

Genetic divergence studies among sand pear (*Pyrus pyrifolia* (Burm) Nakai.) genotypes for yield and yield contributing traits in North-Western Himalayas

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Short Report

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Abstract

Germplasm assets are critical for hereditary breeding, investigation of complex traits and are conducive to the investigation and creation of unused germplasm. In order to effectively measure genetic divergence and character association for sand pear genetic improvement, yield and yield contributing variables were assessed for 125 genotypes during 2018–2021 in three districts of Himachal Pradesh, India (N-W Himalayas). The results indicated that estimates for eye basin, depth stalk cavity depth, fruit stalk length, non reducing sugars and leaf area high had high PCV and GCV values. High heritability and genetic gain both suggests the existence of additive gene action. The fruit's weight, sugar-to-acid ratio, and titratable acidity were reported, these qualities can be enhanced via direct selection. Fruit weight, total sugars, trunk diameter, total soluble solids (TSS), fruit length, fruit breadth, petiole length, and leaf area all have a high direct effect on plant yield, according to studies of association. Therefore, the overall result suggests that there is substantial diversity in the assessed attributes for them to serve as selection indices for genetic improvement of sand pear.

Introduction

Pear belonging to genus *Pyrus*, family Rosaceae is partitioned into two sub group's i.e. Asian and European pears (Zhang et al. 2021). Asian sand pear [*Pyrus pyrifolia* (Burm.) Nakai] has been tamed and developed as an edible fruit in Asia for more than 3000 years with hundreds of cultivars developed for excellent attributes like high yield, early maturation, juiciness, sweetness, freshness, small to very large, gritty fruits and ripeness etc (Xie et al. 2019). Fruits of sand pear are mostly used for fresh consumption or production of jams, juice, beverages and wines (Chandel et al. 2023). The maximum area under sand pear cultivation in India exists in Kashmir valley whereas In Himachal Pradesh, these are found growing as scattered trees in semi-wild state in Mandi, Solan, Sirmour, Shimla, Una, Hamirpur, Bilaspur, Chamba and Kangra districts which exhibit substantial variability in terms of growth, yield and fruit quality parameters.

Sand pear might be the promising crop for low, mid and high hills provinces because of its less chilling requirement, medicinal properties and an economical importance but remained as a neglected or underutilized fruit in North Western Himalayas. This crop can also be substitute in sub temperate zone under the changing climatic scenario where pome and stone fruits are not producing well but there is no availability of systematic research. Introduction and development of new fruit crops and cultivars is the need of an hour. In addition, due to land clearing and restoration of wastelands, the genetic resources of lesser-known fruits, such as sand pears, would diminish at an astounding level. If the current trend continues, it is believed that fruits such as sand pears may go extinct within the next several decades. For the purpose of using elite germplasm in sand pear breeding, the thorough assessment of rich sand pear genetic resources is of paramount importance (Yan et al. 2014). Instinctive and fundamental diversity research in plants require the integration of phenotypic features study (morphological strategy) and biotechnological innovation, as the latter can more precisely reveal the genetic differences of plants (Akhtar et al. 2022; Sapkota et al. 2013). Genetic variability is influenced by the degree and kind of genotypic and phenotypic differences, hence, the parameters on which success of any breeding operation hinges. These should be followed by high heritability, as the degree of heritability represents how reliable it is to detect genotypes based on phenotypic expression (Raina et al. 2014) and regarded as useful index for transfer of traits from parents to progeny. In light of the foregoing, the goal of the current work was to examine genetic factors like heritability, correlation and path coefficient analysis in 125 sand pear genotypes from existing plantations in North-Western Himalayas, in order to obtain desirable selections for direct cultivation that will not only contribute to biological diversity, but also aid in the utilization of genetically superior parents for future breeding programs.

