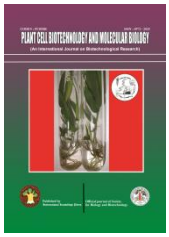

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Principal Component Analysis for Assessing Genetic Variation and Key Traits in Bottle Gourd [*Lagenaria siceraria* (Molina) Standl.] Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out at the Experimental field of Urban Technological Park Habbak, Srinagar, Jammu and Kashmir during *kharif*-2022. The experiment was laid out in Augmented Randomized Block Design with three blocks and plant spacing of 2×1 m for seventy-seven genotypes including two checks, Pusa Naveen and Pusa Santushti. Observations were recorded for growth and yield traits, seed traits and quality parameters. Principal Component Analysis (PCA) was carried out based on twenty-one quantitative and four quality characters in bottle gourd. Six out of the ten principal components, with eigen values above 1.0, explained 69.56% of the total variation. The first PC accounts for the maximum variability in the data i.e., 20.08%. The remaining variability of 17.90%, 10.05%, 8.23%, 6.82% and 6.48% was consolidated in PC2, PC3, PC4, PC5 and PC6 respectively. This population panel can be used for trait improvement in breeding programs for the traits contributing to major variation because the results of the principal component analysis used in the study have shown the high level of genetic variation and the traits contributing to the variation.

Keywords: Bottle gourd; eigen value; PCA.

1. INTRODUCTION

The bottle gourd [*Lagenaria siceraria* (Molina) Standl.] is a well-known member of the "Cucurbitaceae" family and is likely one of the oldest crops grown during the warm season all over the world. Its somatic chromosome number is (2n=2x=22). The Latin word lagena, which means the bottle, is whence the genus Lagenaria gets its name. In various regions of India, it is also known as calabash, white flowered gourd, zucca melon, doodhi, and lauki [1]. It is thought that the bottle gourd originated in Africa. Its cultivation was documented in India's fossil records as early as 200 B.C. In Ethiopia, the Moluccas, and India, wild specimens have been located. The crop spread to the western countries from India and Africa. The bottle gourd was eventually domesticated in Southern Africa; however, it is often grown in tropical and subtropical regions of the world. Six species of the genus Lagenaria can be found in Africa, Madagascar, Indo-Malaysia, and the Neotropics. *Lagenaria siceraria* is an annual, monoecious crop that is currently grown throughout the tropical parts of the world. The five additional species are untamed, perennial, and dioecious, and they can be found in Madagascar and East Africa. Historically, this fruit has been used as a diuretic, aphrodisiac, cardiotonic, cardioprotective medication, antidote to several toxins, and to treat fever, ulcers, and discomfort. In addition to their antibacterial, antifungal, immunoregulatory, anti-allergic, analgesic, anti-inflammatory, antioxidant, and free radical scavenging qualities, bottle gourds also offer memory-boosting and anti-diabetic effects [2].

The success and efficiency of any plant breeding scheme for selecting superior genotypes depends upon the nature and extent of genetic divergence and the extent to heritability of the characters of interest [3]. Better understanding and exploitation of genetic diversity could be helpful to ascertain long term selection gain in plants [4]. Multivariate analysis such as principal component analysis is a useful and effective method for selecting genotypes in any hybridization programme. Principal component analysis (PCA) is an excellent statistical technique that reduces the number of dimensions in a dataset by transforming variables into a smaller set of principal components. PCA is an efficient multivariate technique to identify and determine the independent principal components that governs plant traits separately. Therefore, PCA also helps the plant breeders for genetic improvement of traits such as yield that have low heritability in any crop improvement programme [5,6].

