf width, flag leaf area, filled grains/panicle, total grains/panicle, and days to 50% flowering. As a result, these characters are reliable and can be practiced for further improvement by selection.

3.3 Principal Component Analysis

Principal component analysis (PCA) was used to calculate the effective contribution of various traits based on the corresponding variance in order to comprehend variable independence and balanced loading of traits. Table 2 provide the eigenvalues, percent variability, and cumulative percent variability of various characters. As a potential source of diversity, principal components (PCs) with eigenvalues greater than 1 should be considered (Kaiser, 1960) for study. The first six principal components (PC1 to PC6) in the current investigation, with eigenvalues of 4.443, 3.011, 1.749, 1.524, 1.146, and 1.05, respectively, explained 80.767% of the total variance for all the analysed features. In Table 3, it is shown what percentage of the variables contributed to the principal component axis.

Traits *viz.* flag leaf area, filled grains/panicle, total grains/panicle and biomass yield/plant all contributed more favorably to the PC1, which explained 27.767% of the overall variation. A further 18.822% of the overall variation was accounted for by the PC2, which was mostly influenced by panicles/plant, total tillers/plant, chaffy grains/panicle, spikelet fertility, and seed yield/plant. Likewise, PC3 showed significant loadings for panicles/plant, tillers/plant, chaffy grains/panicle, and spikelet fertility. PC3 described 10.929% of the total variation. The variability for the traits present across the genotypes was finally contributed by the fourth, fifth, and sixth principal components (PC4, PC5 and PC6) which contributed around 9.524, 7.162 and 6.563% of the variability, respectively. The PC4 explained the patterns of variation in panicle length, flag leaf length, filled grains/panicle, and total grains per panicle; while PC5 provided variance through hundred seed weight, flag leaf length and area. The PC6 variability was mostly influenced by the days to 50% flowering, chaffy grains/panicle, harvest index and hundred seed weight. These traits account for a considerable portion of the divergence and also carry the majority of the variability. According to Singh *et al.* (2017) ^[21], characters would contribute more to the divergence the higher the absolute value in the PC. Six major components accounted for 76.4% of the genetic diversity assessed for micronutrient contents and agro-morphological characters of rice (Madhubabu *et al.*, 2020). In Kumari *et al.* (2021) ^[16, 13],

the first three PCs explained 68.69% of the total variation, and PC1 was positively loaded with panicles/plant. A PCA analysis of 217 germplasm lines revealed that PC1 and PC2 accounted for 46.15% of variability and plant height, filled grains/panicle, single plant yield and test weight were significant variables influencing variability (Krishna *et al.*, 2022) ^[12].

Table 2: Eigen values and contribution of variability for the principal component axis

PC	Eigenvalue	Percentage of variance	Cumulative % of variance
PC1	4.443	27.767	27.767
PC2	3.011	18.822	46.588
PC3	1.749	10.929	57.518
PC4	1.524	9.524	67.042
PC5	1.146	7.162	74.204
PC6	1.050	6.563	80.767
PC7	0.950	5.936	86.703
PC8	0.592	3.700	90.403
PC9	0.550	3.439	93.842
PC10	0.452	2.827	96.669
PC11	0.417	2.605	99.273
PC12	0.046	0.284	99.558
PC13	0.034	0.214	99.772
PC14	0.028	0.178	99.95
PC15	0.008	0.050	100

Table 3: Percentage contribution of variables on principal component axis

Variables	PC1	PC2	PC3	PC4	PC5	PC6
DFP	4.291	7.03	1.839	3.117	1.898	11.246
PH	8.491	0.009	0.034	5.915	4.217	8.006
PL	8.143	0.033	0.018	11.191	1.235	0.388
PPP	0.42	19.375	16.815	0.081	2.358	0.074
FLL	7.977	0.083	0.016	14.572	17.898	0.011
FLW	7.657	4.675	2.89	0.326	2.662	3.727
FLA	12.942	1.44	1.372	7.51	14.443	1.695
TTP	0.185	19.344	16.755	0.174	3.281	0.001
FGP	10.428	1.619	9.373	18.197	0	0.254
CGP	3.431	10.236	11.118	7.956	0.543	11.786
TGP	12.301	0.007	2.692	22.626	0.069	0.468
SF	0.001	14.223	23.713	0.023	0.378	9.451
BYP	12.746	1.565	5.131	0.108	5.627	1.873
SYP	8.906	10.882	0.205	0.116	4.966	5.394
HI	0.967	9.323	7.931	0.001	0.181	32.055
HSW	1.115	0.159	0.098	8.087	40.245	13.571