Materials and Methods

Existing genotypes of sand pear plantations served as the subject of the experiment in three districts of Himachal Pradesh, India (North-Western Himalayas) viz., Solan, Sirmour and Shimla over the years 2018–2021. The chosen research area specifically lies within the mild temperate to temperate zone, which spanned from N 30049.701'to N 31017.122'and E 076 047.568' to E 077 056.585' with an elevation range of 850 m to 2200 m above mean sea level (Fig.1). Based on overall fruit quality and input from locals, 125 healthy and productive genotypes of sand pear trees were subjected to selection and further evaluation

Morpho-physical characters was observed as per IBPGR (1983) and UPOV (2000) standard descriptor guidelines. Using an Effigi penetrometer with 7/16" plunger in kg/cm² to measure fruit firmness, an average of five fruit was selected for each of three replications. Fruit's total soluble solids content (TSS) was determined using Erma hand refractometer ranged from 0–32 ° Brix. Ranganna (2009) standard methodology was used to determine the total, reducing and non-reducing sugar contents. Singleton and Rossi's (1965) Folin-Ciocalteu process was used to evaluate the total phenol content. In accordance with Panse and Sukhatme (1985), a statistical analysis was performed using the PAST 4.0, SPSS 16.0 and SPAR 2.0 software to examine different aspects of genetic variability, correlation and path coefficient. Software from PAST3 was used to create a bi-plot depiction of the first two elements of the principal component analysis, which was carried out using SPSS software to show how genotypes and indices, are related

Results and Discussions

For genetic variation, the coefficient of variation is a potential marker which was estimated among 125 genotypes of sand pear by working out various parameters of variability (Fig. 2). The phenotypic traits with the highest coefficients of variance were depth of eye basin (49.54%), depth of stalk cavity (42.81%), length of fruit stalk (41.05%), non-reducing sugars (39.81%), sugar acidratio (31.69%) and leaf area (30.40%) indicating substantial variability in these characters demonstrating numerous opportunities for selection to improve them. Additionally, the genotypic coefficient of variation that was highest was found for depth of eye basin (45.79%), depth of stalk cavity (41.43%), length of fruit stalk (39.21%), non-reducing sugars (39.05 %), width of eye basin (35.72 %), leaf area (30.21%) and sugar acid ratio (30.34%). When compared to their equivalent PCV, the magnitude of the GCV was found to be lower, indicating that the environment had less impact on traits under study (Lal et al. 2022; Saroj et al. 2021). The variation coefficient of depth of eye basin (49.54% & 45.79 %), among 15 numerical traits of 125 sand pear genotypes, was highest while fruit length to diameter ratio was the lowest (13.84 % & 13.82

%) demonstrating the rich genetic diversity of the phenotypic variations of sand pear germplasm. Similar outcomes were seen by Zhang et al. (2022). Heritability (broad sense) was reported to be ranged from 64.56 per cent to 99.92 per cent, being highest in fruit weight, fruit length, diameter and juice content. Genetic gain was between 28.45% and 87.18%. A high degree of genetic gain and heritability were obtained for fruit weight, trunk girth, sugar acid ratio, titratable acidity, leaf area, non-reducing sugars, length of fruit stalk and depth of stalk cavity which are consistent with the conclusions of Bhatt and Dhillon (2015) indicating these as simply inherited characters, less influenced by environment and governed by few major genes, and hence, selecting these characters would improve cultivar performance. Similar findings were also recorded previously in sand pear (Raina et al. 2014). In order to accurately depict the diversity of phenotypic features in sand pears, it is crucial to select out fewer phenotypic traits (Zhang et al. 2022). According to correlation analysis, fruit weight (0.79), length (0.44), breadth (0.39) and trunk girth (0.33) had the largest and most positive associations with yield, indicating their selection would likewise increase production (Table 1). Fruit breadth (0.68), weight (0.59), length to diameter ratio (0.55) and fruit yield (0.44), all demonstrated positive and statistically significant correlations with fruit length. Fruit weight, on the other hand, exhibited a positive and significant correlation with all the analysed characteristics except firmness (-0.01), but it had the strongest correlation with yield per tree (0.79) and juice content (0.19). These findings corroborated investigations of Raina et al. (2014) which showed that increase in fruit length also lead to increase in fruit weight and breadth.

