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Genetic variability among 'Kashmiri Nakh' pear (*Pyrus pyrifolia*): A local variety grown in North- Western Himalayan region of India

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Twenty four (24) 'Kashmiri Nakh' pear (*Pyrus pyrifolia*) genotypes were studied to assess the overall degree of polymorphism, detect similarities among important tree, pomological, fruit quality and yield parameters. Eleven (11) variables were scored and subjected to multivariate analysis. Results show a considerable phenotypic diversity among 'Kashmiri Nakh' pear genotypes and differed significantly for the above traits. The cluster analysis classified the genotypes into two major groups according to their potential characteristics. The first group was found superior in terms of fruits total soluble solids (TSS), TSS/acidity and yield related characteristics and second group in fruits morphological (length, diameter, weight) and tree characteristics attributes. Principal component analysis (PCA) revealed that traits positively related to tree height, tree spread (N-S), tree spread (E-W), yield per tree, fruit weight, fruit length, fruit diameter and acidity, however negatively related to TSS and TSS/acidity. The first principal components expressed 33.58% of the total variation and second PC2 accounted for 23.76% of the total variation. A large proportion of variability observed in genotypes 'TB-3, CHB-4, TBP-3, THP-7, TB-1, THP-1, TBP-1 and TB-2 were found unique for tree, fruit and yield attributing traits during PCA.

Key words: Genetic variability, genotypes, cluster analysis, principal component analysis (PCA).

INTRODUCTION

Pear is the third most important fruit crop grown in temperate region after grapes and apples (Oliveira et al., 1999) in world. In India, it is grown in an area of about 0.4 lakh ha and productivity 8.82 t/ha (FAO, 2012). The genus *Pyrus*, with common name pear, belongs to subfamily Pomoideae, and the family Rosaceae. Geographically, pears are divided in to Occidental and Oriental groups. Occidental pears found in Europe, northern Africa, Asia Minor, Iran, central Asia, and Afghanistan; the majority of cultivars originated primarily from *Pyrus communis*. The Oriental pears grown mainly in Tian-Shan and Hindu-Kush Mountains eastward to Japan and further divided into five groups, that is, Ussurian pear, Chinese white pear, Chinese sand pear, Xinjiang pear (*Pyrus sinkiangensis* Yu) and Japanese pear. Chinese sandpears are botanically *Pyrus pyrifolia*

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Abbreviations: PCA, Principal component analysis; **TSS,** total soluble solids; **PC,** principal components.

and native to China, Japan and Korea. Himalayan region in Asia is known for its biological richness and has always been a botanist's paradise. Several native species that are commonly grown wild are*Pyrus pashia* Buch. & Ham. ex. D. Don (Himalayan Pear, Indian wild pear, Mehal, Mole, Kainath, Soh jhur Shegal, Chhota kainth, wild pear), *P. serotina* Rehd., *Pyrus kumaonii* (Decne.) Stapf., *Pyrus verruculosa* (Indian pear), *Pyrus griffithi* Decne., *Pyrus jacquemontiana* Decne., *Pyrus khasiana* Decne., *Pyrus polycarpa* Hook. F., and *P. pyrifolia* (Burm. F.) Nakai var. culta (Makino) Nakai. In India, pear cultivars commercially grown belong to both *P. pyrifolia* and *P. communis* group. Cultivated occidental pears introduced in the 19th century from Europe and America, where as oriental pears (Chinese sand pears) came from Eastern Asian countries. The 'Chinese Sand Pears' were widely grown in North Western Himalayan region including Jammu and Kashmir, Himachal Pradesh and Uttarakhand. The maximum area under cultivation of 'Chinese Sand Pear' is existed in Kashmir valley. Therefore, it is locally known as 'Kashmiri Nakh". It is also believed that the 'Kashmiri Nakh' is one of the naturalized indigenous cultivar grown since ancient time in India.

Genetic diversity is the key component of any agricultural production system. It plays vital roles for efficient selection of parents for plant 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.

