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Genetic diversity among plum genotypes in North West Himalayan region of India

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ABSTRACT

Twenty three plum (*Prunus* sp.) genotypes were studied to assess the overall degree of polymorphism, detect similarities among important pomological, fruit quality and yield parameters. Sixteen variables were scored and subjected to multivariate analysis. Results showed a considerable phenotypic diversity among plum genotypes. The cluster analysis classified genotypes into two major groups according to their potential characteristics. The first group was found superior in terms of fruit morphological and yield related characteristics and second group in fruit quality attributes. Principal component analysis (PCA) revealed that traits positively related to fruit length, diameter, volume, weight, pulp thickness, stone length, stone diameter, stone weight, reducing sugars and total sugars, and negatively related to fruit firmness, acidity, non reducing sugars, juice content and fruit yield accounted for a large proportion of the observed variability. The genotypes Prune, Grand Duke, Italian Plum, President Plum, Mariposa, Beauty and Santa Rosa were found unique for fruit and yield attributing traits.

Key words: Genetic diversity, North west Himalayan region of india, Plum genotypes

The plums are among the most important stone fruit crop in the world (Bhutani and Joshi 1995). The largest producer is China, with an annual production of 5 664 826 metric tonnes (FAO 2010), accounting for 51.55 % of the world production. It belong to the genus *Prunus* and family Rosaceae. There are two important plum types: European plum (*Prunus domestica*, 2n = 6x = 48) and Chinese plum including both pure Chinese plum (*Prunus salicina*, 2n = 2x = 16) and its hybrids with other diploid plum species, such as *Prunus simonii, Prunus cerasifera, Prunus americana*, and others (Bhutani and Joshi 1985). European plum is used for both drying and fresh markets, while Chinese plum-types are used mainly for fresh market. In India, different plum genotypes are grown in Jammu and Kashmir, Himachal Pradesh, Uttarakhand and Punjab. The total area under plum cultivation is 24 000 ha with an annual production of 74 000 mt and productivity is 3.08 tonnes/ha (Anon. 2014) possess high genetic variability. Genetic variability is the prerequisite for any plant breeding program (Khush 2002). Morphological traits are the primary markers utilized in germplasm management (Karimi *et al*. 2008). These traits are in common use for elucidation of wide genetic diversity in different field and horticultural crops (Blazek 2007).

Leaf, flower and related fruit traits, have been used as main morphological traits in inter-specific hybrids characterization of plum trees (Naotoshi *et al*. 1998, Jakubowski 2002, Ertekin *et al.* 2006). Although, newly developed molecular markers are valuable in gene based diversity studies, however the procedures used for the molecular marker analysis have disadvantage of high cost (Ahmad *et al*. 2004, Bouhadida *et al*. 2005). In contrast, morphological traits could feasibly be used for parental selection and along with molecular techniques are of highly appreciated procedures for description and germplasm classification of plants. Statistical method such as principal component analysis and cluster analysis were employed as powerful options for plant cultivar and accession screenings. Morphological criteria have been widely used as important markers in plant breeding programs (Kaufmane *et al*. 2002, Ogasanovic *et al*. 2007, Karimi *et al*. 2008, Kumar *et al*. 2015). The subject of the present study was to investigate the morphological traits diversity of 23 plum genotypes as an initial step aiming to the national and international germplasm characterization and preservation of these precious fruit trees for future breeding programs. The purpose of this study is to identify promising plum genotypes based on phenological and pomological characteristics that will be useful to harness the economic advantage associated with this valuable crop through survey and collection from potential areas. These elite genotypes further be utilized for crop improvement. The present study will also elucidate relationships among the studied genotypes and their traits.

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Obtained data are necessary to develop adequate phenotypic markers for commercial use and germplasm management and to select the most promising plum genotypes for use in breeding and to identify their desirable fruit and yield characteristics.

