

Genetic diversity among native wild hip rose (*Rosa canina* L.) genotypes collected from Kashmir valley

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ABSTRACT

Thirty six wild hip rose (*Rosa canina* L.) genotypes collected from different areas of Kashmir valley in India were assessed for overall diversity detecting similarities among important pomological, fruit quality and yield parameters. The genotypes differed significantly for these traits. Nine variables were scored and subjected to multivariate analysis. Results showed a considerable phenotypic diversity among hip rose genotypes in bush height (2.45-9.00 m), hip yield (0.75-7.5 kg/bush), fruit diameter (8.05-14.89 mm), fruit length (11.69-24.85 mm), fruit weight (0.46-2.20 g), fruit pulp weight (0.26-1.30 g), fruit: pulp ratio (44.05-89.37), seed number per hip (1-37) and TSS (29.8-39.6°Brix). The cluster analysis classified genotypes into six distinct groups according to their distinct characteristics. The groups I, II and III were found superior in terms of fruit characteristics and tree traits, whereas, I and VI were most diverse. Principal component analysis (PCA) revealed that traits related to fruit diameter, fruit weight, pulp weight, number of seeds per hip accounted for a large proportion of the observed variability and four genotypes, namely, 'RH-PH-1', 'RH-OAF-18' and RH-12 'RH-11' were found superior for yield attributing traits.

Key words: Genetic diversity, hip rose, principal component analysis.

INTRODUCTION

The genus *Rosa* belongs to family Rosaceae, which includes more than 100 species in the temperate and sub-tropical zones of the Northern Hemisphere (Nilsson, 14). Many wild species are naturally growing in abundance in North Western Himalayan states like Jammu & Kashmir, Himachal Pradesh and Uttarakhand and are used by farmers as bio-fence around their agriculture farm and orchards (Dhananjaya *et al.*, 4). Rose bushes are hardy and bear fruits (hips) profusely and generally their fruits are wasted due to lack of knowledge of processing techniques for making value-added products like jam, jelly and dehydrated products etc. The hips are rich source of vitamin C, carotenoids and are essential traits of functional food (Gao *et al.*, 8). These nutritive and medicinal values are derived mainly from their chemical composition in proteins, lipids, tannins, pectin, organic acids, amino acids, essential oils and minerals (Celik *et al.*, 3; Ercisli and Guleryuz, 7). They also act as medicinal supplements, reducing the risk of cardiovascular diseases, different form of cancers and have an anti-inflammatory effect. Conservation and utilization of these resources is required for long term sustainable productions (Tabaei-Aghdai *et al.*, 17). In India, these wild rose shrubs are naturally growing in thousands of

hectares as natural vegetation, producing tonnes of hips annually. Due to lack of suitable genotypes and processing techniques farmers are unable to utilize its vast economic potential. Although, the relevant research in other countries is also very recent. The first selection studies on rose hip germplasm were initiated in Turkey at the end of 1990s in the Northern and Eastern parts of Anatolia (Ercisli, 5). Researchers described several fruit characteristics of promising selections (Ercisli, 5; Gunes, 10). Therefore, purpose of this study is to identify promising rose hip genotypes based on plant and pomological characteristics and would help in developing adequate phenotypic markers for commercial use and germplasm management.

MATERIALS AND METHODS

The study was conducted on 36 diverse wild hip rose genotypes collected from Kashmir valley based on morphological differences (Table 1). The climate of Kashmir valley is varied with annual precipitation ranging 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 with elevation; the average minimum temperature is in the upper regions is -2°C in January, and the average maximum temperature is about 31°C in

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Table 1. List of hip rose genotypes evaluated.