2. MATERIALS AND METHODS

The present research study was carried out at the experimental field of Urban Technological Park, Habbak, Srinagar, Jammu and Kashmir during *kharif*-2022. It is situated at an altitude of 1608 meters above mean sea level lying between 34.16º North latitude and 74.83º East longitude. The climate is temperate characterized by mild summers. The mean minimum and maximum temperatures at the research location are recorded in January and June respectively, indicating a temperate climate. Rainfall is maximum in March and April. The material used for research work consisted seventy-seven

genotypes of bottle gourd which were procured from different sources. The experiment was laid out in accordance with Augmented Randomized Block Design comprising of seventy-seven treatments and three blocks. Recommended agronomic practices were followed to raise a good crop. Observations recorded were node number at which 1st male flower appeared, node number at which 1st female flower appeared, days to appearance of 1st male flower, days to appearance of 1st female flower, days to anthesis of 1st male flower, days to anthesis of 1st female flower, number of male flowers plant^{-1}, number of female flowers plant^{-1}, days to 1st fruit harvest, days to last fruit harvest, vine length (m), number of primary branches, number of fruits plant^{-1}, fruit weight (kg), fruit length (cm), fruit diameter (cm), fruit yield plant^{-1} (kg), fruit yield ha^{-1} (q), number of seeds fruit^{-1}, seed weight fruit^{-1} (g), 100 seed weight (g), TSS (ºBrix), dry matter content (%), vitamin C content (mg100g^{-1}) and total phenols (mg100g^{-1}). The observations on different quantitative and quality parameters were recorded from three randomly selected plants from each germplasm line of all blocks. TSS was calculated using hand-held refractometer. A 100 g of sample of fresh fruit was taken and sun dried followed by oven drying until the entire moisture in the sample was lost for estimation of dry matter content. Using metaphosphoric acid as a stabilizing agent and 2, 6-dichloro phenol indophenol dye, a sample with a known weight was titrated in accordance with the AOAC [7] technique of titration to assess the vitamin C concentration. For total phenols estimation, the fruit samples were extracted in 80 per cent ethanol. The color was developed with FCR and the absorbance of the developed color was noted with a spectrophotometer at wavelength of 650nm. Results were obtained by comparison with a standard curve with catechol as reference [8]. Principal Component Analysis (PCA) was carried out based on twenty-one quantitative and four quality characters in bottle gourd. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an eigen vector for each axis and produces component scores for the characters.

3. RESULTS AND DISCUSSION

The analysis of variance revealed that all the characters under study exhibited highly significant differences among the genotypes thus, suggesting existence of sufficient variability in the germplasm studied [9]. The significance of the largest contributor to the overall variance along each axis of differentiation is revealed using principal component analysis (PCA). This type of analysis, with PCA, is invaluable in understanding the complexity of traits and their interactions in crop improvement. It can guide future breeding strategies, focusing on high-yielding and quality-enhancing traits in bottle gourd cultivation. It is frequently decided by looking at the eigen values how many factors to keep. The number of variables is typically equal to the sum of the eigenvalues. Nearly 69.56% of the overall variation is contributed by the six principal components (PC1 to PC6) that are retrieved from the original data and have latent roots bigger than one. This implies that these six principal component scores could be utilised to condense the original 25 variables in any future data analysis. Eigen value from principal component analysis depicted the first two components accounted for 58.06 cumulative percent of total variation which signifies a high degree of correlation between the analysed traits [10]. Characters in the first principal component with the biggest absolute value that is closest to unity have a greater influence on the clustering than those with a smaller absolute value that is closest to zero, according to Chahal and Gosal [11]. Because of this, rather than a little contribution from each character, the diversification of the genotypes into various clusters in the current study was caused by a relatively substantial contribution from a small number of characters. Table 1 provides the coefficients defining the six principal components of the current data. Consequently, the first principal component contributed 20.08% to the total variance and had a high positive component loading from fruit yield plant^{-1} (0.269434), fruit yield ha^{-1} (0.269206), number of fruits plant^{-1} (0.210961), number of female flowers plant^{-1} (0.187922) and vine length (0.187548) even though other characteristics in this PC did not contribute much, rather their effects were distributed among other PCs. The positive loading indicates that there are positive trends in the correlation between the components and the variables. As a result, the aforementioned characters with high positive load added more to the diversity and served to most clearly distinguish the clusters. The principal component 2 (PC2) contributed 17.90% to the total variance and had a high positive component loading from fruit yield ha^{-1} (0.341256), fruit yield plant^{-1} (0.340775), number of primary branches (0.322577), fruit weight (0.301582) and vine length (0.288801). The share of PC3 in total variance was 10.05% and had a high positive

