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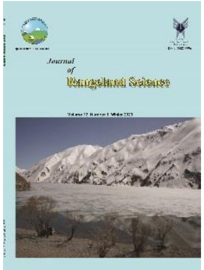

Research and Full Length Article:

Evaluation of Morphological Traits in the Populations of *Coronilla varia* L.

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Abstract. *Coronilla varia* L., crown vetch, has wide adaptation, and desirable morphological characteristics for a grazing plant, tolerates short periods of overgrazing, and accordingly has potential as a forage crop. In this study, 15 traits were investigated to assess the morphological diversity of 52 populations using univariate and multivariate analyses. Crown vetch seeds provided by the Natural Resources Gene Bank of Iran were sown in an experiment field of Research Institute of Forests and Rangelands, Alborz province, over two years (2019–2020). Based on the flowering date, two taxa *C. varia* var. *varia* (as perennial that go to flowering in the first year) and *C. varia* (as perennial that go to flowering in the second year) were identified. However, a close relationship was found between local and exotic crown vetch populations. The populations were significantly variable in all traits. The high variability was found among populations for plant height, plant canopy, internode length, stem number, and biomass yield. Biomass yield was statistically significant ($p < 0.05$) and positively correlated with plant height ($r=0.63$) and plant canopy diameter ($r=0.48$), internode length ($r = 0.57$), stem number ($r=0.66$), and pod length ($r=0.52$). The principal component analysis showed that the variations observed in the populations were mainly caused by traits such as plant height, stem number, the number of days to 50% flowering and seed ripening indicating that their contribution was important in discriminating the populations. Direct selection can also be made for the populations with high biomass yield based on the recorded performance of these populations during the field experiments. In *C. varia*, 12 populations classified in cluster 1 with the highest values for 12 out of 15 traits could be useful for including in future breeding programs. Besides, in *C. varia* var. *varia*, population Bojnurd (for plant height and canopy diameter), population Rezvanshahr (for internode length and stem number), and populations Karaj1 and 2 (for biomass yield) had higher mean values and were recommended for breeding programs.

Key words: Biomass yield, *Coronilla varia*, Principal component analysis, Seed ripening.

Introduction

While it is anticipated that few species will be better adapted to a region than those already commonly grown, continued screening is needed to identify the potential of species in previously untested environments (Beuselinck *et al.,* 1994; Rogers *et al.,* 1997). Marginal areas and reclamation sites that should be established in the permanent cover are of notable concern.

If species adapted to marginal lands can be grazed as pasture or harvested as hay, an economic benefit in addition to soil stabilization benefits can be derived (Clark, 2001). Grasses are generally more tolerant of some stresses than legumes (Rogers *et al.*, 1997); however, legumes are usually more productive and higher in nutritive value than grasses, with the added benefit that nitrogen fixation by the legume also promotes the growth of the associated grass in mixed pastures (Beuselinck *et al.*, 1994; Guldan *et al.*, 2000; Lauriault *et al.*, 2003). While there might be only one or two legume species capable of maximizing production on a given site (Beuselinck *et al.*, 1994), there might be several species capable of providing satisfactory production or other benefits across a variety of soil conditions in an otherwise stable climatic environment (Casler and Walgenbach, 1990; Clark, 2001).

Coronilla varia, crown vetch, is a perennial legume in the pea/legume family (Papilionoideae) which is a native of the Mediterranean area of Europe, Africa, and Asia Minor (Reynolds *et al.*, 1997). Various ecotypes of the species have become adopted throughout much of the eastern United States. Crown vetch has wide adaptation, and desirable morphological characteristics as a grazing plant, tolerates short periods of overgrazing, and accordingly has potential as a forage crop (Seim 1966). Crown vetch has good quality and is highly palatable for ruminant animals such as cattle, horses, goats, and sheep (Burns and Cope, 1974; Arzani et al., 2010; Al-Snafi, 2016).

Crown vetch tolerates a broad range of environmental conditions. It can withstand periods of drought as well as heavy precipitation (up to 165 cm annual precipitation), but it cannot tolerate flooded soil conditions. It is tolerant of cold temperatures (down to –33°C) but it is intolerant of shade (Tu, 2003). Crown vetch is also well adapted to all coarse and medium-textured soils including sands, gravelly-rocky soils, and loams. It does not grow, particularly well in fine-textured soils, but it can survive in silts and clays. It can grow in soils ranging in pH from 5.0–7.5 and it is not tolerant to saline and alkaline soils. Crown vetch reproduces vegetatively by rhizome sprouts and sexually via seeds (Tu, 2003). The number of seeds per plant is 11–1000, and the frequency of sexual reproduction for a mature plant is once a year (GISD, 2021). Crown vetch will typically have a large seed bank stored in the soil, and seeds do not require a period of cold stratification to germinate. Seeds remain viable in the soil for less than a year to 5 years.