S.No.	Genotype	S.No.	Genotype	S.No.	Genotype	S.No.	Genotype	S.No.	Genotype
1	RH-OAF-1	9	RH-OAF-9	17	RH-OAF-17	25	RH-4	33	RH-12
2	RH-OAF-2	10	RH-OAF-10	18	RH-OAF-18	26	RH-5	34	RH-PH-1
3	RH-OAF-3	11	RH-OAF-11	19	RH-OAF-19	27	RH-6	35	RH-PH-2
4	RH-OAF-4	12	RH-OAF-12	20	RH-OAF-20	28	RH-7	36	RH-PH-3
5	RH-OAF-5	13	RH-OAF-13	21	RH-OAF-21	29	RH-8		
6	RH-OAF-6	14	RH-OAF-14	22	RH-1	30	RH-9		
7	RH-OAF-7	15	RH-OAF-15	23	RH-2	31	RH-10		
8	RH-OAF-8	16	RH-OAF-16	24	RH-3	32	RH-11		

July. The primary selection criterion was based on size, colour and bearing of fruits (hips) on the bushes. Individual bushes were marked in the field. The data was recorded at the time of fruit maturity during summer (September) season of the year. Tree related traits like plant height (m) and yield (kg/bush) were recorded in the field. Morphological features and physico-chemical parameters of the fruits were recorded in the laboratory. Fifty fruits from selected plants were randomly chosen and measured. The data were collected on fruit weight (g), fruit diameter (mm), fruit length (mm), pulp weight (g), fruit flesh to seed ratio, number of seeds per fruit and TSS ($^{\circ}$ Brix). The maximum width of the fruit, as measured in the direction perpendicular to the polar axis, is defined as the diameter (Gogu *et al.*, 9). After measuring the fruit size, the seeds were manually separated from the fruits; total seeds and pulp weight per fruit was measured as above. Total soluble solids (TSS) were determined using digital refractometer method (AOAC, 2).

To explore the diversity and relationship among 36 wild hip rose genotypes, their vital morphological characteristics were studied by the multivariate factor analysis. To find out significance level, ANOVA was performed using PROC GLM for clustering of cultivars into similarity groups using the method tree procedure PROC CLUSTER based on average distance (SAS/STAT, 15). In order to identify the patterns of morphological variation and contribution of traits, principal component analysis (PCA) was conducted using PROC PRINCOP in the SAS 9.3 software (SAS Institute, Cary, NC, 16).

RESULTS AND DISCUSSION

The plant and fruit characteristics of the 36 wild hip rose genotypes are given in Table 2 & 3. Plant vigour in terms of plant height is associated with yield and related traits which ranged from 2.45 to 9.00 m in present genotypes. The maximum plant height was recorded in 'RH-12' (9 m) followed by 'RH-10' (8 m)

and 'RH-9' (7.5 m). However, it was found minimum in 'RH-OAF-20' (2.45 m). Yield is as considered the economic potential of a plant and is the most important characters while making selection for crop improvement. A wide range of variability was also noticed among the studied genotypes. It ranged from 0.75 to 7.5 kg/bush. The most productive selection was 'RH-12', which yielded 7.5 kg/bush followed by 'RH-9' (6.2 kg/bush) and 'RH-10' (6.1 kg/bush). The lowest yield was recorded in 'RH-OAF-18' (0.75 kg/bush).

The average weight and dimensions of the fruits in representing hip rose genotypes was estimated. The maximum fruit diameter was recorded in 'RH-11' (14.89 mm) followed by 'RH-OAF-19' (13.45 mm) and 'RH-PH-3' (13.44 mm) with minimum in 'RH-OAF-12' (8.08 mm). Variability in fruit diameter ranged from (8.08-14.89 mm). Fruit length ranged from (11.69 to 24.85 mm) and it was maximum in 'RH-PH-1' (24.85 mm) followed by 'RH-PH-2' (23.02 mm), with minimum in 'RH-OAF-3' (11.69 mm). Fruit weight varied from (0.46-2.20 g); wherein, highest fruit weight was recorded in 'RH-3' (2.20 g) followed by 'RH-11' (2.18 g) and lowest in 'RH-OAF-6' (0.46 g). Fruit pulp weight was found maximum in 'RH-8' (1.30 g) followed by 'RH-PH-2' (1.27 g) and minimum in 'RH-OAF-6' (0.26 g).

