Genetic Diversity Analysis for Yield and Yield-contributing Traits in Pearl Millet [*Pennisetum glaucum* (L.) R. Br.]

ABSTRACT

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is one of the most significant cultivated cereals. It demonstrates remarkable genetic diversity due to its wide distribution across the globe and its adaptability to harsh environmental conditions. A multi-location experiment was conducted in Srikakulam (Location 1), Vizianagaram (Location 2), and Patancheru (Location 3) during 2021 Rainy season to investigate genetic diversity in a world diversity panel of pearl millet based on grain yield and its component traits using principal component analysis (PCA). The PCA revealed that first three principal components with eigen values greater than one accounted for about 69% of the total variation in location 1, 66% in location 2, and two components accounted for 62% in location 3. The first principal component showed high positive loadings for HI and PHI in locations 1 and 2 and for PWT and GYLD in location 3. Traits such as TGWT, PH, and PL contributed positively to the total variation in all three locations. This genetic variability can thus be effectively utilized in pearl millet breeding programs.

Keywords: Pearl millet; principal component analysis; biplot; scree plot; eigen values.

INTRODUCTION

Pearl millet [*Pennisetum glaucum* (L.) R.Br.], ranked as the sixth most important cereal crop after wheat, rice, maize, barley, and sorghum, and is predominantly cultivated in Africa and the Indian subcontinent. India leads in production, with 10.36 million tonnes harvested from 7.54 million hectares (INDIASTAT, 2021). As one of the oldest domesticated cereals (Manning *et al*., 2011), pearl millet plays a crucial role in ensuring food security, nutritional benefits, and economic stability for smallholder farmers (Srivastava *et al*., 2020). It is rich in nutrients, boasting 8-19% protein, significant amounts of starch, fiber, B-complex vitamins, and high levels of iron and zinc (Velu *et al*., 2007 and Govindaraj *et al*., 2013). Additionally, pearl millet serves as a valuable forage crop, offering high levels of protein, calcium, and phosphorus while containing lower levels of hydrocyanic acid, fiber, and lignin, making it superior to sorghum in forage quality. The rising demand for pearl millet is attributed to its remarkable adaptability to various climatic conditions (Tako *et al*., 2015). However, recent studies suggest that pearl millet yields have stagnated over years, highlighting the need to break this plateau to meet the ever-increasing food demands. Hence, there is a need to evaluate the huge variability present in the gene banks for their effective utilization in plant breeding programmes.

Principal Component Analysis (PCA) is a widely used technique for assessing genetic variation and aids in the identification of key traits that differentiate genotypes based on similarities in one or more characteristics. This method is also useful in identifying the minimal number of components that capture the maximum variability within a dataset (Anderson, 1972 and Morrison, 1978) and ranks genotypes according to PCA scores. These components are typically derived from either a correlation or covariance matrix. Thus, in the present study, PCA was employed to examine the huge diversity of pearl millet genotypes concerning grain yield and related traits in the Pearl Millet Inbred Germplasm Association Panel (PMiGAP) of ICRISAT. The objective of this study is to evaluate genotype divergence that can be used for further crop modification.

MATERIALS AND METHODS

In this study, 350 entries, including 345 PMiGAP lines and 5 check varieties, were evaluated across three locations *i.e.*, Srikakulam (Location 1), Agricultural Research Station, Vizianagaram (Location 2), and ICRISAT, Patancheru (Location 3) during *kharif*, 2021. The experiment was laid in alpha lattice design with two replications across 35 blocks. The genotypes were grown in two rows of 2m length with 60x10 cm spacing. All recommended management practices were followed to maintain good crop standard. Observations were recorded on five plants per replication per genotype for plant

height (PH) (cm), panicle length (PL) (cm), thousand-grain weight (TGWT) (g), panicle weight (PWT) (kg/ha), harvest index (HI) (%), and panicle harvest index (PHI) (%). Days to 50% flowering was recorded plot basis. Grain yield (GYLD) was recorded for five plants and then converted to kilograms per hectare. Principal component analysis was performed on the mean of each trait to determine the quantitative traits that contributed most to the observed variations among the genotypes. The analyses were conducted using the Factoextra package of R software version 4.4.0.