The value of genetic diversity, in its various forms has been extensively discussed (Smale, 2006; Rausser and Small, 2011). Moreover, plant breeders require genetic variation (genotypes) for crop/plant improvement. Morphological characters and isozyme analysis have been the two major tools used to assess the genetic variation in *Pyrus* spp. However, isozyme markers and morphological characters are still limited in number (Karimi et al., 2008; Yamamoto et al., 2004). These traits are in common use for elucidation of wide genetic diversity in different field and horticultural crops (Blazek, 2007). Although, newly developed molecular markers are valuable techniques in gene based diversity studies, however the procedures used for molecular analysis have disadvantage of high cost (Ahmad et al., 2004; Bouhadida et al., 2005). The North Western region of Himalayas possesses a high level of heterozygosity created through natural and artificial reproductions (Srivastava et al., 2012). The potential of genetic variability is vast and need to be explored for genetic enhancement of pear genotypes in North West Himalayan region to meet the demand for more food and to find particular characters such as variability in fruit traits especially in size and shape (round, oblong and pyriform) and colour of fruits. 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 have been 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). Keeping in view these facts, the present studies were carried out to investigate the extent of genetic diversity in germplasm based on pomological, yield and quality traits using multivariate analysis.

MATERIALS AND METHODS

This study was conducted during year 2006 to 2009 on 24 diverse genotypes of 'Kashmiri Nakh' pear collected from different sites of Kashmir valley, India (Table 1). The primary selection criterion was based on fruit yield and quality attributes. Individual genotypes were marked in the field. The data were recorded at the time of fruit maturity during summer (August to September) seasons of each year, that is, 2006 to 2009 and data pooled for analysis. Tree height was measured by pole method, and tree spread in N-S and E-W have been recorded by measuring tape. Morphological features and physico-chemical 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), fruit weight (g), fruit diameter (mm), pulp (%) , TSS (^{o} Brix), acidity (%), ascorbic acid (mg/100 g) 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 caliper. The measurement of fruit length was made on the polar axis, that is, 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. Total soluble solids (T.S.S), titrable acidity, and sugars were determined by method given in AOAC (1994). The experiment was conducted under randomized block design replicated three times and pooled data of two years were analyzed as per the method suggested by Gomez and Gomez (1984).

To explore the diversity and relationship among 24 genotypes, their vital morphological characteristics were studied by the multivariate factor analysis. The determination of the states of the morphological and chemical characters was carried out on samples collected. To find out significance level, analysis of variance (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

Analysis of variance showed significant differences among the genotypes for all the characters studied and extent of variability is given in Table 2. The tree height was ranged from 3.15 to 14.15 m and maximum recorded in 'CHB-4' followed by 'TBP-3' and minimum in 'TB-3' m.

Table 1. List of genotypes used in studied.

S/N	Genotype	S/N	Genotype
1	THP-1	13	TBP-3
2	THP-2	14	CB-1
3	THP-3	15	CB-2
4	THP-4	16	CB-3
5	THP-5	17	CHB-4
6	THP-6	18	CB-5
7	THP-7	19	CB-6
8	TB-1	20	CB-7
9	TB-2	21	CB-8
10	TB-3	22	CHB-1
11	TBP-1	23	CHB-2
12	TBP-2	24	CHB-3

Table 2. Tree fruit and yield characteristic of 'Kashmiri Nakh' pear genotypes grown commercially in North West Himalayan region of India.

