

**Taxonomical study of section *Caninae* (*Rosa*) and their hybrids in Iran**

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**Abstract**

The genus *Rosa* has a wide variety in Iran and although some natural hybrids have been found in different regions of the country, but no cultivars have been established so far. In order to optimize use of genetic resources in the country and to create varieties with desirable traits, inter-species relationships and identification of diversity, 45 populations from seven species in section *Caninae* collected from 13 provinces of Iran, were studied. To group the species, 61 qualitative and quantitative characters using the most suitable method of cluster analysis (WARD) were used and their ordination diagram based on the most variable factors for each species and sections were drawn. Cluster analysis of quantitative and qualitative characters showed significant differences between characters. The results of classification confirmed previous taxonomy grouping. Factor analysis of *R. elymatica* populations showed that the hair on pedicels, sepal form, hip length, prickle base and prickle form possessed the highest correlation. Two main groups were formed in *R. boissieri* based on ecological difference between them. Cluster analysis of *R. orientalis* also showed two main groups. Moreover, the results indicated that some populations of *R. canina* such as Polour, Karand, and Siahbishe (Iran), that showed the most variations in qualitative and quantitative characters, could be used to produce interspecific hybrids. Overall, the results of this study revealed that, *R. canina* and *R. pulverulenta* showed the highest variety in the section *Caninae* that is due to the combination of some unusual features in section.

**Keywords:** Cluster analysis, factor analysis, hybrid, morphologic characters, wild roses

**بررسی تاکسونومیک بخش *Caninae* (رز) و هیبریدهای آن در ایران**

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**خلاصه**

جنس رز در ایران بسیار متنوع است و هیبریدهای طبیعی آن شناسایی شده‌اند اما تا کنون هیچ رقمی از آن در کشور تولید نشده است. به منظور استفاده بهینه از منابع ژنتیکی در کشور و ایجاد ارقام با صفات مطلوب، تشخیص روابط گونه‌ها و شناسایی هر گونه تنوع در میان گونه‌های مختلف بخش *Caninae* جنس مذکور، ابتدا جمع‌آوری و مطالعه ۴۵ جمعیت از هفت گونه متعلق به این جنس در ۱۳ استان ایران انجام گرفت. به منظور گروه‌بندی جمعیت‌ها از روش آماری WARD استفاده شد و نمودار رسته‌بندی آن‌ها براساس متغیرترین فاکتورها برای تمامی گونه‌ها و بخش‌ها ترسیم شد. آنالیز خوشه‌بندی صفات کمی و کیفی نشان داد، تفاوت معنی‌داری بین خصوصیات مورد مطالعه وجود دارد. نتایج خوشه‌بندی گونه‌های بخش *Caninae* طبقه‌بندی‌های قبلی را تایید کرد. همچنین، نتایج آنالیز فاکتور جمعیت‌های *R. elymatica* نشان داد که وجود مو روی دمگل، فرم کاسبرگ، طول هیپانتیوم، قاعده و فرم دم‌برگ بیشترین ارتباط را با یکدیگر نشان می‌دهند. دو گروه اصلی در *R. boissieri* به دلیل اختلاف شرایط اکولوژیک بین جمعیت‌ها مشخص شده است. آنالیز خوشه‌ای دو گروه اصلی را در جمعیت‌های جنس *R. orientalis* نشان داد. برخی از صفات کمی و کیفی توانست جمعیت‌های مختلف گونه *R. canina* را از هم جدا کند، اما برخی مناطق مانند پلور، کوند و سیاه بیشه بیشترین تنوع را برای ایجاد هیبریدهای بین‌گونه‌ای نشان دادند. در نهایت، نتایج بررسی گونه‌های بخش *Caninae* نشان داد که *R. canina* و *R. pulverulenta* بیشترین تنوع را داشتند که این مسئله می‌تواند به دلیل ساختار کروموزومی ویژه در *Caninae* باشد.

**واژه‌های کلیدی:** آنالیز خوشه‌بندی، آنالیز فاکتور، خصوصیات مورفولوژیک، دورگه، رزهای وحشی

## Introduction

There are more than 120 species in genus *Rosa* harboring different growth forms, from semi-evergreen to deciduous. Most of roses have different growth habitat in Asia, east of Africa, North America and Europe (Rehder 1940, Gu & Robertson 2003). A quarter of rose species host in Europe and North America, although, approximately half of them appear in Asia. Interestingly, Fouge`re-Danezan *et al.* (2015) found that based on phylogeny and biogeography of wild roses, most of survived American species are the results of a later recolonization from Asia. There are different rose classifications because of wide variation in phenotypic characters. Wissemann's (2003) divided the genus *Rosa* into four subgenera. There are many researches about subgenus *Rosa*, harbors about 95% of all species distributed into ten sections (Rehder 1940, Klasterky 1968, Gudin 2000). Dog-roses (section *Caninae*) are conventionally divided into six subsections; the three larger of these (*Caninae*, *Rubigineae*, and *Vestitae*) are unambiguously differentiated and each contains several less clear-cut microspecies (Henker 2000) but all of rose species in Iran belong to *Caninae* subsection.

