Genetic Diversity Among Sumac Accessions Collected From Five Areas of Iran

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Abstract

Sumac (*Rhus coriaria* L.) has been used in human nutrition as herbal drug to treat different diseases for centuries. In recent years, its genetic improvement has engrossed more consideration because of its substantial portion to human health and nutrition. Middle East region, including Iran being its origin. However, the diffused cultivation of sumac, endangers its existence in the future, so its protection and genetic improvement may cause extensive cultivation. This investigation aims to determine the genetic variation among 23 sumac accessions. Of 18 different traits, consist of four descriptive characters were used. Analysis of variance demonstrated significant differences for all of the morphological characters, and the coefficient of variation ranged from 3.6% in seed length to 37.9% in the weight of the bunch. Results of mean comparison through LSD test indicated that accessions YA6, AB1, and AB2 following to YA10, KB1, KB2, KB3, and AB3 were the best performing accessions for most of the morphological traits. The cluster analysis classified accessions into four groups as Cluster-I can be regarded for the weight of ten fruit while Cluster-IV can be regarded for the weight of the bunch. The accessions of Cluster-II and Cluster-III had relatively good or average magnitudes for most of the studied charters, and they can be used for improving these sumac traits considering goals of the breeder. The factor analysis explained 74.81% (39.71% and 35.10% by factor-1 and factor-2, respectively) of the total variation. Traits leaf length, leaf width, terminal leaflet length, and terminal leaflet width are positively correlated based plot of the first two factors. Accessions YA6, AB1, and AB2 were the best performing accessions in terms of studied traits and are worth germplasm for next genetic improvement projects in sumac because they can be selected as parents for crossing and breeding new sumac cultivars in the future.

Introduction

Nowadays, people pay more attention to green products due to health concerns, and global demand for such products increases day by day. Such massive demand for greens influences their production, which will make the production a vital necessity in the future (Sütyemez et al. 2019). Green products can play an important role in the improvement of both human health and nutrition properties, and such characteristics have been reported by various investigations in sumac (*Rhus coriaria* L.). Its leaves were used as a drug to the therapy of mouth sores and skin cracking. Genus *Rhus*, containing sumac, belongs to the family Anacardiaceae, which is dispersed over temperate areas of east and south Asia while some species native to North and Central America (Yi et al. 2004; Rayne and Mazza, 2007). It consists of about 150 deciduous species, which occur as pioneer species on disturbed zones, but they are intolerant of shade and cannot compete with invading trees while they are tolerant of poor soils as well as drought stress (Tilki and Bayraktar, 2013). Genus *Rhus*, is recommended as an ornamental shrub for open zones in arid and semi-arid environments, and its establishment is accessible in any soil conditions which provide proper cover for birds and animals.

For increasing sumac production, which will be a necessity soon, it should be reached by establishing dense sumac fields using high yielding, which have high-quality. Until now, small sources have been identified for sumac breeding, and a little effort has been performed to study the characteristics of sumac in the world; thus, it is necessary to conduct breeding programs to focus on its extensive cultivation (Fereidoonfar et al. 2018). The most important targets of breeding programs are the tolerance to environmental stresses, having good quality, resistance to biotic stresses, but such breeding effort aiming to obtain a new variety in sumac, which is high costing and time-consuming project (Valiollahi et al. 2014). Most of the genetic improvement projects on sumac had been accomplished in the Turkey and Iran, with little effort being performed in the other areas of the world. Also, the evaluations on the genetic variation are being done in Turkey and Iran, where there is a good collection of plant

materials as native landraces (Fereidoonfar et al. 2018; Sütyemez et al. 2019). Efficient characterization of the plant materials requires knowledge about the collections from different aspects, especially for morphological traits (Sabaghnia et al. 2015).

Rawashdeh et al. (2009) studied molecular variation among sumac accessions from three locations of Jordan and classified them into two main groups. Fereidoonfar et al. (2018) assessed the diversity of 136 sumac genotypes from the center of Iran (one province) and they showed high variations for most traits, and identified only 20 genotypes as the best for the fruit traits. Mohammadi-Alaghoz et al. (2021a) investigated morphological diversity in five populations of Iran and reported the high coefficients of variation for diameter at breast height, number of sprouts, and collar diameter. Sütyemez et al. (2019) studied the genetic diversities among 24 sumac accessions by SRAP and ISSR markers and they found sumac genotypes showing high genetic variations will be used in the programs. Multivariate statistical procedures are helpful for classification of plant materials when a number of genotypes are to be evaluated for several agronomical traits. The usefulness of multivariate methods for morphological evaluation of diversity has been demonstrated in many plant species (Sabaghnia et al. 2014; Nouraein et al. 2020). Such investigations provide relevant information which can be helpful to identify groups of genotypes that have good traits for different breeding purposes, cross-pollination, and study of the variation pattern. Therefore, this investigation was performed to detect the extent of genetic variation and diversity for accessions management in sumac populations in west and northwest of Iran and proper utilization in future breeding programs.