Table 1: Correlation coefficients between phenotypic and genotypic variables in several sand pear genotypes

		2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	G	-0.01	-0.03	0.08	0.12	0.24*	0.18*	0.17	0.25*	-0.13	0.04	-0.01	0.09	0.01	-0.20*	-0.13	-0.01	0.01
	P	-0.01	-0.02	0.08	0.11	0.24*	0.18*	0.11	0.25*	-0.12	0.04	0.01	0.09	0.01	-0.18*	-0.12	-0.01	-0.01
2	G		0.61*	0.39*	0.44*	-0.00	-0.00	-0.00	-0.13	0.04	-0.04	0.02	0.11	-0.07	-0.12*	0.01	0.03	0.01
	P		0.52*	0.28*	0.35*	-0.01	-0.01	-0.00	-0.11	0.04	-0.03	-0.06	0.00	-0.06	-0.11	-0.03	0.03	-0.01
3	G			0.28*	0.41*	-0.06	-0.00	-0.08	-0.03	0.03	-0.18*	0.01	0.11	-0.02	-0.01	-0.02	-0.13	0.01
	P			0.21*	0.33*	-0.06	-0.01	-0.08	-0.03	0.06	-0.14*	-0.00	0.13	-0.02	0.01	-0.03	-0.11	0.01
4	G				0.26*	0.01	-0.18*	0.21*	-0.12	-0.09	-0.00	0.01	0.10	0.03	-0.03	-0.01	-0.06	0.01
	P				0.25*	0.01	-0.17*	0.21*	-0.12	-0.10	-0.01	0.03	0.06	0.03	-0.02	0.01	0.06	0.01
5	G					0.11	0.00	0.17*	0.04	0.11	-0.16*	0.17*	-0.06	-0.03	-0.18*	0.01	-0.02	0.01
	P					0.11	0.00	0.17*	0.04	0.11	-0.16*	0.16*	-0.06	-0.03	0.18*	0.02	-0.02	0.01
6	G						0.68*	0.55*	0.58*	-0.06	0.08	0.09	0.07	0.15*	-0.02	-0.04	0.03	-0.01
	P						0.68*	0.55*	0.59*	-0.06	0.07	0.09	0.05	0.15	-0.01	-0.03	0.03	-0.01
7	G							-0.22*	0.48*	-0.02	0.08	0.20*	0.10	0.12	0.03	-0.19*	0.04	-0.01
	P							-0.22*	0.48*	-0.02	0.08	0.19*	0.07	0.13	0.04	-0.17*	0.04	-0.01
8	G								0.23*	-0.06	0.04	-0.09	0.01	0.05	-0.06	0.16*	-0.00	0.01
	P								0.23*	-0.06	0.05	-0.08	0.00	0.05	-0.07	0.16*	0.00	0.01
9	G									0.08	0.04	0.18*	0.06	0.19*	-0.01	0.04	0.01	0.01
	P									0.07	0.04	0.18*	0.05	0.19*	-0.01	0.05	0.01	0.01
10	G										-0.12	0.21*	-0.15*	-0.01	0.12	0.17*	-0.04	0.01
	P										-0.10	0.19*	-0.11	-0.05	0.11	0.15*	-0.03	0.01
11	G											0.02	0.09	0.12	0.10	0.07	0.14	0.01
	P											0.00	0.10	0.12	0.08	0.06	0.14*	-0.01
12	G												0.18*	0.19*	0.03	-0.03	0.08	0.01
	P												0.06	0.17*	0.10	-0.00	0.07	0.01
13	G													0.19*	0.17*	0.11	-0.09	0.01
	P													0.18*	0.13	0.05	-0.09	0.01
14	G														0.49*	0.10	0.05	0.01
	P														0.46*	0.10	0.05	0.01
15	G															0.21*	0.14*	0.01
	P															0.19*	0.12	0.01
16	G																0.09	0.01
	P																0.08	0.01
17	G																	0.01
	P																	0.01
18	G																	
	P																	
19	G																	
	P																	
20	G																	
	P																	
21	G																	
	P																	

