Research Article

Diversity in Pomegranate (*Punica granatum* L.) Genotypes of India as Revealed by Principal Component Analysis and Cluster Analysis

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Abstract

Pomegranate (*Punica granatum* L.), belonging to the family Lythraceae, is one of the oldest and beloved fruit crops cultivated widely in several tropical and subtropical countries. In the recent past pomegranate cultivation is gaining immense popularity in India owing to its dietary and nutraceutical benefits. The present study was conducted with an objective of determining diversity present in the popular pomegranate genotypes of India for different morphological and biochemical traits and to detect the association between the genotypes using Principal Component Analysis (PCA) and Cluster Analysis (CA). Results suggest presence of considerable phenotypic and genetic diversity in the studied pomegranate genotypes. Fruit and aril traits like fruit weight, dry weight of 100 arils, fruit volume, fruit length, peel weight, aril weight and fruit diameter were found to be the most discriminating traits of the Indian pomegranate germplasm under study.

Keywords: Pomegranate, Diversity, Principal Component Analysis, Cluster Analysis

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Introduction

Pomegranate (*Punica granatum* L.), belonging to the family Lythraceae, is one of the oldest and beloved fruit crops cultivated widely in several tropical and subtropical countries. It is an excellent fruit crop for valorising marginal lands and saline waters without special care and is considered to be the native of region circumventing Iran and Northern India [1]. Pomegranate fruits are consumed both as fresh as well as processed in the form of juice, squash, wine and as an acidulant product commonly known as anardana [2]. India is one of the leading producers of pomegranate in the world with a total production of 20.90 Lakh tones from an area of 2442 thousand hectares and a productivity of 11.70 MT/ha sharing 1.5% of total fruit production of the country [3]. It is commercially cultivated in Maharashtra, which is the leading state in India in terms of area and production, Karnataka, Gujarat, Andhra Pradesh, Madhya Pradesh, Tamil Nadu and Rajasthan [3].

India is considered to be the home of many wild type pomegranates locally known as Daru types which are deciduous, hardy, seedling origin trees characterized by small and highly acidic fruits with thick rinds and smaller arils, found gregariously growing in gravel and boulder deposits of dry ravines in the foothills of Himalayas [4-6]. Several introductions have been made to India through National Bureau of Plant Genetic Resource which are being maintained, characterized and conserved in the field gene banks at NBPGR Regional Stations and other research institutes like National Research Centre, pomegranate and State Agriculture Universities. However, very few of these introductions could be utilized in the pomegranate improvement programme while many failed to establish owing to the warm climatic conditions prevailing in India. The Indian varieties, mostly originating from active breeding programs, are characterized by low-acid, sweet flavour, small to medium sized fruit with soft seed, more juice and thin rind. Although, the country has been bestowed with rich genetic diversity of pomegranate and the varieties obtained through breeding programmes add to this richness, their full potential is yet to be explored by pomegranate researchers, growers and industrialists.

Since, both fresh market and processing industries drive the pomegranate consumption, a comprehensive characterization of germplasm for different fruit traits contributing to its fresh market and processing attributes will be paramount to satisfy the quality demands of different markets [7]. In the characterization of a germplasm, it is important to evaluate the traits which show variation in the population in order to identify the traits of interest and variations therein. This becomes complex while dealing with large number of traits at a time. In general, the yield attributing traits as well as traits with bearing on the quality of produce exhibit polygenic or complex inheritance and are highly influenced by the environmental conditions. Under such circumstances, Principal Component Analysis (PCA) is one of the most efficient approaches to find out the variations being explained by different traits thus reducing the variables under study. Pomegranate germplasm have been characterized in several countries for different

economic traits [8-11]. However, to the best of our knowledge, there is negligible information available on the characterization of the pomegranate genotypes of India. The objective of this study was to determine the diversity present in the pomegranate genotypes of India for different morphological and biochemical traits and to detect the association between the genotypes using PCA and Cluster Analysis (CA).