The coefficient of correlation between any two vectors representing variables in a biplot analysis is given by the cosine of the angle between the two vectors. Any angle between a vector representing a variable and an axis representing a PC is also an indication of correlation between two variables (Jolliffe and Cadima, 2016) ^[9]. Each trait's vector length shows how much it contributed to overall divergence; the longer the vector length, the greater the contributing traits were (Krishna *et al.*, 2022) ^[12]. This study used PC1 and PC2 to perform variable biplot analysis for 16 yield-related factors in order to examine how they interacted with one another (Fig. 1). Indicating its contribution to the overall divergence, the trait flag leaf area had the highest vector length, which was followed by biomass yield/plant, total grains/panicle, filled grains/panicle, seed yield/plant, panicles/plant, and total tillers/plant. The variable biplot

shown in Fig. 1 clearly demonstrates the sign difference in loading values of variables with regard to PC1 and PC2. With the exception of harvest index, every one of the 16 investigated variables had a positive connection with PC1. Likewise, for PC2, all traits except chaffy grains/panicle, days

to 50% flowering, flag leaf width, flag leaf area, and hundred seed weight exhibited positive association. For several yield-attributing features in rice, Fathima *et al.* (2021) [6] and Krishna *et al.* (2022) [12] revealed comparable findings.

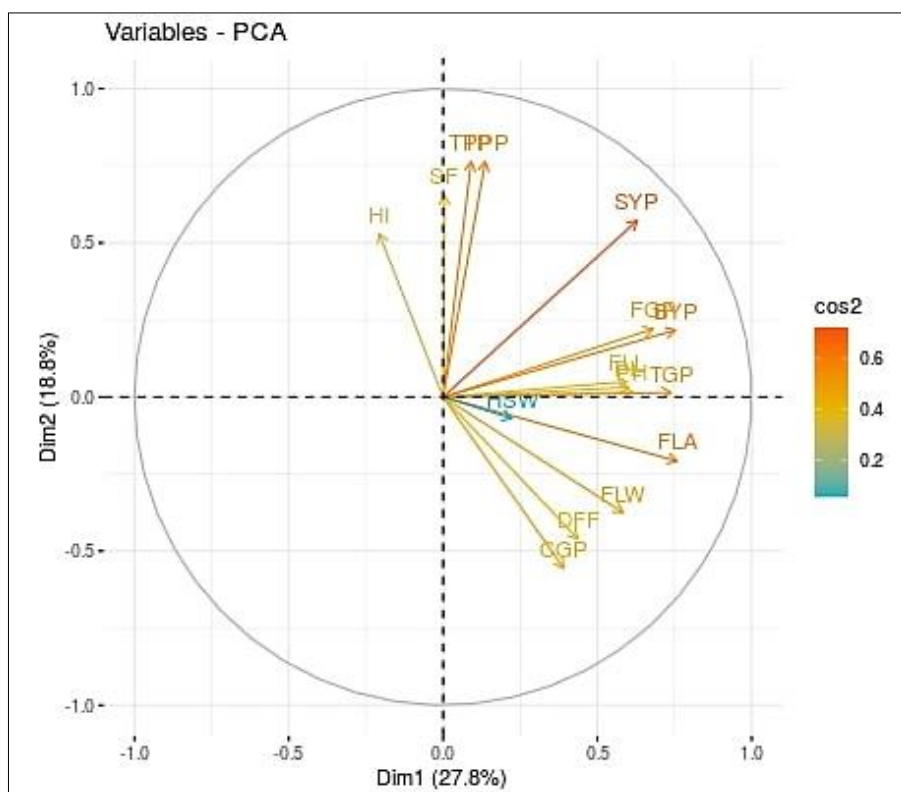


Fig 1: Biplot of 16 yield-related traits across the first two principal components

4. Conclusion

The current study highlighted the variability that existed across the 339 genotypes in the 3k rice panel including check varieties. The results of heritability and genetic advance demonstrated the predominance of additive gene action in the expression of panicle length, number of panicles per plant, flag leaf length, width, and area, number of tillers per plant, number of filled grains per panicle, number of total grains/panicle, and seed yield/plant, so selection based on these traits could contribute significantly to the improvement of rice. Using the principal component analysis method, the 16 variables in the data set were efficiently reduced to 6 principal components with eigenvalues greater than 1, accounting for 80.767% of the overall variability. It explains the pattern of useable variation in the current set of genotypes from the 3k rice panel. Principal components and variable biplot served as the foundation for identifying traits (such as flag leaf area, biomass yield/plant, total grains/panicle, filled grains/panicle, seed yield/plant, panicles/plant, and total tillers/plant) influencing phenotypes and undertaking selection, which will be effective for yield improvement. Thus, future breeding programs will benefit from selecting traits with high variability.

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