Genotype	Tree height (m)	Tree spread (m) N-S	Tree spread (m) E-W	Fruit weight (g)	Fruit length (mm)	Fruit Diameter (mm)	TSS (°Brix)	TSS/Acidity ratio (%)	Acidity (%)	Vit-C (mg/100 gm pulp)	Yield/tree (kg)
THP-1	10.25	12.25	10.25	115.07	61.65	58.84	13.1	52.40	0.25	4.94	250
THP-2	9.45	10.25	8.45	128.58	65.39	60.66	13.2	37.71	0.35	2.86	210
THP-3	10.45	10.56	9.58	124.41	60.76	58.43	12.9	67.89	0.19	2.34	510
THP-4	8.78	9.45	8.45	128.61	61.90	61.9	13.3	110.83	0.12	1.17	600
THP-5	3.45	2.45	3.45	119.91	60.23	60.77	15.7	65.41	0.24	2.21	240
THP-6	4.45	4.46	5.12	105.92	58.65	58.31	16.5	91.66	0.18	3.25	280
THP-7	3.58	4.58	5.45	137.18	66.44	62.71	16.5	68.75	0.24	1.95	215
TB-1	6.25	7.16	6.89	122.37	62.11	61.79	15.9	66.25	0.24	2.73	315
TB-2	11.15	10.13	9.45	93.95	54.96	57.45	15.7	82.63	0.19	1.69	800
TB-3	3.15	3.09	4.56	58.82	46.17	51.56	16.5	71.73	0.23	2.73	245
TBP-1	11.45	11.07	10.58	114.35	58.37	60.17	17.8	136.92	0.13	2.73	1600
TBP-2	12.25	14.45	11.25	116.80	59.41	59.71	13.8	125.45	0.11	2.34	815
TBP-3	13.55	15.56	14.20	96.01	56.28	57.65	13.4	33.50	0.4	2.34	1614
CB-1	8.45	6.78	7.14	115.03	65.32	52.13	14.4	120.00	0.12	2.73	250
CB-2	10.15	7.89	8.10	126.26	58.13	42.14	17.2	95.55	0.18	2.99	230
CB-3	6.45	8.46	7.45	125.13	52.14	58.21	16.3	95.88	0.17	2.34	280
CB-4	9.45	10.25	9.45	111.10	60.34	52.42	13.4	78.82	0.17	1.69	514
CB-5	6.47	11.45	10.45	119.50	62.12	60.31	14.6	63.47	0.23	1.69	612
CB-6	4.48	4.45	5.46	96.34	62.31	55.24	15.6	141.81	0.11	3.25	210
CB-7	11.13	10.25	10.25	98.42	42.35	48.34	17.4	145.00	0.12	3.12	330
CB-8	7.45	6.58	7.45	112.31	48.14	47.21	16.3	135.83	0.12	2.73	220
CHB-1	8.75	8.45	8.46	119.12	52.13	55.14	14.2	88.75	0.16	2.08	190
CHB-2	9.12	8.46	8.41	96.52	58.14	52.33	15.2	89.41	0.17	2.73	230
CHB-3	14.15	12.25	12.25	116.21	60.24	58.34	14.3	110.00	0.13	2.47	280
CD at 5%	3.13	3.16	2.87	15.74	4.23	2.89	1.23	30.65	0.09	1.16	60.76

The tree spread measured as North-South and East-West extension. The North-South spread ranged from 2.45 to 15.56 m and maximum in genotype 'TBP-3' followed by 'TBP-2' and minimum in 'THP-5'; whereas, East-West tree spared ranged from 3.45 to 14.20 m and maximum in genotype 'TBP-3' followed by 'CHB-3' and minimum in 'THP-5'. The findings were in agreement with (Prakash 2000; Singh et al*.*, 2001).

The maximum fruit weight was recorded in 'THP-7' (137.18 g) followed by 'THP-4' (128.61 g) and minimum in 'TB-3' (58.82 g); wherein, fruit length was ranged between 42.35 to 66.44 and maximum measured in

Table 3. Descriptive statistics for eleven tree, fruit quality, and yield traits of 24 'Kashmiri Nakh' pear genotypes.

Variable	Range	Mean	Std. Dev	CV	Skewness	Kurtosis	Bimodality
Tree height (m)	3.15-14.15	8.51	3.17	37.25	-0.19	-0.80	0.39
Tree spread (m) N-S	2.45-15.56	8.78	3.40	38.72	-0.09	-0.39	0.33
Tree spread (m) E-W	3.45-14.20	8.44	2.55	30.21	0.06	0.02	0.29
Fruit weight (g)	58.82-137.18	112.41	16.38	14.57	-1.55	3.80	0.47
Fruit length (mm)	42.35-66.44	58.07	6.08	10.47	-1.12	0.93	0.51
Fruit Diameter (mm)	42.14-62.71	56.32	5.23	9.29	-1.14	0.91	0.53
TSS	12.9-17.80	15.13	1.51	9.98	0.05	-1.28	0.47
TSS/acidity ratio (%)	33.5-145	90.65	32.12	35.43	0.14	-0.81	0.39
Acidity (%)	0.11-0.40	0.19	0.07	36.84	1.33	1.96	0.51
Vit-C (mg/100 gm)	1.17-4.94	2.55	0.74	29.02	1.17	4.00	0.32
Yield/tree (kg)	190-1614	460.00	398.93	86.72	2.20	4.44	0.74