Crown vetch can invade and dominate a variety of vegetation types. It is a serious threat to many natural areas because of its prolific seeding ability and rapid rate of vegetative spread via its rhizomes, which can create densely, single-species stands. The character of a natural area can be transformed from a richly diverse habitat into just another weedy track (Symstad, 2009; LOsure *et al.*, 2009). However, crown vetch has been extensively cultivated for erosion control along many roads, highways, and disturbed areas in the USA. It has also been widely planted for ground cover, mine reclamation, and as a cover crop, it provides nitrogen to the soil through its association with cyanobacteria (USDA, 2007).

Some research has been conducted to find alternatives to alfalfa for use in hay and pasture systems (Berg, 1990; Bolger and Matches, 1990). As a forage crop, crown vetch compares quite favorably with alfalfa and *Lotus corniculatus* in total digestible nutrient and digestible protein. In contrary to other forage legumes that have been compared to alfalfa, crown vetch has no limitations such as low initial stand density or slow stand development that leads to low yields early in the stand life (Ruffner and Hall, 1963; Guldan *et al.,* 2000; Gucker Corey, 2009; Zarabiyan *et al*., 2013; Irani *et al*., 2016). Arzani *et al.* (2010) by comparing six species, including two grasses (*Bromus tomentellus* and *Dactylis glomerata*), two forbs (*Ferula ovina* and *C. varia*), and two shrubs (*Salsola rigida* and *Artemisia aucheri*) reported that *Coronilla varia* had the highest amount of crude protein (CP) and dry matter digestibility (DMD), and the lowest amount of acid detergent fiber (ADF) in the first growth stage. They concluded *C. varia* had the highest forage quality among the six studied species (Arzani *et al.*, 2010).

Although there is a widespread distribution of crown vetch in Iran, no significant effort has been made to assess the diversity of the species. Therefore, in this study, the diversity of 52 crown vetch populations consisted of seven exotic and 45 wild populations from different regions of Iran were evaluated for morphological traits. Thus, a field experiment was conducted aiming to 1) develop an important database for the support of gene bank management, and 2) make a preliminary selection of promising ecotypes for further research studies in breeding programs.

Material and Methods

Plant Material

A total of 52 crown vetch, *Coronilla varia*, populations consisted of seven exotic and 45 wild populations that were collected from different geographic regions of Iran were provided from Natural Resources of Gene Bank of Iran (Table 1). Thirty seeds from each crown vetch population were planted in seedling pots (December 2018). Planting and maintenance operations were carried out in the field at the research field of Research Institute of Forests and Rangelands, Alborz province, Iran (2019–2020). The experimental layout was a completely randomized block design with three replications. Each replicate consisted of 15 plants. The row and plant spacings were 100 and 40 cm, respectively.

Morphological traits

Fifteen different quantitative traits were evaluated at harvest time. Ten plants (normal growth, uniform performance, disease- and insect pest-free) from each population were randomly selected for recording. Characters included day to sprout, days to 50% flowering, days to seed ripening, seed length (mm), seed width (mm), seed index (seed length/ width), plant height (at 50% flowering, cm), the plant canopy diameter (cm), internode length (second internode at 50% flowering, cm), stems number, pod length (cm), pod width (cm), pod index (Pod length/width), biomass yield (plant fresh weight) (g), and plant dry weight (g) (Burns and Cope, 1974; Arzani et al., 2010).

Data analysis

Data were subjected to analysis of variance (ANOVA) using SAS software system (SAS, 2001). For the determination of superior populations, a means comparison for every 15 traits was made in DMRT Duncan test. Pearson correlation was determined using SPSS v.21. To evaluate the information contained in the collected morphological data, principal component analysis (PCA) was carried out by Minitab software (version 15). PCA was used to identify the most important traits in the data set. Mean values per populations were used to create a correlation matrix from which the standardized PCA scores were extracted and a scatter plot on the first two PCA was performed. Cluster analysis was performed using Ward’s methods and Euclidean distance and a dendrogram was calculated.