1-Trunk girth 2- Leaf bade length 3- Leaf blade width 4- Petiole length 5- Leaf area 6- Fruit length 7- Fruit breadth 8- Fruit length to diameter ratio 9- Fruit weight 10- Length of fruit stalk 11- Depth of stalk vaity12 Depth of eye basin 13- Width of eye basin 14- Juice content 15- Firmness 16- TSS 17- Titratable acidity 18- Total sugars 19- Reducing sugars 20- Non reducing sugars 21- Sugar-acid ratio 22- Yield.

*Significant at 0.05%

Table 2: Estimated effects of various traits, both directly and indirectly, on the yield of various sand pear genotypes

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	<u>0.14</u>	0.00	0.00	0.00	0.00	0.01	0.00	-0.01	0.21	0.01	0.00	0.00	0.00	0.00	0.02	-0.01	0.00	-0.05	0.00
2	0.00	<u>-0.11</u>	0.00	0.00	0.00	0.00	0.00	0.00	-0.11	0.00	0.00	0.00	0.01	0.00	0.01	0.00	-0.01	0.05	-0.01
3	0.00	-0.07	<u>0.00</u>	0.00	0.00	0.00	0.00	0.01	-0.03	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.04	0.00	-0.01
4	0.01	-0.04	0.00	<u>0.01</u>	0.00	0.00	0.00	-0.02	-0.10	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
5	0.02	-0.05	0.00	0.00	<u>0.01</u>	0.00	0.00	-0.01	0.03	-0.01	0.01	0.00	0.00	0.00	0.01	0.00	0.01	0.02	-0.01
6	0.03	0.00	0.00	0.00	0.00	<u>0.03</u>	0.01	-0.05	0.46	0.01	0.00	0.00	0.00	-0.01	0.00	0.00	-0.01	-0.02	0.00
7	0.03	0.00	0.00	0.00	0.00	0.02	<u>0.01</u>	0.02	0.39	0.00	0.00	0.00	0.00	-0.01	0.00	-0.01	-0.01	-0.09	0.00
8	0.02	0.00	0.00	0.00	0.00	0.02	0.00	<u>-0.08</u>	0.19	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.07	-0.01
9	0.04	0.01	0.00	0.00	0.00	0.02	0.01	-0.02	<u>0.80</u>	-0.01	0.00	0.00	0.00	-0.01	0.00	0.00	0.00	0.04	-0.01
10	-0.02	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.06	<u>-0.09</u>	0.01	0.00	0.01	0.00	-0.01	0.01	0.01	0.16	-0.01
11	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	<u>-0.05</u>	0.00	0.00	-0.01	-0.01	0.00	-0.04	0.01	0.00
12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.15	-0.02	0.00	<u>-0.01</u>	-0.01	-0.01	0.00	0.00	-0.03	0.01	0.00
13	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.01	-0.01	0.00	<u>-0.04</u>	-0.01	-0.01	0.01	0.03	0.05	-0.01
14	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.00	-0.01	0.00	-0.01	<u>-0.06</u>	-0.04	0.01	-0.02	0.10	-0.01
15	-0.03	0.01	0.00	0.00	0.00	0.00	0.00	0.01	-0.01	-0.01	-0.01	0.00	-0.01	-0.03	<u>-0.07</u>	0.01	-0.04	0.15	-0.01
16	-0.02	0.00	0.00	0.00	0.00	0.00	0.00	-0.01	0.04	-0.02	0.00	0.00	0.00	-0.01	-0.02	<u>0.07</u>	-0.03	0.36	-0.01
17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	-0.01	0.00	0.00	0.00	-0.01	0.01	<u>-0.30</u>	0.09	-0.01
18	-0.01	-0.01	0.00	0.00	0.00	0.00	0.00	-0.01	0.05	-0.02	0.00	0.00	0.00	-0.01	-0.02	0.04	-0.04	<u>0.61</u>	-0.01
19	-0.02	-0.02	0.00	0.00	0.00	0.00	0.00	-0.01	0.04	-0.02	0.00	0.00	0.00	-0.01	-0.02	0.03	-0.02	0.52	<u>-0.01</u>
20	0.01	0.01	0.00	0.00	0.00	0.00	0.00	-0.01	0.02	-0.01	-0.01	0.00	-0.01	0.00	-0.01	0.02	-0.05	0.35	-0.01
21	0.00	-0.01	0.00	0.00	0.00	0.00	0.00	-0.01	0.04	-0.01	0.00	0.00	0.00	-0.01	0.00	0.02	0.22	0.31	-0.01