contribution from fruit weight (0.311960), number of seeds fruit^{-1} (0.263714), days to 1st fruit harvest (0.254156), days to last fruit harvest (0.248377) and 100 seed weight (0.240434). Similarly, the contribution of PC4 in the total variation was 8.23%. The characteristics that made a greater contribution to PC4 were number of seeds fruit^{-1} (0.444733), seed weight fruit^{-1} (0.417463), total phenols (0.380785), vitamin C (0.303026) and TSS (0.285346). PC5 contributed 6.82% to total variation. The high positive contributors among the studied traits in PC5 were seed weight fruit^{-1} (0.462083), number of seeds fruit^{-1} (0.357324), number of primary branches (0.181033), fruit length (0.166550) and node number at which 1st female flower appeared (0.156857). The overall variation contributed by PC6 was 6.48%. the characteristics with a high positive contribution to the PC6 were fruit diameter (0.459675), node number at which 1st female flower appeared (0.342523), days to 1st fruit harvest (0.162659), number of female flowers plant^{-1} (0.145015) and number of fruits plant^{-1} (0.138458).

Table 1. Latent vectors for twenty-five traits in bottle gourd [*Lagenaria siceraria* (Molina) Standl.] genotypes

Parameters	Eigen vectors					
	Prin1	Prin2	Prin3	Prin4	Prin5	Prin6
NMA	0.103216	0.122968	0.002096	-0.183331	0.105916	-0.144465
NFA	0.036561	0.007402	0.022074	-0.059823	0.156857	0.342523
DAPMF	-0.345014	0.252847	-0.165377	0.061665	0.050828	0.007188
DAPFF	-0.339226	0.264122	-0.152348	0.057731	0.051805	0.017995
DAMF	-0.346767	0.250975	-0.153319	0.058348	0.056945	0.013797
DAFF	-0.347841	0.256187	-0.125590	0.051682	0.059357	0.015001
NOMF	0.071764	0.096814	-0.318083	-0.189138	-0.120965	0.106448
NOFF	0.187922	0.088775	-0.414754	0.146796	0.104861	0.145015
DFFH	-0.256737	0.221590	0.254156	-0.057087	-0.129250	0.162659
DLFH	-0.252356	0.192171	0.248377	-0.059905	-0.147710	0.110450
VL	0.187548	0.288801	-0.011194	-0.142303	0.142374	0.025489
NOPB	0.146112	0.322577	0.030245	-0.133363	0.181033	0.046086
NOFPP	0.210961	0.087952	-0.437388	0.132746	0.148387	0.138458
FW	0.161580	0.301582	0.311960	-0.115745	0.007884	-0.086328
FL	0.012556	0.092310	0.009849	-0.110812	0.166550	-0.658546
FD	0.148177	0.054452	0.236742	0.150746	-0.063335	0.459675
FYPP	0.269434	0.340775	0.039959	-0.051318	0.073308	-0.002675
FYPH	0.269206	0.341256	0.038555	-0.051375	0.074139	-0.005266
NOSPF	0.006135	-0.004695	0.263714	0.444733	0.357324	-0.040602
SWPF	-0.019425	-0.035738	0.155162	0.417463	0.462083	-0.006733
100SW	0.067675	0.090377	0.240434	-0.177666	-0.082831	0.100080
TSS	0.128895	0.108474	-0.075380	0.285346	-0.242418	-0.030812
DM	0.110201	0.125839	-0.028405	0.232867	-0.465930	-0.246314
VITC	0.103341	0.140349	-0.003317	0.303026	-0.348091	0.073593
TP	0.062038	0.179555	0.057985	0.380785	-0.158621	-0.191933
Eigen value	5.02000651	4.47517427	2.51138841	2.05730230	1.70612094	1.62102865
Percentage variance	20.08	17.90	10.05	8.23	6.82	6.48
Cumulative percentage variance	20.08	37.98	48.03	56.26	63.08	69.56