Table 1. The list of studied 52 crown vetch populations

Taxon	Code	Abbre. code	Origin, province	Longitude		Latitude		Altitude (m asl)
C. varia	5798	VArak	Markazi, Arak	49°	51´	34°	36´	1,708
	38085	VArdabil	Ardabil	47°	43´	38°	28´	1,750
	19804	VBaneh	Kordestan, Baneh	46°	8´	35°	57´	1,790
	34151	VBrujen	Chahar Mahaal and Bakhtiari, Brojen	50°	59´	31°	46´	2,600
	43875	VDastjer	Qom, Dastjerd	50°	11´	34°	41´	1,697
	42	VDizin1	Tehran, Dizin	51°	25´	36°	25´	3,800
	115	VDizin2	Alborz, Shemshak Dizin	51°	27´	36°	13´	3,800
	13689	VGom	Qom	50°	6´	34°	43´	2,280
	19935	VGorgan1	Golestan, Gorgan	54°	19´	36°	51´	65
	2677	VGorgan2	Golestan, Gorgan	54°	18´	36°	50´	70
	38817	VHameda1	Hamedan	48°	27´	34°	47´	2,015
	19369	VHameda2	Hamedan	48°	37´	34°	41´	2,050
	18231	VIsfahan	Isfahan	51°	39´	32°	39´	1,571
	256	VKaleyba	East Azarbaijan, Kaleybar	47°	22´	38°	51´	1,345
	33	VKaraj1	Alborz, Karaj	50°	59´	35°	46´	1,380
	590	VKaraj2	Alborz, Karaj	50°	59´	35°	46´	1,380
	228	VKaraj3	Alborz, Karaj	50°	59´	35°	46´	1,380
	38066	VKhalkh1	Ardabil, Khalkhal	48°	27´	37°	26´	1,795
	42422	VKhalkh2	Ardabil, Khalkhal	48°	27´	37°	26´	1,725
	42372	VKhalkh3	Ardabil, Khalkhal	48°	26´	37°	30´	1,915
	38101	VKhalkh4	Ardabil, Khalkhal	48°	27´	37°	26´	2,217
	38076	VKosar	Ardabil, Kosar	48°	28´	37°	52´	2,037
	44541	VMeshki1	Ardabil, Meshkinshahr	47°	23´	38°	28´	1,889
	36608	VMeshki2	Ardabil, Meshkinshahr	47°	22´	38°	19´	1,730
	43434	VNir	Ardabil, Nir	48°	37´	37°	26´	1,732
	9915	VSananda	Kordestan, Sanandaj	46°	58´	35°	10´	1,322
	42719	VSemirom	Isfahan, Semirom	51°	38´	31°	32´	2,400
	3387	VShahrko	ChaharMahaal V Bakhtiari, Shahrkord	50°	39´	31°	58´	2,066
	35778	VSoltan1	Zanjan, Soltanie	48°	49´	36°	19´	2,050
	40363	VSoltan2	Zanjan, Soltanie	48°	49´	36°	19´	2,050
	551	VTehran1	Tehran	51°	23´	35°	41´	1,368
	33605	VTuyserk	Hamedan, Tuyserkan	48°	25´	34°	36´	1,980
	19277	VZanjan1	Zanjan	48°	30´	36°	40´	1,638
	19279	VZanjan2	Zanjan	48°	30´	36°	40´	1,638
	16405	VZirab	Mazandaran, Zirab	52°	53´	36°	4´	1,592
	534	VForein1	Exotic*					
	20496	VForein2	Exotic*					
	20713	VForein3	Exotic*					
	20714	VForein4	Exotic*					
	20716	VForein5	Exotic*					
	3287	VForein6	Exotic*					
	541	VForein7	Exotic*					
C. varia var.*varia*	37835	VvAstar1	Gilan, Astare	48°	35´	38°	26´	1,416
	37834	VvAstar2	Gilan, Astare	48°	37´	38°	24´	689
	1555	VvBojnur	North Khorasan, Bojnurd	57°	64´	37°	28´	1,380
	329	VvKaraj1	Alborz, Karaj	50°	59´	35°	46´	1,380
	186	VvKaraj2	Alborz, Karaj	50°	59´	35°	46´	1,380
	117	VvKaraj3	Alborz,Karaj	50°	59´	35°	46´	1,380
	38579	VvOrumie	West Azarbaijan, Oromiye	50°	21´	41°	47´	1,878
	44243	VvRezvan	Gilan, Rezvanshahr	48°	47´	37°	31´	1,490
	25563	VvTalegh	Alborz, Taleghan	50°	45´	36°	10´	2,226
	37836	VvTalesh	Gilan, Talesh	48°	47´	38°	1´	829