MATERIALS AND METHODS

This study was conducted during the year 2009 to 2013 on 23 diverse plum genotypes, viz. Meriposa, Santa Rosa, President Plum, Kubio-26, Grand Duke, Prune, Kubio, Kanto-5, Monarch, Au-Cherry, Methley, Green Gage, Red Plum, Tarcol, Beauty, Italian Plum, Red Beauty, Au-Rosa, Black Beauty, Frontier, Krassivica, Burbank and Black Amber collected from ICAR-National Bureau of Plant Genetic Resources (NBPGR) , New Delhi, India at research farm of ICAR-Central Institute of Temperate Horticulture (CITH) , Srinagar on morphological, chemical and yield attribute differences in plum. The climate of Kashmir valley is varied with annual precipitation is about 750 mm which is much higher as compared to Ladakh (90 mm), derived partially from the summer monsoon and partially from storms associated with winter low-pressure systems. Snowfall often is accompanied by rain and sleet. Temperatures vary considerably by elevation; the average minimum temperature is “2°C in January, and the average maximum is about 31°C in July. The valley is surrounded by Himalayas on all sides and spring is the wettest season while autumn is the driest.

The primary selection criterion was based on fruit and yield attributes of the genotypes. Individual genotypes were marked in the field. The data were recorded at the time of fruit maturity during summer (Aug-September) seasons of the each year, i.e. 2008 -2012 and data pooled for analysis. Morphological features and physicochemical parameters of the fruits were recorded in the laboratory. Twenty fruits from each genotype were randomly chosen and measured. The data were collected on fruit length (mm), weight (g), diameter (mm), volume (ml) , pulp thickness (mm), fruit firmness index, stone length (mm), stone diameter (mm), stone weight (g), TSS (^{o} Brix), acidity (%), reducing sugars, non reducing sugars, total sugars, juice (%) and fruit yield (kg/plant). Weight was measured by Sartorius balance of accuracy of 0.001 g. The length and diameter of the fruit was measured with a digital vernier calipers. The measurement of fruit length was made on the polar axis, i.e. between the apex and the end of stem. The maximum width of the fruit, as measured in the direction perpendicular to the polar axis, is defined as the diameter. After measuring the whole fruit size, the stone was manually separated from the fruits, and traits were measured as above. Fruit firmness index recorded using digital firmness meter. Total soluble solids (TSS), titrable acidity, and sugars were determined by method given in AOAC (1994). The experiment was conducted under randomized block design with three replications and pooled data of four years were analyzed as per the method suggested by Gomez and Gomez (1984).

Study of genetic divergence among the available genetic resources play a vital role for selection of better parents for plum improvement in which genetically diverse parents are likely to contribute desirable segregants and or to produce high heterotic crosses. Parents identification based on divergence are more promising for any breeding program (Arunachalam 1981). Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. Therefore, biometrical descriptive analysis was performed. To explore the diversity and relationship among 23 genotypes, their vital morphological characteristics were studied by the multivariate factor analysis. The determination of the status of the morphological and chemical characters was carried out on samples collected. To find out significance level, ANOVA performed using PROC GLM, clustering of genotypes into similarity groups was performed using the method tree procedure PROC CLUSTER based on average distance. In order to identify the patterns of morphological variation and contribution of traits, principal component analysis (PCA) was conducted as PROC PRINCOP in the SAS 9.3 software (SAS Institute, 2012 Cary, NC).

RESULTS AND DISCUSSION

Yield is the economic potential of plants considered most important while making selection and further improvement. A wide range of variability was noticed among the 23 genotypes which range from 0.580 to 34.18 kg. The most productive selections Beauty yielded 34.18 kg/plant followed by Santa Rosa (26.52 kg/plant) and Red Plum (22.76 kg/plant) and lowest (0.850 kg/plant) was in Black Beauty genotype.