genotype 'THP-7' followed by 'THP-2' and lowest in 'CB-7'. Fruit diameter also varied considerably from 42.14 to 62.71 and maximum in genotype 'THP-7' followed by 'TB-1' and least in 'CB-2'. The total soluble solids (TSS) ranged from 12.90 to 17.80 °Brix and maximum TSS expressed by genotype 'THB-1' followed by 'CB-7', 'CB-2' least in 'THP-3'. However, fruit acidity was varied from 0.11 to 0.40% and maximum found in 'TBP-3' followed by 'THP-2' and least in 'TBP-2'. The sugar acid ratio ranged from 33.50 to 145 and maximum in 'CB-7' and lowest in 'TBP-3'. Ascorbic acid varied between 1.17 to 4.94 mg/100 g of pulp and highest was recorded in 'THP-1' followed by 'THP-6' and 'CB-6' and lowest in 'THP-4'. These results are in agreement with the values reported by (Nergiz and Yildiz, 1997; Robertson et al., 1992) in European plum and (Prakash 2000; Singh et al., 2001) in pear genotypes.

Yield is the economic potential of plants considered most important while making selection and further improvement. A wide range of variability noticed among the twenty three genotypes which range from (190 to 1614 kg/tree). The most productive selections 'TBP-3' yielded 1614 kg/tree followed by 'TBP-1' (1600 kg/tree)' and 'TB-2 (800 kg/tree)'. Low yielding genotype 'CHB-1' produces only 190 kg/plant. Previous studies on pear also reported a high variability among pear cultivars for above, these parameters and findings are in conformity with (Mann and Singh, 1985; Prakash, 2000; Singh et al., 2001).

Data on extent of diversity for eleven pomological, chemical and yield variables are presented in Table 3. The variability of each trait was expressed by standard deviation and the coefficients of variation. Studied genotypes showed highest coefficient of variation for fruit yield (86.72) followed by tree spread N-S (38.72), tree height (37.25), acidity (36.84), tree spread E-W (30.21) and lowest in fruit diameter (9.29). Maximum standard deviation was recorded in fruit yield (398.93) followed by TSS/Acidity (32.12), fruit weight (16.38); however, lowest in acidity (0.07). These results are in line with the findings of Brown and Walker (1990) and Chen et al. (2007) who reported genotypic variations for fruit quality in apricots and pear cultivars, respectively. Skewness describes the symmetrical distribution pattern with respect to its dispersion from the mean. The positive skewness was recorded for the traits like tree spread (m) E-W, TSS, TSS/acidity, acidity, vitamin C and fruit yield per plant and negative skewness in traits like tree height , tree spread, tree spread (m) N-S, fruit weight, fruit length and fruit diameter. Kurtosis tells the weight of the tails of a distribution. In the present set of data it was recorded that platykurtic distribution pattern for the traits like tree spread, tree height, TSS, TSS/acidity, however lepto-kurtic distribution for the traits like tree spread, fruit weight, fruit length, fruit diameter, acidity, vitamin C and yield per plant. Bimodality of genetic admixture values provides evidence of strong isolation between two morphological and genetic clusters, supporting the existence of a sympatric genotypes pair within the gene pool. It clearly showed that these genotypes existed in the same geographic area and thus regularly encounters one another. An initially interbreeding population that splits into two or more distinct species sharing a common range exemplifies sympatric speciation. Such speciation may be a product of reproductive isolation which prevents hybrid offspring from being viable or able to reproduce, thereby reducing gene flow that results in genetic divergence.