*The country origin of the population is unknown

Results

Significant (p<0.01) variation was revealed for morphological and phonological traits among crown vetch germplasm (Table 2). The number of days to 50% flowering varied significantly, ranging from 110 days to 625 days; this grouped the populations into *C. varia* var. *varia* based on the first year flowering and *C. varia* in the second year flowering. In each taxon, three 50% flowering categories including early (110 days in *C. varia* var. *varia*, and 435 days in *C. varia*), mid (125 days in *C. varia* var. *varia* and 558 days in *C. varia*), and late (150 days in *C. varia* var. *varia* and 625 days in *C. varia*) 50% flowering were observed. Days to seed ripening also corresponded to 50% flowering, which ranged from 139-165 days in *C. varia* var. *varia*, and 454-638 days in *C. varia*; thus in terms of seed yield, there were earlier and late-maturing populations in *C. varia* var. *varia*, and early, mid, and late-maturing populations in *C. varia* (Table 3). There was a wide range of values in plant height (*C. varia* var. *varia*: 37-88 cm, and *C. varia:* 30-109 cm), the plant canopy diameter (*C. varia* var. *varia*: 27-58 cm, and *C. varia:* 37-125 cm), and internode length (*C. varia* var. *varia*: 6.5-9 cm, and *C. varia:* 5-12.5 cm), stem number (*C. varia* var. *varia*: 4-8.88, and *C. varia*: 4.7-10.5) and biomass yield (*C. varia* var. *varia*: 56-179 g, and *C. varia:* 14.5-303 g), which are resulting from the ecotype of the populations. Other traits such as seed and pod size (though had a fairly narrow range)differed significantly (p<0.01) among the populations, indicating highly significant variation. Results indicated that in *C. varia* var. *varia*, the highest amounts of plant height (88 cm) and plant canopy diameter (58 cm) in population VvBojnur, internode length (9 cm) and stem number (8.88) in population VvRezvan, and biomass yield (179 g) in populations VvKaraj1 and 2 were observed. In *C. varia*, population VGorgan showed the highest amount of plant height (109 cm), population VForein2 had the highest value of plant canopy diameter (125 cm), population VKhalkh4 showed the highest amounts of internode length (12.5 cm) and biomass yield (303 g), and the highest value of stem number (10.5 in) was estimated population in population VKaleybar (Table 3). Means comparison of different traits between two taxon indicated that amounts of almost all traits are significantly higher in *C. varia* (Table 3).

The relationships between traits (Table 4) showed that biomass yield was positively correlated with day to 50% flowering (r = 0.29), seed ripening (r=0.29), plant height (r=0.64) and plant canopy diameter (r=0.48) internode length (r=0.57), stem number (r=0.66), pod length (r=0.53), and pod width (r=0.27) (Table 4). Day to 50% flowering was positively correlated with days to seed ripening (r=0.99), seed length (r=0.31), plant height (r=0.25), plant canopy diameter (r=0.49), stem number (r=0.42), pod length (r=0.45), and biomass yield (r=0.29) (Table 4).

The principal component analysis (PCA) of the 15 quantitative traits is summarized in Table 5. The first six PCs had eigenvalues > 1 and they explained 84.5% of the total variation for the morphological traits. Plant height, stems number, pod length, biomass yield, dry weight and canopy diameter were loaded highly in PC1 and they accounted for 33.6% of the total variation.

In PC2, days to 50% flowering and seed ripening accounted for 15.4% of the total of variation.

In PC3, the traits such as seed width, seed index, and pod index accounted for 12% of the total variation. PC4 contributed 11.4% of the total morphological variation in these populations with seed length and index, and pod width and index loading highly. PC5 accounted for 7% of total variation with seed length and width.

Generally, for the 15 morphological traits studied, PC1 and PC2 constituted 49.1% of the total morphological variation with most vegetative traits and seeds-related traits. This indicated that these traits can be used to classify the populations under study. Two-dimensional principal component analysis showing the relationship among quantitative traits of studied populations is presented in Fig 1. Populations *C. varia* var. *varia* and *C. varia* were separated partially by PC2; traits related to this separation are mainly the day to 50% flowering and seed ripening.

