Eco. Env. & Cons. 28 (October Suppl. Issue) : 2022; pp. (S104-S107)
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ISSN 0971–765X

http://doi.org/10.53550/EEC.2022.v28i06s.0017

Principal Component Analysis for Yield and Yield Related Traits in Pearl Millet Cultivars

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(Received 18 January, 2022; Accepted 9 March, 2022)

ABSTRACT

A set of 40 pearl millets genotypes were evaluated with a view of studying genetic parameters for eight quantitative characters. In the experimental materials, analysis of variance revealed significant differences for all analyzed traits. The study identified 3 Principal Components (PCs) with Eigen value greater than 1.00 which accounted for 82.3% of the total variation for discriminating the lines. From principal component analysis, PC1 showed highest amount of variance (36.2%) with mostly related to traits like yield per plant, productive tillers per plant, and fodder yield per plot. As a result, the first component mainly identifies the characters responsible for yield. PC2 showed second highest amount of variance (29.9%) with cumulative variance (66.1%) with mostly related to traits like days to maturity, days to 50% flowering, and panicle diameter. Third highest variance (16.2%) with cumulative variance (82.3%) with mostly related to traits plant height and panicle length was observed in PC3. Elbow type line is seen after PC3 showing little variation after PC3. Highest Eigen value is shown by PC1. From biplot, PC1 components showed negative relationship with plant height and Days to 50% flowering, days to maturity showed slightly negative with PC1. PC2 had negative relationship with traits like productive tillers per plant and slightly negative yield per plant and both components showed positive relation with panicle diameter, panicle length and fodder yield per plot.

Key words: *Pearl millets, RBD, Principal component analysis, Eigen values, Biplot*

Introduction

Pearl millet [*Pennisetum glacum* (L). R.Br], is a warm-season grain crop, which was consumed by millions of people in the tropics of dry and semi-arid places (Kapila *et al.*, 2008). It's a hardy, fast-growing variety with high yield potential and good tillering ability. Many cereal crops, such as maize and sorghum, are unable to produce high yields in challenging agro-climatic conditions, yet the pearl millet crop thrives and performs better. It is the world's eighth most important cereal crop, after wheat, rice, maize, and sorghum, and India's fourth most common crop (Khairwal *et al.*, 1999 and Sowmiya *et al.*, 2016). It is grown on over 30 million hectares in over 30 nations, with the majority of this land in Asia (>10 million hectares), Africa (nearly 18 million hectares), and the Americas (>2 million hectares) (Gupta *et al.*, 2015). India is a top grower of pearl millet, each in terms of geography and production. With 43.3 percent of the world's land area and 42 percent of the world's production. It is primarily farmed on a total of 9.16 million hectares in the states of Rajasthan, Maharashtra, Gujarat, Madhya Pradesh, Karnataka, Andhra Pradesh, Uttar Pradesh, and Tamil Nadu, with an annual production of 8.01 million tonnes. Because of its extensive spread over the world, adaptability to hard environmental conditions, and cross pollination method with protogynous flowering, it has a lot of genetic variation (Satyavathi *et al.*,

2013 and Singh *et al.*, 2013). Landrace genetic variation is critical for breeding initiatives attempting to develop enhanced landrace-based cultivars for difficult growing situations and for better yields and nutrient content (Yadav *et al.*, 2001). Climate change will affect a genotype's overall performance, and if the traits' heritability is higher, the selection process will be easier, and the responsiveness to selection may be better (Larik *et al.*, 2000; Soomro *et al.*, 2008). To begin an efficient breeding programme, it is necessary to understand the type and extent of variability, genetic variations among yield factors, and the interrelationship of different traits (Izge *et al.*, 2006). The objective of this project is to evaluate genotype divergence that can be used for further crop modification.

Materials and Methods

The study included a total of 40 pearl millet genotypes. A field trial was conducted at the Agricultural Research Station at Palem, PJTSAU, in 2017. The genotypes are listed in greater detail in Table 1. Using the Randomized Block design, the test was repeated three times. Seeds of forty pearl millet genotypes were immediately sown at a 45 x 15 cm spacing inside the plot. To symbolize each genotype, 6 rows of each genotype were employed, each 6 metres long. Appropriate agronomic approaches were used to raise a good crop. Days to 50% flowering, days to maturity, plant height, productive tillers per plant, panicle diameter, panicle length, yield per plant, and other economically important biometrical parameters were observed. Banfield's (1978) recommended protocol was used to measure the PCA. The statistical analysis was done by using STAR software. The 40 genotypes were presented in (Table 1).