NMA: Node no. at which first male flower appears, NFA: Node no. at which first female flower appears, DAPMF: Days to appearance of first male flower, DAPFF: Days to appearance of first female flower, DAMF: Days to anthesis of first male flower, DAFF: Days to anthesis of first female flower, NOMF: No. of male flowers plant^{-1}, NOFF: No. of female flowers plant^{-1}, DFFH: Days to first fruit harvest, DLFH: Days to last fruit harvest, VL: Vine length (m), NOPB: No. of primary branches, NOFPP: No. of fruits plant^{-1}, FW: Fruit weight (kg), FL: Fruit length (cm), FD: Fruit diameter (cm), FYPP: Fruit yield plant^{-1} (kg), FYPH: Fruit yield ha^{-1} (q), NOSPF: No. of seeds fruit^{-1}, SWPF: Seed weight fruit^{-1} (g), 100SW: 100 seed weight (g), TSS: Total soluble solids (ºBrix), DM: Dry matter content (%), VIT C: Vitamin C content (mg100g^{-1}), TP: Total phenols (mg100g^{-1})

Fig. 1 represents the relationship among 25 characters in bottle gourd genotypes by 2D scatter for first and second principal components. Fig. 2 depicts the relationship among 25 characters in bottle gourd genotypes by 2D scatter for first and third principal components. In Fig. 1, the parameters lying towards the right (towards the value 1) on the horizontal axis are the ones contributing more positively towards PC 1. Similarly, the parameters inclined more towards the left (towards the value -1) on the same axis are those whose negative contribution towards PC 1 is more. On the other hand, more positive contribution towards PC 2 is observed from those parameters which lie towards 1 on the vertical axis and the ones that are close to -1 on the same axis are those that contribute more negatively towards PC 2. Fig. 2 can be comprehended in a similar manner with component 3 replacing component 2. Fig. 3 denotes the relationship among 77 bottle gourd genotypes represented by a 2D scatter for first three principal components based on 25 characters. The scattered plot of the PCs showed that the genotypes were scattered in all the quarters, which is also a representative that high level of genetic variability is present among the evaluated genotypes, providing a resource in order to develop improved varieties in future breeding programme. More the distance between the genotypes, more likely are they to be genetically distant from each other and thus can be successfully employed in crossing programmes for developing high yielding bottle gourd varieties in the future.

The results of the current inquiry are supported by the findings of Kalyanrao et al*.* [12], who observed five principal components PC1, PC2, PC3, PC4 and PC5 with Eigen values 3.89, 2.75, 1.75, 1.47 and 1.36, respectively, accounting for 80.28% of the total variation. The first two principal components PC1 and PC2 with a proportion of 27.84% and 19.60%, respectively, contributed more to the overall variation. In further support to our findings, Shubha et al. [13] reported that the first two components were responsible for 36.77% of the phenotypic variability. The first principal component (PC1) accounted for 24.11% followed by second principal component (PC2) which accounted for 12.64% of the total variability. Similar results have also been reported by Jatav et al. [14] and Mehta et al. [15] in bitter gourd.