From the above result, it can be concluded that all the 24 pear genotypes are having wide variability for studied traits. Genetic variability in 'Kashmiri Nakh' is probably due to heterogeneity, diversity in environments and hybrid progeny (Katayama and Uematsu, 2006). The obtained evidences as a result of the present study indicated prospects of some accessions to exploit for commercialization and use in breeding programmes for improvement of existing and evolution of new cultivars. The dendrogram generated from the average linkage cluster analysis based on average distance, classified 24 genotypes in to two major groups at 2.23 NRMS distance

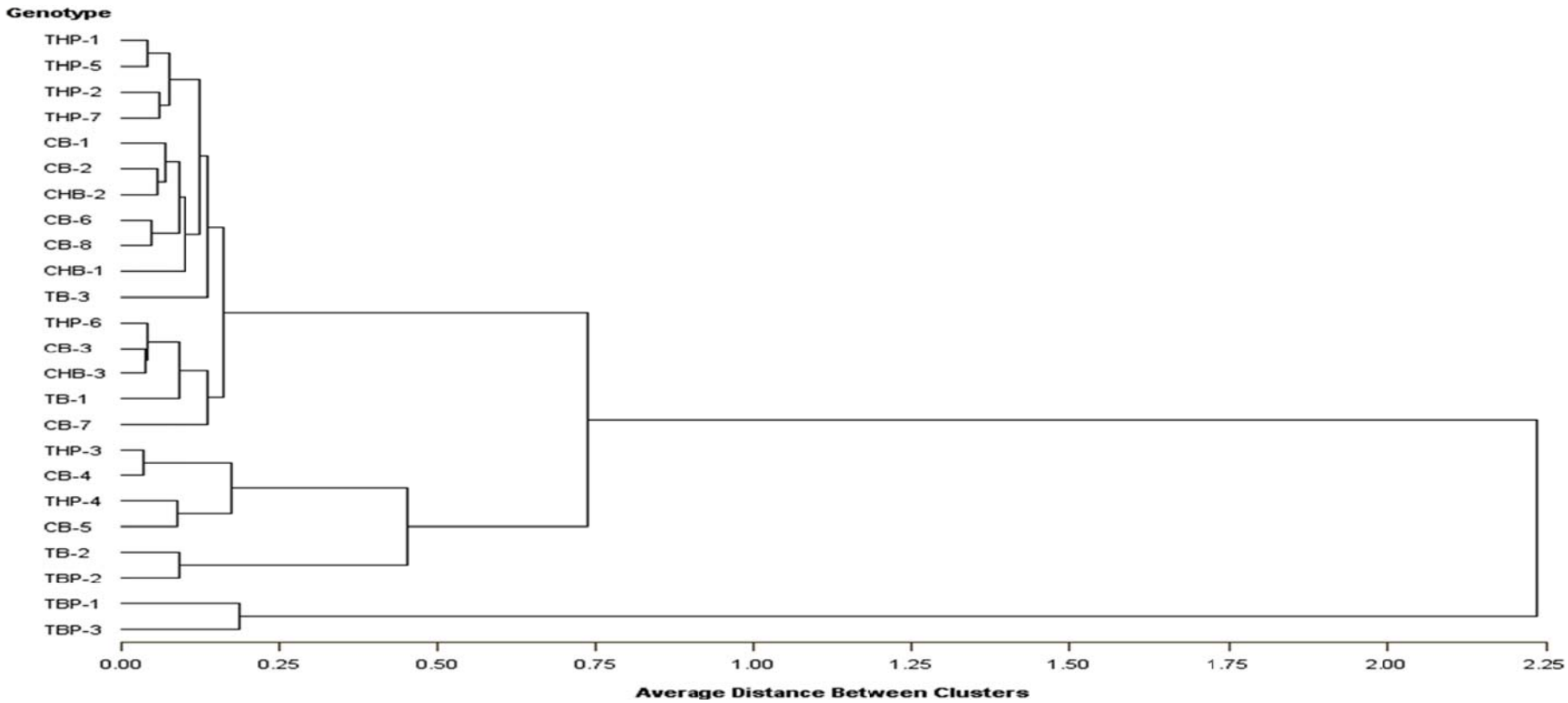

Figure 1. Dendrogram of 24 'Kashmiri Nakh'pear *genotypes* obtained by average distance between cluster analyses based on 11 tree, pomological, fruit quality, and yield traits.