The distribution of *Rosa* species in Iran was reported in Flora of Pakistan (Ali & Qaiser 2009), Flora Iranica (Zielinski 1982), Flora of Turkey (Davis 1985), and the latest Flora of Iran (Khatamsaz 1992). In flora of Iran, *Rosa* genus has 14 species through two subgenera. They were included *R. persica* Michx. ex Juss as an only member of *Hulthemia* subgenus. The other species (subgenus *Rosa*) were grouped in three sections, namely, *Pimpinellifoliae* (*hemisphaerica* Herrmann, *R. foetida* Herrmann, and *Pimpinellifolia* L.), *Cinnamomeae* (*R. beggeriana* Schrenk, and *R. webbiana* Wall.), *Caninae* subsection *Caninae* (*R. elymaitica* Boiss & Hausskn, *R. villosa* L., *R. orientalis* Dupont, *R. pulverulenta* M.B., *R. canina* L., *R. iberica* Stev., and *R. boissieri* Crépín.), and *Synstylae* (*R. moschata* Herrmann) as well as eight natural hybrids have been reported from all over the country. Most of the species are concentrated in the northwest of Iran. Moreover,

Arjmandi *et al.* (2015) reported a new species for the flora of Iran, *Rosa freitagii* Ziel. of *Cinnamomeae* section from South Khorasan province, and Sharghi *et al.* (2014) introduced *Rosa kokanica* of *foetideae* section from Binalood mountains.

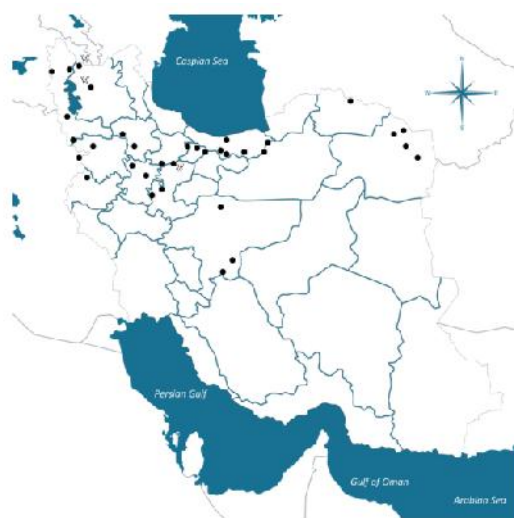
In our previous investigation, some populations of two species of section *Caninae*; and *R. foetida* Herrmann. and *R. hemisphaerica* Herrmann., belonging to the section *Pimpinellifoliae* were studied in order to show inter and intra-section variation (Koobaz *et al.* 2008). In this manner, taxonomical study of *Pimpinellifoliae* was done and introduced a new species from Iran named *Rosa abrica* (Koobaz *et al.* 2010).

Genetic variation among nine wild rose species from different regions of Iran were analyzed by Samiei *et al.* (2010) and SSR markers showed good aggregation with the traditional botanical classification and horticultural Literature. Section *Caninae* evolved by multiple hybridization events (Wissemann 1999, 2000, Ritz *et al.* 2005). Dog-roses are tetra- to hexaploid but pentaploid cytotypes are most frequent (Pachl 2011). They originated by allopolyploidy and are characterized by unbalanced meiosis producing polyploid egg cells (usually 4x) and haploid sperm cells (1x). Ploidy level estimation of some species in the research by flow cytometry could differentiate some of species but, karyotype formulae for all the species were 7n and could not properly display the diversity among the species, which in part could be attributed to their small symmetric chromosomes (Jowkar *et al.* 2008).

Morphological and AFLP-based differentiation within the taxonomical complex section *Caninae* (subgenus *Rosa*) showed that, the taxa and subsections of the dog-roses are distinguishable by a set of well-defined morphological characters. However, the large and consistent overlap of the morphologically defined groups indicates the occurrence of inter subsectional and specific hybridization that results in a combination of intermediate, transgressive and species-specific characters (De cock *et al.* 2008). Morphological traits are

affected by environmental factors, it is assumed that, the adaptation of intra-and intra-species morphological diversity to genetic studies such as number of chromosomes, genomic size, karyological traits, and molecular analyzes can be made. There were not complete reports on the biosystematics of section

*Caninae* in Iran and their interspecies hybrids. Therefore, the aim of present study is to investigate the morphological diversity and interbred wild roses of section *Caninae* in Iran to help us in reaching new and important genetic reservoirs that contain desirable traits in breeding roses.



**Fig. 1.** Geographical distribution of *Rosa* species collected from different provinces of Iran.

### Materials and Methods

In this study, 45 populations of seven *Rosa* species (including *R. elyptica* Boiss & Hausskn, *R. villosa* subspecies *villosa* L., *R. orientalis* Dupont, *R. pulverulenta* M.B., *R. canina* L., *R. iberica* Stev., and *R. boissieri* Crépin.) and some hybrids of different *Caninae* species were labeled and collected in two seasons to get flower and mature hips during 2008–12 from 13 provinces of Iran along with their morphological studies (Fig. 1). Details of the localities and codes are presented in table 1. For each individual, at least 20 measurements and for each population 3–6 individuals were studied. Voucher specimens were identified by a botanist (Khatamsaz 1992) and deposited in the Herbarium of the Research Institute of Forests and Rangelands (TARI). Based on the Flora of Iran (Khatamsaz *l.c.*), and our own field studies, 61 quantitative and qualitative morphological characters were selected (Table 2).

