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Short Communication

Principal component analysis of JNPT lines of rice for the important traits responsible for yield and quality

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Abstract

In present study, 67 JNPT (Jawahar New Plant Type) lines were evaluated for 28 morphological and quality traits planted in RCBD with three replications. Principal Component Analysis (PCA) revealed that out of 28, only eight PCs exhibited more than 1.0 eigen value and showed about 81.84% total variability. For selecting the high yielding genotypes in rice, the characters *viz.,* spikelet density, spikelet fertility, number of tillers plant^{-1} and panicle weight plant^{-1} may be considered. On the basis of high PC score ten most prominent lines namely JNPT-1059-9, JNPT-1059-10, JNPT1062-1, JNPT-1062-2, JNPT-1064-9, JNPT-1065-1, JNPT-1065-2, JNPT1065-3, JNPT-1066-52 and JNPT-1068-65 were identified for yield and quality traits.

Key words: Eigen values, JNPT lines, PC score, rotated component matrix, scree plot ion

Principal component analysis (PCA) is a multivariate technique that is commonly used for compression, reduction and transformation of data. Its goal is: to extract the essential data from the table, to represent it as a set of new orthogonal variables called principal components and to show the pattern of similarity of the observations and of the variables as points in maps. Further, PCA identifies the minimum number of components, which can explain maximum variability out of the total variability (Anderson 1972; Morrison 1982) and also to rank genotypes on the basis of PC scores. Several researchers have characterized rice germplasm including the landraces, varieties and advance materials of diverse nature for morphological and physical-chemical quality parameters (Bollinedi et al. 2020; Madhubabu et al. 2020) and reported a wide range of variability. Considering the importance of PCA, an investigation was carried out on 67 JNPT lines to dissect componential traits for yield and quality to obtain precise information and to rank genotypes.

The experimental material consisted of 67 new JNPT (Jawahar New Plant Type) lines derived from *indica* x *japonica* subspecies crosses (F_8-F_9 BC_3 generation) was developed by Rice Improvement Project, JNKVV, Jabalpur. The materials were grown during *kharif* season of 2018 at Seed Breeding Farm, JNKVV, Jabalpur (M.P.), India. These lines were planted in Randomized Complete Block Design with three replications. Twenty-one days old seedlings were transplanted in five rows in each replication with spacing of 15 cm between plant to plant and 20 cm between the rows, keeping single seedling per hill. Gap filling was done within a week so as to keep uniform plant population. The standard agronomic practices were adopted for normal crop growth. Twenty-eight quantitative and quality characteristics were used to characterize and assess the genetic diversity of JNPT lines as per rice DUS guidelines. Five plants were randomly chosen from each replication in each genotype for yield assessment and quality attributed/ traits. The observations were recorded as per the standard procedure and subjected to statistical analysis using mean values. The statistical analysis of data on individual characters was carried out using mean values of randomly selected plants from each

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genotype in each replication. Principal components are generally estimated either from correlation matrix or covariance matrix. When the variables are measured in different units, scale effects can influence the composition of derived components. In such situations it becomes desirable to standardize the variables. In the present investigation correlation matrix was used to extract the principal components. PCA analysis was done using the methodology given by Massy (1965) and Jolliffe (1986).

Genetic variability and Principal Component Analysis (PCA)

PCA was performed using phenological, yield and quality components on rice germplasm. Out of twenty-eight, eight principal components (PCs) exhibited more than 1 Eigen value and showed about 81.84% total variability. The PC1 showed 20.82% while, PC2, PC3, PC4, PC5, PC6, PC7 and PC8 accounted 13.31%, 11.99%, 10.88%, 9.50%, 6.72%, 4.56% and 4.04% variability, respectively among the genotypes for the traits under study. Shoba et al. (2019) reported that out of nine PCs, four exhibited more than 1.0 eigen values and showed 70.14 per cent total variability among nine traits of sixty-seven rice germplasm lines. Jeevanpriya et al. (2019) reported that out of sixteen traits studied in one twenty-six rice genotypes which include new restorer lines of hybrid rice, 6 PCs exhibited more than 1.0 eigen values and showed about 70.20% total variability among the characters studied. The present findings are in agreement of previous findings.

Scree plot graph depicted in Fig. 1 explained the percentage of variance associated with each PCs obtained by drawing a graph between Eigen values and principal component numbers. PC1 showed 20.825% variability with Eigen value 5.831, which then declined gradually.