Materials and Methods

The study was carried out at University of Horticultural Sciences, (UHS) Bagalkot, Karnataka. Bagalkot is located in the northern region of Karnataka and positioned at 16°12′N, 75°45′E the average elevation in this area reaches approximately 610 m. The climate is warm and dry throughout the year and rainfall is scarce with an average annual rainfall of 518 mm and is characterized as semi-arid region.

Plant material

A total of 23 pomegranate genotypes were selected for this study which included commercial Indian cultivars (viz. AmLidana, Bhagwa, CO-1, Dholka, Early Bhagwa, G-137, Ganesh, Kabul Yellow, KRS, Mridula, P-23, P-26, Phule Arakta, Ruby, Super Bhagwa, Tobesto, Yercaud), an exotic variety (Wonderful), an indigenous variety (Kaladagi Local) and four mutant lines (UHSP 23, UHSP 57, UHSP 81, UHSP 125) developed at UHS, Bagalkot.

Phenotypic characterization

Fruits obtained during hastha-bahar (Feb-April, 2017) were selected for this study since it is the most preferred bahar under Northern Karnataka region owing to lesser incidence of bacterial blight. Three plants were randomLy selected per genotype with three fruits from each plant. Thus, nine fruits of each genotype were individually analysed for morphological and biochemical characters. The details of morphological and biochemical parameters studied is provided in **Table 1**.

Table 1 List of observations recorded for morphological and biochemical characters

Sl. No.	Characters	Abbreviations	Particulars
	Morphological parameters		
1	Fruit weight (g)	FW	Precision balance
2	Fruit length (mm)	FL	Digital Vernier calipers with 0.001mm accuracy
3	Fruit diameter (mm)	FD	Digital Vernier calipers with 0.001mm accuracy
4	Fruit length/width	FS	Ratio calculated
5	Fruit volume (cm^3)	FV	Liquid displacement methods
6	Fresh wt. of 100 arils (g)	FreshW	Precision balance
7	Dry wt. of 100 arils (g)	DryW	Precision balance
8	Moisture %	MP	Oven drying arils at 60°C until constant weight
9	Crown length (mm)	CRL	Digital Vernier calipers with 0.001mm accuracy
10	Peel weight (g)	PW	Precision balance
11	Aril weight (g)	AW	Precision balance
12	Total No. of Arils/fruit	TNA	Manual counting
13	Aril length (mm)	AIL	Digital Vernier calipers with 0.001mm accuracy
14	Aril width (mm)	AW	Digital Vernier calipers with 0.001mm accuracy
15	Seed length (mm)	SL	Digital Vernier calipers with 0.001mm accuracy
16	Seed width (mm)	SW	Digital Vernier calipers with 0.001mm accuracy
17	Rind thickness (mm)	RT	Digital Vernier calipers with 0.001mm accuracy
	Biochemical parameters	TSS	
18	Titratable Acidity (%)	TA	Titration method with 0.1 N NaOH (pH 8.1)
19	pH of the Juice	pH	pH-meter
20	Fruit Juiciness % (per 100gm aril wt.)	FJ	Extracted juice from 100 arils and measured as weight/weight with aril wt.
21	TSS (°Brix)		Refractometer

Statistical Analysis

The traits studied were subjected to Analysis of Variance (ANOVA) which revealed significant variation between

genotypes for almost all the traits at 1% level of significance. Further, mean values recorded for each trait were used to perform PCA and clustering of cultivars into similarity groups using UPGMA (Unweighted Pair Group Method, Arithmetic Average). Data processing was performed using the SPSS software.

Results and Discussions

Mean value with their standard error mean (SEm) for different morphological and biochemical characters of pomegranate genotypes used in the study has been presented in **Table 2(a&b)**. The data reveals large variability between genotypes for all the characters.