The characters were used for phonetic analysis and binary/multistate codes. Variables were standardized (mean=0, variance=1) for multivariate statistical analyses (Chatfield *et al.* 1995, Sheidai *et al.* 2010). Cluster analysis was used in order to identify species with morphological similarities using UPGMA (un-weighted paired group mean average) and WARD (minimum variance spherical clusters) (Everitt 1986). In this manner, ordination based on principal component analysis (PCA) was also performed (Sneath & Sokal 1973) and squared Euclidean distance was used as dissimilarity coefficient in cluster analysis of morphological data. Factor analysis based on principal components analysis (PCA) to determine the most variable morphological characters among the species and populations was performed. Invariable characters were omitted before factor analysis. Multivariate statistical analyses were done by IBM SPSS Ver. 22 (2013) software.

**Table 1.** The *Rosa* species along with its related data in Iran

Taxa	Code	Altitude (m)	Locality (province)	Collector	Voucher specimen
<i>R. elimatica</i>	Sb	1730	Mazandaran	Koobaz, Khatamsaz, Hosseini	102912
	Kar	1346	Kordestan	Koobaz, Khatamsaz, Hosseini	102913
	Ar	1918	Markazi	Koobaz, Khatamsaz, Hosseini	102909
	Ga	1749	Hamedan	Koobaz, Khatamsaz, Hosseini	102910
	Po	2160	Mazandaran	Koobaz, Khatamsaz, Hosseini	102911
	Khan	2300	Markazi	Koobaz, Khatamsaz, Hosseini	102908
<i>R. villosa</i>				Koobaz, Khatamsaz & Zarshenas	102937
	O	1620	W Azarbaijan Mazandaran	Koobaz, Khatamsaz, Hosseini	102942
	Ch	2026	Mazandaran	Koobaz, Khatamsaz	102943
	Too	2155	Mazandaran Esfahan		
<i>R. canina</i>	O	1400	W Azarbaijan	Koobaz, Khatamsaz, Hosseini	102900
	M	1300	Khorasan	Koobaz, Khatamsaz	102898
	Ga	1749	Hamedan	Koobaz, Khatamsaz, Hosseini	102897
	She	2190	Mazandaran	Koobaz, Khatamsaz, Hosseini	102901
	D	1800	Tehran	Koobaz, Khatamsaz, Hosseini	102954
	Sb	1600	Mazandaran	Koobaz, Khatamsaz, Hosseini	102955
	Se	1700	Semnan	Koobaz, Khatamsaz, Hosseini	102906
	Ar	1918	Markazi	Koobaz, Khatamsaz, Hosseini	102904
	Kar	1170	Kordestan	Koobaz, Khatamsaz, Hosseini	102956
	Ta	1860	E Azarbaijan	Koobaz, Khatamsaz, Zarshenas	102899
	Ab	1870	Zanjan	Koobaz, Khatamsaz, Hosseini	102957
	Sn	1373	Kordestan	Koobaz, Khatamsaz, Hosseini	102958
<i>R. iberica</i>	O	1620	W Azarbaijan	Koobaz, Khatamsaz, Zarshenas	102915
	Se	1750	Semnan	Koobaz, Khatamsaz, Hosseini	102919
	Ch	2100	Mazandaran	Koobaz, Khatamsaz, Hosseini	102914
	She	2190	Mazandaran	Koobaz, Khatamsaz, Hosseini	102959
	Sb	1680	Mazandaran	Koobaz, Khatamsaz, Hosseini	102917
	Ta	1240	E Azarbaijan	Koobaz, Khatamsaz, Zarshenas	102918
	Po	1800	Mazandaran	Koobaz, Khatamsaz, Hosseini	102916
<i>R. boissieri</i>	M	1300	Khorasan R.	Koobaz, Khatamsaz	102988
	SB	1800	Mazandaran	Koobaz, Khatamsaz, Hosseini	102989
	TA	1240	E Azarbaijan	Koobaz, Khatamsaz, Hosseini	102938
	She	2190	Mazandaran	Koobaz, Khatamsaz, Hosseini	102941

**Table 2.** Morphological characters and their coding key

Character code	Character	Coding key for the character	Character code	Character	Coding key for the character
	<b>Qualitative characters (1-52)</b>		31	Prickles on hypanthium	(0) prickly (1) glabrous
1	Form of shrub	(0) erect (1) patent (2) repent (3) inclining	32	Form of sepal	(0) entire (1) dentate (2) dentate rarely entire (3) lanceolate
2	Color of branch	(0) reddish yellow (1) reddish green (2) red (3) brown (4) green (5) brownish green	33	Hair on sepal	(0) hairy (1) glabrous
3	Hair on prickle	(0) hairy (1) glabrous	34	Prickles on sepal	(0) prickly (1) glabrous