(Figure 1). The first group included two genotypes (TBP-1, TBP-3) contributes 8.33% of the total genotypes in this population. It had the maximum fruit yield per plant and high TSS and TSS/Acidity. The second group comprised 22 genotypes (THP-1, THP-5, THP-2, THP-7, CB-1, CB-2, CHB-2, CB-6, CB-8, CHB-1, TB-3, THP-6, CB-3, CHB-3, TB-1, CB-7, THP-3, CB-4, THP-4, CB-5, TB-2, TBP-2) contributes 91.66% of the total genotypes. This group further divided in to two major clusters at 0.73 NRMS distance. In first cluster, six genotypes exist and contributes 25.00% of the total genotypes which is further divided in to two sub clusters at 0.45 NRMS distance in which first sub cluster comprised two genotypes which possess medium fruit length, fruit diameter, fruit weight, TSS, mid to high fruit yield and lower fruit acidity however second sub-cluster consists four genotypes that is, THP-3, CB-4, THP-4, CB-5 having lowest fruit acidity, high tree spread, tree height, high fruit weight, medium fruit length. The second cluster also further divided into two sub clusters segregated at 0.16 NRMS distance comprised 16 genotype (THP-1, THP-5, THP-2, THP-7, CB-1, CB-2, CHB-2, CB-6, CB-8, CHB-1, TB-3, THP-6, CB-3, CHB-3, TB-1, CB-7) contributes 66.66% of the total genotypes.

The first sub cluster consists five genotype, that is, (CB-7, TB-1, CHB-3, CB-3 and THP-6) and possess medium to high tree height, TSS, TSS/-acidity and low fruit yield attributes however second sub cluster comprised 11 genotypes in 2 sub-sub clusters. The second sub cluster divided

Table 4. Principal component analysis of the "Kashmiri Nakh' pear genotypes showing the eigen vectors, eigen values and percentage total variance accounted for by the eleven principal component axes.

Parameter	Eigen vector										
	PRIN1	PRIN2	PRIN3	PRIN4	PRIN5	PRIN6	PRIN7	PRIN8	PRIN9	PRIN10	PRIN11
Tree height (m)	0.406022	0.326143	0.050758	0.181451	-0.033762	0.104402	0.068807	0.347342	0.742690	-0.008537	0.064772
Tree spread (m) N-S	0.479381	0.200321	0.010391	0.095263	0.006716	0.029149	-0.169550	0.049329	-0.446632	-0.055181	0.697339
Tree spread (m) E-W	0.457938	0.267753	-0.019804	0.060031	-0.006041	0.072890	-0.073575	0.198018	-0.415908	0.113716	-0.691896
Yield/tree (kg)	0.336776	0.165463	-0.080281	-0.507138	0.410679	-0.042198	0.325698	-0.511623	0.107660	-0.209418	-0.042997
Fruit weight (g)	0.130493	-0.259580	0.528155	0.203767	0.092763	0.643076	-0.197203	-0.352975	0.059309	-0.039011	-0.066699
Fruit length (mm)	0.158184	-0.421594	0.331439	0.180502	0.230292	-0.167720	0.672541	0.310847	-0.144694	0.046448	0.040098
Fruit Diameter (mm)	0.201869	-0.387988	0.175355	-0.284337	0.362074	-0.379036	-0.590803	0.218787	0.143896	0.054954	-0.041343
TSS °B	-0.341807	0.205363	-0.045366	-0.278608	0.503672	0.490445	0.004516	0.491999	-0.116154	-0.076557	0.075206
TSS/Acidity ratio (%)	-0.188391	0.435174	0.435338	-0.010566	0.175608	-0.199654	0.017933	-0.163422	-0.003026	0.694358	0.075036
Acidity (%)	0.197839	-0.348471	-0.538057	-0.052657	0.057030	0.302102	0.058178	-0.049448	0.072748	0.659314	0.082543
Eigen value	3.694005	2.613585	1.569189	1.136287	0.76194	0.575275	0.357612	0.138637	0.08329	0.05411	0.016071
Difference	1.08042	1.044396	0.432902	0.374347	0.186665	0.217663	0.218975	0.055348	0.029179	0.038039	
Proportion	0.3358	0.2376	0.1427	0.1033	0.0693	0.0523	0.0325	0.0126	0.0076	0.0049	0.0015
Cumulative	0.3358	0.5734	0.7161	0.8194	0.8886	0.9409	0.9734	0.986	0.9936	0.9985	1