Dendrogram for complete linkage cluster analysis of the traits is presented in Fig 2. The results indicated that the populations were grouped into five major clusters. Cluster 1 contained 12 populations, four exotic from an unknown origin and 8 local from Iran, belonging to *C. varia*. They are characterized by the highest values of seed size, plant height, and plant canopy diameter, internode length, stem number, pod size, biomass yield, and dry weight. Also, these populations had longer 50% flowering and seed ripening periods that were classified as late flowering and seed ripening populations (Table 6). Cluster 2 contained 13 populations: 10 from Iran and three exotic from unknown origin belong to species *C. varia*. Cluster 3 contained 6 populations belonging to *C. varia var. varia*. They are also characterized by the highest amount of pod index and have the widest seed size compared to all other populations. Cluster 4 contained six populations: three belong to species *C. varia*, three belong to *C. varia* var. *varia*.

These were classified with the lowest plant height and canopy and the smallest pod size compared with other clusters. Cluster 5 was the largest one with 16 populations, 15 from Iran, and one exotic with unknown origin, belonging to species *C. varia*. These were classified as early 50% flowering and seed ripening populations. Results indicated no relationship between studied traits and the origin of populations.

Table 2. Analysis variance of 15 morphological traits of 52 crown vetch populations

S.O.V.	d.f.	Seed length	Seed width	Seed index	Plant height	Plant canopy diameter	Internode length	Stem number	Pod length	Pod width	Pod index	Biomass yield	Dry weight
Taxon	1	1.745**	0.382**	0.124ns	2481.06**	38684.71**	0.576^{ns}	51.827**	16.529**	0.0055**	5.749^{ns}	42442.9**	6.204^{ns}
Population	51	0.669**	0.11**	0.601**	2909.14**	2622.34**	12.785**	9.082**	1.545**	0.0058**	186.52**	22130.05**	1342.57**
Error	280	0.1509	0.015	0.122	161.07	115.75	1.68	0.564	0.387	0.0003	24.11	193.95	20.131
CV%		9.768	8.56	12.59	17.36	15.64	16.4	10.3	12.54	10.24	17.82	9.13	13.2

*, ** significant at 0.05 and 0.01 levels, respectively; ^{ns} not significance.

Table 3. Means comparison of 15 traits of 52 populations of *C. varia* (with prefix V) and *C. varia* v. *varia* (with prefix Vv)

Population	Day to sprout	Days to 50% flowering	Days to seed ripening	Seed length (mm)	Seed width (mm)	Seed index	Plant height (cm)	Canopy diameter (cm)	Internode length (cm)	Stem number	Pod length (cm)	Pod width (cm)	Pod index	Biomass yield (g)	Dry weight (g)
VArak	20	435	454	3.96e-n	1.45e-m	2.73c-k	47.2p-t	36.6u-x	6.9h-p	5.20pq	-	-	-	59.20rs	13.00st
VArdabil	21	435	454	4.02c-k	1.48c-l	2.72c-k	67.5i-o	101.25b	8.12d-l	6.75h-n	4.76e-o	0.2a	23.81h-m	97.12op	20.87o-r
VBaneh	20	435	454	3.84h-n	1.43f-n	2.70d-k	82.44c-i	102.22b	8.5c-j	7.88e-h	5.43a-i	0.2a	27.16e-k	120.6k-n	29.77k-m
VBrujen	19	435	454	4.18b-i	1.41h-p	2.99a-e	52.77l-s	45.88p-w	5.611n-p	7.33f-l	4.77e-o	0.155b	33.61c-g	110.5l-o	27.33k-o
VDastjer	17	435	454	4.08b-j	1.40i-p	2.91b-h	60.55j-q	83.55c-i	6.166l-p	7.00g-m	5.11b-l	0.2a	25.55h-l	197.8f	45.22ef
VDizin1	24	435	454	3.84h-n	1.55a-f	2.49i-l	67.22i-o	90.55b-g	7.5e-n	8.00e-g	4.50h-p	0.2a	22.5i-m	107.4m-o	25.11l-p
VDizin2	18	596	610	4.67a	1.41g-o	3.31a	70.00h-n	60.05j-o	5.00op	6.00m-p	4.00m-r	0.2a	20k-m	14.5t	2.60u
VGom	18	435	454	3.96e-n	1.41h-p	2.82c-i	90.22a-g	100.11bc	8.38c-k	8.66c-e	4.9d-n	0.2a	24.5h-l	237.5d	50.55de
VGorgan1	15	435	454	3.88f-n	1.42f-o	2.73c-k	108.55a	76.88g-k	9.94b-d	9.22b-d	5.133b-l	0.2a	25.66g-l	169.4gh	29.40k-m
VGorgan2	20	435	454	4.23b-h	1.38j-p	3.08a-d	100.55a-c	83.88c-i	8.52c-j	7.88e-h	5.54a-g	0.2a	27.72e-k	199.8ef	46.66ef