Higher number of seeds per fruit is desired for oil extraction, while lesser is ideal for juice making and other value-added products. Wide range of variability was recorded for number of seeds per fruit (1-37) in the genotypes evaluated. Maximum seeds per hip (37) were recorded in 'RH-11' followed by RH-8 (31) with minimum in 'RH-PH-1' (1). Total soluble solids in pulp were recorded highest (39.6 $^{\circ}$ Brix) in 'RH-OAF-4' and 'RH-OAF-8', while it was lowest in 'RH-OAF-3' (29.8 $^{\circ}$ Brix). Fruit pulp: seed ratio is the important parameter determining the suitability of genotypes for processing, which ranged from 44.05 to 89.37%. Genotype 'RH-PH-1' record the highest value (89.37%) followed by 'RH-OAF-18' (72.3%)

Table 2. Tree and fruit characteristic of hip rose genotypes from Kashmir valley.

Genotype	Fruit Dia. (mm)	Fruit length (mm)	Fruit wt. (g)	Pulp wt. (g)	No. of seeds per fruit	TSS (°Brix)	Fruit pulp: seed ratio	Plant height (m)	Yield/ bush (kg)
RH-OAF-1	12.45	16.95	1.47	0.99	20.2	38.0	67.45	5.12	3.50
RH-OAF-2	12.04	15.92	1.18	0.69	20.2	35.8	58.28	3.75	2.10
RH-OAF-3	9.56	11.69	0.64	0.33	18.8	29.8	50.79	2.50	2.20
RH-OAF-4	12.03	14.39	1.11	0.59	23.8	39.6	55.27	5.14	4.50
RH-OAF-5	9.88	13.90	0.79	0.52	22.4	35.6	65.79	2.50	1.50
RH-OAF-6	8.22	12.65	0.46	0.26	21.6	35.8	53.66	3.75	2.70
RH-OAF-7	8.29	15.64	1.06	0.54	20.6	38.6	50.93	2.55	1.56
RH-OAF-8	9.45	11.99	1.12	0.72	24.6	39.6	65.31	5.12	4.59
RH-OAF-9	9.04	17.05	1.46	0.67	20.2	38.8	46.87	3.14	2.20
RH-OAF-10	9.08	16.79	1.69	0.75	21.0	39.0	44.05	5.16	3.69
RH-OAF-11	9.76	13.59	1.36	0.79	22.6	39.0	59.52	5.14	4.58
RH-OAF-12	8.08	17.02	1.29	0.66	22.6	38.0	51.04	2.50	2.12
RH-OAF-13	9.68	17.39	1.55	1.00	24.6	36.6	65.57	3.25	2.69
RH-OAF-14	9.27	15.92	1.37	0.84	23.4	38.0	61.38	5.56	4.12
RH-OAF-15	9.61	15.14	1.49	0.91	22.8	37.6	61.10	2.56	1.82
RH-OAF-16	9.22	17.38	1.51	0.88	17.8	37.0	58.94	2.57	1.50
RH-OAF-17	10.31	15.43	1.51	0.92	27.8	38.0	61.62	2.54	1.20
RH-OAF-18	11.12	18.53	1.18	0.85	12.6	37.8	72.28	2.50	0.75
RH-OAF-19	13.46	17.91	1.66	1.03	23.6	37.2	62.86	2.59	2.10
RH-OAF-20	12.44	18.90	1.55	0.94	22.0	38.2	60.79	2.45	2.20
RH-OAF-21	12.35	19.01	1.54	1.06	25.8	34.6	70.59	2.52	3.10
RH-1	12.86	15.25	1.49	0.85	22.8	36.2	57.13	3.10	1.50
RH-2	12.24	15.31	1.33	0.78	24.4	36.8	58.32	4.50	4.00
RH-3	14.18	19.17	2.21	1.29	30.6	33.6	58.59	4.50	2.00
RH-4	13.08	16.32	1.60	0.92	26.8	36.8	57.37	5.10	5.00
RH-5	12.79	15.26	1.53	0.82	27.4	38.4	53.82	7.00	5.00
RH-6	12.49	16.31	1.81	1.18	30.8	36.8	65.17	6.00	2.50
RH-7	11.69	17.33	1.61	0.99	23.8	36.0	61.89	4.50	1.50
RH-8	12.59	16.68	2.12	1.30	31.2	35.6	61.55	4.00	1.20
RH-9	12.18	17.17	1.85	1.12	28.6	34.4	60.56	7.50	6.20
RH-10	12.43	16.76	1.87	1.16	26.6	36.0	61.95	8.00	6.10
RH-11	14.89	16.83	2.19	1.23	37.0	38.8	56.09	6.00	3.20
RH-12	12.76	15.45	1.47	0.86	24.4	39.2	58.28	9.00	7.50
RH-PH-1	10.75	24.85	1.12	0.99	1.0	35.6	89.38	5.12	3.50
RH-PH-2	12.97	23.02	2.06	1.27	22.8	36.0	61.70	3.25	2.60
RH-PH-3	13.44	14.33	1.54	0.90	25.6	35.2	58.74	3.56	3.20
CD at 5%	1.60	1.93	0.31	0.20	7.04	3.05	12.25	0.845	0.90