Materials And Methods

Accessions

This investigation was performed to study the morphological variations of 23 population of sumac from five different zones of the west and northwest Iran, including three west areas, Yasinabad, KaniBid, Kolseh in West Azarbaijan province and two northwest areas, AqBoraz and Tabestanaq, in East Azarbaijan province, as some of their geographical properties with some descriptive traits are given in Table 1. Identification of samples was performed by a botanist from the Research Institute of Forests and Rangelands, Tehran, Iran. The accessions of these areas were tagged, numbered and used for recording the morphological traits and then the full ripened fruits were harvested.

Traits

The accessions were measured in terms of 14 morphological traits via the visiting at several growth stages based on five replications, and each replication was the mean values of ten samples. Measured traits were LL, leaf length; LW, leaf width; TLL, terminal leaflet length; TLW, terminal leaflet width; LD, leaf density; LN, leaf number; BW, bunch width; BL, bunch length, WB, the weight of the bunch; FDB, fruit density per bunch; FL, fruit length; FW, fruit width; SL, seed length; and WTF, the weight of ten fruit. The quantitative traits like length and width were measured by digital caliper and weight was measured by digital lab scale while qualitative traits like fruit density per bunch were counted. Also, some traits such as the height of the first branch, stem diameter, fruit taste, and fruit color were measured, and explained descriptively (Table 1).

Analysis

The dataset was examined for normality by the Anderson and Darling method using Minitab 17 (2014) software and then was subjected to analysis of variance using the appropriate statistical model as a randomized complete

block design. The mean values of traits for accessions were compared using the least significant difference (LSD) test via SAS 9.1 (SAS, 2004). Phenotypic correlation coefficients between measured traits were calculated for all possible comparisons via the Pearson correlation coefficient. The means of 14 agronomic traits on 23 accessions were used for clustering analysis via squared Euclidean distance. Ward's method for clustering was used to classify the accessions via the SPSS 14.0 (SPSS, 2004). The overall patterns among accessions and traits were investigated via factor analysis based on correlation matrix to define the pattern of variations. The factor analysis reduces a large number of correlated traits to a much smaller number items, which called factors, and the obtained matrix rotated based on a varimax orthogonal rotation.

Results

Analysis of variance showed significant differences for all of the measured traits of 23 sumac accessions (Table 2). These results indicate a large variation among accessions, which reflects a good chance for genetic improvement of sumac. The phenotypic coefficient of variation (CV) ranged from 3.6% in seed length to 37.9% in the weight of the bunch (Table 2), which verifies the existence of considerable high variation among sumac accessions.

The mean leaf length was 17.7 cm and varied from 11.5 to 22.8 cm, which accessions YA3, YA5, and YA11 had high values for leaf length (Table 3). The mean leaf width was 8.6 cm and varied from 4.7 to 12.0 cm, whereas accessions YA3, YA5, and YA11 had high values for leaf width (Table 3). All of these superior accessions were belonging to Yasinabad in the west of Iran. Accession YA2 had the highest magnitudes of terminal leaflet length and terminal leaflet width while the mean values were 4.7 and 2.4 mm for TLL and TLW, respectively (Table 3). The mean bunch width was 26.6 mm and varied from 12.9 to 59.9 mm, whereas accession YA7 had high values for leaf length (Table 3). The superior accessions for all of the mentioned traits were from Yasinabad in the west of Iran. Accession YA1, YA3, YA4, YA5, YA9, YA10, KB1, KB4, and KO2 had the highest magnitudes of leaf density while YA7, YA11, and KB4 had the highest values of leaf number (Table 3). Accession YA7 had the highest values for bunch length, the weight of the bunch, fruit density per bunch, fruit length, fruit width and seed length while accession TA following YA6, AB1, and AB2 accessions had the highest values for the weight of ten fruit (Table 4). Thus, accession YA7 showed good performance for bunch and fruit related traits except yield. Generally, accessions YA6, AB1, and AB2 following to YA10, KB1, KB2, KB3, and AB3 had highest or relatively highest values for most of the measured morphological traits.

To determine in the most precise manner the interrelation of traits, correlation coefficients were established (Table 5) and showed there were not significant positive correlations between the weight of ten fruit and all of the measured traits while leaf length, leaf width, terminal leaflet length and terminal leaflet width indicated significant negative correlations with the weight of ten fruit. Similar results for traits associations were reported by Mohammadi-Alaghoz et al. (2021a) in study of morphological traits of sumac in five different populations in Iran. Seed length and fruit width had significant positive correlation with each other and with leaf number, bunch width, the weight of the bunch, fruit density per bunch and fruit length (Table 5). Fruit length indicated negative correlations with leaf length, leaf width and terminal leaflet width and positive correlations with leaf number, bunch width, the weight of the bunch, fruit density per bunch (Table 5). The weight of the bunch and fruit density per bunch had significant positive correlation with each other and with leaf length, leaf width, bunch width, bunch length (Table 5). Bunch length showed significant positive correlations with leaf length, leaf width, terminal leaflet length, terminal leaflet width, leaf density and bunch width (Table 5). Leaf length and leaf width traits had significant positive correlation with each other and with terminal leaflet length and terminal leaflet width (Table 5). Similarly, Fereidoonfar et al. (2018) found relatively similar results in investigation of morphological traits in some