Table 2 (contd)

4	Settlement of prickles on branch	(0) equal (1) unequal	35	Glands on sepal	(0) glandular (1) glabrous
5	Form of prickles	(0) regular (1) irregular	36	Hair on stigma	(0) hairy (1) glabrous
6	Shape of prickles	0) erect or curved (1) curved or thistle (2) erect (3) thistle	37	Sepal permanency	(0) deciduous (1) not deciduous (2) deciduous or not deciduous
7	Base of prickle	(0) wide (1) narrow (2) wide or narrow	38	State of sepal on hypanthium	(0) erect (1) recurved (2) erect or recurved (3) leveler
8	Form of surplus to stipule	(0) with surplus (1) without surplus (2) without stipule	39	State of stamen	(0) separate (1) attached
9	Surplus of stipule	(0) surpluser (1) glabrous	40	Hair on style	(0) hairy or glabrous (1) hairy (2) glabrous
10	Base of leaflet	(0) roundish (1) cuneate (2) roundish or cuneate	41	Edge of sepal	(0) entire (1) has lobe (2) lanceolate
11	Stipule	(0) stipular (1) without stipule	42	Color of hips	(0) Brownish purple (1) red (2) blackish purple (3) reddish orange (4) brownish orange (5) yellow (6) brownish red
12	Edge of stipule	(0) hairy and glandular (1) glabrous	43	Prickles on hips	(0) prickly (1) glabrous
13	Hair on adaxial surface of leaflet	(0) hairy or glabrous (1) glabrous (2) hairy	44	Hair on hips	(0) hairy (1) glabrous
14	Hair on abaxial surface of leaflet	(0) hairy or glabrous (1) glabrous (2) hairy	45	Glands on hips	(0) glandular (1) glabrous
15	Glands on adaxial surface of leaflet	(0) glandular or glabrous (1) glabrous (2) glandular	46	Hip shape	(0) roundish (1) roundish or ovate (2) apiculate
16	Glands abaxial surface of leaflet	(0) glandular or glabrous (1) glabrous (2) glandular	47	Petal color	(0) yellow (1) white (2) pink or white
17	Leaflet shape	(0) obovate or elliptic (1) elliptic or ovate (2) ovate or orbicular (3) elliptic	48	Petal shape	(0) emarginated (1) truncate

Table 2 (contd)

18	Leaflet tip	(0) acute or obtuse (1) obtuse or truncate (2) obtuse or round (3) acute or apiculate	49	Color leaf	(0) green (1) dark green (2) green attend to blue
19	Leaflet margin	(0) serrate or double-serrate (1) serrate (2) double-serrate	50	State of achenes in hypanthium	(0) center (1) attached to wall
20	Number of leaflets	(0) 5 (1) 7 (2) 5 or 7	51	State of leaflet base	(0) symmetric (1) asymmetric (2) symmetric or asymmetric
21	Prickles on petiole	(0) prickly (1) glabrous	52	Leaflet symmetry	(0) symmetric (1) alternative (2) symmetric or alternative
22	Hair on petiole	(0) hairy (1) glabrous	<b>Quantitative characters (53–61)</b>		
23	Glands on petiole	(0) glandular (1) glabrous	53	Length of shrub	
24	Form of inflorescence	(0) singular (1) single or double (2) panicle (3) singular, triplet or fivelet (4) corymb or raceme (5) singular or raceme	54	Leaflet length	
25	Glands on pedicel	(0) glandular (1) glabrous	55	Leaflet width	
26	Hair on pedicel	(0) hairy (1) glabrous	56	Pedicel length	
27	Status of prickle on each other	(0) attached (1) separate	57	Hip length	
28	Involucres	(0) without involucres (1) with involucres	58	Hip width	
29	Hair on hypanthium	(0) hairy (1) glabrous	59	Flower diameter	
30	Glands on hypanthium	(0) glandular (1) glabrous	60	Petal length	
			61	Petal width	

## Results and Discussion

The section harbors the highest number of species. Cluster analysis and ordination based on PCA factors of morphological traits on all seven species in the section, as the biggest section of *Rosa* genus, were performed. The results of each species were shown separately.