Table 2(a) Mean values for individual morphological and biochemical traits of different pomegranate genotype

Treatment	Fruit weight (g)	Fruit Length (mm)	Fruit diameter (mm)	Fruit Length/ width	Fruit Volume (cm^3)	Fresh wt. of 100 arils	Dry wt. of 100 arils	Moisture %	Crown length (mm)	Peel weight (g)
AmLidana	187.56	70.57	72.80	0.97	189.44	32.55	8.03	75.33	20.05	34.00
Bhagwa	285.33	90.12	76.33	1.18	260.56	24.67	5.48	77.79	10.77	95.89
CO-1	148.65	59.24	65.97	0.90	115.00	22.50	5.86	73.96	13.06	65.00
Dholka	207.50	71.16	75.99	0.94	231.67	20.67	4.14	79.97	19.44	67.00
Early Bhagwa	350.22	100.34	85.70	1.17	358.33	32.33	7.34	77.30	15.13	121.56
G-137	227.03	67.07	73.50	0.91	235.00	22.33	5.61	74.88	19.04	95.00
Ganesh	505.00	112.35	95.87	1.17	527.78	46.89	9.62	79.48	12.83	192.44
Kabul Yellow	134.44	61.37	64.61	0.95	141.95	30.00	7.59	74.70	13.30	45.00
Kaladagi Local	94.70	55.44	57.44	0.97	105.00	17.17	4.05	76.41	15.83	31.67
KRS	186.10	67.03	68.40	0.98	151.67	14.67	3.53	75.94	12.63	50.33
Mridula	96.93	50.52	56.55	0.89	113.33	16.67	3.35	79.90	12.61	30.00
P-23	134.89	59.39	61.98	0.96	112.11	32.22	6.79	78.93	13.20	53.89
P-26	179.78	67.35	69.20	0.98	182.28	36.44	6.59	81.92	13.74	79.22
PhuleArakta	374.22	94.50	86.41	1.09	377.78	32.22	5.91	81.66	8.92	118.67
Ruby	135.56	61.77	64.54	0.96	139.17	15.53	2.54	83.64	19.36	54.67
Super Bhagwa	306.45	97.86	94.14	1.07	313.89	30.56	5.54	81.87	13.60	110.89
Tobesto	225.60	72.00	67.50	1.07	279.67	35.00	7.19	79.46	12.80	70.00
UHSP 23	56.01	47.06	45.85	1.03	62.00	15.01	1.70	88.67	10.48	24.33
UHSP 57	145.76	52.96	54.25	0.98	148.33	23.98	1.62	93.22	12.51	38.67
UHSP 81	79.87	47.41	42.43	1.12	96.67	11.45	1.70	85.15	10.89	30.33
UHSP 125	71.50	53.93	51.43	1.05	93.33	16.97	1.15	93.22	13.78	29.00
Wonderful	202.67	67.72	76.60	0.89	196.67	32.00	6.65	79.22	18.81	80.67
Yearcaud	170.22	64.84	71.18	0.91	173.61	25.45	5.33	79.06	16.31	58.78
C.D.	30.10	7.74	9.60	0.11	34.71	2.88	0.36	2.57	2.41	9.47
SE(m)	10.52	2.71	3.36	0.04	12.14	1.01	0.13	0.90	0.84	3.31

Correlation analysis

Correlation analysis was done to find out reliance of the variables (**Table 3**). A positive correlation was observed between fruit weight and other traits like total aril weight (r = 0.98), total peel weight (r = 0.95), fruit volume (r = 0.98), fruit length (r = 0.96), fruit diameter (r = 0.91), total number of arils (r = 0.88), fresh weight of aril (r = 0.72) and dry weight of aril (r = 0.98). Total aril weight correlated with total peel weight (r = 0.90), volume of juice (r = 0.84), 100-aril fresh weight (r = 0.70), 100-aril dry weight (r = 0.97), fruit length (r = 0.96), fruit volume (r = 0.97) and fruit diameter (r = 0.89) suggesting that aril weight had a positive relationship with fruit size. A positive correlation was observed between total peel weight and total aril weight (r = 0.90), total number of arils (r = 0.88), aril length (r = 0.44), aril width (r = 0.46), seed length (r = 0.50), fruit length (r = 0.92), fruit diameter (r = 0.87) and fruit volume (r = 0.94). Similar results have been reported by Mohammad *et al.* (2018) [12] in pomegranate accessions of Iraq. Also, there was a positive correlation between volume of juice and fruit length (r = 0.42) and fruit width (r = 0.39) suggesting that large fruits might be better for making juice. Mekni *et al*. (2019) [13] reported positive correlation between fruit weight and total number of arils per fruit ($r = 0.913$, $p < 0.01$). The results imply that arils play a major role in determining the pomological quality of pomegranates and that the varieties with maximum