The average weight and dimensions of the fruits representing selections were measured as minimum, maximum and average values. The fruit length ranged from 19.87 mm to 63.09 mm with standard deviation and coefficient and maximum recorded in Grand Duke (63.09 mm) followed by ‘Kubio-26’ (55.24 mm) and minimum in Prune (19.87 mm) whereas fruit diameter was recorded maximum in Mariposa (49.43 mm), followed by Santa Rosa (48.98 mm) and Grand Duke (46.80 mm) and minimum in ‘Prune’ (21.11 mm). Diversity in fruit diameter range from 21.11-49.43 mm with standard deviation 7.96 and coefficient of variation 21.47%. Fruit volume ranged from 5.60 ml to 81 ml and maximum volume recorded in genotype Grand Duke followed by President plum and Santa Rosa however, minimum in Red Beauty with standard deviation of 21.77 and coefficient of variation 67.47%. Fruit weight varied from 5.72 -81.36 g with standard deviation 22.02 and coefficient of variation 60.49 %; wherein, highest fruit weight recorded in Grand Duke (81.36 g) followed by Santa Rosa (71.38 g) and least in Prune (5.72 g). Fruit pulp thickness is the important parameter determined the value of genotypes for processing which ranged from 6.84 to 17.14 % and measured highest in Grand Duke (17.14 %) followed by Santa Rosa (16.39 %) and lowest in Prune (6.84 %) with standard deviation 3.41 and coefficient of variation 27.44 %. Similarly, fruit firmness is also very important characters which is responsible for shelf-life of fresh fruit which varied from 22.00 to 75.46 with standard deviation 14.22 and coefficient of variation 28.20. Maximum fruit firmness index was recorded in Frontier followed by Burbank and least in Italian plum. Stone length ranged from 12.40-32.12 and standard deviation 4.81 and coefficient of variation 22.56. Stone diameter and stone weight ranged from 9.27-19.82 and 0.380-3.38 with standard deviation of 2.22, 0.699 and coefficient of variation 14.70, 56.66%, respectively. Maximum stone diameter and stone weight was recorded in genotype President Plum (19.82 and 3.38) followed by Kubio -26 (17.92 and 2.36) and Santa Rosa (17.21 and 1.86) and least in Prune (9.27 and 0.38). The total soluble solids (TSS) ranged from 19.16 to 24.93 with standard deviation 3.37 and coefficient of variation 19.37%. Maximum TSS measured in genotype Grand Duke (24.93) followed by President Plum (23.06), Italian Plum (22.23) and least in Kubio-26 (9.16). However, fruit acidity varied from 0.33 to 1.0 and maximum was found in Black Beauty (1.0) followed by Red Plum (0.95) and least in Au Rosa (0.33) with standard deviation 0.17 and coefficient of variation 29.01%. Reducing sugars varied between 7.21-19.53 with standard deviation 3.50 and coefficient of variation 30.24. Highest reducing sugars recorded in Grand Duke (19.53) followed by President Plum (18.14) and Frontier (17.95) and lowest in Beauty (7.21). Whereas, non-reducing sugars ranged from 1.26 to 3.73 with standard deviation 0.615 and coefficient of variation 25.87. Highest non-reducing sugar were recorded in Prune (3.73) followed by Red Plum (3.06) and least in Frontier (1.26). Total sugar also varied greatly between 9.43-21.04 with standard deviation 3.20 and coefficient of variation 22.92 and maximum estimated in Grand Duke (21.04) followed by President Plum (20.45) and Frontier (19.21) and minimum in Monarch (9.43) (Table 1). Results are similar with the values reported by Nergiz and Yildiz (1997) and Robertson *et al.* (1992).

Juice content of genotypes ranged between 24.80-58.90 with standard deviation of 9.88 and coefficient of variation 22.80. Highest juice content was recorded in Red Plum (58.90) followed by Beauty (54.90) and Frontier (53.30) however, lowest in Krassivica (24.80). Previous studies on plum also reported a high variability among plum cultivars for these parameters (Paunovic and Misic 1975; Nergiz and Yildiz 1997).