sumac accessions in a central province of Iran. Considering the dendrogram (Fig. 1), the 23 sumac accessions are classified into four distinct clusters, which is the cutting point was determined via Wilks' lambda statistic of multivariate ANOVA (results are not shown). In Cluster-I, six accessions (AB2, AB4, AB5, KO1, TA, and YA8) were grouped while in Cluster-II, three accessions (KB1, YA9, and YA10) were grouped. In Cluster-IV, three accessions (YA1, YA7, and Y11) were grouped and other remined accessions were grouped as Cluster-III with eleven accessions (Fig. 1). The mean values of each cluster for measured traits are given in Table 6. The Cluster-I had lowest values for all traits expect the weight of ten fruit while The Cluster-IV had lowest values for all traits expect the weight of ten fruit (Table 6). Cluster-II and Cluster-III had high values for some traits, low values for other traits and moderate values for some other traits. It is obvious that accessions of Cluster-I and Cluster-IV are the distinct groups and maybe genetically different heterotic groups, which can be used in crossing planning. Also, accessions of Cluster-I can be considered for potential for the weight of ten fruit while the accessions of Cluster-IV can be considered for potential for the weight of the bunch. The accessions of Cluster-II and Cluster-III had high or average values for the most of the characters and can be used for improving these traits of sumac regarding targets of breeder. The accessions of Cluster-I can be regarded from good potential for the weight of ten fruit while the accessions of Cluster-IV can be regarded from good potential for the weight of the bunch. The accessions of Cluster-II and Cluster-III had high or average magnitudes for the most of the traits and can be applied for improving these traits in sumac considering breeders' goals.

Figure 2 indicated the distribution of the 23 areas of origin of the accessions along the first two axes of the factor analysis. The factor analysis explained 74.81% (39.71% and 35.10% by factor-1 and factor-2, respectively) of the total variation, which this percentage indicates the complexity of the associations among the accessions. The first factor axis separated accessions to two left and right groups and the second factor axis separated them to four groups; left-up group consist on KO1, KO2 and YA8; left-down group consist on AB1, AB2, AB3, AB4, AB5, KB4, and TA; right-down group consist on YA7 and YA11; and right-up group consist on the other remined accessions (Fig. 2). Some of the results can be verified from the cluster analysis (Fig. 1) but some are not consistent with the data and such mentioned discrepancies are expected because the first two factors usually explain less than 100% (in this case, about 75%) rather than 100% of the total variation.

To better grasp the association among the sumac traits they are graphically presented as a plot of Factor 1 versus Factor 2 (Fig. 3). In this figure, for each trait, a vector is dragged from the plot origin to simplify embodiment of the association between and among the traits by the cosine of the angle between vectors. Two traits are positive correlated if the angle between vectors is 0°, independent if the angle is 90° and negative correlated if the angle is 180°. Thus, regarding angle 0° between and among TLW, TLL, LL, and LW, they are positively correlated as well as between and among FDD, WB, and BW traits and between and among FL, FW and SL traits (Fig. 3). The association between FDD, WB, and BW traits with TLW, TLL, LL, and LW traits is independent due to the angle of 90° between their vectors. Also, interrelationship between WTF with TLW, TLL, LL, and LW traits is negative due to the angle of 1800° between their vectors (Fig. 3). Most of the above predictions on traits' association can be verified from the original data but some are not consistent with the data due to less explanations of two factors than the total variation. In this plot, traits with taller vectors are more reactionary, while traits with shorter vectors are less reactionary to the accessions; and those assessed at the plot origin are not reactionary at all, and most of our sumac traits had taller vectors and so they are more reactionary to the 23 sumac accessions.

Discussion

In this investigation, the analysis of variance and mean comparison via LSD test based on 14 morphological traits showed significant differences among the 23 sumac accessions and identified the most favorable accessions. Multivariate analysis using cluster analysis and factor analysis are revealed some internal relationships among traits and accessions. The cluster analysis separated the accessions into four distinct groups, which were in match with their properties. The obtained results are in agreement with the clustering result Fereidoonfar et al. (2018) and indicated, when the correct cluster algorithm is applied. Also, the clustering result according to measured traits is comparable to the other reports. Such diverse accessions might be useful in genetic improvement projects to retain and wide genetic variation in the new registered cultivars. So far, Iran is one of the production areas of sumac in the world and pervious investigations showed there was large genetic variation among Iranian accessions (Mohammadi-Alaghoz et al. 2021a). Similarly, our results demonstrated that there existed a notable genetic diversity among Iranian accessions in most traits.

Awareness of the trait genetic variation not only simplices breeding program but also aids to detect the requirements for future collections of germplasm. One of the main targets of this investigation was to furnish information, which is suitable for the examination of genetic variation and to assess association in the 23 sumac accessions. Our findings showed that there was high genetic variation in Iranian sumac accessions types and its magnitude could be useful for germplasm management and breeding programs. Finally, accessions YA6, AB1, and AB2 following to YA10, KB1, KB2, KB3, and AB3 had high magnitudes for most of the morphological traits of sumac.

