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Principal Component Analysis of Yield Attributing Traits in Derived Lines of Katarni Rice

Divya Mahto[1], P.K. Singh[2], Sareeta Nahakpam[3] and Mankesh Kumar[1]*

[1]Department of Plant Breeding and Genetics,
Bihar Agricultural University Sabour (Bihar), India.
[2]Director Seed and Farms, Bihar Agricultural University Sabour (Bihar), India.
[3]Department of Plant Physiology and Biochemistry,
Bihar Agricultural University Sabour (Bihar), India.

(Corresponding author: Mankesh Kumar)*
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ABSTRACT: In, the traditional aromatic non-basmati Katarni rice is grown in the few blocks of Bihar Bhagalpur, Banka, and Munger, districts. However, it matures late, has weak straws, is tall, and is prone to lodging. With the objective of developing a semi-dwarf and early maturing variety, Katarni was crossed with three semi-dwarf high yielding cultivars namely Rajendra Sweta, IR 64 and BPT5204. The generation was advanced to the F_6 generation and 54 derived lines of Katarni were examined in this study on the basis of 14 morphological parameters. Seventy percent of the entire variability was accounted for by five principal components, all of which had Eigen values above one. Between the first PC (23.31%) and second PC (35.59%), the total variation was 63.90%. Trait biplot analysis revealed substantially favorable genotypes for plant height and also found to be strongly positively. The genotypes biplot analysis showed that entries KIR-46, KIR-48, KRS-30, KRS-32, KRS-40 KRS-43, KRS-14, KRS-15, KRS-16, KRS-17, KRS-9, KRS-25 and KMTU-54 were found to be diverse and can be used further for varietal development.

Keywords: Eigenvalue, Hybridization, Katarni, Principal component.

INTRODUCTION

In more than 39 nations, rice (*Oryza sativa* L.) provides around 32–59% of the dietary calories and 25–44% of the dietary protein consumed by more than 2.7 billion people (Tannidi *et al.,* 2016; Prabhu *et al.,* 2017). The traditional Basmati and developed Basmati varieties form a significant portion of the Basmati gene pool of the Indian subcontinent, according to (Nagaraju *et al.,* 2002), which claims that the aromatic Basmati lies on a distinct group between indica and japonica. A traditional non-basmati cultivar of aromatic rice from the Bihar district of Bhagalpur is called Katarni. One of India's most well-known fine-grained aromatic rices, this rice is noted for its distinct scent, distinctive grain, and exceptional cooking properties. It blooms from the end of October to the beginning of November, maturing in December. According to (Smriti *et al.,* 2016), its height ranges from 140 to 160 cm. In April 2018, Katarni rice received a geographical indicator due to its distinctiveness. The available Katarni, however, has low yields (25–30 t/ha), weak straws, a tall variety, and is late maturing. It is also readily lodging-prone (Kumar *et al.,* 2018). The most common method for estimating the relative contribution of different features to overall variability is principal component analysis (PCA), which makes it simple to pinpoint the fewest factors that contribute the most variability. Also, it demonstrates the pattern of similarities and relationships between the qualities. Moreover, PCA determines the smallest number of components that can account for the greatest amount of variability out of all variability (Anderson 1972) and also ranks genotypes based on PC scores. Rice germplasm has been characterized by a number of researchers for morphological and physical-chemical quality characteristics, including landraces, varieties, and advance materials of various natures (Bollinedi *et al.,* 2020; Madhubabu *et al.,* 2020), and a wide range of variability has been recorded. A segregating population was produced by crossing Katarni with R. Sweta IR-64 and MTU-7029, and this population was used as study material for the current experiment. The entries in segregating generation were selected on the basis of semi-dwarf plant height with early maturity and good yielding ability. The principal component analysis was used to identify a promising line which can be used in next breeding programmes, on the basis of diversity of morphological parameters.

MATERIALS AND METHODS

The experimental material included 54 Katarni derived families along with two rice genotypes as aromatic checks i.e. Sabour Surbhit and Rajendra Suwasini—and four parental checks—Katarni, R. Sweta, IR-64, and MTU-7029. During Kharif 2019, the derived lines of Katarni were grown in an alpha lattice pattern with two replications at the rice section of the Bihar Agricultural University, Sabour, Bhagalpur. The segregating genotypes of Katarni × R. Sweta, Katarni × IR64, and Katarni × MTU7029 were designated as KRS, KIR, and KMTU, respectively, for convenience. Morphological data were recorded for fourteen quantitative and qualitative traits.