Results and Discussion

In principal component analysis, the number of variables is reduced to linear functions called canonical vectors which accounts for most of the variation produced by the characters under study. The Eigen values, per cent variance, per cent cumulative variance and factor loading of different characters studied are presented in (Table 2 and 3). The study identified 3 Principal Components (PCs) with Eigen value greater than 1.00 which accounted for 82.3% of the total variation for discriminating the lines.From principal component analysis, PC1 showed highest amount of variance (36.2%) with mostly related to traits like yield per plant (0.575), productive tillers per plant (0.544), and fodder yield per plot(0.400). As a result, the first component mainly identifies the characters responsible for yield. PC2 showed second highest amount of variance (29.9%) with cumulative variance (66.1%) with mostly related to traits like days to maturity (0.578), days to 50% flowering (0.568), and panicle diameter (0.370), therefore the PC2 mainly identifies the characters related with flowering and maturity. Third highest variance (16.2%) with cumulative variance (82.3%) with mostly related to traits plant height (0.583) and panicle length (0.411). Characters that show both positive and negative impacts on PCs are said to be the key source of variability and mainly contributed for the divergence of genotypes. Scree plot showed the association of PCs with eigen values and variance% was presented in (Figure 1).Elbow type line is seen after PC3.One of the most commonly used criteria for solving the number of components problemis the eigen value-one, also known as the Kaiser's (1960) criterion. Highest eigen value is shown by PC1 was shown in (Table 2). The out-

Table 1. Pearl millet lines tested in the study

S. No	Millet lines	S. No	Millet lines	S. No	Millet lines	S. No	Millet lines
1	Fe-101-1	11	Fe-111-30	21	Fe-121-34	31	Fe-131-29
2	Fe-102-37	12	Fe-112-9	22	Fe-122-20	32	Fe-132-2
3	Fe-103-28	13	Fe-113-16	23	Fe-123-11	33	Fe-133-4
4	Fe-104-24	14	Fe-114-6	24	Fe-124-35	34	Fe-134-36
5	Fe-105-17	15	Fe-115-18	25	Fe-125-39	35	Fe-135-31
6	Fe-106-15	16	Fe-116-10	26	Fe-126-26	36	Fe-136-19
7	Fe-107-27	17	Fe-117-25	27	Fe-127-12	37	Fe-137-38
8	Fe-108-3	18	Fe-118-32	28	Fe-128-8	38	Fe-138-13
9	Fe-109-23	19	Fe-119-33	29	Fe-129-14	39	Fe-139-22
10	Fe-110-5	20	Fe-120-40	30	Fe-130-7	40	Fe-140-21

Table 2. Standard deviation, Variance, Cumulative variance and Eigen values of 8 principal components.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Standard deviation	1.702	1.546	1.139	0.806	0.706	0.456	0.210	0.109
Proportion of Variance	0.362	0.299	0.162	0.081	0.062	0.026	0.006	0.001
Cumulative Proportion	0.362	0.661	0.823	0.905	0.967	0.993	0.999	1.000
Eigen values	2.8973	2.3916	1.2983	0.6502	0.4989	0.2076	0.0441	0.0119

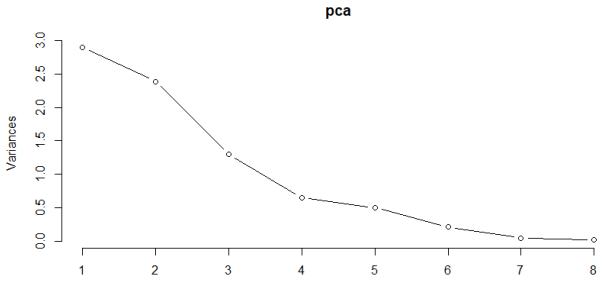

Fig. 1. Scree plot showing Eigen values against respective principal components

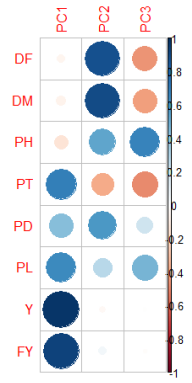

Fig. 2. Correlation plotted against different characters with respective principal components