The utilization of crosses between distant genetic materials may generate higher variation, better genetic recombination in next generations, and result in varieties with a wide genetic base (Morshedloo et al. 2018; Mohammadi-Alaghoz et al. 2021b).Three of five accessions of AqBoraz (AB2, AB4, and AB5) and Tabestanaq accession were from East Azarbaijan province and are grouped as Cluster-I and all of accessions from East Azarbaijan province expect KO1 and YA8 are grouped as clusters II, III and IV. In contrast, in plot of the first two factors, all accessions East Azarbaijan province are grouped in same section and so it seems that factor analysis can distinguish accessions and areas better than cluster analysis. Also, factor analysis grouped accessions of Yasinabad, KaniBid and Kolseh in distinct sections expect accessions of YA7, YA8, and YA11, which are grouped separately.

Factor analysis revealed association among TLW, TLL, LL, and LW as well as FDD, WB, and BW besides FL, FW, and SL traits with longer vectors, which demonstrated their high responsive properties and significance. In contrast we did not find any significant relation between main economic traits, WTF (the weight of ten fruit), with other measured traits. Yield as a complex quantitative trait has high interaction with other factors like environment and selection of accessions based on performance in single environment is not effective (Shrestha et al. 2012), thus it is essential to perform selection based on average performance in multiple environmental conditions. Therefore, it can be concluded that there is a requirement for molecular markers to complement investigation of morphological traits, which it would decrease the quantity of plant material as well as the costs of projects.

However, high magnitudes of genetic diversity were observed among sumac accessions, which can be used for genome mapping projects. However, the grouping discovered for these accessions, based on morphological will be a hopeful for sumac breeders to design crosses for superior traits by choosing accessions with proper variation. The current study verified the importance of morphological traits, to specify genetic variation among accessions with the aim to pick out various parents in new crossing systems. From germplasm maintenance aspect, management of the dispensation areas will be necessary to hold landraces *in situ* while *ex situ* tasks should also be

done to keep this valuable martial via seed production. It is obvious that using seeds is better than it would be the least harmful to the local landraces and would put the broad range of genetic diversity.

Conclusions

Our results on sumac accessions indicate a large variation of morphological traits, which provide a broad range for selection of the favorable accessions. Also, it processes facility to choose accessions with specific traits for domestication or genetic improvement. Sumac is used as a medicine and spice in Middle East areas and recently is introduced as a new medicinal spice in Europe, thus its breeding is essential. Most of the accessions indicated high potential in measured traits, accessions YA6, AB1 and AB2 following to YA10, KB1, KB2, KB3 and AB3 were superior in terms of the morphological traits and are worth germplasm for future breeding programs in sumac.

Declarations

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

Formal consent For this type of study formal consent is not required.

Human participants This paper does not contain any studies with human participants performed by any of the authors.

Informed consent Additional informed consent was obtained from all individual participants for whom identifying information is included in this paper.

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Tables

Table 1. Geographical properties and some characteristics of the sumac (*Rhus coriaria* L.) accessions, which were collected from different areas

Code	Region	Latitude	Longitude	Altitude	HFB†	ST‡	Fruit taste	Fruit color
YA1	Yasinabad	36°11'82"N	45°54'89"E	1263	13.0	24.97	Sour	Light brown
YA2	Yasinabad	36°11'78"N	45°54'93"E	1236	68.0	21.76	Sour	Light brown
YA3	Yasinabad	36°11'81"N	45°54'88"E	1314	68.2	21.76	Sour	Light brown
YA4	Yasinabad	36°11'76"N	45°55'09"E	1303	68.5	21.76	Sour	Light brown
YA5	Yasinabad	36°11'80"N	45°54'94"E	1267	68.3	21.76	Sour	Light brown
YA6	Yasinabad	36°11'82"N	45°55'06"E	1239	68.0	21.67	Sour	Light brown
YA7	Yasinabad	36°11'74"N	45°54'95"E	1269	35.0	12.67	Sour	Light brown
YA8	Yasinabad	36°11'85"N	45°54'90"E	1280	10.2	30.01	Sour	Light brown
YA9	Yasinabad	36°11'79"N	45°54'84"E	1247	24.0	45.64	Sour	Light brown
YA10	Yasinabad	36°11'25"N	45°54'49"E	1285	17.3	33.61	Sour	Light brown
YA11	Yasinabad	36°11'32"N	45°55'02"E	1279	18.0	34.00	Sour	Light brown
TA	Tabestanaq	39°00'33"N	47°25'19"E	1094	58.0	31.98	Slightly sour	Crimson
KB1	KaniBid	36°12'34"N	45°52'51"E	1415	51.3	10.42	Sour	Light brown
KB2	KaniBid	36°12'09"N	45°52'16"E	1431	23.0	15.14	Sour	Light brown
KB3	KaniBid	36°12'15"N	45°52'84"E	1424	21.4	8.68	Sour	Light brown
KB4	KaniBid	36°12'18"N	45°52'54"E	1389	21.0	12.63	Sour	Light brown
KO1	Kolseh	36°05'45"N	45°33'05"E	1291	30.0	8.60	Sour	Light brown
KO2	Kolseh	36°05'14"N	45°33'26"E	1331	37.0	11.23	Sour	Light brown
AB1	AqBoraz	39°00'39"N	47°23'34"E	1050	23.5	9.13	Slightly sour	Crimson
AB2	AqBoraz	39°01'23"N	47°39'10"E	1074	33.0	26.21	Slightly sour	Crimson
AB3	AqBoraz	39°01'10"N	47°39'56"E	1093	16.1	10.41	Slightly sour	Crimson
AB4	AqBoraz	39°01'00"N	47°39'04"E	1132	48.0	18.59	Slightly sour	Crimson
AB5	AqBoraz	39°01'26"N	47°39'74"E	1088	28.0	6.00	Slightly sour	Crimson