By linearly transforming the original variables, principal component analysis can reduce a huge data set into a smaller number of uncorrelated variables, or principal components. Genotypic means were employed in the current study to identify genetic variability for the attributes in PCA. SAS (Statistical Analysis System) version 9.2 was used to analyze each set of data. Eigen values, which specify the amount of overall variation shown on the PC axis, were initially determined for PCA. After then, loading values were standardized so that the sum of square of loadings within a PC was equal to 1. The loading values showed how each trait contributed to its corresponding principal component.

RESULT AND DISCUSSION

The results of the analysis of variance showed a significant variation for the characteristics, like number of tillers per plant, and plant height indicating genetic diversity. To determine the major components, their contributing characteristics, and the genotypes within each component, principal component analysis were used. Upon analysis, seven major components were identified by the PCA (PC1 to PC7) out of which, five of the seven PCs—PC1 (3.64), PC2 (2.41), PC3 (1.38), PC4 (1.19), PC5 (1.09), PC6 (0.94), and PC7 contributed 80% of the total variability (0.82). The cumulative variation shown by the first PC (25.98%) and second PC (43.16%) was found to be 69.14%. Tables 1 and 2 list the principal components, Eigen values, factor loading values, percentage contributions of each variable to the total variance, and key qualities that contribute to each main component. Kernel length, length to breadth ratio were significant variables and contributed substantial sources of variation in PC1. Contrarily, main source of variability were imparted by flag leaf length and plant height in PC2, alkali spreading value and the number of tillers per plant in PC3 (Table 2), kernel breadth in PC4, leaf aroma score, and alkali spreading value in PC5. The programme for crop improvement must include traits with considerable variability (Nachimuthu *et al.,* 2014). Consequently, in present study, the selection of diverse genotypes from a certain principal component can be based on the length and breadth ratio, number of tillers per plant, panicle length, and plant height. The results of this study agreed with those of (Sao *et al.,* 2019; Ojha *et al.,* 2017; Gour *et al*., 2017). The factor loading value was found to be at its highest for grain yield per plant in PC6 (0.56) and kernel length (0.88) in PC1, flag leaf length (0.75) in PC2, alkali spreading value (0.53) in PC3, kernel breadth (0.70) in PC4, and leaf aroma score (0.81) in PC5. In PC1, genotype KIR-46 had the most variability (11.51%), followed by KIR-48 (6.87%), and KRS-39 (5.50%) (Table 3).

In PC2, however, genotype KRS-17gave the most variability (10.43%), followed by KRS-15 (7.44%), and KRS-16 (7.25%). The main contributions to variability in PC3 were KRS-33 (20.94%), KMTU-54 (7.25%) and KRS-31(6.40%), in PCA4, they were KRS-33 (31.46%), KRS-37 (5.90%). Genotypes KRS-31 (9.89%) and KRS-28 (6.00%) made up the majority of the variability in PC5. Katarni (10.52%) was the check that contributed the major variability to PCA5 among the others (Table 3).

The results of PCA on the F_6 lines of Katarni would be very helpful in choosing promising and diversified breeding lines for upcoming rice development programmes. The Scree plot was used to describe the percentage of variation by graphing the eigen values and cumulative variability (%) on the Y axis and the mean value of the 14 characters being studied on the × axis (Fig. 1). Each PC's proportion of variance and its Eigen values were explained by the scree plot. According to the graph, the top three PCs produced the majority of the variations. The scores for the 14 various characters in the scree plot were distributed differently, indicating a significant amount of diversity. Genotype by Trait (GT) biplot, which highlights those genotypes that are particularly outstanding in certain traits, allows for genotype comparison on the basis of assessed multiple factors. Effectively, the GT biplot can be utilised as a genotype selection criterion that is independent of yield (Yan and Rajcan 2002). A trait's vector length, or distance from the biplot origin, is a sign of how that characteristic is represented in the biplot. A short vector suggests that the trait's genotype-to-genotype variance is either modest or poorly represented in the biplot due to the trait's weak or absent connection with other traits (Yan and Fregeau-Reid 2018). In the biplot analysis, PC1 and PC2 variables demonstrated both positive and negative relationship among the attributes. Since the axes recorded an angle smaller than 900 plant height, had a strong positive correlation (Fig. 2). The Flag leaf length, panicle length, length breadth ratio with kernel length, kernel breadth, with alkali spreading value and amylose content with grain yield per plant were also positively associated as these parameters showed axis angles smaller than 900. Some features, such as number of grains per panicle with number of tillers per plant with days to 50% flowering, were negatively correlated because they are positioned at a roughly 1800-degree angle on the PC1 and PC2 axes. In a similar vein, the