Population	Day to sprout	Days to 50% flowering	Days to seed ripening	Seed length (mm)	Seed width (mm)	Seed index	Plant height (cm)	Canopy diameter (cm)	Internode length (cm)	Stem number	Pod length (cm)	Pod width (cm)	Pod index	Biomass yield (g)	Dry weight (g)
VHameda 1	30	435	454	3.69j-o	1.43f-n	2.58g-l	57.00k-q	55.00m-t	9.5b-e	6.60i-o	4.82e-o	0.16b	34.1c-f	101.6n-p	19p-s
VHameda 2	19	435	454	3.82h-n	1.62ab	2.36kl	50.77n-s	47.77p-v	8.11d-l	6.22k-p	5.08b-l	0.2a	25.44h-l	98.7op	21.66n-q
VIsfahan	15	435	454	4.198b-i	1.52b-i	2.77c-j	103.33ab	57.22l-s	6.83i-p	6.88g-m	5.88a-d	0.2a	29.44e-i	173.6gh	33.33i-k
VKaleyba	14	591	610	3.73j-n	1.31n-s	2.88c-i	90a-g	92.5b-g	9.00c-g	10.5a	6.05ab	0.2a	30.25e-i	262.5bc	65.00b
VKaraj1	15	435	454	3.93e-n	1.49c-k	2.64e-l	90.22a-g	98.66b-d	9.44b-e	8.88c-e	5.08b-l	0.2a	25.44h-l	216.8e	57.66c
VKaraj2	14	594	607	4.05c-k	1.62ab	2.49i-l	97.5a-d	82.5d-i	10.33bc	6.66i-n	5.46a-i	0.2a	27.33e-k	279.0b	67.18b
VKaraj3	12	596	616	3.84h-n	1.41g-o	2.72c-k	104.37ab	76.75g-k	10.93ab	9.62a-c	5.68a-e	0.2a	28.43e-j	247.7cd	55.87cd
VKhalkh1	21	435	454	4.18b-i	1.41h-p	2.96a-g	31.33t	39.16t-x	6.50j-p	5.83m-p	4.63f-p	0.2a	23.16h-m	129.8j-l	19.61p-r
VKhalkh2	26	435	454	4.11b-j	1.43e-n	2.87c-i	45.00q-t	41.66r-x	7.03f-n	5.66n-q	4.33j-q	0.166b	28.33e-j	179.0g	44.00e-g
VKhalkh3	29	435	454	4.06c-k	1.49b-k	2.75c-j	30.00t	45.00q-w	4.93p	4.66qr	3.50qr	0.1c	35.00b-e	126k-m	23.33m-p
VKhalkh4	17	625	638	3.85g-n	1.28p-s	3.02a-e	92.50a-f	71.50h-l	12.50a	10.0ab	6.25a	0.2a	31.25d-h	302.5a	80.00a
VKosar	17	558	573	4.30b-f	1.39i-p	3.1a-c	87.50b-h	91.00b-g	7.5e-n	9.5a-c	5.25b-k	0.2a	26.25f-l	237.5d	37.5h-j
VMeshki1	18	435	454	3.96e-n	1.54a-h	2.55h-l	57.50k-q	52.50n-u	6.37k-p	6m-p	5.00c-m	0.2a	25.00h-l	104.0no	22.00n-q
VMeshki2	13	558	573	4.008c-l	1.57a-e	2.55h-l	71.25g-m	62.0k-p	9.87b-d	7.75e-i	5.30a-j	0.2a	26.5f-l	129.25j-l	33.75i-k
VNir	35	435	454	3.57m-o	1.50b-j	2.40j-l	62.4j-q	40.40s-x	5.8m-p	6.8h-n	-	-	-	70.00q-s	15.60q-t
VSananda	17	594	607	4.40a-d	1.44e-n	3.07a-d	99.16a-c	65.00j-o	8.5c-j	8.66c-e	5.68a-e	0.2a	28.41e-j	177.1g	40.66f-h
VSemirom	30	435	454	4.34a-e	1.43e-n	3.02a-e	51.66m-s	70.00h-m	8.5c-j	5.66n-q	3.76p-r	0.1c	37.66b-d	111.8k-o	25.00l-p