RESULTS AND DISCUSSION

Principal component analysis (PCA) is a powerful tool for assessing the significance and contribution of each component to the overall variability, as well as to understand the degree to which each original variable contributes to each principal component. This approach retains all essential information from the original dataset and helps to minimize redundancy in experimental data (Amy and Pritts, 1991). As a multivariate analysis technique, PCA reduces complex datasets to lower dimensions, providing insights into the importance and contribution of each component to the total variance.

In this study, PCA was conducted on eight quantitative traits of pearl millet genotypes. Among the principal components, first three principal components (PCs) had eigen values greater than 1.0, accounting for 68.71% of the total variability in location 1, 65.70% in location 2, while, first two principal components accounted for 62.19% of the total variability in location 3 (Fig. 1). The first principal component (PC1) was the most significant, accounting for 34.9%, 34.6%, and 42.2% of the variation in locations 1, 2, and 3, respectively. The primary contributors to the variation observed in PC1 were PL, TGWT, and PWT in location 1; PH, GYLD, HI, and PHI in location 2; and all traits in location 3. Variances of 16.9% and 13.5% were extracted from the second and third principal components in locations 1 and 17.4% and 13.5% from location2, respectively. A variance of 19.9% was extracted from the second PC in location 3. The variations in PC2 were primarily due to PH, PL, TGWT, and PHI in locations 1 and 2, while DFF, PH, PL, and PWT contributed to the variation in location 3. Similarly, the main contributors to the variation observed in PC3 were DFF, PH, TGWT, PWT, GYLD, and HI in location 1; DFF, PH, TGWT in location 2; and PL, PWT, GYLD, and HI in location 3 (Tables 1, 2).

PC1 emerged as the most critical component, with eigen values of 2.799, 2.77, and 3.376 in locations 1, 2, and 3, respectively. PC2 had eigen values of 1.356, 1.398, and 1.598 in locations 1, 2, and 3, respectively, while PC3 had eigen values of 1.082 and 1.087 in locations 1 and 2, respectively. These results highlight the specific traits contributing most to genetic divergence, helping to discriminate between pearl millet genotypes. The findings of this study are consistent with the PCA analyses conducted by Animasaun *et al*. (2017), Sangwan *et al*. (2019) and Mithlesh *et al*. (2020) in pearl millet. Similar results were also reported by Rasitha *et al*. (2020) and observed 63.81% of total variability by the first three PCs.

Table 1. Eigen values and contribution of variability for the principal components

Location	Component	Eigen values	Variance explained (%)	Cumulative (%)
Location1	**PC1**	2.799	34.997	34.997
	PC2	1.356	16.960	51.957
	PC3	1.082	13.527	65.485
Location2	**PC1**	2.770	34.630	34.630
	PC2	1.398	17.485	52.116
	PC3	1.087	13.596	65.712