genotypes biplot research (Fig. 3) showed that the entries KIR-46, KIR-48, KRS-30, KRS-32, KRS-40 KRS-43, KRS-14, KRS-15, KRS-16, KRS-17, KRS-9, KRS-25, KMTU-54, and Katarni are far from the axes' origins, showing their variety in comparison to other genotypes under consideration. As a result, the present study's different genotypes can be used to initiate a hybridization breeding programme. These diverse genotypes include selection of plant height, number of tillers per plant, panicle length, and kernel length, length breadth ratio of the kernel.

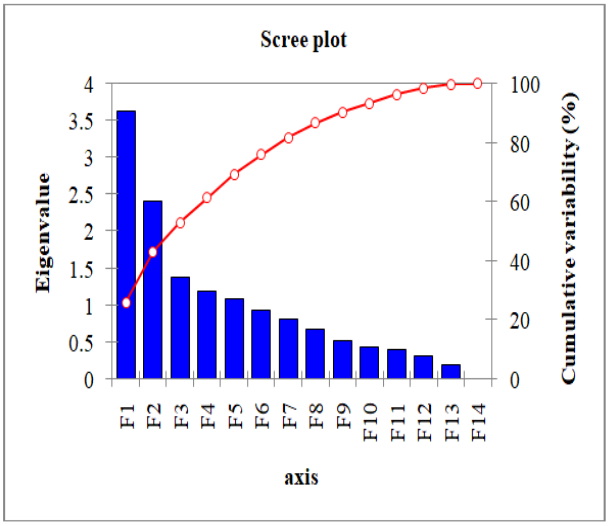

Fig. 1. Scree plot of different components with Eigen values.

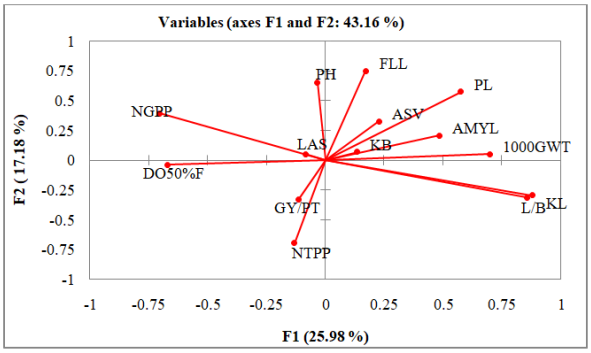

Fig. 2. Biplot of 14 different morphological characters.

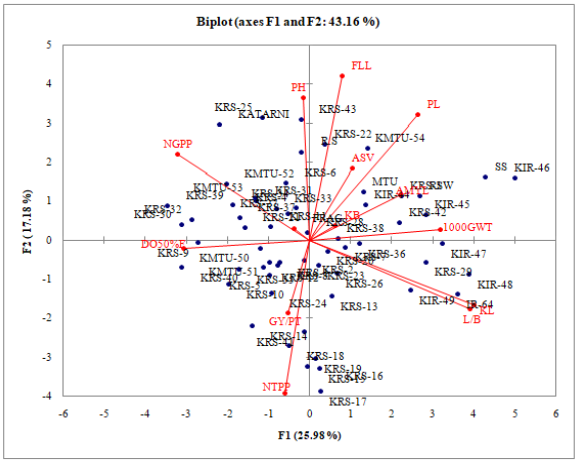

Fig. 3. Biplot of 60 genotypes including checks.

Table 1: Eigen value, percentage of variance and Eigen vector of Katarni derived lines.