number of arils and thick peel will be suitable not only in terms of eating quality but also for transportation. Wetzstein *et al.* (2011) [14] opined that the size of pomegranate fruit does not necessarily increase the proportion of the edible part; it is rather the number and the mass of the seeds which directly contribute to the improvement of the pomological quality of pomegranate fruits.

Table 2(b) Mean values for individual morphological and biochemical traits of different pomegranate

Treatment	Aril Wt. (g)	Total no. of arils/ fruit	Aril Length (mm)	Aril width (mm)	Seed length (mm)	Seed width (mm)	Rind thickness (mm)	TSS (°Brix)	Titratable Acidity (%)	pH of the Juice	Fruit Juiciness %
AmLidana	153.56	317.44	9.63	6.72	5.89	3.04	1.44	15.56	1.09	2.53	54.89
Bhagwa	189.44	656.11	8.11	4.51	6.84	3.32	3.66	13.22	0.21	3.67	60.22
CO-1	83.65	320.33	5.02	2.52	7.09	2.85	4.10	14.53	0.05	3.54	58.37
Dholka	140.50	685.33	9.03	5.32	7.76	2.48	3.42	11.55	0.07	3.29	62.67
Early Bhagwa	228.67	710.00	8.33	6.75	7.53	2.86	4.18	13.95	0.19	3.70	68.00
G-137	132.03	559.67	9.00	5.47	7.18	3.04	4.33	12.47	0.15	3.07	39.40
Ganesh	312.55	1077.89	11.48	8.63	7.28	2.89	4.19	15.53	0.19	3.99	66.22
Kabul Yellow	89.44	283.00	9.74	6.99	5.59	2.62	2.73	14.40	0.13	3.55	62.44
Kaladagi	63.03	351.83	8.36	5.85	6.66	2.73	2.91	14.30	0.06	3.26	66.67
Local											
KRS	135.77	574.33	8.66	5.28	5.77	2.66	3.83	12.50	0.05	3.49	61.52
Mridula	66.93	330.33	8.72	4.81	7.52	2.89	4.06	10.52	0.08	3.54	56.00
P-23	81.00	465.22	9.56	6.84	6.73	3.21	2.29	14.83	0.06	3.26	64.00
P-26	100.56	383.37	10.08	6.38	6.61	3.11	3.90	13.67	0.07	3.40	59.67
Phule	255.55	767.78	8.08	4.59	6.84	2.76	2.18	14.75	0.18	3.78	72.44
Arakta											
Ruby	80.89	499.78	7.58	4.27	7.11	2.74	4.37	9.62	0.13	3.90	71.55
Super	195.56	671.89	9.81	7.14	6.61	2.92	3.85	12.55	0.18	3.70	61.33
Bhagwa											
Tobesto	155.60	231.33	9.85	8.00	6.77	3.25	4.30	15.55	0.06	3.55	41.54
UHSP 23	31.67	168.67	6.41	3.75	4.85	2.88	2.66	11.65	0.42	3.34	29.07
UHSP 57	107.10	187.67	7.11	4.17	4.85	2.60	2.58	11.13	0.46	3.35	52.07
UHSP 81	49.54	157.67	7.46	4.76	6.02	3.13	2.46	12.86	0.64	3.13	50.65
UHSP 125	42.50	150.67	8.48	4.81	6.32	3.10	2.96	12.44	0.47	3.64	46.95
Wonderful	122.00	502.33	10.35	7.57	6.82	2.97	3.73	17.95	0.12	3.59	77.33
Yearcaud	111.44	382.67	8.82	5.69	6.86	3.07	3.89	12.43	0.12	3.02	60.00
C.D.	32.15	70.15	0.79	0.96	0.55	0.41	1.08	1.17	0.05	0.17	6.80
SE(m)	11.24	24.53	0.28	0.33	0.19	0.14	0.38	0.41	0.02	0.06	2.38