Location3	**PC1**	3.376	42.207	42.207
	PC2	1.598	19.986	62.193

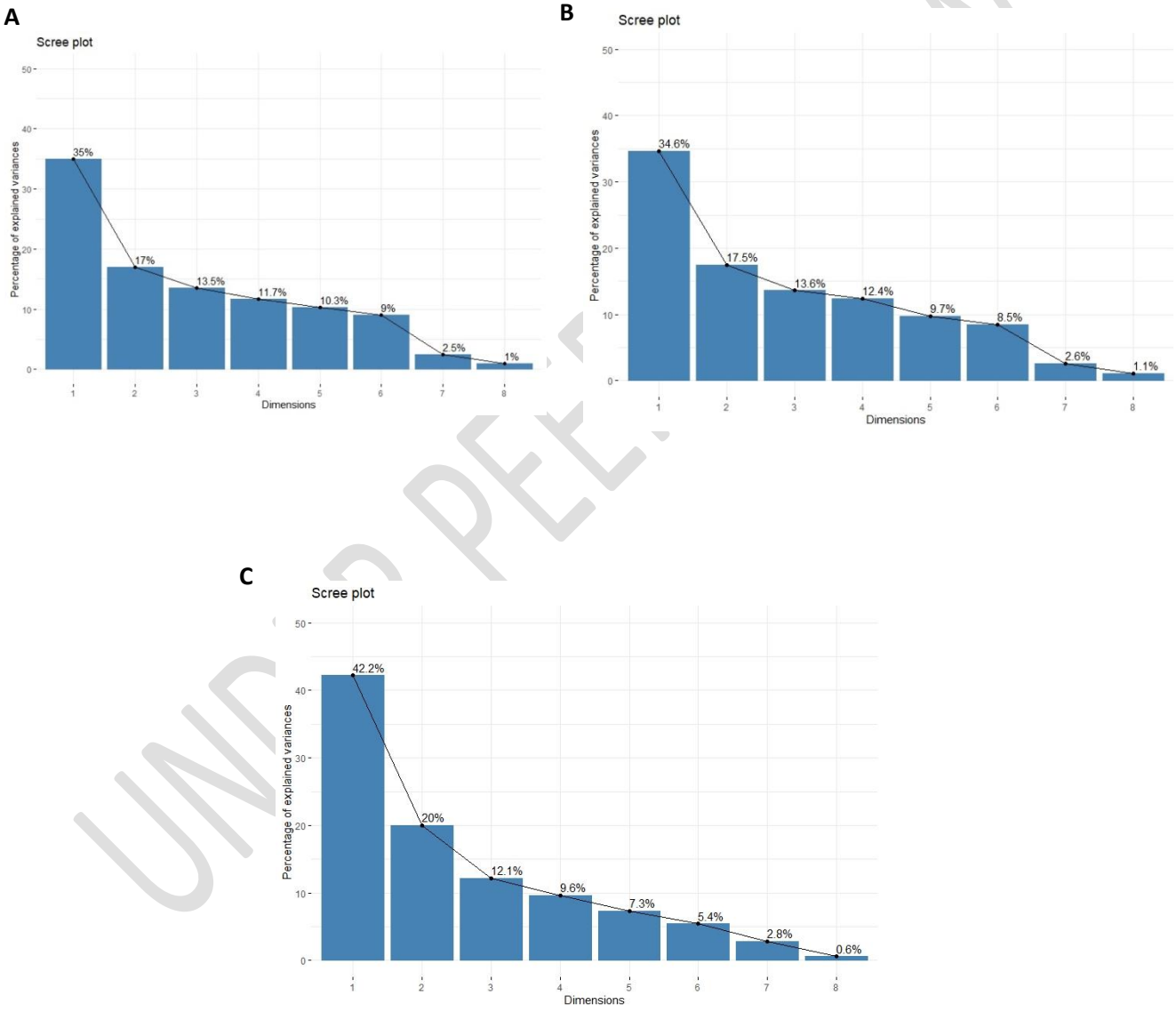

Figure 1. Scree plot diagram of principal components of PMiGAP panel in (A) Location1 (B) Location2 and (C) Location3.

A scree plot was created using the percentage of explained variances for each principal component, as shown in Fig. 1. In this plot, the black line represents the cumulative variability percentage from PC1 to PC8. The graph clearly illustrates that the maximum variance was captured by PC1 and PC2 across all locations. Additionally, a biplot was generated between PC1 and PC2 using the variability of all agro-morphological traits to examine the interaction between these two components. The biplot graph confirmed the grouping of genotypes based on PC1 and PC2 (Fig. 2). This biplot analysis, focused on the two major principal components (PC1 and PC2), accounted for 52%, 52.1%, and 62.2% of the total variability in locations 1, 2, and 3, respectively. The results of this study align with the findings of Kumar *et al*. (2015), Ramya *et al*. (2017) and Triki *et al*. (2023).

A correlation matrix of the eight yield and yield-contributing traits against the eight principal components is presented in Fig. 3. The first principal component (PC1) exhibited high positive loadings for HI and PHI in locations 1 and 2, and for PWT and GYLD in location 3, making them the primary contributor towards variability. The second principal component (PC2) showed high loadings for PH in locations 1 and 2, and for HI in location 3. PC3 had high loadings for DFF across all three locations.