†HFB, height of the first branch

‡SD, stem diameter

Table 2. Analysis of variance for 14 measured traits in 23 sumac accessions

SOV†	DF‡	LL	LW	TLL	TLW	LD	LN	BW
Replication	4	3.51^{ns}	0.40^{ns}	0.214^{ns}	0.257^{ns}	2.75^{ns}	0.32^{ns}	6.5^{ns}
Genotype	22	56.74^{**}	19.57^{**}	7.602^{**}	2.345^{**}	14.90^{**}	18.19^{**}	488.7^{**}
Error	88	1.61	0.68	0.620	0.143	1.49	1.60	40.8
CV⸙		7.2	9.6	16.6	15.7	8.2	15.1	24.0
SOV	DF	BL	WB	FDB	FL	FW	SL	WTF
Replication	4	0.45^{ns}	3.06^{ns}	136.7^{ns}	0.027^{ns}	0.008^{ns}	0.018^{ns}	0.000591^{*}
Genotype	22	71.18^{**}	156.1^{**}	27280.1^{**}	2.910^{**}	2.115^{**}	1.389^{**}	0.005965^{**}
Error	88	3.47	8.55	829.4	0.041	0.039	0.017	0.000233
CV		21.7	37.9	22.3	4.0	4.8	3.6	6.8

Abbreviations: LL, leaf length; LW, leaf width; TLL, terminal leaflet length; TLW, terminal leaflet width; LD, leaf density; LN, leaf number; BW, bunch width; BL, bunch length, WB, the weight of the bunch; FDB, fruit density per bunch; FL, fruit length; FW, fruit width; SL, seed length; WTF, the weight of ten fruit.

†SOV, source of variation

‡DF, degrees of freedom

⸙CV, coefficient of variation

** and ns, significant at 0.01 probability level and non- significant

Table 3. Mean values comparison of seven morphological traits in 23 sumac accessions using Least Significant Difference (LSD) test

	LL	LW	TLL	TLW	LD	LN	BW
YA1	19.83	9.83	5.32	2.50	16.20	7.00	36.33
YA2	19.67	10.33	8.33	4.00	11.20	7.20	26.13
YA3	21.67	12.00	4.33	2.50	15.80	4.80	29.82
YA4	20.33	9.50	5.17	2.33	16.20	5.80	29.84
YA5	22.80	11.33	6.33	3.17	17.00	7.20	29.47
YA6	19.50	10.00	6.00	3.50	14.00	8.00	37.30
YA7	15.00	7.00	4.00	2.00	15.00	11.00	59.90
YA8	17.00	7.50	5.00	3.00	13.00	5.00	12.97
YA9	19.00	9.33	5.33	2.83	15.80	8.20	23.45
YA10	19.50	10.50	5.00	2.50	17.00	10.00	30.27
YA11	22.00	11.00	6.00	3.00	15.00	11.00	37.21
TA	12.00	4.67	3.17	1.17	12.60	9.20	20.57
KB1	19.33	9.83	5.00	2.83	16.20	9.00	31.34
KB2	18.50	8.75	5.00	2.50	15.00	7.00	23.00
KB3	19.50	9.25	5.00	2.50	15.00	6.80	23.52
KB4	17.00	8.00	4.00	2.00	17.00	12.00	22.98
KO1	18.50	9.10	4.70	2.40	15.40	7.40	19.38
KO2	19.40	9.10	4.40	2.14	16.40	9.40	20.50
AB1	16.47	7.20	3.20	1.60	15.20	9.80	26.03
AB2	13.00	6.17	3.50	1.83	14.00	9.00	17.84
AB3	13.17	6.40	3.07	1.33	13.20	9.80	19.35
AB4	11.50	6.25	3.15	1.60	14.00	7.80	19.49
AB5	12.00	5.50	4.00	2.00	11.00	10.00	15.78
LSD†	1.597	1.040	0.990	0.475	1.534	1.592	8.026

†LSD, Least Significant Difference

Abbreviations: LL, leaf length; LW, leaf width; TLL, terminal leaflet length; TLW, terminal leaflet width; LD, leaf density; LN, leaf number; BW, bunch width.