and lowest in 'RH-OAF-10' (44.1%). The above findings are in agreement with the earlier reports (Ercisli, 5; Misirli *et al.*, 13; Ercisli and Esitken, 6). Descriptive statistics revealed the maximum standard deviation for fruit flesh to seed ratio (7.83) followed by number of seeds per fruit (4.37) and minimum for pulp weight (0.24). The data were normally skewed to the tune of less than ± 2 . However, positive skewness was recorded for fruit pulp: seed ratio, fruit length, plant height, yield, number of seeds per fruit, while it was negative for TSS, pulp weight, fruit weight and fruit diameter. In the present set of data, platykurtic distribution pattern was recorded for fruit diameter alone, however leptokurtic distribution for fruit: pulp ratio, TSS, fruit length, number of seeds per fruit, fruit weight, yield, plant height and pulp weight. 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 (Arunachalam, 1). In the present study, values are near to zero, explains the closeness amongst genotypes for the traits under study.

The dendrogram generated from the linkage cluster analysis based on average distance, classified 36 hip rose genotypes into six major groups (Fig. 1). The first group formed at normalized root mean square (NRMS) distance of 2.30, which included only one genotype (RH-PH-1) contributing 2.78% of the total genotypes studied. It had the maximum fruit length and fruit flesh ratio but the medium fruit diameter, TSS, plant height, number of seeds per fruit, pulp weight and low fruit weight. The second group was separated at NRMS distance 1.40 and again comprised of one genotype (RH-OAF-18) contributing 2.78% of the total genotypes that possessed minimum

Table 3. Descriptive statistics for nine pomological, fruit quality and tree traits of wild hip rose genotypes.

Variable	Minimum	Maximum	Std Dev	CV%	Skewness	Kurtosis	Bimodality
Fruit dia. (mm)	8.080	14.894	1.845	16.333	-0.165	-1.121	0.4769
Fruit length (mm)	11.698	24.850	2.585	15.692	1.058	2.953	0.3403
Fruit weight (g)	0.464	2.202	0.390	26.588	-0.345	0.681	0.2829
Pulp weight (g)	0.256	1.302	0.249	28.413	-0.433	0.270	0.3351
No. of seeds per fruit	12.600	37.000	4.370	18.237	0.480	1.971	0.2345
TSS ($^{\circ}$ Brix)	29.800	39.600	1.965	5.3286	-1.327	3.441	0.4111
Fruit: pulp ratio (%)	44.046	89.376	7.832	13.026	1.221	4.794	0.3087
Plant height (m)	2.450	9.000	1.744	40.762	0.921	0.336	0.5119
Yield/bush (kg)	0.750	7.500	1.590	52.183	0.941	0.499	0.4998

Table 3. Principal component analysis of the wild hip rose genotypes using nine principal component axes.