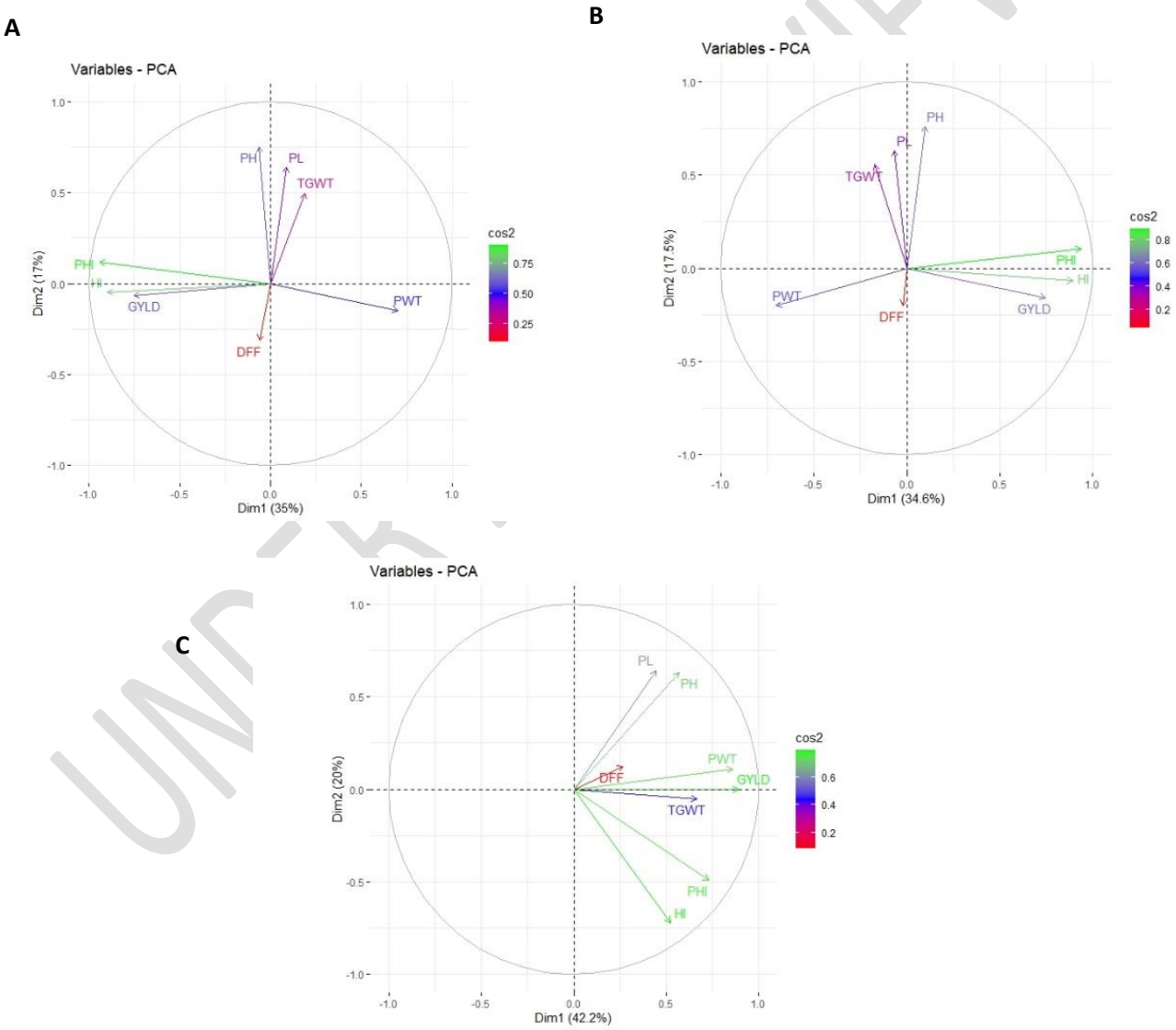

Figure 2. Biplot against PC1 and PC2 for studied characters of PMiGAP from three locations.