Descriptive statistics revealed the maximum standard deviation for fruit weight (22.02) followed by fruit volume (21.77) and least for acidity (0.177). Similarly, coefficient of variation was found maximum for fruit yield (71.74) followed by fruit volume (67.47). Skewness describes the symmetrical distribution pattern with respect to its dispersion from the mean. The skewness values showed that the data are normally skewed which are less than +2. However, positive skewness was recorded for fruit length, fruit volume, fruit weight, pulp thickness, fruit firmness, stone length, stone weight, TSS, acidity, reducing sugars, non reducing sugars, total sugars and fruit yield (Table 2). Kurtosis tells the weight of the tails of a distribution. In the present set of data it was recorded platykurtic distribution pattern for fruit length, fruit diameter, fruit volume, fruit weight, pulp thickness, fruit firmness, non-reducing sugar and juice content, however leptokurtic distribution for stone length, stone diameter, stone weight, TSS, acidity, reducing sugar, total sugars and fruit yield. Bimodality of genetic admixture values provide evidence of strong isolation between two morphological and genetic clusters, supporting the existence of a sympatric genotypes pair within the gene pool. In the present study values are near to zero, explains the closeness among the genotypes for the traits under study. Results are in accordance with the finding of Sarkhosh *et al*. (2007) and Usenik *et al*. (2008).

The dendrogram generated from the average linkage cluster analysis based on average distance, classified 23 genotypes in to two major groups at 1.35 NRMS distance (Fig 1). The first group included 5 genotypes (Meriposa, Santa Rosa, President Plum, Kubio-26 and Grand Duke) contributes 16.66 % of the total genotypes in this population. The genotypes in the first group had the maximum fruit length, fruit diameter, fruit volume, fruit weight, pulp thickness, medium to high fruit firmness, stone length, stone diameter, stone weight, low to medium in acidity, reducing sugars, non-reducing sugars, total sugars and fruit yield. The second group was comprised rest other 18 genotypes (Prune, Kubio, Kanto-5, Monarch, Au-Cherry, Methley, Green Gage, Red Plum, Tarcol, Beauty, Italian Plum, Red Beauty, Au-Rosa, Black Beauty, Frontier, Krassivica, Burbank, Black Amber) contributing 78.26% of the total genotypes. This group further divided into two major clusters at 0.87 NRMS distance. In first cluster there were seven genotypes contributing 30.43% of the total genotypes which is further divided in to two sub-clusters at 0.76 NRMS distance in which first sub cluster comprised six genotypes which posses medium fruit length, fruit diameter, fruit weight, pulp thickness, stone length, diameter, stone weight, TSS, high fruit firmness, sugars, juice content and mid to high

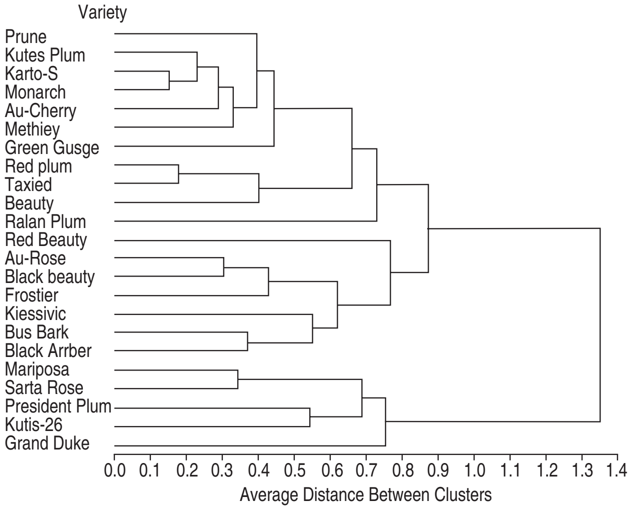

Fig 1 Dendrogram of 23 *Prunus* genotypes obtained by average distance between cluster analyses based on 16 phenological, fruit quality, and yield traits

Table 1 Fruit and yield characteristic of plum genotypes grown commercially in North West Himalayan region of India