PCA / Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigenvalue	3.64	2.41	1.38	1.19	1.09	0.94	0.82
Variability (%)	25.98	17.18	9.84	8.52	7.80	6.73	5.85
Cumulative %	25.98	43.16	53.00	61.52	69.32	76.05	81.90
Component matrix	**Factor Loading Value**						
PH	-0.03	0.65	-0.08	-0.17	0.20	0.48	0.22
DO50%F	-0.67	-0.04	-0.04	-0.21	0.10	-0.05	0.52
FLL	0.17	0.75	0.12	0.10	-0.22	0.09	-0.12
PL	0.58	0.57	0.24	-0.05	0.22	0.04	0.01
NTPP	-0.13	-0.70	0.47	-0.10	0.19	0.18	-0.01
NGPP	-0.70	0.39	-0.10	-0.05	-0.31	0.05	-0.16
1000 GWT	0.70	0.05	-0.34	0.04	0.05	0.39	-0.13
GY/PT	-0.12	-0.33	0.29	0.58	0.08	0.56	0.08
ASV	0.23	0.33	0.53	0.39	0.33	-0.37	-0.13
AMYL	0.48	0.21	0.45	-0.24	-0.11	-0.06	0.50
LAS	-0.09	0.05	-0.37	-0.15	0.81	-0.07	-0.06
KL	0.88	-0.30	-0.14	-0.11	-0.09	-0.03	0.06
KB	0.13	0.07	-0.47	0.70	-0.03	-0.20	0.40
L/B	0.86	-0.31	-0.13	-0.15	-0.12	-0.05	0.04

Table 2: Contribution of each trait in different principal components.

PCA / Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
PH	0.03	17.47	0.42	2.45	3.56	24.74	6.06
DO50%F	12.41	0.06	0.13	3.54	0.85	0.22	32.82
FLL	0.80	23.35	1.07	0.85	4.26	0.77	1.79
PL	9.10	13.64	4.13	0.25	4.26	0.14	0.00
NTPP	0.48	20.16	15.76	0.87	3.30	3.38	0.01
NGPP	13.62	6.38	0.73	0.22	8.68	0.25	3.32
1000GWT	13.38	0.10	8.34	0.15	0.23	16.49	1.99
GY	0.36	4.56	6.20	28.16	0.54	33.46	0.85
ASV	1.41	4.44	20.57	12.97	10.23	14.82	2.22
AMYL	6.41	1.80	14.39	4.68	1.17	0.38	30.44
LAS	0.20	0.11	9.94	1.81	60.77	0.56	0.39
KL	21.18	3.64	1.46	0.99	0.72	0.08	0.38
KB	0.50	0.19	15.73	41.17	0.09	4.44	19.49
L/B	20.11	4.11	1.15	1.89	1.32	0.27	0.22

Table 3: Contribution of each genotype in different principal components.