CONCLUSIONS

Principal component analysis (PCA) is commonly used to assess the contribution of different quantitative traits to total variability. In the current study, PCA reduced a dataset of eight variables into three principal components, explaining 65.4% and 65.7% of the cumulative variability in locations 1 and 2, respectively. In location 3, the eight variables were reduced to two principal components, accounting for 62.1% of the cumulative variability. The key traits identified within each principal component as significant contributors towards total variability tend to cluster together, making them effective for selection in crop breeding programs. Across all three locations, traits such as TGWT, PH, and PL contributed positively to the total variation, indicating their potential utility in selection in pearl millet breeding programs.

Table 2. Factor loadings (Eigen vectors) for yield and its component traits for the principal components from three locations

	Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
LOC1	DFF	-0.0362	-0.2680	0.7308	-0.2442	0.4926	0.2987	-0.0248	-0.0265
	PH	-0.0382	0.6439	0.1122	-0.0433	-0.2665	0.7056	0.0141	0.0189
	PL	0.0521	0.5484	-0.1758	0.2148	0.7682	-0.1657	-0.0433	0.0079
	TGWT	0.1139	0.4266	0.5983	-0.0207	-0.3014	-0.5922	-0.0716	0.0094
	PWT	0.4189	-0.1266	0.1510	0.6669	-0.0571	0.1502	-0.0928	-0.5536
	GYLD	-0.4487	-0.0557	0.1972	0.5866	-0.0211	0.0031	0.5408	0.3459
	HI	-0.5364	-0.0413	0.0411	0.2617	-0.0398	0.0171	-0.7958	0.0722
	PHI	-0.5631	0.1002	-0.0338	-0.1862	0.0088	-0.1093	0.2402	-0.7533
LOC2	DFF	-0.0123	-0.1702	0.8005	-0.2536	0.4372	-0.2707	0.0227	-0.0277
	PH	0.0592	0.6412	0.0823	0.1840	-0.2265	-0.7022	-0.0143	0.0059
	PL	-0.0409	0.5312	-0.3194	-0.2627	0.7245	0.1413	0.0120	-0.0078
	TGWT	-0.1033	0.4684	0.4880	0.3754	-0.1177	0.6119	0.0399	0.0309
	PWT	-0.4213	-0.1708	-0.0908	0.5899	0.2970	-0.1499	0.0872	-0.5646
	GYLD	0.4486	-0.1343	-0.0212	0.5165	0.3225	-0.0420	-0.5360	0.3469
	HI	0.5364	-0.0582	-0.0286	0.2264	0.1318	-0.0103	0.7978	0.0538
	PHI	0.5635	0.0880	0.0513	-0.1608	-0.0958	0.1216	-0.2573	-0.7457
LOC3	DFF	0.1448	0.0980	-0.9414	-0.2198	0.0956	0.1602	-0.0050	0.0020
	PH	0.3093	0.4978	-0.0769	0.2167	-0.0929	-0.6936	-0.3373	-0.0160
	PL	0.2426	0.5066	0.1810	0.1592	0.6996	0.3401	0.1410	-0.0379
	TGWT	0.3633	-0.0416	-0.0691	0.6691	-0.4314	0.4628	-0.1160	0.0087
	PWT	0.4674	0.0871	0.1941	-0.4614	-0.1908	0.1357	-0.0425	0.6832
	GYLD	0.4855	-0.0006	0.1587	-0.4067	-0.2087	0.0721	0.0904	-0.7188
	HI	0.2842	-0.5706	0.0230	0.0169	0.4467	-0.0352	-0.6256	-0.0239
	PHI	0.3969	-0.3886	-0.0831	0.2305	0.1648	-0.3723	0.6720	0.1190