Population	Day to sprout	Days to 50% flowering	Days to seed ripening	Seed length (mm)	Seed width (mm)	Seed index	Plant height (cm)	Canopy diameter (cm)	Internode length (cm)	Stem number	Pod length (cm)	Pod width (cm)	Pod index	Biomass yield (g)	Dry weight (g)
VShahrko	15	435	454	3.98d-m	1.46e-m	2.73c-k	64.44i-q	86.11b-h	5.57n-p	7.33f-l	5.37a-i	0.2a	26.88f-k	200.5ef	47.90e
VSoltan1	17	435	454	3.69j-o	1.60a-d	2.32l	33.75st	48.00p-v	7.37f-n	6.75h-n	4.12l-r	0.15b	30.00e-i	95.7op	19.50p-r
VSoltan2	21	435	454	4.41a-c	1.48c-l	2.98a-f	53.75l-r	96.25b-f	6.32k-p	7.00g-m	4.82e-o	0.1c	48.25a	114.9k-o	28.08k-n
VTehran1	19	435	454	4.02c-k	1.37k-p	2.98a-f	67.00i-p	81.00e-j	6.94g-o	8.00e-g	5.15b-k	0.2a	25.77g-l	127.8kl	24.85m-p
VTuyserk	20	435	454	3.89f-n	1.55a-f	2.52i-l	76.66e-k	69.83h-m	8.08d-l	8.33d-f	5.61a-f	0.2a	28.08e-k	212.1ef	47.33e
VZanjan1	17	435	454	3.64k-o	1.43e-n	2.54h-l	46.4q-t	80.00f-j	7.2f-n	6.2l-p	4.96d-n	0.2a	24.8h-l	66.0q-s	12.00t
VZanjan2	21	435	454	3.84h-n	1.53b-i	2.52i-l	82.5c-i	67.5i-n	7.75e-m	5.5o-q	5.5a-h	0.2a	27.5e-k	115k-o	25.00l-p
VZirab	19	435	454	3.32o	1.20rs	2.76c-j	35.6r-t	43.0q-x	7.5e-n	6.00m-p	4.44i-q	0.16b	30.2e-i	156.0hi	23.82m-p
VForein1	15	435	454	3.79j-n	1.46e-m	2.60f-l	62.22j-q	58.77l-q	7.166f-n	6.77h-n	4.63f-p	0.166b	29.27e-i	100.4op	18.33p-s
VForein2	18	435	454	4.27b-g	1.67a	2.58g-l	99.44a-c	125.0a	10.22bc	8.88c-e	5.46a-i	0.2a	27.33e-k	239.8d	56.44c
VForein3	15	435	454	3.70j-o	1.35l-q	2.79c-i	100.0a-c	96.66b-e	8.38c-k	8.77c-e	5.27a-k	0.2a	26.38f-l	270.4b	36.88h-j
VForein4	13	435	454	3.94e-n	1.53b-i	2.57h-l	95.0a-e	72.22h-l	8.44c-j	8.00e-g	4.92d-n	0.2a	24.61h-l	147.07ij	31.44j-l
VForein5	15	435	454	4.32a-e	1.62a-c	2.67e-l	99.77a-c	83.88c-i	5.77m-p	6.88g-m	5.46a-i	0.2a	27.33e-k	131.7jk	21.66n-q
VForein6	21	435	454	4.04c-k	1.32n-r	3.06a-d	72.00g-l	98.75b-d	7.75e-m	7.50f-j	4.92d-n	0.2a	24.62h-l	126.8k-m	24.26m-p
VForein7	13	594	610	4.47ab	1.36k-p	3.27ab	60.75j-q	53.87m-t	8.68c-i	6.75h-n	5.40a-i	0.2a	27.00f-k	112.8k-o	27.5k-o
VvAstar1	19	125	139	4.007c-l	1.54a-h	2.60f-l	73.75f-k	41.62r-x	8.12d-l	6.37j-o	4.52g-p	0.11c	42.03ab	166.9gh	46.87ef
VvAstar2	20	110	139	3.64k-o	1.36k-p	2.67e-l	53.75l-r	33.0v-x	7.12f-n	6.00m-p	3.96n-r	0.21a	18.74ml	76.62qr	18.74p-s