### - *R. elymatica*

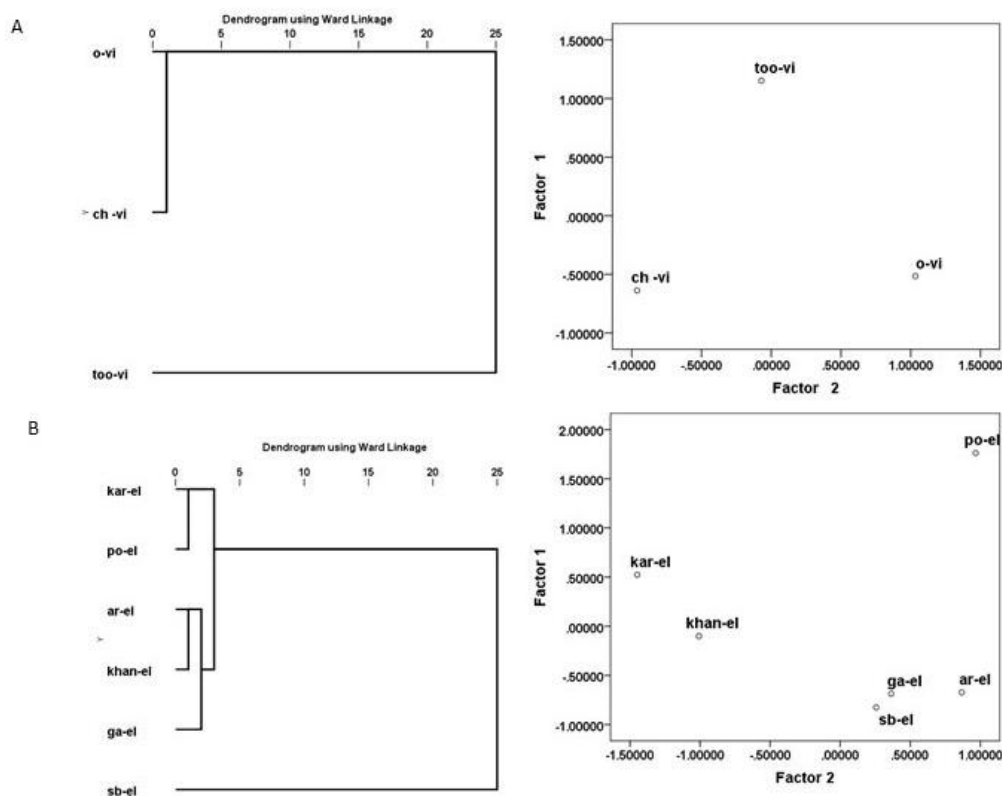
Morphological traits of six populations of *R. elymatica* were analyzed by cluster analysis and ordination based on PCA factors (Fig. 2a). Populations of Siahbishe, Arak and Hamedan showed similarities and formed the first group but samples collected from Karand and Khansar were distinctly separated from first group.

The Polour population was interestingly separated. Factor analysis of morphological characters revealed that, the first four factors embraced about 89% of the total variations, characters like hair on pedicels, sepal form, hip length, base of prickle, hair on pedicel, prickle form, leaflet form, color of branch, and sepal permanency possessed the highest correlation ( $>0.70\%$ ) (Fig. 2a).

#### - *R. villosa*

Three populations of *R. villosa* from Orumieh, Chalooos, and Tooyserkan were analyzed by cluster

analysis and the third group separated from the others due to very different ecologic situations (Fig. 2b). Factor analysis of morphological characters revealed that, the first two factors embraced about 100% of the total variations, in which the first one embraced 60% of total variations such as color of branch, form of prickles, base of prickle, form of surplus to stipule, leaflet margin, gland on pedicel, hair on sepal and petal width showed significant correlation. The results of ordination based on PCA factors confirmed cluster analysis (Fig. 2b).



**Fig. 2.** Cluster analysis and PCA of *Rosa elymatica* and *R. villosa* on morphological characters (population codes as in table 1).

#### - *R. boissieri*

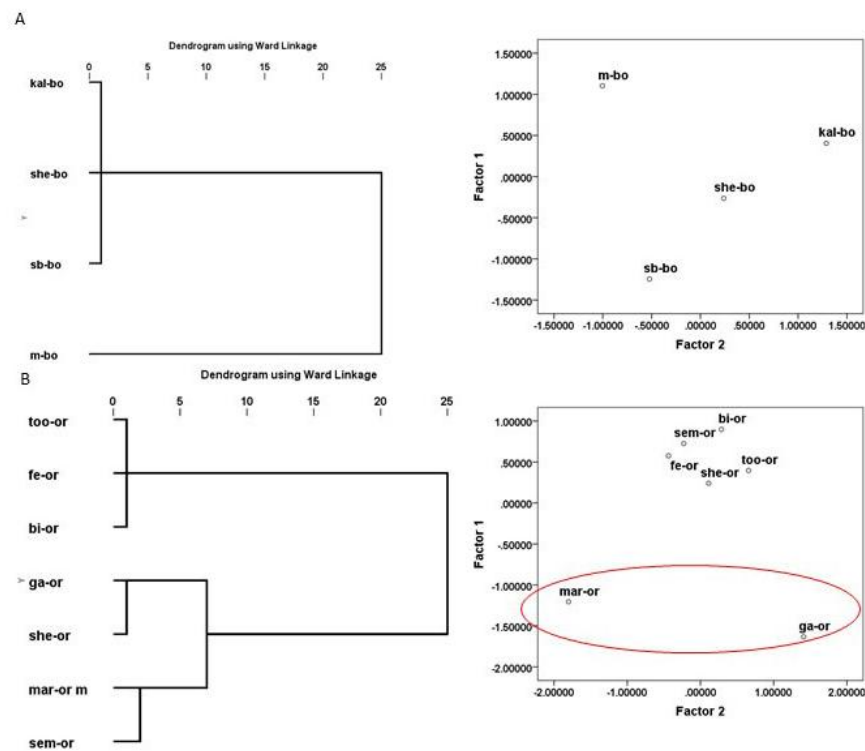
Cluster analysis and ordination based on PCA factors of morphological traits on four populations of *R. boissieri* were done (Fig. 3a). Two main clusters/groups were formed in *R. boissieri*; samples collected from Kalibar, Shahrestanak and Siahbishe (kal, sh and sb) formed the first group while samples from Mashhad (m) formed the second group. Factor analysis revealed that, the first three factors embraced 100% of