Table 4. Mean values comparison of the other seven morphological traits in 23 sumac accessions using Least Significant Difference (LSD) test

	BL	WB	FDB	FL	FW	SL	WTF
YA1	12.67	10.77	253.2	4.55	3.82	3.41	0.182
YA2	9.17	6.75	93.2	4.40	3.70	3.50	0.202
YA3	12.33	10.25	130.0	4.36	3.84	3.36	0.220
YA4	9.67	8.14	93.2	4.62	3.71	3.52	0.218
YA5	13.67	11.50	120.0	4.76	3.76	3.42	0.228
YA6	14.00	14.67	140.0	4.58	3.82	3.47	0.260
YA7	15.00	24.90	320.0	8.07	6.84	5.98	0.220
YA8	3.00	0.68	30.0	4.51	4.02	3.45	0.150
YA9	12.33	9.83	173.2	4.89	3.98	3.56	0.220
YA10	11.00	10.24	175.0	4.82	3.87	3.66	0.240
YA11	11.00	15.84	280.0	5.45	4.22	3.85	0.180
TA	5.83	3.23	56.8	5.67	4.64	3.98	0.320
KB1	10.33	9.50	160.0	5.18	3.80	3.86	0.232
KB2	9.00	5.25	112.2	5.01	4.46	3.81	0.238
KB3	7.00	6.52	120.0	4.93	4.16	3.55	0.230
KB4	7.00	6.61	140.0	4.72	3.84	3.51	0.220
KO1	6.60	3.02	73.0	4.47	3.80	3.38	0.218
KO2	7.40	4.77	114.0	4.74	3.63	3.47	0.180
AB1	5.97	5.27	128.4	5.05	4.13	3.83	0.268
AB2	3.17	2.11	53.2	5.51	4.38	3.68	0.260
AB3	4.50	3.50	90.0	5.25	3.93	3.85	0.238
AB4	4.50	2.86	70.0	5.58	4.14	3.66	0.226
AB5	2.50	1.09	40.0	5.23	3.86	3.50	0.220
LSD†	2.340	3.676	36.20	0.254	0.249	0.166	0.1446

†LSD, Least Significant Difference

Abbreviations: BL, bunch length, WB, the weight of the bunch; FDB, fruit density per bunch; FL, fruit length; FW, fruit width; SL, seed length; WTF, the weight of ten fruit.

Table 5. Pairwise correlation coefficients between 14 morphological traits of 23 sumac accessions

	LL	LW	TLL	TLW	LD	LN	BW	BL	WB	FDB	FL	FW	SL
LW	0.96												
TLL	0.72	0.72											
TLW	0.73	0.75	0.95										
LD	0.58	0.55	0.00	0.03									
LN	-0.35	-0.35	-0.32	-0.38	0.04								
BW	0.33	0.35	0.24	0.22	0.32	0.22							
BL	0.68	0.71	0.51	0.51	0.52	-0.06	0.82						
WB	0.44	0.46	0.32	0.33	0.38	0.23	0.97	0.88					
FDB	0.40	0.40	0.21	0.19	0.46	0.36	0.87	0.75	0.89				
FL	-0.48	-0.47	-0.39	-0.41	-0.12	0.51	0.55	0.11	0.48	0.44			
FW	-0.34	-0.37	-0.29	-0.29	-0.09	0.32	0.60	0.21	0.54	0.47	0.93		
SL	-0.30	-0.31	-0.25	-0.27	-0.04	0.44	0.68	0.27	0.61	0.55	0.95	0.95	
WTF	-0.41	-0.40	-0.41	-0.45	-0.12	0.24	-0.03	-0.08	-0.09	-0.22	0.22	0.18	0.15

Critical values of correlation $P < 0.05$ and $P < 0.01$ (df = 21) are 0.40 and 0.51, respectively

Abbreviations: LL, leaf length; LW, leaf width; TLL, terminal leaflet length; TLW, terminal leaflet width; LD, leaf density; LN, leaf number; BW, bunch width; BL, bunch length, WB, the weight of the bunch; FDB, fruit density per bunch; FL, fruit length; FW, fruit width; SL, seed length; WTF, the weight of ten fruit.

Table 6. The mean values of the measured traits for each of four identified clusters

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV
LL	14.00	19.28	18.91	18.94
LW	6.53	9.89	9.26	9.28
TLL	3.92	5.11	4.98	5.11
TLW	2.00	2.72	2.51	2.50
LD	13.33	16.33	15.09	15.40
LN	8.07	9.07	7.98	9.67
BW	17.67	28.35	26.18	44.48
BL	4.27	11.22	9.06	12.89
WB	2.17	9.86	7.57	17.17
FDB	53.83	169.40	116.45	284.40
FL	5.16	4.96	4.77	6.02
FW	4.14	3.88	3.91	4.96
SL	3.61	3.69	3.57	4.41
WTF	0.25	0.23	0.23	0.19