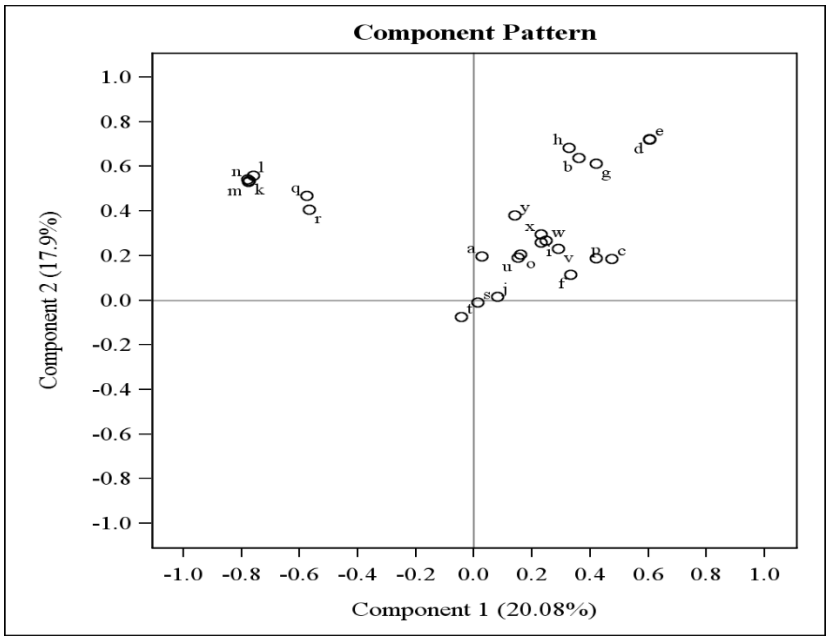

Fig. 1. Relationship among 25 characters in bottle gourd [*Lagenaria siceraria* (Molina) Standl.] germplasm by 2D scatter for first two principal components

a- Fruit length (cm), b- Fruit weight (kg), c- No. of fruits plant^{-1}, d- Fruit yield plant^{-1} (kg), e- Fruit yield ha^{-1} (q), f- Fruit diameter (cm), g- Vine length (m), h- No. of primary branches, i- Node no. at which male flower appears, j- Node no. at which female flower appears, k- Days to appearance of 1st male flower, l- Days to appearance of 1st female flower, m- Days to anthesis of 1st male flower, n- Days to anthesis of 1st female flower, o- No. of male flowers plant^{-1}, p- No. of female flowers plant^{-1}, q- Days to 1st fruit harvest, r- Days to last fruit harvest, s- No. of seeds fruit^{-1}, t- Seed weight fruit^{-1}(g), u- 100 seed weight (g), v- TSS (ºBrix), w- Dry matter content (%), x- Vitamin C content (mg100g^{-1}), y- Total phenols (mg100g^{-1})