total variance. Characters such as form of shrub, color of branch, hair on abaxial leaf, leaflet form, leaflet margin, leaflet length and width, petal length and width possessed the highest correlation ( $>70\%$ ). Therefore, these characters are considered the most variable morphological characters amongst them. There is significant ecological difference between these two population groups and it could be a reason that quantitative traits separate them.

### - *R. orientalis*

Figure 3 illustrates that, cluster analysis created two main groups in *R. orientalis*. The first group contained four populations with higher similarity, but samples from Marivan and Hamedan formed the second group. The second group was distributed in lower altitude compared to the populations of the first group. The red ring in PCA analysis separated first group of cluster (Fig. 3b). Altitude is a well-known severity gradient that shifts along elevation. For instance, decreases of specific leaf area with elevation (Fajardo *et al.* 2011, Scheepens *et al.* 2010) and differences in

growth were shown within species. It has been suggested to explain the functional trait variation at diverse biological levels (Milla *et al.* 2009) but there are some problems to scale up it (Ackerly & Cornwell 2007, Albert *et al.* 2012). Factor analysis of morphological characters revealed that, the first four factors embraced about 80% of the total variations, in which color of branch, leaflet form, hair on pedicel, glands on hypanthium, color of petal, leaflet width, gland on pedicel, sepal permanency, petal width and pedicel length possessed the highest correlation (>0.70%).



**Fig. 3.** Cluster analysis and PCA of *Rosa boissieri* and *R. orientalis* based on morphological characters (population codes as in table 1).

### - *R. pulverulenta*

About 66 quantitative and qualitative morphological characters of *R. pulverulenta* harboring six populations from Shahrestanak, Tabriz, Semnan, Afjeh, Orumieh and Polur were analyzed by cluster analysis and ordination based on PCA factors (Fig. 4a). The four first populations were formed as first group and

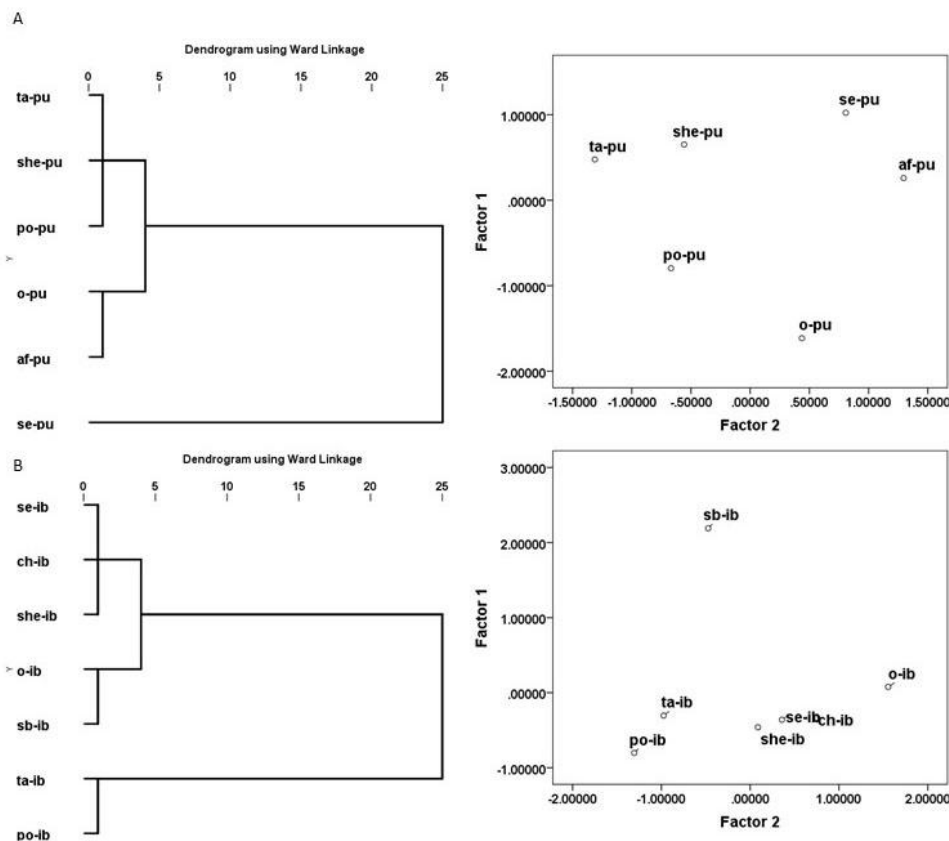
last two populations separated as the second group. Factor analysis of morphological characters revealed that, the first four factors embraced about 92% of the total variations, in which form of prickles, hair on adaxial leaflet, Petal shape, base of prickle, flower diameter, petal length, and petal width possessed the highest correlation (>0.70%).