Residual effect = 0.24

1-Trunk girth 2- Leaf bade length 3- Leaf blade width 4- Petiole length 5- Leaf area 6- Fruit length 7- Fruit breadth 8- Fruit length to diameter ratio 9- Fruit weight 10- Length of fruit stalk 11- Depth of stalk cavity 12 Depth of eye basin 13- Width of eye basin 14- Juice content 15- Firmness 16- TSS 17- Titratable acidity 18- Total sugars 19- Reducing sugars 20- Non reducing sugars 21- Sugar-acid ratio 22- Yield.

Note: values with bold and underline are depicting direct effect.

To measure the direct and indirect cause of association and formulating effective breeding strategies to develop elite genotype, path analysis was calculated using fruit yield per plant as dependent variable and other component characteristics as independent variable (Table 2). The most significant direct positive effects on fruit yield was demonstrated by fruit weight (0.80); total sugars (0.61) and trunk girth (0.14) where fruit weight had a favourable indirect on trunk girth (0.04); total sugars (0.04); fruit length (0.02) and leaf blade length (0.01). These results concurred with those of Carra et al. (2018) indicating direct effect of fruit weight on yield. Unaccounted-for effects in path coefficient analysis are classified as residual effects, and their low frequency at genotypic level suggested that the traits in the current study accounted for the majority of the variation in the dependent variable (fruit yield) (Chauhan et al. 2020).

In order to assess the pattern of variation in sand pear genotypes principal components (PC) analysis was done by considering all twenty two variables simultaneously. The PCA revealed that eight principle components with Eigen value greater than one explained 71.40 per cent of variation among 125 genotypes, with the first three components accounting for more than 39.39 per cent of the observed variability (Fig 3.). 14.47% of the overall variation was accounted for by the first PC, while fifteen out of twenty two traits exerted positive effects on this component and rest exerted negative effect of different magnitudes. The second element was responsible for 13.96% of total variation primarily illustrate the pattern of variation in trunk girth, fruit weight, length, yield, diameter, length to diameter ratio and juice content which were found to have positive impact on second component while leaf length, width and petiole length had negative coefficients. The third PC accounted for 10.96% of total variation, alluded with the variations in trunk girth, leaf length, area, width, petiole length and fruit length exhibiting positive effect while rest parameters with negative effect. Fig. 4 displays the scores for the first, second and third

principal components and the bi-plot of PC1 vs. PC2 is displayed in Fig. 5. Similarly, Zavisic et al. (2017) also reported 54.78% variation explained by first two PC when fruit and leaf characters were analysed together.