Table 3 Pearson's Correlation coefficient (19 df) for analyzed parameters

Correlation		FW	FL	FD	FS	FV	FreshW	DryW	MP	CRL	PW
1	FW	1									
2	FL	.968***	1								
3	FD	0.91***	0.931***	1							
4	FS	0.557***	0.613***	0.291	1						
5	FV	0.984***	0.948***	0.878***	0.577***	1					
6	FreshW	0.727***	0.695***	0.708***	0.268	0.733***	1				
7	DryW	0.984***	0.947***	0.882***	0.566***	0.999***	0.766***	1			
8	MP	0.284	0.293	0.441***	-0.204	0.224	0.268	0.231	1		
9	CRL	-0.077	-0.06	0.174	-0.508	-0.058	0.006	-0.054	0.294	1	
10	PW	0.959***	0.92***	0.873***	0.509***	0.942***	0.715***	0.943***	0.259	-0.072	1
11	AW	0.987***	0.96***	0.898***	0.564***	0.973***	0.708***	0.971***	0.288	-0.077	0.901***
12	TNA	0.884***	0.87***	0.872***	0.373	0.839***	0.507***	0.83***	0.369	0.076	0.882***
13	AIL	0.455***	0.455***	0.518***	0.085	0.504***	0.665***	0.525***	0.244	0.27	0.441***
14	AW	0.481***	0.493***	0.516***	0.196	0.536***	0.736***	0.56***	0.299	0.228	0.462***
15	SL	0.432***	0.438***	0.521***	-0.003	0.444***	0.228	0.436***	0.444***	0.334	0.501***
16	SW	0.011	0.05	-0.051	0.28	0.016	0.215	0.032	0.013	-0.158	0.064
17	RT	0.291	0.281	0.346	-0.034	0.297	0.078	0.286	0.243	0.171	0.425**
18	TSS	0.37	0.344	0.37	0.119	0.351	0.664***	0.381**	0.436***	0.02	0.352
19	TA	-0.165	-0.15	-0.257	0.204	-0.141	-0.087	-0.14	-0.32	0.082	-0.295
20	pH	0.443***	0.459***	0.352	0.407**	0.438***	0.194	0.428**	-0.157	-0.37	0.529***
21	FJ	0.397**	0.429**	0.52	-0.016	0.332	0.318	0.337	0.336	0.205	0.379**

Table 3 Continues

Correlation		AW	TNA	AIL	AW	SL	SW	RT	TSS	TA	pH	FJ
1	FW											
2	FL											
3	FD											
4	FS											
5	FV											
6	FreshW											
7	DryW											
8	MP											
9	CRL											
10	PW											
11	AW	1										
12	TNA	0.853***	1									
13	AIL	0.447***	0.427**	1								
14	AW	0.474***	0.367	0.917***	1							
15	SL	0.377**	0.573***	0.251	0.192	1						
16	SW	-0.019	-0.152	0.189	0.207	0.105	1					
17	RT	0.204	0.346	0.112	0.11	0.583***	0.052	1				
18	TSS	0.366	0.19	0.441***	0.592***	0.082	0.298	-0.164	1			
19	TA	-0.086	-0.344	-0.102	-0.08	-0.498	0.171	-0.661	0.025	1		
20	pH	0.378**	0.463***	0.048	0.056	0.291	-0.164	0.498***	-0.032	-0.537	1	
21	FJ	0.392**	0.556***	0.285	0.259	0.441	-0.288	0.092	0.302	-0.337	0.375**	1

** Significant at 0.1%, *** Significant at 0.05%

Principal Component Analysis (PCA)

PCA is a variable reduction technique aiming at reduction of a larger set of variables into smaller set of uncorrelated variables, known as 'principal components' (PCs), such that these principal component accounts for most of the variance present in the original variables. Thus, PCA helps in identification of characters explaining as much of total variation in the original variables but with a very few components, reducing the dimension of the problem [15]. A total of 21 traits which included both morphological as well as biochemical parameters were subjected to principal component analysis (PCA). Grouping of pomegranate genotypes using PCA was based mainly on the first three PCs that accounted for 72.61% of the variability observed wherein PC1 accounted for 47.90%, PC2, 12.64% and PC3, 12.05% of total variation (**Table 4**).