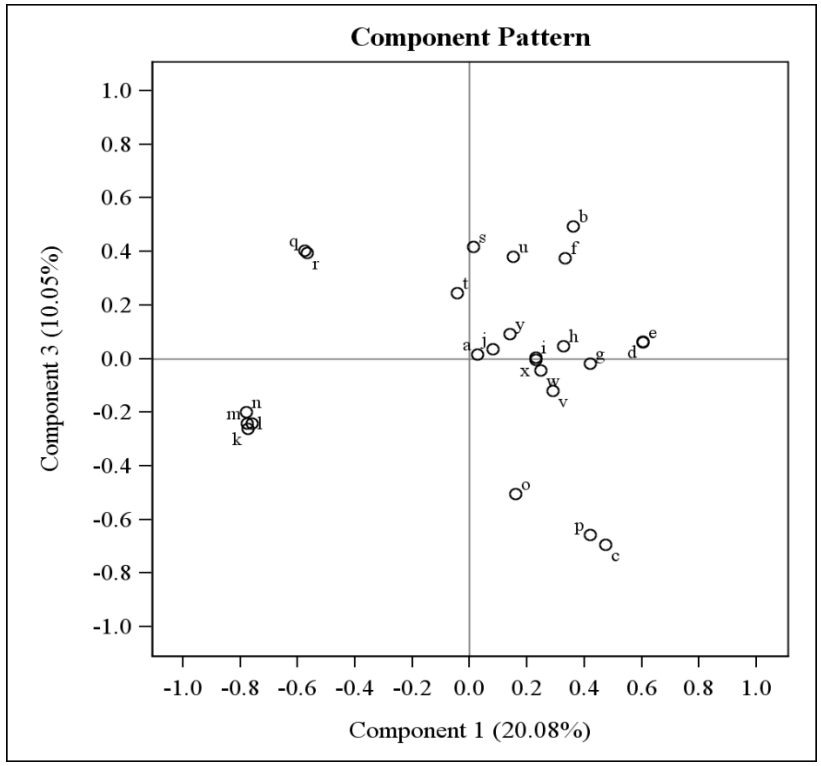

Fig. 2. Relationship among 25 characters in bottle gourd [*Lagenaria siceraria* (Molina) Standl.] germplasm by 2D scatter for first and third principal components

a- Fruit length (cm), b- Fruit weight (kg), c- No. of fruits plant^{-1}, d- Fruit yield plant^{-1} (kg), e- Fruit yield ha^{-1} (q), f- Fruit diameter (cm), g- Vine length (m), h- No. of primary branches, i- Node no. at which male flower appears, j- Node no. at which female flower appears, k- Days to appearance of 1st male flower, l- Days to appearance of 1st female flower, m- Days to anthesis of 1st male flower, n- Days to anthesis of 1st female flower, o- No. of male flowers plant^{-1}, p- No. of female flowers plant^{-1}, q- Days to 1st fruit harvest, r- Days to last fruit harvest, s- No. of seeds fruit^{-1}, t- Seed weight fruit^{-1}(g), u- 100 seed weight (g), v- TSS (ºBrix), w- Dry matter content (%), x- Vitamin C content (mg100g^{-1}), y- Total phenols (mg100g^{-1})