Genotypes	Fruit length (mm)	Fruit dia. (mm)	Fruit volume (cm^3)	Fruit wt. (g)	Pulp thickness (mm)	Fruit firmness index	Stone length (mm)	Stone dia. (mm)	Stone wt. (g)	TSS (°Brix)	Acidity (%)	Reducing sugars	Non-reducing sugars (%)	Total sugar (%)	Juice (%)	Fruit yield (kg/tree)
Prune	19.87	21.11	6.00	5.72	6.84	43.67	12.4	9.27	0.38	17.28	0.42	9.47	3.73	13.20	43.60	5.96
Red Plum	37.43	39.10	32.40	31.36	11.56	44.08	17.48	16.00	0.60	18.22	0.53	10.89	3.06	13.95	58.90	22.76
Red Beauty	45.82	44.87	56.89	56.36	15.51	63.28	23.68	16.83	1.86	18.20	0.95	11.95	2.08	14.03	51.20	12.85
Kubio Plum	31.15	30.12	15.62	15.42	8.75	42.23	17.11	12.75	0.78	18.90	0.57	11.89	2.31	14.20	35.90	6.78
Methley	25.52	24.34	10.12	9.90	7.00	38.30	23.77	16.53	1.76	15.60	0.40	8.34	2.86	11.20	47.30	15.39
Au-Cherry	32.98	32.19	20.00	19.74	10.70	39.16	19.27	13.55	0.86	15.10	0.74	8.56	3.13	11.69	50.50	12.19
Kanto-5	27.8	26.62	12.40	12.08	7.73	45.73	18.43	13.05	0.80	15.36	0.87	8.74	2.69	11.43	46.70	8.27
Au-Rosa	43.69	40.61	44.37	43.76	8.60	59.70	22.43	15.49	1.20	15.83	0.33	8.89	2.80	11.69	36.50	12.6
Mariposa	49.16	49.43	71.64	70.32	13.82	58.56	23.42	16.39	1.74	15.03	0.80	8.94	2.37	11.31	50.80	9.00
Monarch	30.96	29.16	16.90	16.04	8.85	44.33	18.0	13.16	0.82	14.66	0.60	7.98	1.45	9.43	43.30	7.73
Krassivica	35.97	34.79	27.22	26.76	9.77	53.20	16.15	13.39	0.76	18.66	0.73	11.74	2.77	14.51	24.80	4.60
Beauty	37.6	35.92	27.20	26.92	9.54	38.76	19.33	14.48	1.16	13.66	0.67	7.21	2.73	9.94	54.90	34.18
Black Beauty	44.45	41.65	45.42	45.00	12.32	65.16	23.87	16.43	1.53	17.46	1.00	11.98	2.47	14.45	43.70	0.58
Bur Bank	36.01	40.97	38.00	37.68	14.62	75.03	17.89	13.71	0.74	16.76	0.62	9.96	2.07	12.03	28.50	20.30
Frontier	45.08	42.59	49.80	49.20	13.55	75.46	22.64	15.51	1.62	21.16	0.55	17.95	1.26	19.21	53.30	5.65
Black Amber	33.05	36.12	26.75	26.34	14.07	70.80	17.44	13.93	0.70	14.96	0.57	9.06	2.78	11.84	38.10	17.01
Green Gage	31.14	27.38	14.50	14.20	7.30	62.66	20.03	14.13	1.18	17.30	0.55	10.09	2.60	12.69	48.20	4.27
Grand Duke	63.09	46.80	81.75	81.36	17.14	28.53	31.17	17.72	2.18	24.93	0.44	19.53	1.51	21.04	35.20	14.64
Tarcol	37.87	37.39	33.10	32.64	11.47	50.30	19.03	14.95	1.22	18.73	0.64	13.93	1.48	15.41	57.80	16.97
President Plum	54.71	45.42	70.20	64.48	11.85	46.63	32.12	19.82	3.38	23.06	0.50	18.41	2.04	20.45	29.10	7.86
Kubio-26	55.24	42.36	58.15	57.32	15.18	37.50	29.25	17.92	2.36	19.16	0.58	13.61	2.08	15.69	29.20	3.09
Italian Plum	39.84	35.36	24.15	23.30	10.65	22.00	21.59	15.44	1.62	22.23	0.35	16.08	2.61	18.69	38.10	1.00
Santa Rosa	50.15	48.98	71.75	71.38	16.39	54.99	23.98	17.21	1.86	17.91	0.61	11.61	1.80	13.41	50.68	26.52
CD (P=0.05)	4.07	3.80	0.78	6.74	1.51	11.72	2.38	1.40	0.33	2.39	0.03	0.94	1.15	0.75	1.03	1.28