comes of the present study are in agreement with earlier findings of Kumar *et al.,* 2015 and Ramya *et al.,* 2017. Top 10 PC scores were mentioned genotype wise in (Table 4) in 3 principal components. These scores can be used for the purpose of precised selection indices whose intensity is based on the variability showed by the respective components. High score for a particular genotype in particular principal component indicates the high variability for a particular character of that principal component. Based on specific goals of a particular breeding programme the genotypes based on PC scores were selected for respective character. Correlation matrix of 8 yield and yield contributing traits were plotted against the 3 principal components was presented in (Figure 2) and biplot between PC1 and PC2 for 8 characters of 40 genotypes was presented in (Figure 3). From correlation matrix the red dots show the

Table 3. Principal components scores for 8 yield contributing traits

Characters	PC1	PC2	PC3
DF	-0.0298	**0.568928**	-0.38964
DM	-0.03989	**0.57817**	-0.36807
PH	-0.0836	0.336467	**0.583599**
PT	**0.400699**	-0.24082	-0.41393
PD	0.249726	**0.370741**	0.175866
PL	0.37485	0.17818	**0.41193**
Y	**0.575268**	-0.02263	-0.00788
FY	**0.544208**	0.033608	-0.01

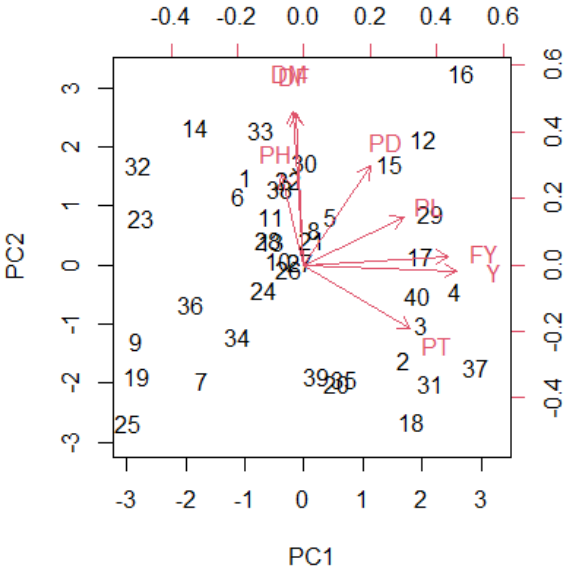

Fig. 3. Biplot against PC1 and PC2 for studied characters of 40 genotypes

negative relationship between the respective characters with components and blue dot shows the positive relationship. From biplot analysis revealed that genotypes are diverse for the characters under PC1 and PC2. PC1 components showed negative relationship with plant height and Days to 50% flowering, days to maturity showed slightly negative with

Table 4. Top 10 Genotypes which have variability for particular characters according to respective principal components

S. No.	PC1	PC2	PC3
1	Fe-137-38	Fe-116-10	Fe-127-12
2	Fe-116-10	Fe-114-6	Fe-120-40
3	Fe-104-24	Fe-133-4	Fe-122-20
4	Fe-131-29	Fe-112-9	Fe-112-9
5	Fe-129-14	Fe-130-7	Fe-125-39
6	Fe-112-9	Fe-115-18	Fe-135-31
7	Fe-103-28	Fe-132-2	Fe-134-36
8	Fe-117-25	Fe-101-1	Fe-108-3
9	Fe-140-21	Fe-122-20	Fe-130-7
10	Fe-118-32	Fe-138-13	Fe-101-1

PC1. PC2 had negative relationship with traits like productive tillers per plant and slightly negative yield per plant and both components showed positive relation with panicle diameter, panicle length and fodder yield per plot. From biplot of PC1 and PC2 genotypes like 16, 37, 18, 25, 19, 23, 32, and 14 were highly diverse.

Acknowledgement

Necessary facilities provided by Regional Agricultural Research Station in Palem, PJTSAU are acknowledged.

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