Rotated component matrix

Rotated component matrix presented in Tables 1 and 2 revealed that the PC1 which accounted for the highest variability (20.825%) among other 28 PCs. The PC2, PC4, PC5 and PC7 accounts for yield contributing traits whereas PC1 and PC3 dominated with yield as well as quality traits. The PC6 accounts for only quality traits. The PC1 accounts for spikelet fertility and thousand grain weight as well as quality related traits i.e. grain width and decorticated grain width. The PC2 was mostly dominated by yield contributing traits *viz*., number of spikelets panicle^{-1}, number of fertile spikelets panicle^{-1}, spikelet density, panicle index, harvest index and grain yield plant^{-1}. The present findings are in favour of Yang et al. (2009). Madhubabu et al. (2020) reported the results of principal component analysis (PCA)

Table 1. Rotated component matrix for different traits of JNPT lines of rice

Traits	Principal components						
	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DTF	-0.508	-0.135	-0.274	0.656	-0.021	0.165	-0.089
DTM	-0.470	-0.146	-0.226	0.717	0.017	0.168	-0.028
TPP	0.430	0.308	0.124	0.623	0.272	-0.010	0.240
PTPP	0.434	0.300	0.119	0.622	0.271	-0.009	0.244
PH	-0.353	-0.111	0.130	-0.276	0.817	0.057	0.121
SL	-0.306	-0.108	0.056	-0.195	0.832	0.021	0.152
PL	-0.355	-0.054	0.397	-0.488	0.245	0.189	-0.099
CT	-0.306	-0.127	0.329	0.311	0.056	0.187	-0.411
FLL	-0.488	0.045	-0.113	-0.188	0.491	-0.011	-0.058
FLW	-0.060	0.308	-0.088	-0.604	0.163	-0.299	0.260
BYPP	0.052	0.342	0.737	0.253	0.319	0.052	-0.064
PWPP	0.128	0.567	0.675	0.163	0.107	-0.220	-0.210
NSPP	-0.741	0.490	0.146	-0.218	-0.232	0.090	-0.074
FSPP	-0.590	0.597	0.144	-0.137	-0.255	0.089	0.184
SF	0.547	0.066	-0.050	0.153	0.074	-0.015	0.514
SD	-0.706	0.525	0.053	-0.103	-0.313	0.042	-0.037
TGW	0.729	-0.330	0.266	-0.253	-0.071	0.112	-0.106
PI	0.478	0.541	-0.230	-0.014	-0.025	0.022	0.161
HI	0.241	0.507	-0.131	-0.103	-0.285	-0.313	-0.138
GL	0.193	-0.437	0.662	-0.054	-0.333	0.107	0.066
GW	0.763	-0.100	0.027	-0.183	0.149	0.056	-0.301
DGL	0.247	-0.545	0.669	-0.069	-0.165	0.033	0.092
DGW	0.724	0.109	-0.283	-0.100	0.260	0.116	-0.411
DLBR	-0.379	-0.420	0.633	0.050	-0.293	-0.086	0.333
HP	0.339	0.412	-0.017	-0.190	-0.177	0.617	0.055
MP	0.426	0.275	-0.006	-0.291	-0.124	0.705	0.206
HRR	-0.256	0.101	0.078	0.135	0.166	0.723	-0.031
GYPP	0.233	0.669	0.578	0.146	0.107	-0.209	-0.164

Colored value represents more related traits in each principal component

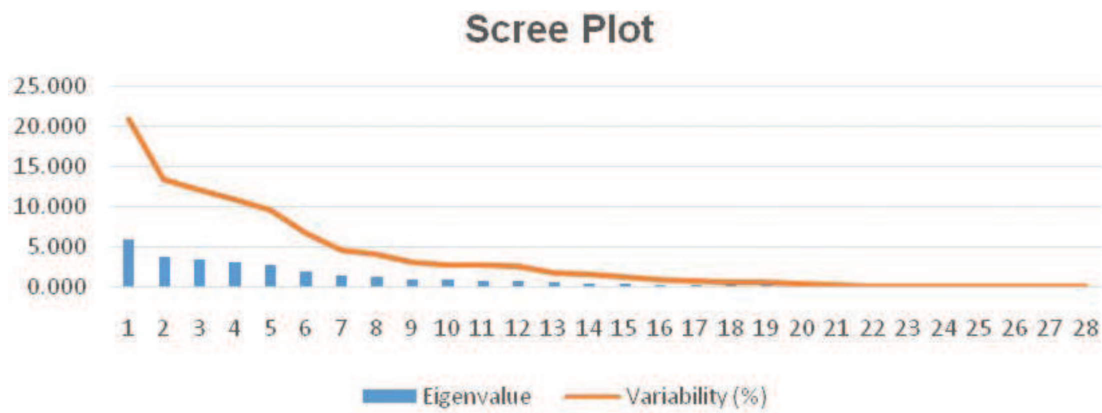

Fig. 1. Scree plot of principal component analysis for JNPT lines of rice between their Eigen value and the number of principal component