Table 2 Descriptive statistics for sixteen phenological, fruit quality, and yield traits of 23 plum genotypes

Characteristics	Range		Mean	Std. dev	CV%	Skewness	Kurtosis	Bimodality
Fruit length (mm)	19.870	63.090	39.503	10.456	26.46888	0.3881	-0.0887	0.3416
Fruit dia. (mm)	21.110	49.430	37.099	7.966	21.47228	-0.3139	-0.7478	0.4055
Fruit volume (ml)	6.000	81.750	32.276	21.779	67.47738	0.8385	-0.1550	0.5158
Fruit weight. (g)	5.720	81.360	36.403	22.022	60.49501	0.5346	-0.8193	0.4874
Pulp thickness (mm)	6.840	17.140	11.444	3.141	27.4467	0.1906	-1.1053	0.4407
Fruit firmness index	22.000	75.460	50.437	14.224	28.20152	0.0963	-0.5127	0.3428
Stone length (mm)	12.400	32.120	21.325	4.811	22.56038	0.7212	0.4817	0.3859
Stone dia. (mm)	9.270	19.820	15.116	2.223	14.70627	-0.3529	1.1658	0.2433
Stone weight. (g)	0.380	3.380	1.353	0.699	51.66297	1.1147	1.6976	0.4351
TSS (^{o}Brix)	13.660	24.930	17.398	3.371	19.37579	0.1216	1.1662	0.2195
Acidity (%)	0.330	1.000	0.610	0.177	29.01639	0.5809	0.0425	0.3822
Reducing sugars	7.210	19.530	11.600	3.508	30.24138	1.0258	0.1567	0.5679
Non-reducing sugars	1.260	3.730	2.377	0.615	25.87295	-0.0534	-0.2300	0.3108
Total sugars	9.430	21.040	13.982	3.206	22.92948	0.9337	0.1731	0.5156
Juice (%)	24.800	58.900	43.317	9.880	22.8086	-0.2871	-0.9378	0.4297
Fruit yield (kg/plant)	0.580	34.180	11.748	8.429	71.74838	1.0008	0.8830	0.4612

fruit yield, however second sub-cluster consists only one genotypes, i.e. Red Beauty having lowest fruit volume and juice content and high acidity. The second cluster also further divided in to two sub-clusters segregated at 0.72 NRMS distance comprised 10 genotype (Prune, Kubio, Kanto-5, Monarch, Au-Cherry, Methley, Green Gage, Red Plum, Tarcol, Beauty) contributes 47.82 % of the total genotypes. These two sub-cluster further divided into two sub-sub cluster at 0.68. The first sub-sub cluster consists only one genotype, i.e. Italian plum and posses high TSS, sugars and lowest in yield attributes however second sub-sub cluster comprised 10 genotypes in two categories, one characterized by lowest fruit length, fruit diameter, fruit volume, fruit weight, fruit thickness, fruit firmness, acidity, sugars, juice content and yield. Second category characterized by high fruit length, fruit diameter, fruit volume, fruit weight, fruit thickness, fruit firmness, acidity, sugars, juice content and maximum fruit yield.

The dissimilarity level in terms of genetic distance ranged from 0.153-1.35 indicating a high degree of dissimilarity between genotypes and high genetic distance between genotypes and if chosen for hybridization program, may give high heterotic F_1s and broad spectrum of variability in segregating generations.