Trait	Eigen vector								
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9
Fruit dia. (mm)	0.425	-0.029	-0.139	-0.211	0.096	0.849	0.145	-0.037	-0.001
Fruit length (mm)	0.264	-0.434	0.345	0.197	-0.473	-0.091	0.586	-0.078	-0.026
Fruit wt. (g)	0.466	-0.070	-0.263	0.274	-0.224	-0.119	-0.357	0.090	0.657
Pulp wt. (g)	0.488	-0.208	-0.025	0.121	0.018	-0.150	-0.425	0.109	-0.697
No. of seeds per fruit	0.383	0.183	-0.383	-0.096	0.454	-0.412	0.531	0.054	-0.003
Plant height (m)	0.293	0.493	0.287	-0.142	-0.127	-0.117	-0.107	-0.724	-0.003
TSS ($^{\circ}$ Brix)	-0.000	0.273	0.226	0.842	0.338	0.202	0.089	0.003	-0.031
Fruit: pulp ratio	0.155	-0.351	0.606	-0.229	0.566	-0.084	-0.147	0.043	0.282
Yield/kg per bush	0.189	0.535	0.377	-0.183	-0.239	-0.011	0.045	0.664	0.001
Eigen value	3.559	2.055	1.191	1.001	0.503	0.383	0.190	0.112	0.001
Proportion	0.395	0.228	0.132	0.111	0.056	0.042	0.021	0.012	0.001
Cumulative	0.395	0.623	0.756	0.867	0.923	0.966	0.987	0.999	1.000

(PC = Principal component)

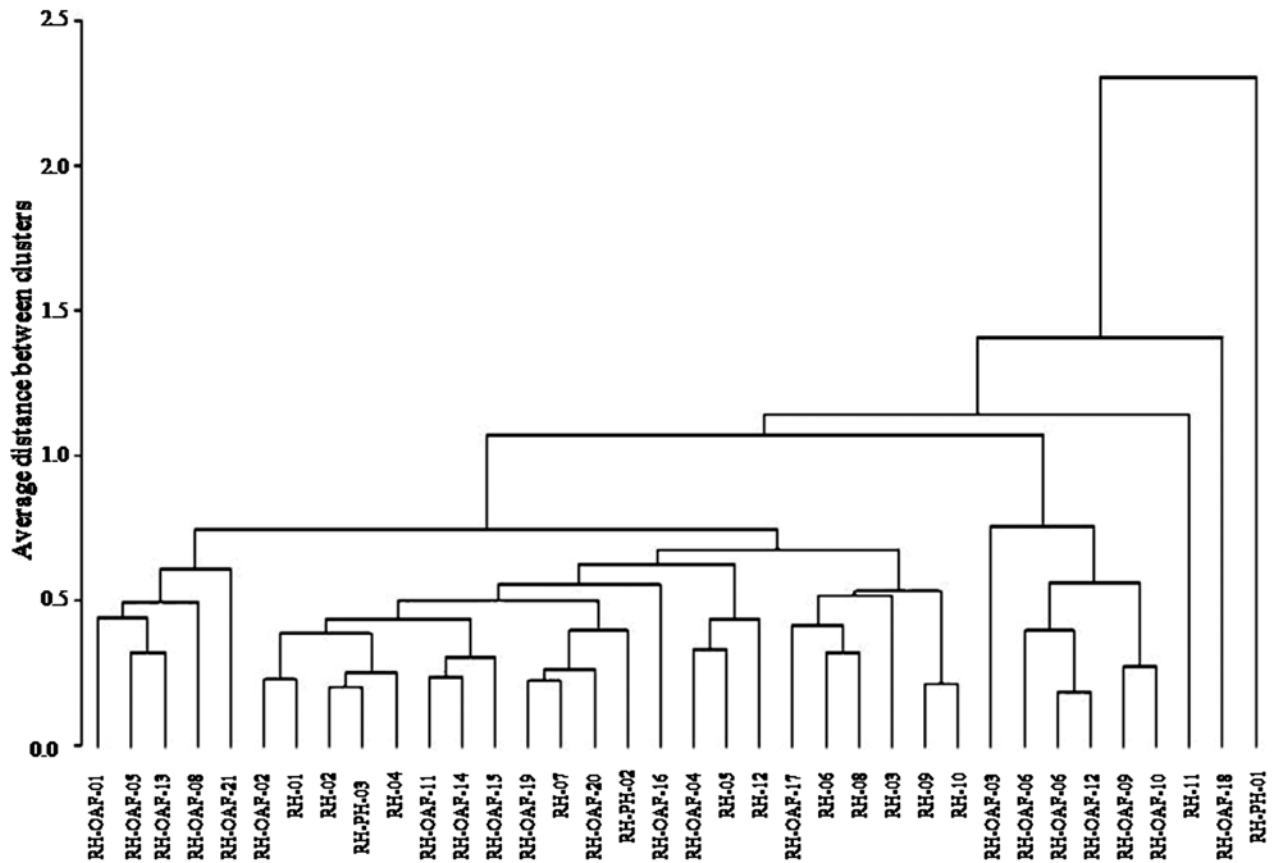


Fig. 1. Dendrogram of 36 wild hip rose genotypes obtained by average distance between cluster analyses based on 9 fruit quality and tree traits.