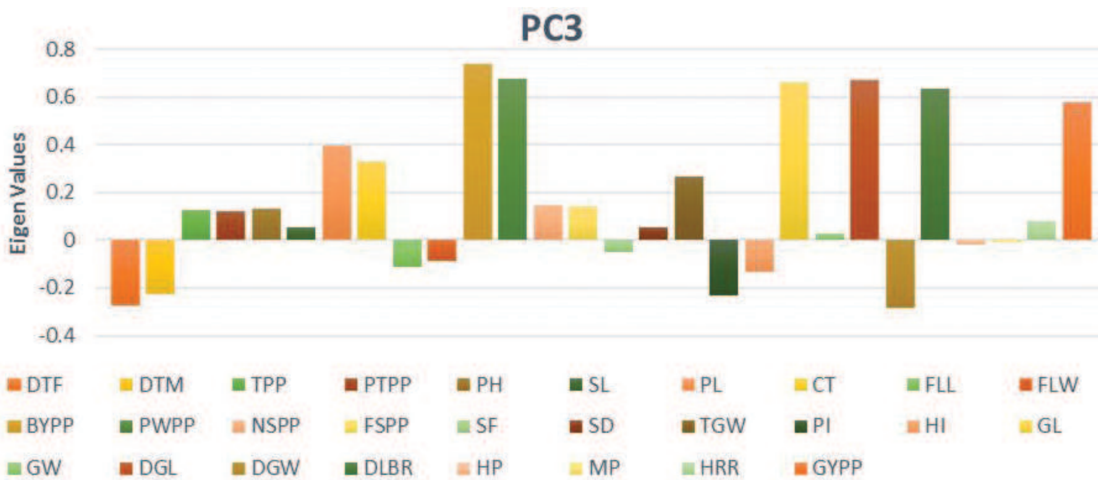

Fig. 2. Graphical representation of rotated component matrix for different traits in PC3

Table 2. Interpretation of rotated component matrix for the traits having highest value in each PCs

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Traits	SF	NSPP	PL	DTF	PH	HP	FLW
	TGW	FSPP	CT	DTM	SL	MP	
	GW	SD	BYPP	TPP	FLL	HRR	
	DGW	PI	PWPP	PTPP			
		HI	GL				
		GYPP	DGL				
			DLBR				

DTF = Days to 50% flowering, DTM = Days to maturity, TPP = Number of tillers per plant, PTPP = Productive tillers per plant, PH = Plant height, SL = Stem length, PL = Panicle length, CT = Culm thickness, FLL = Flag leaf length, FLW = Flag leaf width, BYPP = Biological yield per plant, PWPP = Panicle weight per plant, NSPP = Number of spikelet per panicle, FSPP = Fertile spikelet per panicle, SF = Spikelet fertility, SD = Spikelet density, TGW = Thousand grain weight, PI = Panicle index, HI = Harvest index, GL = Grain length, GW = Grain width, DGL = Decorticated grain length, DGW = Decorticated grain width, DLBR = Decorticated length breadth ratio, HP = Hulling percentage, MP = Milling percentage, HRR = Head rice recovery, GYPP = Grain yield per plant

that 6 PCs accounted for approximately 72.8% of variance. Discriminatory power of PCs as inferred from PCA was high for PC1 (>19%), whereas PC2 explained only 14.2% of variation positively correlated with test weight, grain length and grain width while negatively correlated with total tiller number and effective tiller number in rice.