**- *R. iberica***

Cluster analysis and ordination of *R. iberica* populations produced similar results (Fig. 4b). There were two groups in cluster. The second group harbored distinctly separated population (Siabhishe). Factor analysis of morphological characters revealed that, the first three factors embraced about 73% of the total variations, in which gland on color of branch, leaflet form, State of leaflet length achenes in hypanthium, leaflet shape flower diameter, petal length and petal

width, prickle form, base of leaflet and form of inflorescence possessed the highest correlation (>0.70%). Therefore, these characters were considered the most variable morphological characters among *R. iberica* populations. There are different reasons for variation such as trait convergence between species at lower elevations, where water shortage may have a stronger environmental filtering effect than colder temperatures at higher altitudes (Pescador *et al.* 2015).



**Fig. 4.** Cluster analysis and PCA of *Rosa pulverulenta* (A) and *R. iberica* (B) based on morphological characters (population codes as in table 1).

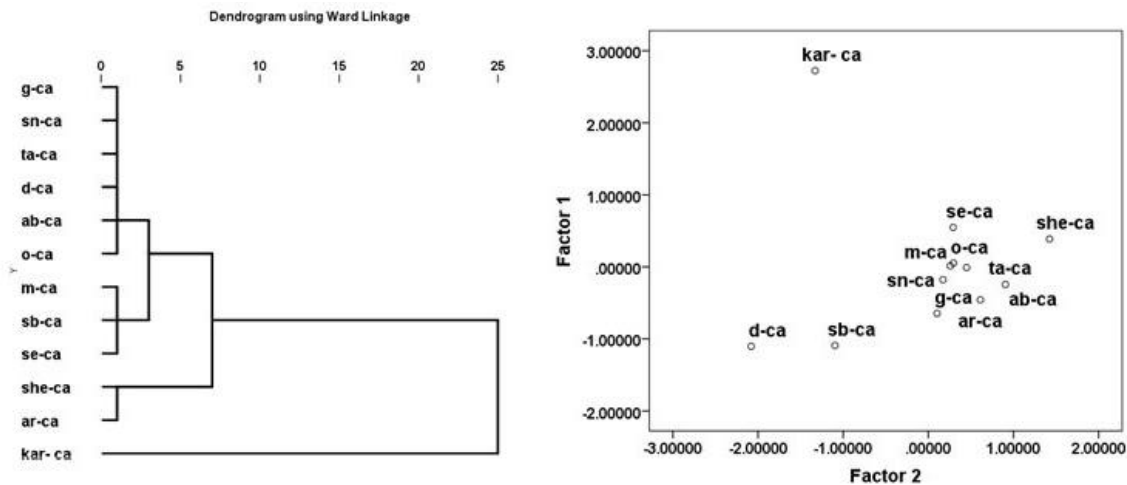
**- *R. canina***

Morphological characters of 12 *R. canina* populations, the last species of section *Caninae*, were analyzed by Cluster analysis and ordination method. As shown in figure 11, samples collected from Siabhishe and Damavand formed the second subgroup and the other populations settled in the first subgroup. Samples from Karand were distinctly separated in the second group far from the other groups in ordination based PCA analysis

(Fig. 5). There was great dissimilarity between different populations due to different time of pollination of plants within this species. The variation in morphological studies has also shown in other experiments (De cock *et al.* 2008). Qualitative characters such as number of leaflet, sepal form, gland on hypanthium, form of inflorescence, leaflet form, sepal in petiole and quantitative characters including leaflet width, petal length and petal width could differentiate some

populations of *R. canina*. Some populations such as Polour, Karand and Siahbishe have interpopulation

variation, thus are suitable candidates to produce interspecific hybrids.

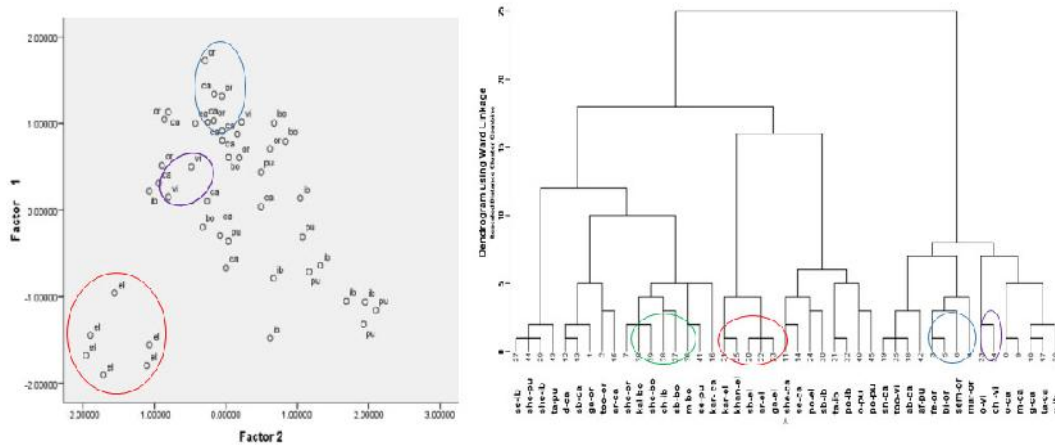


**Fig. 5.** Cluster analysis and PCA of *Rosa canina* based on morphological characters (population codes as in table 1).