Principal components analysis is a way of identifying patterns in data, which expresses data in such a way as to highlight their similarities and differences (Mattos *et al.* 2010, Milosevic and Milosevic 2010). Therefore, it was carried out to determine the characters more strongly contributed to the principal components. Principal components analysis reduced the original 16 characters in experiment to 4 principal components. The first four principal components with eigen values >1 explained 81% of variation among 23 accessions (Table 3) and other PCs had eigen values <1 and have not been interpreted.

The first PC, which is the most important component, explained 49.66% of total variation and was positively related to fruit length, fruit diameter, fruit volume, fruit weight, pulp thickness, stone length, stone diameter, stone weight, reducing sugars and total sugars and negatively related to fruit firmness, acidity, non-reducing sugars, juice content and fruit yield in which PC1 is a weighted average of these four characters. The PC2 accounted of 15.38% of the total variation and the characters with the greatest weight on this component was acidity. The PC3 accounted for 8.44 % and positively related to only fruit firmness. However, PC4 is accounted for only 7.61% and weighted for TSS, juice content and yield (kg/plant). This situation confirms the suitability of using phenology as a basis for selecting parental sources; nevertheless, studies through several years must be conducted before parental selection for a possible plant breeding. The PC analysis provided a simplified classification of the plum genotypes for collecting and breeding. The biplot axes also shows geometrical distances among cultivars that reflect similarity among them in terms of variables measured. The first three principal component scores were plotted to aid visualization of accessions grouping. The derived cluster and subgroups are very similar to those identified from average distance between cluster analyses. More interesting genotypes were Prune, Grand Duke, Italian Plum, President Plum, Mariposa, Beauty, and Santa Rosa, that were disposed in gaps and are the most promising ones. Genotype Prune characterized by smallest fruit length, fruit diameter, fruit volume and fruit weight and pulp thickness however Grand Duke is characterized by highest fruit length, fruit volume, fruit weight, pulp thickness, TSS and total sugars. However, President plum had the maximum stone length, stone diameter and stone weight; Italian Plum possessed least acidity, Mariposa has highest fruit weight, Beauty has highest fruit yielding capacity and Santa Rosa having better fruit and quality traits. So, it can be intended for further utilization for introducing these

Table 3 Principal component analysis of the plum genotypes showing the eigen vectors, eigen values and percentage total variance accounted for by the 16 principal component axes