Furthermore, the component matrix of PCA analysis from extraction method, indicated that the first component (PC1) related to 11 characters (Table 4), including fruit weight, fruit volume, fruit length, fruit diameter, peel weight, aril weight, total number of arils, fresh weight of 100 arils, dry weight of 100 arils, aril length, aril width accounting for 47.90% of the total variation. The highest positive loading was exhibited by fruit weight followed by dry weight of 100 arils, fruit volume, fruit length, peel weight, aril weight and fruit diameter with loading values greater than 0.90. The second principal component (PC2) which explained 12.64 % of total variation, showed positive loadings for traits like titratable acidity and fruit shape while negative loading for rind thickness, seed length and seed width. Moreover, the characters like crown length, moisture percentage, fruit shape and pH comprised the third main factor (PC3) and explained 12.05% of the total variance. The variation in aril length and width was found to be explained by both PC1 and PC3 with higher loading in PC1. Mars and Marrakchi (1999) [8] studied 30 pomegranate accessions of Tunisia and found fruit size, colour and juice characteristics to be most discriminating characters for their germplasm. Dandachi et al. (2017) [16] found hermaphrodite flowers, petal width as well as fruit weight, diameter and length, in addition to juice pH and sugar/acid ratio, to be the most discriminating traits for assessment of Lebanese pomegranate. PCA and cluster analysis has been reported to be effective tools for assessing phenotypic and genetic diversity in pomegranate germplasm of Iran [11], Italy [17] and India [18].

Hierarchical Cluster Analysis

Hierarchical Cluster Analysis **(**HCA), groups the samples based on similarities without considering the class membership. HCA analyses the inter point distances (or correlation) between all samples using defined metric such as Euclidian distance, Manhattan distance etc. [15]. In order to understand the associations among Indian pomegranate genotypes, HCA was performed using the morphological and biochemical parameters (listed in Table 1). The result obtained from HCA has been presented as a dendogram (**Figure 1**). The pomegranate genotypes were grouped into 3 main groups (1, 2 and 3). The First main group (group 1) comprised a total of 6 pomegranate genotypes divided

among two subgroups (1A and 1B), wherein sub-group 1A accommodated 3 genotypes and the second sub-group, 1B comprised of 3 genotypes. The third main group (group 3) comprised of 16 genotypes divided into 3 subgroups. The second main group (group 2) was a solitary group comprising only of genotype Ganesh (Figure 1).

Table 4 Loadings, eigenvalues and percent of cumulative variance for the first three principal components

Parameters	Components		
	1	2	3
FW	.968		-.150
Dry W	.963	.144	-.113
FV	.959	.128	-.142
FL	.957		-.151
PW	.952		-.171
AW	.941	.152	-.132
FD	.935		
TNA	.889	-.216	-.112
Fresh W	.782	.311	.284
AW	.620	.261	.530
AIL	.593	.172	.529
FJ	.498	-.369	.171
TA	-.286	.740	
RT	.367	-.654	-.133
SL	.539	-.574	.131
CRL		-.350	.678
pH	.475	-.313	-.595
FS	.476	.509	-.556
MP	.376	-.322	.531
TSS	.451	.358	.499
SW		.417	.146
Eigenvalues	10.060	2.656	2.532
%Cumulative variance	47.907	60.555	72.610