#### - Section *Caninae*

Cluster analysis of all section *Caninae* showed an extensive variance between seven Iranian species of the section. There are two major cluster; populations of *R. boissieri* and *R. elymatica* separated from the others in the first cluster. The second cluster contained some sub-clusters that separated most of the populations of *R. orientalis* and *R. villosa*. Population of *R. canina*, *R. iberica*, and *R. pulverulenta* distributed in both of main groups and multivariate statistical data could not segregate them. Polyploidy and cross pollination resulted different hybrids between some species of section *Caninae* as one of the extensive variation. The results of ordination confirmed cluster analysis data (Fig. 6). Factor analysis of morphological characters revealed that, the first seven factors embraced about 60% of the total variations, in which gland on adaxial leaflet, form of sepal, hair on the adaxial leaflet, and pedicel form could separate *R. boissieri*, *R. elymatica*, *R. orientalis*, and *R. villosa*. Similarity between *R. boissieri*, *R. elymatica*, *R. orientalis*, and *R. villosa* was also considered by Flora of Iran (Khatamsaz 1992). Morphometric data showed

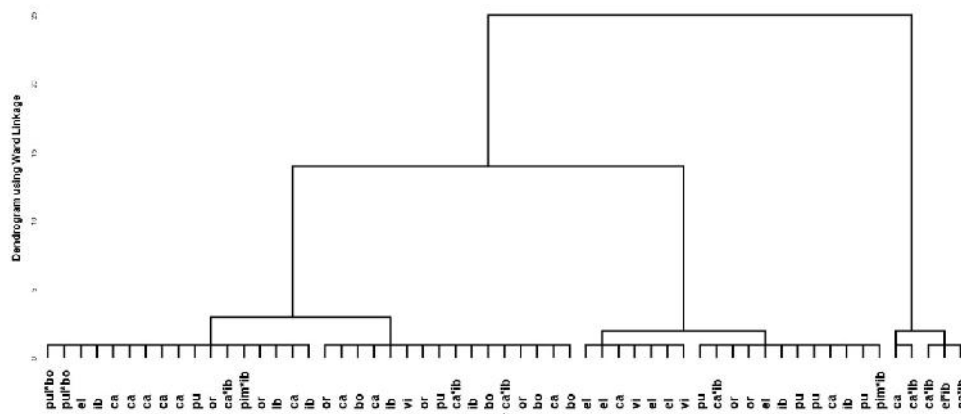
some diversity in *R. pulverulenta* but in Flora of Iran these species are placed near to each other which is not supporting our data. Jokar *et al.* (2008) reported *R. pulverulenta* is a hexaploid species. Moreover, there are some reports on hybrids of *R. pulverulenta* and other species such as *R. pimpinellifolia* (Khatamsaz 1992), and *R. boissieri*. These data confirmed the diversity of *R. pulverulenta* as our data showed. Morphological and molecular studies between two subsections of *Rosa* showed that, when different closely related dog-rose species are present at the same growth site, the genetic structure may show more differentiation between localities than between taxa as it was shown in some populations of *R. pulverulenta* in morphological characters (De cock *et al.* 2008). From an evolutionary point of view, the *canina* meiotic system has probably developed fairly recently (Lim *et al.* 2005), supporting the idea that, the dog-roses are rather young (Atienza *et al.* 2005). Hexaploid base of *R. Pulverulenta* caused to get equal molecular characters from their parents (not maternal) and it could be reason of broad variation of their populations.



**Fig. 6.** Cluster analysis and PCA of section *Caninae* based on morphological characters (population codes as in table 1).

The hybrids of section *Caninae* were collected and confirmed by Mrs. Khatamsaz (the author of Flora of Iran). Hybrid of *R. canina* × *iberica* was reported in Flora of Iran by Khatamsaz (1992) and hybrids of *R. pulverulenta* × *boissieri*, *R. elyomatica* × *iberica*, and *R. pimpinelifolia* × *iberica* were recently reported from Iran by Koobaz et al. (2017). These hybrids have some qualitative characters specially one of parents. Due to the allopolyploid constitution, skewed maternal inheritance and ongoing hybridization, the taxonomy of section *Caninae* is notoriously difficult. Schanzer & Kufunina

(2010) studied morphologic and molecular characters of some wild roses section *Caninae* and their hybrids and their results indicated the hybrid nature of the specimens is confirmed by molecular data, however, they are not intermediate between the parental species as to their morphology. The hybrids either demonstrate novel combinations of diagnostic characters or coincide morphologically with one of the parents. The hybrids were shown in figure 7 with the highest diversity between all genotypes of section *Caninae*. Using these fertile hybrids can help us to improve our gene pool and introduce them to rose breeding.



**Fig. 7.** Cluster analysis of section *Caninae* and their hybrids based on the first two PCA axes characters (population codes as in table 1).

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