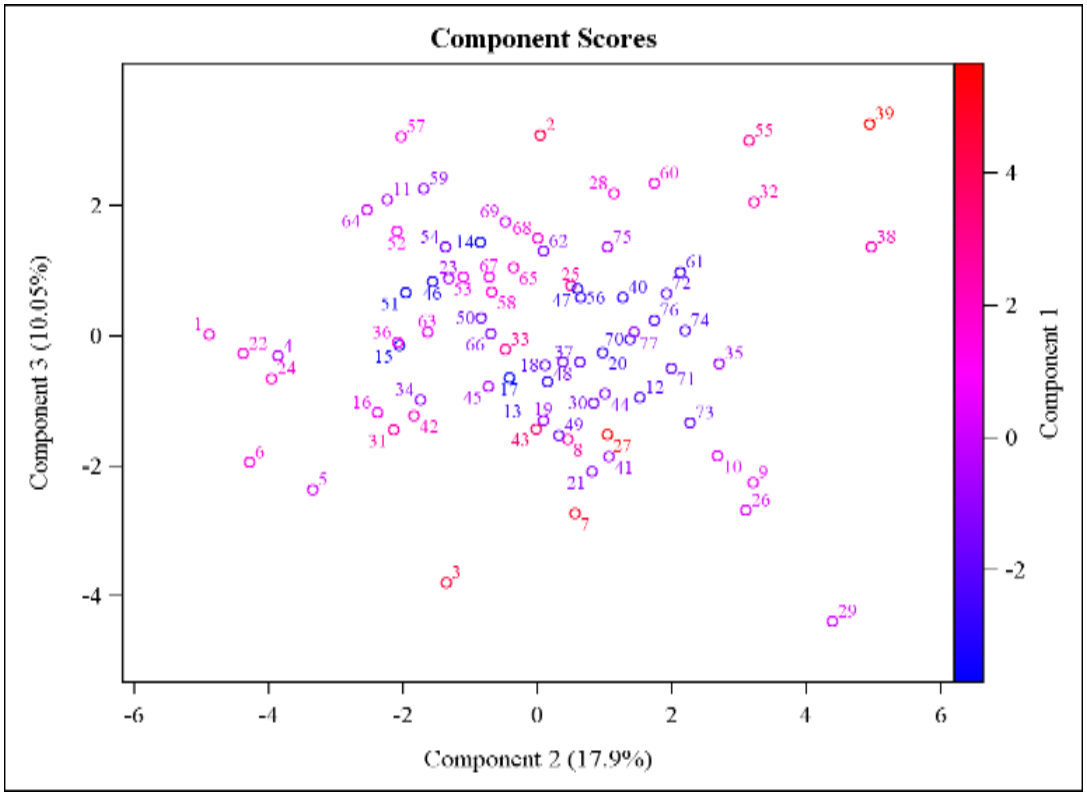

Fig. 3. Relationship among 77 bottle gourd [*Lagenaria siceraria* (Molina) Standl.] genotypes shown by a 2D scatter for first three principal components based on quantitative and qualitative characters

1-Pusa Naveen, 2-Pusa Santushti, 3- SKUA-BG-4, 4- SKUA-BG-5, 5- SKUA-BG-6, 6- SKUA-BG-7, 7-SKUA-BG-3, 8-SKUA-BG-1, 9- SKUA-BG-8, 10-IC-047045, 11-IC-262868, 12-IC-256053, 13-IC-256052, 14-IC-256051, 15-IC-256043, 16-IC-284953, 17-IC-284895, 18-IC-284874-1, 19-IC-284874, 20-IC-284816, 21-IC-276552, 22-IC-276153, 23-IC-294891, 24-IC-94891-1, 25-IC-319460, 26-IC-316017-1, 27-IC-318883-1, 28-IC-310206-1, 29-IC-310206, 30-SKUA-BG-2, 31-IC-307077, 32-IC-310188, 33-IC-306422, 34-IC-297846, 35-IC-306128-A, 36-IC-418491, 37-IC-385816, 38-IC-382258, 39-IC-371747-1, 40-IC-371747, 41-IC-392392, 42-IC-522868-1, 43-IC-371697, 44-IC-522866, 45-IC-522856, 46-IC-426990, 47-IC-424502, 48-IC-411915, 49-IC-522868, 50-IC-522876, 51-IC-522878, 52-IC-385816-1, 53-IC-394736, 54-IC-394857, 55-IC-398541, 56-IC-417705, 57-IC-421962, 58-IC-418491-A, 59-IC-342078, 60-IC-321121, 61-IC-341390, 62-IC-339209, 63-IC-536894-1, 64-IC-331981, 65-IC-330999, 66-IC-321460, 67-IC-325973, 68-IC-321559, 69-IC-321412, 70-IC-321414, 71-IC-312410-1, 72-IC-321410, 73-IC-330987, 74-IC-331121, 75-IC-342080, 76-IC-546151, 77-IC-536594

4. CONCLUSION

Principal component analysis has identified few characters that plays prominent role in classifying the variation existing in the germplasm set. The first six principal components accounted for 69.56 % to the total variation. Principal component analysis reflects the importance of largest contributor in each principal component. The first PC accounts for the maximum variability in the data i.e., 20.08%. The remaining variability of 17.90%, 10.05%, 8.23%, 6.82% and 6.48% was consolidated in PC2, PC3, PC4, PC5 and PC6 respectively. The analysis identified that fruit yield plant^{-1}, fruit yield ha^{-1}, fruit weight, number of seeds fruit^{-1}, seed weight fruit^{-1} and fruit diameter in different principal components are the most important for classifying the variation. Thus, the PCA results revealed significant genetic variation among the genotypes, with specific traits contributing to this variation. This population panel can thus be effectively utilized in breeding programs to improve traits with major variations.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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