Sr. No.	Genotypes	PCA1	PCA2	PCA3	PCA4	PCA5	PCA6	PCA7
1.	KIR-44	0.84	0.56	2.38	0.00	0.00	1.92	0.16
2.	KIR-45	3.68	0.29	3.36	3.83	0.44	0.07	0.81
3.	KIR-46	11.51	1.73	0.08	3.11	0.05	3.67	3.72
4.	KIR-47	4.78	0.00	1.54	2.57	1.68	0.59	3.14
5.	KIR-48	6.87	0.53	0.44	0.09	0.01	0.93	0.03
6.	KIR-49	2.78	1.15	1.85	3.62	5.72	0.93	0.34
7.	KMTU-50	0.66	0.03	0.15	0.11	0.26	0.00	1.53
8.	KMTU-51	0.43	0.22	0.49	0.07	0.00	0.44	3.75
9.	KMTU-52	1.87	1.41	0.01	0.18	0.80	7.21	0.02
10.	KMTU-53	0.82	0.81	1.11	2.16	2.24	1.24	0.90
11.	KMTU-54	0.91	3.83	7.25	1.36	2.08	0.07	0.27
12.	KRS-1	0.25	0.22	1.27	0.65	1.68	1.40	4.14
13.	KRS-10	1.80	0.87	2.96	0.15	3.54	0.27	0.00
14.	KRS-11	0.41	0.08	1.15	3.93	0.82	4.23	0.59
15.	KRS-12	0.59	0.33	0.19	2.27	3.61	0.04	1.75
16.	KRS-13	0.13	1.45	0.52	0.16	0.12	0.00	0.10
17.	KRS-14	0.91	3.35	0.03	0.60	2.99	0.84	0.41
18.	KRS-15	0.03	7.44	2.76	0.41	0.32	1.83	0.10
19.	KRS-16	0.00	7.25	1.95	1.51	1.38	0.33	2.37
20.	KRS-17	0.03	10.43	0.07	0.02	1.28	0.79	0.69
21.	KRS-18	0.12	5.09	1.46	1.29	0.88	2.31	0.11
22.	KRS-19	0.01	6.41	0.04	0.11	0.02	0.25	0.00
23.	KRS-2	0.01	0.18	0.75	0.23	0.47	1.58	2.28
24.	KRS-20	0.09	0.05	2.29	2.84	0.98	0.20	1.37
25.	KRS-21	1.16	0.08	1.44	0.30	5.11	0.19	2.42
26.	KRS-22	0.06	4.16	0.00	0.60	0.34	2.84	0.20
27.	KRS-23	0.02	0.29	0.09	0.13	0.53	1.34	0.56
28.	KRS-24	0.40	1.29	1.11	4.49	0.11	3.35	0.11
29.	KRS-25	0.61	6.82	1.76	2.15	0.15	0.68	0.01
30.	KRS-26	0.21	0.51	2.23	0.01	2.08	1.24	0.63
31.	KRS-27	0.13	0.32	1.96	2.18	1.08	2.38	0.16
32.	KRS-28	0.00	0.03	0.68	0.13	6.00	2.72	0.12
33.	KRS-29	3.66	0.22	1.45	0.29	0.89	0.99	2.35
34.	KRS-3	2.28	0.88	0.04	1.96	1.51	4.39	0.20
35.	KRS-30	4.47	0.11	0.04	0.07	2.92	0.19	2.96
36.	KRS-31	0.77	0.71	6.40	0.07	9.89	0.33	1.25
37.	KRS-32	3.81	0.20	2.78	0.13	0.74	0.07	6.25
38.	KRS-33	0.30	0.44	20.94	31.46	1.20	6.94	13.56
39.	KRS-34	1.61	0.58	0.62	0.57	0.59	1.00	0.02
40.	KRS-35	1.37	0.40	1.36	0.00	0.05	0.87	0.30
41.	KRS-36	0.67	0.01	0.02	0.53	0.41	0.82	1.68
42.	KRS-37	1.34	0.22	0.98	5.90	2.05	0.54	1.88
43.	KRS-38	0.21	0.00	0.01	0.01	1.09	1.17	6.26
44.	KRS-39	5.50	0.54	0.09	0.02	0.01	0.42	0.05
45.	KRS-4	0.05	0.48	2.75	0.71	3.88	2.17	0.47
46.	KRS-40	4.43	0.34	2.01	0.38	0.60	0.31	1.28
47.	KRS-41	0.01	3.83	0.90	0.02	0.61	0.05	6.58
48.	KRS-42	2.21	0.14	3.18	0.06	0.20	5.54	0.04
49.	KRS-43	0.02	6.61	2.70	1.16	0.73	11.03	3.37
50.	KRS-5	0.44	0.56	0.18	1.82	0.28	0.13	0.00

51.	KRS-6	0.15	1.50	1.72	2.28	0.77	1.66	0.53
52.	KRS-7	0.34	0.02	2.37	1.81	1.34	0.37	1.17
53.	KRS-8	0.28	0.29	1.02	0.02	2.97	0.56	2.97
54.	KRS-9	3.38	0.00	1.68	1.00	0.26	0.13	0.34
55.	MTU7029	0.78	1.04	0.08	0.01	0.06	0.29	1.72
56.	IR-64	5.93	1.33	0.09	1.83	2.20	0.05	3.97
57.	Katarni	2.23	6.07	0.03	5.36	10.52	10.65	6.56
58.	R. Sweta	0.02	3.55	0.00	0.92	5.68	0.37	0.79
59.	R. Suwasini	3.29	0.89	2.95	0.33	1.73	2.94	0.01
60.	S. Surbhit	8.34	1.84	0.23	0.02	0.06	0.12	0.65

PH: Plant height, DO50%F: Days to 50% flowering, FLL: Flag leaf length, PL: Panicle length, NTPP: Number of tillers/plant, NGPP: Number of grains/panicle, 1000GWT: 1000-grain weight, ASV: Alkali spreading value, AMYL: Amylose content, LAS: Leaf aroma score, KL: Kernel length, KB: Kernel breadth, LB: L/B ratio and GY/PT: Grain yield/plant

CONCLUSIONS

Significantly advantageous genotypes for the trait plant height were found via trait biplot analysis. Several genotypes that can be employed further for varietal development were identified by the genotypes biplot analysis, including KIR-46, KIR-48, KRS-30, KRS-32, KRS-40, KRS-43, KRS-14, KRS-15, KRS-16, KRS-17, KRS-9, KRS-25, and KMTU-54.

FUTURE SCOPE

In investigating under multiple locations trials, promising lines will be advanced in order to generate dwarf, early maturing, high yielding stable genotypes for varietal development.

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Conflict of Interest. None.

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