Conclusion

There exists an extensive variation among all the sand pear genotypes from existing plantation in Himachal Pradesh (North-Western Himalayas). The majority of the studied characters exhibited high and moderate phenotypic coefficient of variation, indicating the presence of significant diversity among these characters and providing abundant opportunity for their improvement through selection. Fruit weight, sugar acid ratio, and titratable acidity showed high heritability and high values of genetic advance as percentage means in the genotypes under study, indicating that these characters were strongly influenced by additive gene action and hence a straightforward selection process based on phenotypic expression of these features would be more trustworthy. The direct positive impacts on fruit yield were noted by fruit weight, total sugars trunk girth, TSS and fruit length. Hence, more emphasis should be given to these traits while selecting a genotype as compared to those showing negative direct effect with fruit quality. These findings provide an insight into available diversity among sand pear genotypes and leads to selection of 13 superior genotypes excelling in one or more horticulturally desirable traits which was field conserved. It would be worthwhile to field test these selected superior sand pear genotypes under suitable agro-climatic conditions for isolating better performing genotypes having commercial potential.

Declarations

Conflict of interest:

The authors declare that they have no conflict of interest.

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Figures

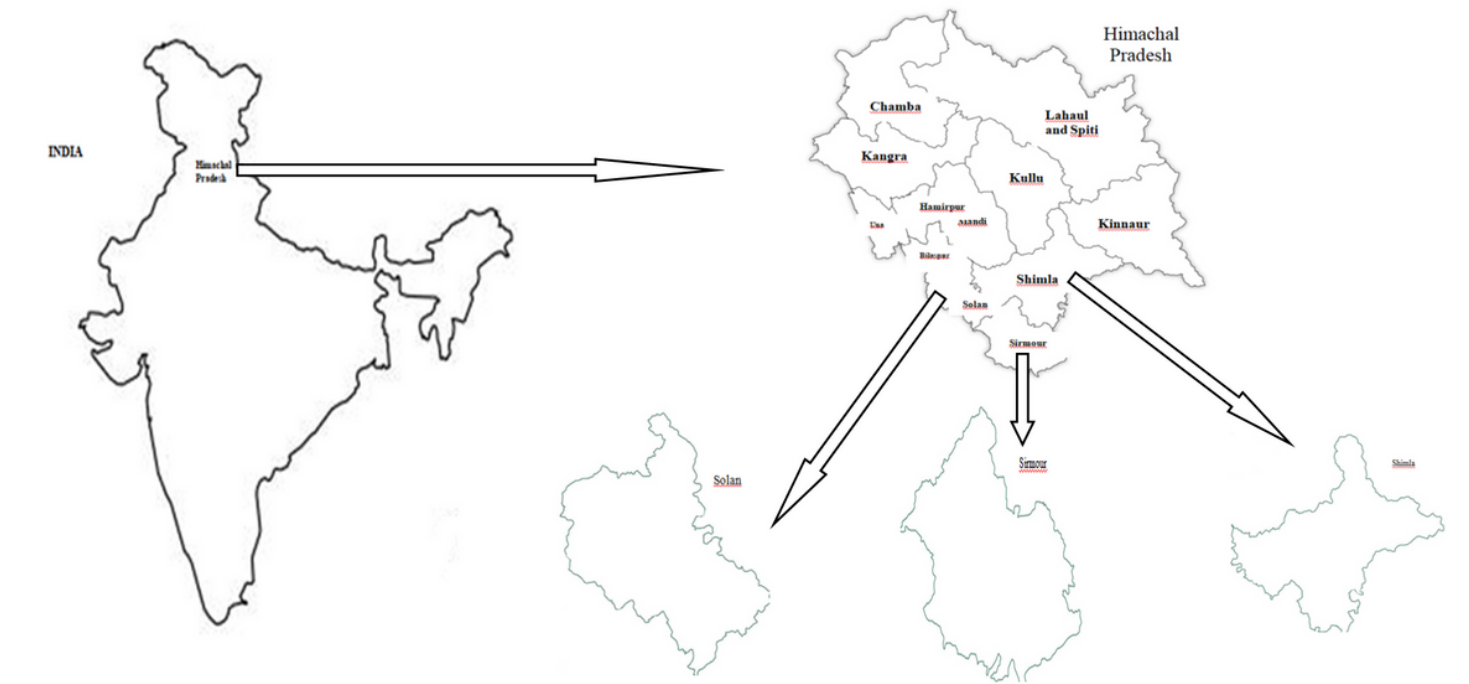


Figure 1

Geographic locations of area surveyed in North-Western Himalayas

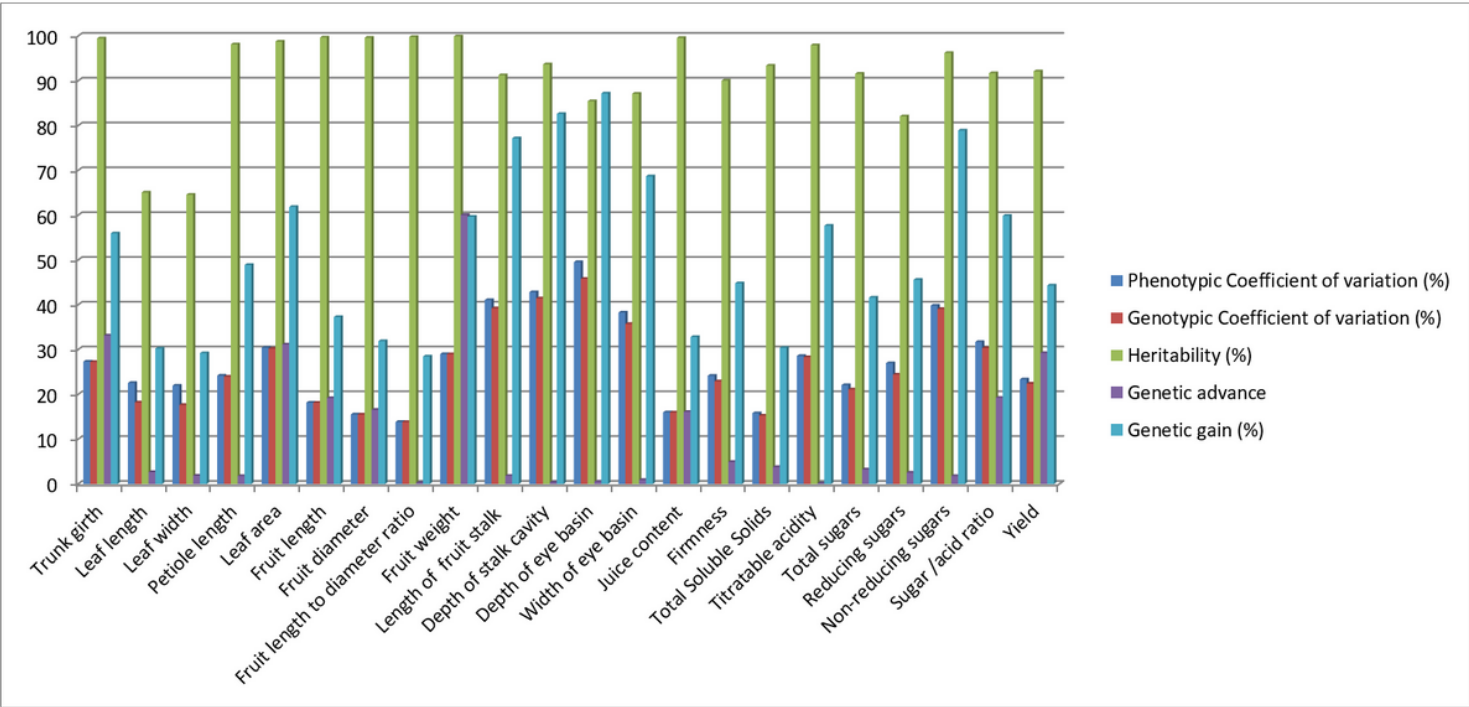


Figure 2

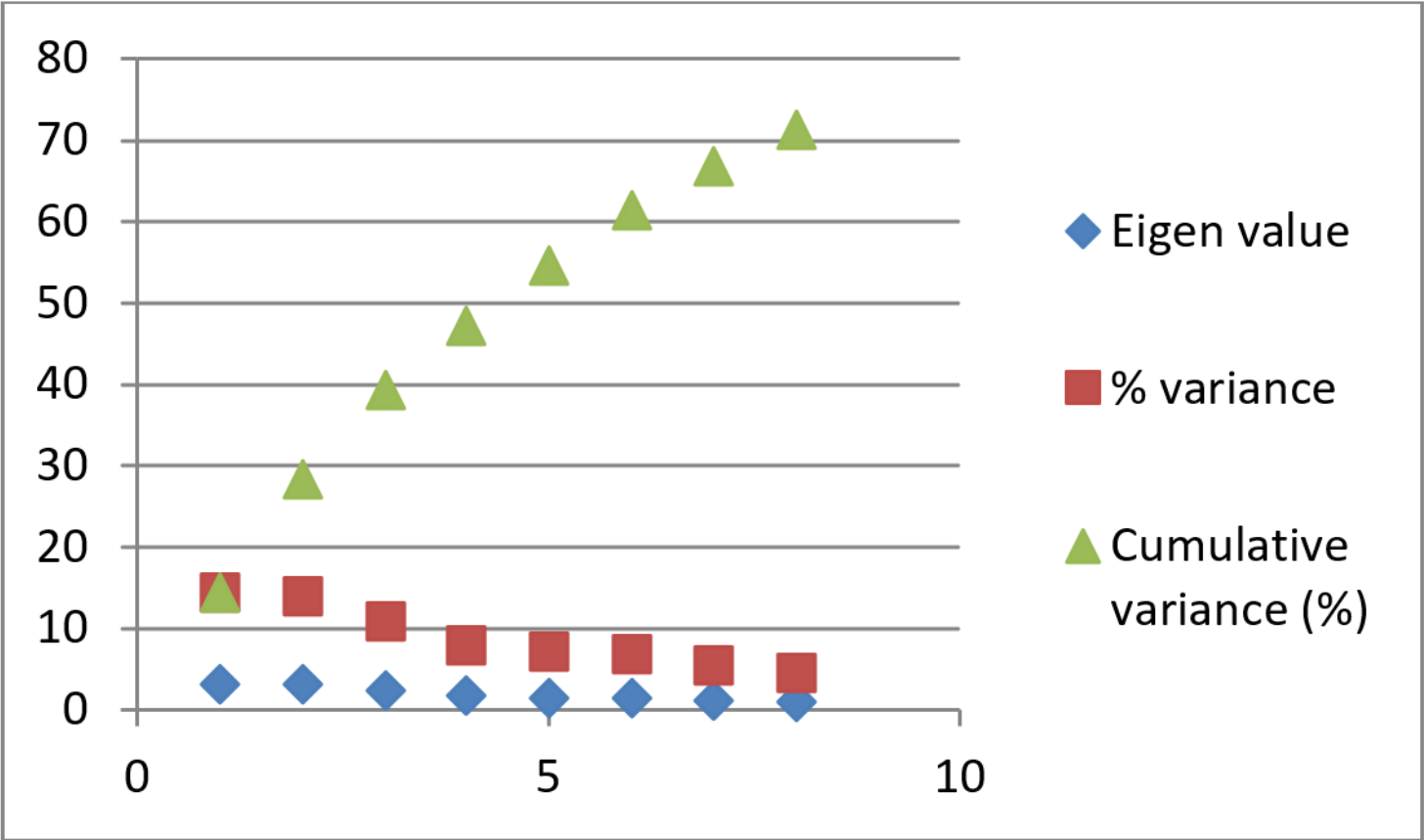


Figure 3

125 genotypes' principal components based on 22 characteristics