into two sub-sub clusters. The first sub-sub cluster includes only single genotypes TB-3 which is characterized by lowest tree height, tree spread, fruit weight, fruit length but high in TSS, vitamin C and yield per plant whereas second sub-sub cluster consists 10 genotypes (THP-1, THP-5, THP-2, THP-7, CB-1, CB-2, CHB-2, CB-6, CB-8, CHB-1) which were characterized by moderate to high in tree height, tree spread, fruit weight, length, diameter, TSS, TSS/acidity, vitamin C and low to moderate in fruit yield per plant.

The dissimilarity level in terms of genetic distance ranged from (0.0.33 to 2.236) based on NRMS (Figure 1) 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 (Mratinić et al., 2007). This grouping pattern of genotypes based on pomological and yield attributes confirmed the results obtained by cluster analysis and that the crosses involving parents belonging to the maximum divergent clusters were expected to manifest maximum heterosis and also wide variability in genetic architecture. The results of present study are thus useful as it gives information about the groups where certain traits are more important allowing breeder to conduct specific breeding programme.

Principal components (PC) analysis is a way of identifying patterns in data, which expresses data in such a way as to highlight their similarities and differences (Milosevic and Milosevic, 2010). Therefore, PC was carried out to determine the characters more strongly contributed to the principal components. Principal components analysis reduced the original 11 characters in experiment to 4 principal components. The first four principal components with Eigen values >1 explained 81.94% of variation among 24 accessions (Table 4). Other PCs had Eigen values <1 and have not been interpreted.

The first PC, which is the most important component, explained 33.58% of the total variation and was positively related to tree height, tree spread (N-S), tree spread (E-W), yield per tree, fruit weight, fruit length, fruit diameter and acidity however PC1 negatively related to TSS and TSS/acidity. The PC2 accounted of 23.76% of the total variation and the characters with the greatest weight on this component was TSS. The PC3 accounted for 14.27% and highest positively related to TSS/acidity. However, PC4 is accounted for only 10.33%. This situation confirms the suitability of using morphology as a basis for selecting parental sources; nevertheless, studies through several years must be conducted