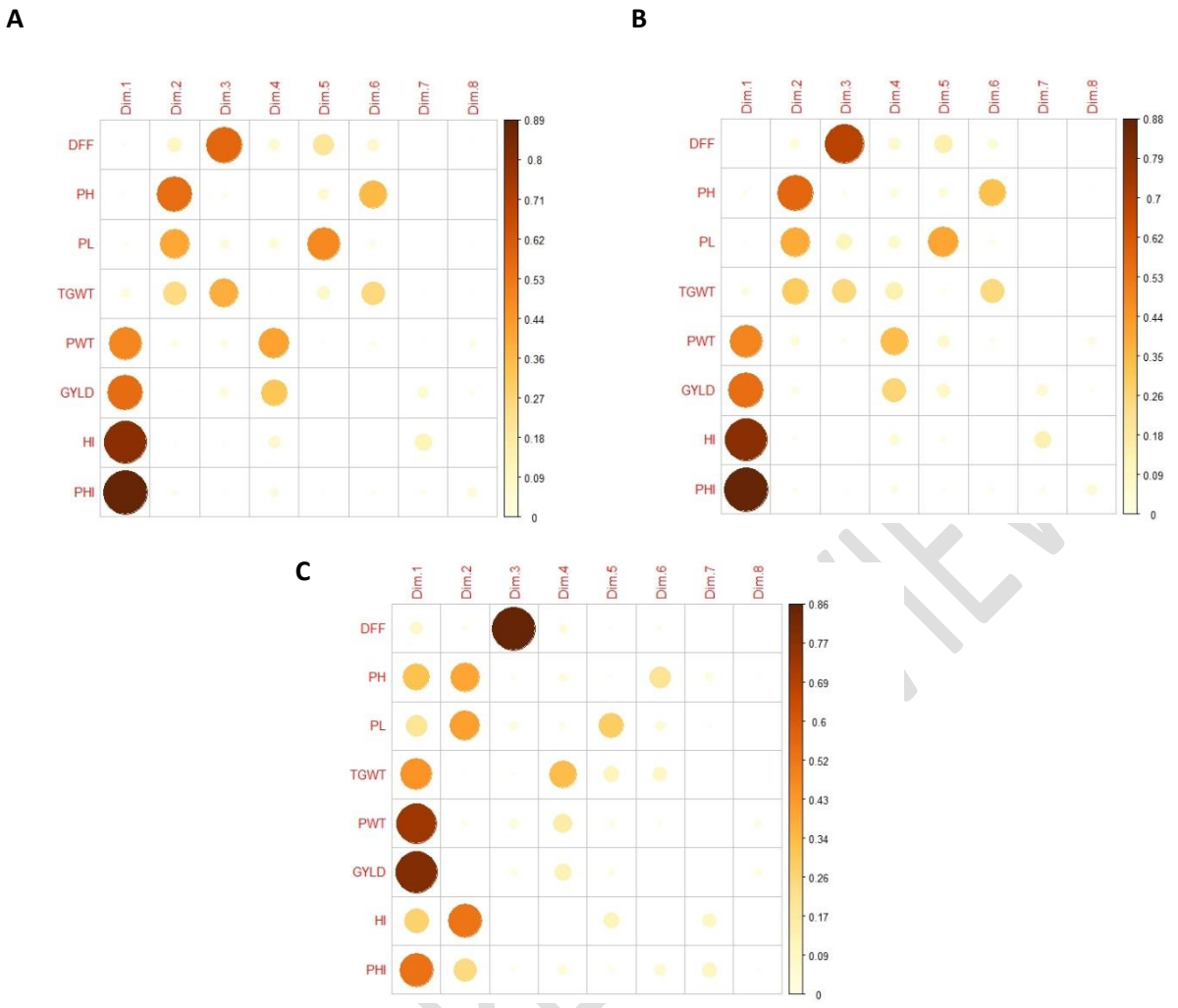

Figure 3. Biplot against PC1 and PC2 for studied characters of PMiGAP from three locations.

References

Amy EL, Pritts MP. Application of principal component analysis to horticultural research. Horticultural Science. 1991; 26(4): 334–338.

Anderson TW. An introduction to multivariate analysis. Wiley Eastem Pvt. Ltd. New Delhi. 1972.