Abbreviations: LL, leaf length; LW, leaf width; TLL, terminal leaflet length; TLW, terminal leaflet width; LD, leaf density; LN, leaf number; BW, bunch width; BL, bunch length, WB, the weight of the bunch; FDB, fruit density per bunch; FL, fruit length; FW, fruit width; SL, seed length; WTF, the weight of ten fruit.
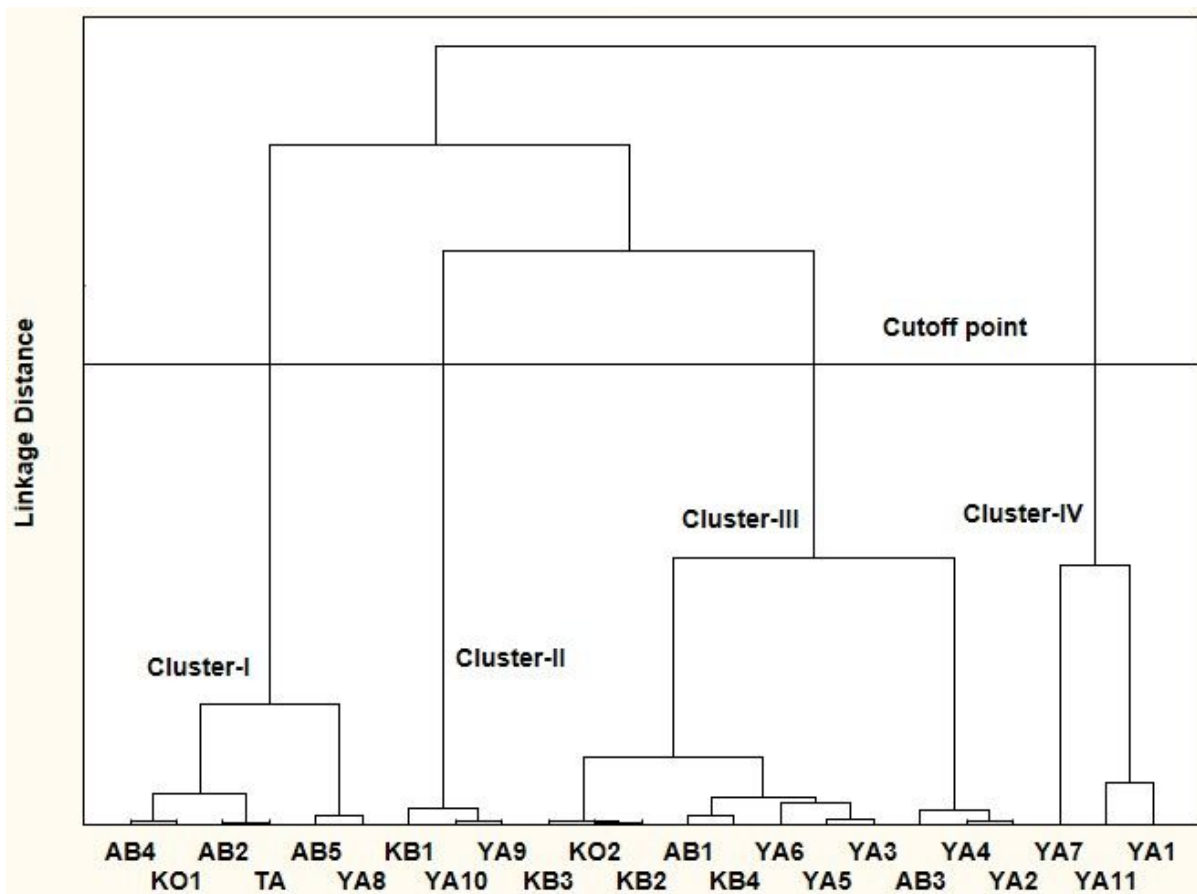
Figures