Characteristics	Eigen vectors															
	PRIN1	PRIN2	PRIN3	PRIN4	PRIN5	PRIN6	PRIN7	PRIN8	PRIN9	PRIN10	PRIN11	PRIN12	PRIN13	PRIN14	PRIN15	PRIN16
Fruit length (mm)	0.34020	0.08479	-.05637	-.07938	-.04053	0.11706	-.076328	-.13556	-.031068	-.243493	0.271512	0.28191	0.371034	0.2762	0.6327	-.01405
Fruit dia. (mm)	0.30464	0.26769	0.05308	0.04140	-.13972	0.15777	0.081184	.10944	-.039959	-.439799	0.236117	0.04884	-.376815	0.3777	-.47975	0.00068
Fruit volume (ml)	0.30935	0.04640	-.08498	0.00101	-.26737	0.10277	0.018256	-.30795	-.525960	0.491991	0.072653	-.430891	-.054394	0.0415	0.0581	-.00129
Fruit weight (g)	0.32661	0.19094	-.00448	-.01605	-.10249	0.12705	0.044904	-.159855	-.142571	-.046823	-.149296	0.46758	0.041653	-.71898	-.14214	0.00778
Pulp thickness (mm)	0.27377	0.26078	0.12558	0.08623	-.19895	0.19964	-.261442	-.052297	0.515418	0.080609	-.582042	-.202904	-.056797	0.1017	0.1327	-.00078
Fruit firmness index	-.00181	0.34027	0.55308	0.01463	-.19200	-.38422	0.574148	0.029183	0.102767	0.155328	0.064412	0.01795	0.127954	0.0338	0.0800	-.00125
Stone length (mm)	0.31226	-.03808	-.21845	-.24438	0.18877	-.14721	0.104671	0.105169	-.002866	0.147368	-.243029	0.06085	0.580752	0.2755	-.46537	0.00561
Stone diameter (mm)	0.30462	0.07781	-.24063	-.12657	0.20806	-.12514	0.253685	0.199995	0.126287	-.373294	0.099720	-.595068	-.004358	-.35338	0.1402	0.004233
Stone weight (g)	0.30005	-.07567	-.19303	-.22572	0.25998	-.18655	0.202551	0.195821	0.019508	0.293993	-.143608	0.31622	-.590106	0.1533	0.2346	-.00376
TSS (°Brix)	0.16504	-.33505	0.21923	0.48987	0.02660	0.18354	0.235186	0.342802	-.388782	-.229041	-.376634	-.001298	0.042439	0.0936	0.0958	-.00098
Acidity (%)	-.01222	0.38553	0.36836	-.19327	0.47671	0.44710	-.176582	0.361769	-.169255	0.185636	0.141860	-.061431	0.034080	-.02518	-.011876	-.00061
Reducing sugars (%)	0.28097	-.31231	0.18995	0.18894	0.08174	0.02236	-.072128	-.012583	0.263686	0.175447	0.298538	-.001978	0.013472	-.07136	-.086106	0.73283
Non-reducing sugars (%)	-.22824	-.08221	-.22659	-.17907	-.13318	0.64729	0.589122	-.059940	0.205349	0.086699	-.017771	0.02293	0.041027	0.0343	0.025670	0.12769
Total sugar (%)	0.26335	-.35805	0.16231	0.17191	0.06506	0.14608	0.035850	-.022854	0.329051	0.209218	0.317265	-.002128	0.022930	-.08676	-.109936	-.66806
Juice (%)	-.07681	0.26405	-.16889	0.51483	0.58991	-.01998	0.172179	-.488790	0.043441	0.061056	-.061736	0.00575	0.022938	0.0571	0.024140	-.00072
Fruit yield (Yield/kg)	-.00979	0.34983	-.44287	0.46654	-.26315	-.01599	-.034705	0.514475	0.079148	0.228470	0.233503	0.10097	0.068227	-.00633	-.021016	0.00024
Eigen value	7.94506	2.46031	1.34980	1.21705	0.92817	0.59541	0.523045	0.336236	0.269626	0.119481	0.098655	0.08439	0.054443	0.0132	0.00509	0.000002
Difference	5.48475	1.11051	0.13275	0.28887	0.33276	0.07236	0.186808	0.066611	0.150144	0.020827	0.014263	0.02994	0.041243	0.00811	0.005087	
Proportion	0.4966	0.153	0.084	0.076	0.05	0.037	0.0327	0.021	0.0169	0.0075	0.0062	0.0053	0.0034	0.0008	0.0003	

traits in desired genotypes. Identification and description of the genetic variability available in the genotypes of *Prunus* sp. are preliminary requirements for the exploitation of useful traits in plant breeding.

The multivariate analysis was found useful for detection of phenotypic differences among the plum genotypes. The results of the present work may also help breeders in selecting the most diverse accessions with similar pomological, fruit quality and yield related traits to begin crossing and breeding programs which may result in increased desired traits. The results are certainly representative and valuable, and will provide some guidance for screening of breeding resources for improving fruit quality and serve as a base for economically valuable phenotypes. The cluster analysis classified genotypes into two major groups and further in clusters according to their potential characteristics. The first group genotypes were superior in terms of fruit yield related traits and second group genotypes in quality attributes. Genotypes and high genetic distance between genotypes and if chosen for hybridization program, may give high heterotic F_1s and broad spectrum of variability in segregating generations PC analysis may help in selection of a set of genotypes with better fruit qualities, which, in present study, were observed in Prune, Grand Duke, Italian Plum, President Plum, Mariposa, Beauty, and Santa Rosa.

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