Animasaun DA, Morakinyo JA, Krishnamurthy R, Mustapha OT. Genetic divergence of Nigerian and Indian pearl millet accessions based on agronomical and morphological traits. Journal of Agricultural Sciences. 2017; 62: 115-131.

Govindaraj M, Rai KN, Shanmugasundaram P, Dwivedi SL, Sahrawat KL, Muthaiah AR. Combining ability and heterosis for grain Iron and Zinc densities in pearl millet. Crop Science. 2013; 53: 507-517.

Gupta D, Khandelwal V. Principal component analysis for yield and its attributing characters of pearl millet (*Pennisetum glaucum* [L.] R.Br.). Annals of Plant and Soil Research. 2022; 24(3):408-414.

INDIASTAT. 2021. INDIASTAT Database. https://www. indiastat.com/table/agriculture-data/2/agricultural production/225/7267/data.aspx.

Kumar R, Verma U, Malik V, Vart D. Multivariate analysis for selection of diverse genotypes in pearl millet germplasm. Forage Research. 2015; 41(2): 73-77.

Manning K, Pelling R, Higham T, Schwenniger JL, Fuller DQ. 4500-year-old domesticated pearl millet (*Pennisetum glaucum*) from the Tilemsi valley, Mali: new insights into an alternative cereal domestication pathway. Journal of Archaeological Science. 2011; 38(2): 312-322.

Mithlesh Kumar, Kirti Rani BC, Ajay MS, Patel KD, Mungra, MP, Patel. Multivariate Diversity Analysis for Grain Micronutrients Concentration, Yield and Agro-morphological Traits in Pearl millet (*Pennisetum glaucum* (L) R. Br.). International Journal of Current Microbiology and Applied Sciences. 2020; 9: 2209 2226.

Morrison DE. Multivariate statistical methods 2nd ed 4th Print, McGraw Hill Kogakusta Ltd. 1978.

Ramya AR, Ahamed ML, Srivastava RK. Genetic diversity analysis among inbred lines of pearl millet [Pennisetum glaucum (L.) R. Br.] based on grain yield and yield component characters. International Journal of Current Microbiology and Applied Sciences. 2017; 6(6): 2240-2250.

Rasitha R, Iyanar k, Ravikesavan R, Senthil N. Assessment of Genetic Diversity in Parental Lines of Pearl Millet [*Pennisetum glaucum* (L). R. Br] for Yield and Yield Related Traits. International Journal of Current Microbiology and Applied Sciences. 2020; 9(12): 1575-1582.

Sangwan S, S Yashveer, R Kumar, Hemender, S Sharma, N Redhu. Multivariate analysis reveals substantial diversity in pearl millet [*Pennisetum glaucum* (L). R. Br.] inbred lines. International Journal of Current Microbiology and Applied Sciences. 2019; 7: 358-375.

Shashibhushan D, Kumar CVS, Kondi RKR. Principal Component Analysis for Yield and Yield Related Traits in Pearl Millet Cultivars. Ecology Environment and Conservation. 2022; 28:104-107.

Srivastava RK, Singh RB, Pujarula VL, Bollam S, Pusuluri M, Chellapilla TS, Yadav RS, Gupta R. Genome - wide association studies and genomic selection in pearl millet: Advances and prospects. Frontiers in Genetics. 2020; 10: 1389.

Tako, E., S. M. Reed, J. Budiman, J. J. Hart and R. P. Glahn, 2015. Higher iron pearl millet (Pennisetum glaucum L.) provides more absorbable iron that is limited by increased poly penolic content. *Journal of Nutrition* 14: 11-18.

Triki T, Bennani L, Boussora F, Tlahig S, Ali SB, Gasmi A, Yahia H, Belhouchette K, Loumerem M, Guasmi F. Characterization and Trait Association Analysis of 27 Pearl Millet Landraces in Southern Tunisia. Agronomy. 2023; 13: 1-17.

Velu G, KN Rai, V Muralidharan, VN Kulkarni, T Longvah, TS Raveendran. Prospects of breeding biofortified pearl millet with high grain iron and zinc content. Plant Breeding. 2007; 126: 182-185.