Figure 1

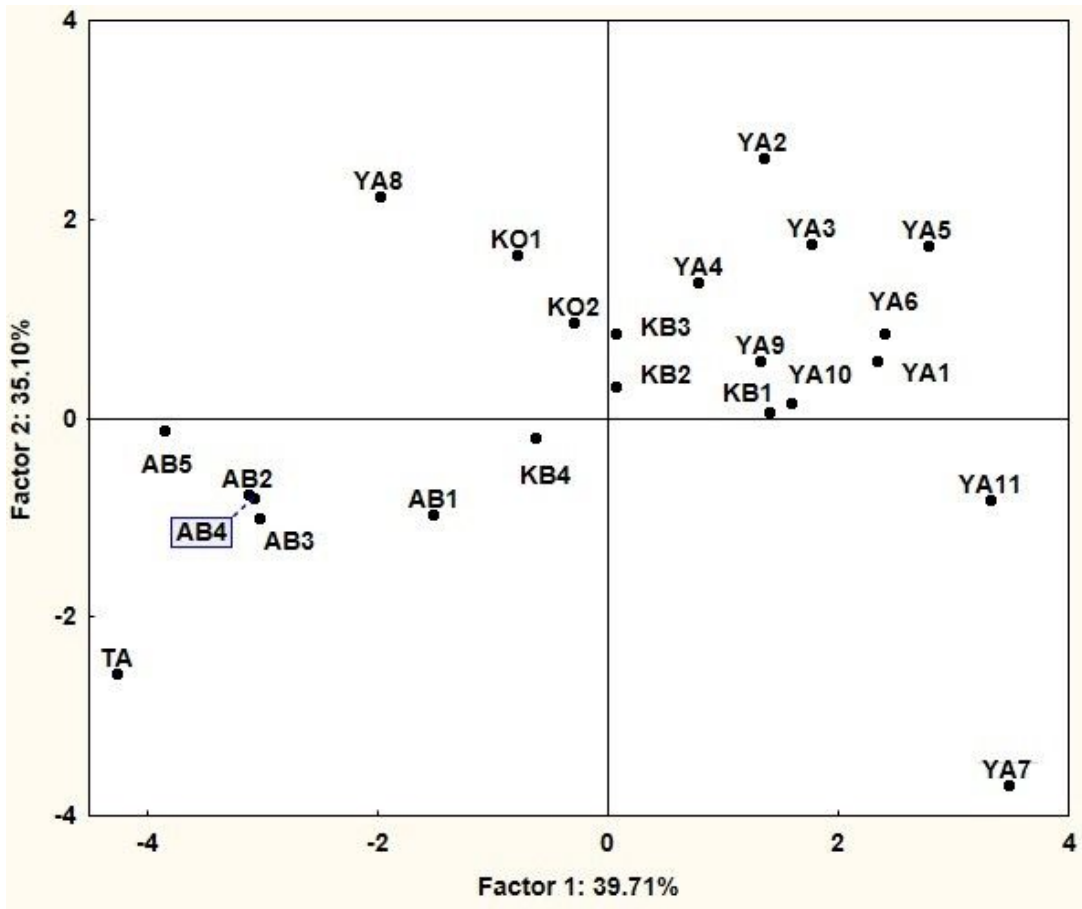Dendrogram for clustering 23 sumac accessions on the basis of morphological traits

Figure 2

Plot of two first factor analysis for 23 sumac accessions based on 14 morphological traits. For abbreviation of traits refer to Table 1.
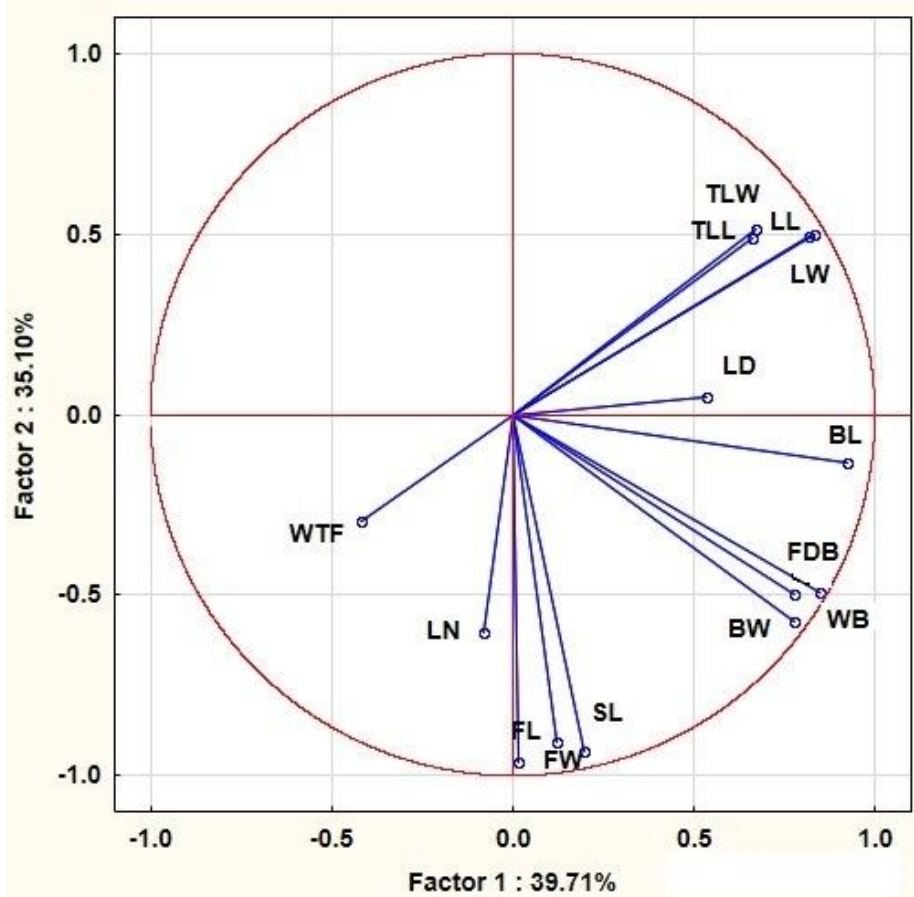
Figure 3

Plot of two first factor analysis for 14 morphological traits, which were measured on 23 sumac accessions. Abbreviations: LL, leaf length; LW, leaf width; TLL, terminal leaflet length; TLW, terminal leaflet width; LD, leaf density; LN, leaf number; BW, bunch width; BL, bunch length, WB, the weight of the bunch; FDB, fruit density per bunch; FL, fruit length; FW, fruit width; SL, seed length; WTF, the weight of ten fruit.