Extraction Method: Principal Component Analysis

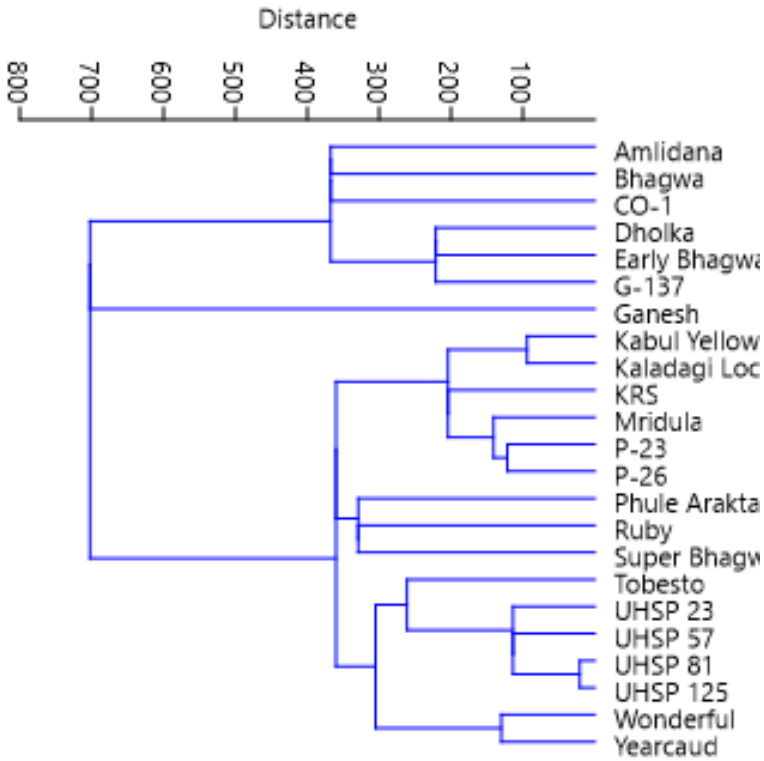

Figure 1 UPGMA (Paired) with Euclidean Distance (Cophen Correlation value=0.3284)

The grouping of genotypes in different groups was mostly based on the morphological characters or the method of cultivar development, for example all the four mutants included in the study (UHSP 23, UHSP 57, UHSP 81, UHSP 125) were present in the sub-sub group $3A_1$. The mutants used in this study are derived from Bhagwa and Ganesh, and the grouping of these mutants separately from their parents suggests that mutation has created sufficient genetic diversity in these genotypes. Sub-sub group $3A_3$ comprised of 6 genotypes where, Kaladagi Local and Kabul Yellow were in one group while Mridula, P-26 and P-23, in the other group. The third sub-sub group of group 3 ($3A_3$) had only one genotype KRS. Ganesh which was the solitary inhabitant of group 2 is one of the most popular and commercial cultivars of India and is characterized by largest sized fruits among all the studied genotypes (Table 2). The genotype, G-137, is a selection from Ganesh and its presence in a different group than Ganesh, suggests that they are genetically diverse, similarly the clustering of Bhagwa and its clone Super Bhagwa in different groups confirms the genetic distance between the two. However, Bhagwa and its another clone early Bhagwa were grouped together suggesting that the genetic distance between these two is lesser than that between Bhagwa and Super Bhagwa (Figure 1).

Conclusion

Principal Component Analysis and Cluster Analysis have revealed a considerable variability in the pomegranate genotypes used in this study. The variability in germplasm is expected due to recombination (resulting from outcrossing) combined with sexual and vegetative propagation, for a long period of time. It can be concluded that among the fruit characteristics measured, fruit and aril traits like fruit weight, dry weight of 100 arils, fruit volume, fruit length, peel weight, aril weight and fruit diameter which were explained by the first PC with loading values greater than 0.90 are the most discriminating traits of the Indian pomegranate germplasm under study. The phenotypic characterization of the pomegranate germplasm of India indicates the diversity status prior to molecular characterization that can provide a much clear picture of genetic diversity present in India for pomegranate. Comprehensive understanding of the genetic diversity of Indian pomegranate germplasm is of great significance to management and conservation of pomegranate genetic resources and improving varietal diversity.

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