numbers of seed per fruit, plant height and yield per plant. The third group segregated at 1.13 NRMS distance only in single genotype (RH-11) contributing 2.78% of the total genotypes in the population and characterized by highest fruit diameter and number of seeds per fruit. The fourth group distanced at 1.07, which comprised of six genotypes (RH-OAF-10, RH-OAF-9, RH-OAF-12, RH-OAF-7, RH-OAF-6 and RH-OAF-3) contributing 16.67% of the total genotypes. These genotypes had low to medium fruit length, fruit weight, pulp weight, number of seeds per fruit, plant height, TSS and yield along with lowest fruit diameter. The fifth group was the largest group comprising of 22 genotypes (RH-10, RH-9, RH-3, RH-8, RH-6, RH-OAF-17, RH-12, RH-5, RH-OAF-4, RH-OAF-16, RH-PH-2, RH-OAF-20, RH-7, RH-OAF-19, RH-OAF-19, RH-OAF-15, RH-OAF-14, RH-OAF-11, RH-4, RH-PH-3, RH-2, RH-1 and RH-OAF-2) contributing 61% of total genotypes and characterized by maximum fruit weight, yield per plant, plant height and TSS. This cluster also showed lowest dissimilarity level (0.236) among 'RH-OAF-7' and 'RH-OAF-12' revealing their

close relationships. The sixth group comprised of five genotypes (RH-OAF-21, RH-OAF-8, RH-OAF-13, RH-OAF-5 and RH-OAF-1) contributing 13.88% of the total genotypes that had medium value for most of the traits. The dissimilarity level in terms of genetic distance ranged from 0.236-2.30 indicating a high degree of dissimilarity and high genetic distance between the genotypes. The maximum inter-cluster distance was measured between clusters I & VI followed by II & VI, III & VI suggesting their suitability as parents for hybridization programme, which may give rise to high heterotic F_1 s and broad spectrum of variability in the 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.*, 11; Milosevic Milosevic, 12). Principal components analysis reduced the original nine characters in the experiment to 4 principal components. The first four components with eigen values >1 explained 85% of variation among 36 genotypes (Table 3). Other PCs had Eigen values <1

and have not been interpreted. The first PC, which is the most important component, explained 39.55% of total variation and was positively related to fruit diameter, fruit weight, pulp weight, number of seeds per fruit and negatively related to TSS, in which PC1 is a weighted average of the four characters. The PC2 accounted of 22.84% of the total variation and the characters with the greatest weight on this component were plant height and yield per kg. The PC3 accounted for 13.24% and positively related to fruit length and fruit flesh ratio. However, PC4 accounted for 11.1% and weighted for only TSS. This situation confirms the suitability of using phenology as a basis for selecting parental genotypes. 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 hip rose genotypes for collecting and breeding. The biplot axes (Fig. 2) also shows geometrical distances among genotypes that reflect similarity among them in terms of variables measured. The first three principal component scores were plotted to aid visualization of accessions grouping (Fig. 2).

The derived cluster and sub-groups were very similar to those identified from average distance between cluster analyses. The multivariate analysis was found useful for detection of phenotypic differences among the wild hip rose genotypes. The cluster analysis classified cultivars into six groups according to their potential characteristics. The groups I, II and III of the genotypes were superior in terms of fruit quality and tree related traits, whereas I & VI were found most diverse to each other. Full PC analysis would help in selection of a set of genotypes with better fruit qualities, which in our study, were observed in 'RH-PH-1', 'RH-OAF-18' RH-12 and 'RH-11'. The cluster analysis classified genotypes into six distinct groups according to their potential characteristics. The groups I, II and III were found superior in terms of fruit characteristics and tree traits; whereas I and VI were most diverse. Principal component analysis (PCA) revealed that traits related to fruit diameter, fruit weight, pulp weight, number of seeds per fruit accounted for distinct variability for different traits.