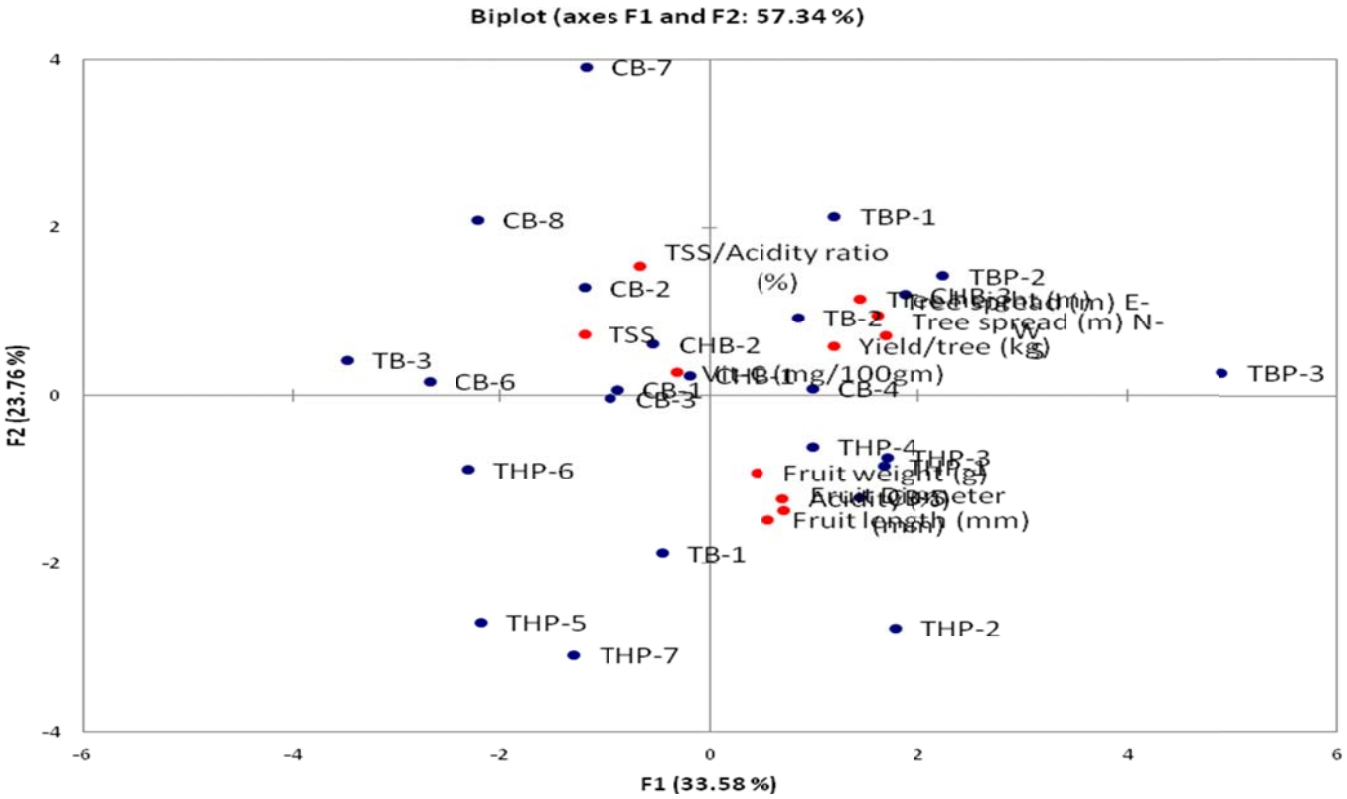

Figure 2. Segregation of 24 'Kashmiri Nakh' pear genotypes according to their fruit quality and yield characteristics determined by principal component analysis (PCA). Vectors represent the loadings of phenological, quality and yield traits data along with the principal component scores.

before parental selection for a possible plant breeding.

The PC analysis provided a simplified classification of the pear genotypes for collecting and breeding programme. 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 (Figure 2). The derived cluster and subgroups are very similar to those identified from average distance between cluster analyses. More interesting genotypes were 'CHB-4, THP-3, THP-7, THP-1, TBP-1 and TB-2,' that were disposed in gaps means more diverse than others and are the most promising ones. Genotype 'TB-3' characterized by smallest tree height minimum plant spread minimum fruit weight and fruit length however 'TBP-3' is characterized by highest tree height of the tree. Genotype 'TBP-1' had the maximum TSS and TBP-3 highest yield per plant. THP-1 was richest in vitamin C however TBP-3 in acidity. The THP-7 genotype had highest fruit weight and fruit diameter compared to others genotypes.

So, it can be intended for further utilization for introducing these 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 pear 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 results in increased in desired traits. The results are certainly representative and valuable, and will provide some guidance for screening 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 (TBP-1 and TBP-3) genotypes were superior in terms of fruit yield and second group (22) 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 our study, were observed in 'TB-3, CHB-4, TBP-3, THP-7, TBP-3, THP-1, TBP-1 and TB-2. They can be used as directly new cultivars or potential may be utilized for desirable crop improvement programme to breed a

variety with high yield and fruit quality.

Conflict of Interests

The author(s) have not declared any conflict of interest.

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