The PC3 contributed for panicle length, stem thickness, biological yield plant^{-1}, panicle weight plant^{-1} and some quality traits *viz*., grain length, decorticated grain length and L/B ratio of decorticated grain. The PC4 was dominated with some phenological traits *viz*., days to 50% flowering and days to maturity

Table 3. PC scores of NPT genotypes having positive values >1.0 in each PC

PC1	PC2	PC3	PC4	PC5	PC6	PC7
JNPT-1065-3 (6.245)	JNPT-1062-2(4.063)	JNPT-1059-10(6.924)	JNPT-1068-65(4.806)	JNPT-1068-64(3.656)	JNPT-1066-56(2.326)	JNPT-1068-67(2.284)
JNPT-1065-1(4.252)	JNPT-1059-10(3.656)	JNPT-1051(3.527)	JNPT-1059-12(4.416)	JNPT-1059-10(3.567)	JNPT-1063-32(2.261)	JNPT-1068-65(2.156)
JNPT-1066-52 (3.778)	JNPT-1062-1(3.32)	JNPT-1059-9(2.544)	JNPT-1068-64(3.557)	JNPT-1063-34(3.179)	JNPT-1056(2.242)	JNPT-1064-9(2.073)
JNPT-1065-2(3.689)	JNPT-1068-65(2.892)	JNPT-1054(2.442)	JNPT-1058(3.403)	JNPT-1063-33(2.797)	JNPT-1063-36(2.148)	JNPT-1059-9(1.785)
JNPT-1065-5 (3.493)	JNPT-1064-4(2.748)	JNPT-1064-4(2.115)	JNPT-1061-25(3.078)	JNPT-1060-16(2.675)	JNPT-1064-9(1.991)	JNPT-1064-8(1.724)
JNPT-1068-66 (3.401)	JNPT-1060-15(2.635)	JNPT-1062-1(1.923)	JNPT-1061-26(2.859)	JNPT-1068-65(2.63)	JNPT-1062-1(1.854)	JNPT-1052(1.677)
JNPT-1065-4 (3.123)	JNPT-1065-3(2.624)	JNPT-1066-55(1.895)	JNPT-1060-24(2.851)	JNPT-1063-31(2.453)	JNPT-1058(1.851)	
JNPT-1064-7(3.003)	JNPT-1059-9(2.337)	JNPT-1066-53(1.890)	JNPT-1056(2.614)	JNPT-1063-36(2.393)	JNPT-1059-9(1.810)	
JNPT-1067-5 (2.836)	JNPT-1060-19(2.164)	JNPT-1061-26(1.888)	JNPT-1055(2.33)	JNPT-1059-9(1.734)	JNPT-1063-35(1.694)	
JNPT-1068-63 (2.617)	JNPT-1064-7(2.095)	JNPT-1053(1.839)	JNPT-1059-10(2.259)	JNPT-1065-3(1.674)	JNPT-1060-23(1.614)	
JNPT-1068-67(2.384)	JNPT-1067-4(1.963)	JNPT-1052(1.570)	JNPT-1061-27(1.844)	JNPT-1063-32(1.593)	JNPT-1065-2(1.547)	

PCA score of each NPT lines given in parentheses ()

and some yield contributing traits like number of tillers plant^{-1} and number of productive tillers plant^{-1}. PC5 included plant height, stem length and flag leaf length were recorded. Many important quality traits like hulling percentage, milling percentage and head rice recovery were found in PC6, whereas PC7 was linked to the trait flag leaf width. These results were in partial conformation with Ashfaq et al. (2012), Gour et al. (2017) and Choudhary et al. (2018).

The genotypes under study were selected on the basis of PC scores and presented in Table 3. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal component. High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype (Singh and Chaudhary 1977). Top PC scores of positive values >1.5 in each PC for all the rice genotypes were selected in 7 principal components.

The genotypes such as JNPT-1059-9, JNPT-1059-10, JNPT-1062-1, JNPT-10622, JNPT-1064-9, JNPT-1065-1, JNPT-1065-2, JNPT-1065-3, JNPT-1066-52 and JNPT-1068-65, fell in yield as well as quality associated PCs with high PC scores hence these lines had high value for yield as well as quality. On the basis of PC scores which is found to be common in yield as well quality associated PCs, maximum positive value recorded in JNPT-1059-10 (6.924). It can be concluded that PC analysis highlights the characters with maximum variability. So, intensive selection procedures can be designed to bring about rapid improvement of yield and quality attributing traits.

Authors' contribution

Conceptualization of research (PKU, GK, YS); Designing of the experiments (PKU, GK, SR); Contribution of experimental materials (GK, YS); Execution of field/lab experiments and data collection (SR, YS, GK); Analysis of data and interpretation (PKU, GK, SR); Preparation of manuscript (SR, PKU, YS).

Declaration

The authors declare no conflict of interest.

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