The promising genotypes identified were 'RH-11', 'RH-PH-1', 'RH-PH-2' and 'RH-12' that were disposed

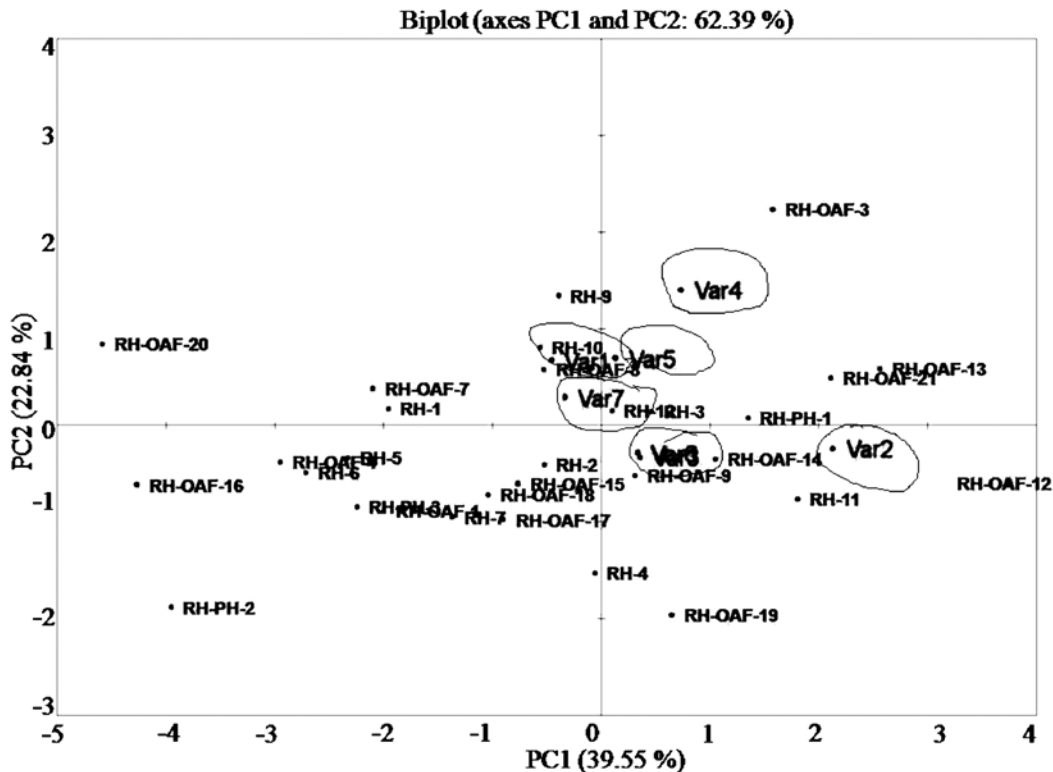


Fig. 2. Segregation of 36 wild rose genotypes according to their fruit quality and tree characteristics determined by principal component analysis. Vectors represent the loading of morphological and quality traits data along with the principal component scores. Abbreviations in biplot are: Var1: Fruit diameter; Var2: fruit length; Var3: fruit weight; Var4: pulp weight; Var5: number of seeds per fruit; Var6: plant height; Var7: TSS; Var8: fruit flesh ratio; Var 9: Yield/kg per bush.

in gaps. Genotype 'RH-11' was characterized by highest fruit diameter and number of seeds per fruit. While 'RH-PH-1' had the maximum fruit length and fruit: flesh ratio. Genotype 'RH-PH-2' possessed higher pulp weight and 'RH-12' having tallest plants with higher TSS and yield, hence it may be intended for further utilization for introducing these traits in desired genotypes. Identification and description of the genetic variability available in the hip rose genotypes of *Rosa canina* L. are preliminary requirements for the exploitation of useful traits in plant breeding.

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