Population	Day to sprout	Days to 50% flowering	Days to seed ripening	Seed length (mm)	Seed width (mm)	Seed index	Plant height (cm)	Canopy diameter (cm)	Internode length (cm)	Stem number	Pod length (cm)	Pod width (cm)	Pod index	Biomass yield (g)	Dry weight (g)
VvBojnur	19	125	139	4.006c-l	1.50b-k	2.70d-k	87.77b-h	49.77o-u	8.94c-h	6.11m-p	4.76e-o	0.218a	22.18i-m	172.1gh	46.89ef
VvKaraj1	19	125	139	3.55no	1.29o-s	2.77c-j	79.0d-j	36.0u-x	8.92c-h	6.00m-p	5.10b-l	0.2a	25.54h-l	178.5g	46.42ef
VvKaraj2	20	110	139	3.58l-o	1.19s	3.01a-e	63.5i-q	48.0p-v	7.16f-n	6.33k-p	4.27k-r	0.23a	21.06j-m	178.3g	49.16e
VvKaraj3	19	125	139	3.94e-n	1.48d-l	2.66e-l	46.8q-t	31.0wx	6.5j-p	4.60qr	3.86o-r	0.1c	38.6bc	83.00pq	24.00m-p
VvOrumie	13	125	139	3.69j-o	1.55a-g	2.39j-l	79.00d-j	54.00m-t	7.5e-n	7.0g-m	6.00a-c	0.2a	30.00e-i	125k-m	37.5h-j
VvRezvan	19	125	139	4.04c-k	1.23q-s	3.29a	76.00e-k	58.44l-r	9.11b-f	8.88c-e	4.5h-p	0.2a	22.5i-m	157.7hi	38.44g-i
VvTalegh	15	125	139	3.98e-n	1.41h-p	2.83c-i	36.50r-t	32.37v-x	7.43e-n	7.37f-k	3.96n-r	0.1c	39.62bc	55.60s	14.87r-t
VvTalesh	31	150	165	4.11b-j	1.32m-r	3.10a-c	48.33o-t	26.66x	7.5e-n	4.00r	3.36r	0.2a	16.83m	56.68s	16.55q-t
C. varia	19.24a	468.12a	486.33a	4.00a	1.46a	2.77a	71.79a	72.24a	7.83a	7.35a	5.04a	0.19a	27.83a	154.25a	33.23a
C.varia v.varia	21.80 b	130.10b	146.80b	3.86b	1.39b	2.81a	64.44b	41.09b	7.84a	6.27b	4.43b	0.17b	27.71a	125.07b	33.95a

Different letters indicate significant differences among different populations for the same species. $P < 0.05$.

Table 4. Simple correlation matrix for the 15 traits of vetch populations

Traits	Day to sprout	Days to 50% flowering	Days to seed ripening	Seed length	Seed width	Seed index	Plant height	Canopy diameter	Internode length	Stem number	Pod length	Pod width	Pod index	Biomass yield
Days to 50% flowering	-0.289*													
Days to seed ripening	-0.288*	1**												
Seed length	-0.088^{ns}	0.307*	0.303*											
Seed width	-0.033^{ns}	0.165^{ns}	0.166^{ns}	0.208^{ns}										
Seed index	-0.019^{ns}	0.079^{ns}	0.074^{ns}	0.563**	-0.687**									
Plant height	-0.37**	0.248**	0.243^{ns}	0.137^{ns}	0.105^{ns}	0.017^{ns}								
Canopy diameter	-0.253^{ns}	0.493**	0.494**	0.215^{ns}	0.153^{ns}	0.035^{ns}	0.575**							
Internode length	-0.236^{ns}	0.17^{ns}	0.165^{ns}	-0.167^{ns}	-0.065^{ns}	-0.061^{ns}	0.544**	0.293*						
Stem number	-0.376**	0.422**	0.423**	0.002^{ns}	-0.113^{ns}	0.112^{ns}	0.665**	0.638**	0.55**					
Pod length	-0.295*	0.454**	0.452**	-0.045^{ns}	0.19^{ns}	-0.19^{ns}	0.685**	0.477**	0.36**	0.607**				
Pod Width	-0.191^{ns}	0.204^{ns}	0.202^{ns}	-0.117^{ns}	-0.08^{ns}	-0.006^{ns}	0.51**	0.282*	0.256^{ns}	0.333*	0.541**			
Pod index	0.054^{ns}	-0.018^{ns}	-0.017^{ns}	0.116^{ns}	0.196^{ns}	-0.095^{ns}	-0.198^{ns}	-0.057^{ns}	-0.085^{ns}	-0.042^{ns}	-0.056^{ns}	-0.859**		
Biomass yield	-0.401**	0.291*	0.286*	-0.057^{ns}	-0.115^{ns}	0.064^{ns}	0.639**	0.484**	0.57**	0.66**	0.529**	0.268*	-0.02^{ns}	
Dry weight	-0.342*	0.141^{ns}	0.134^{ns}	-0.058^{ns}	-0.086^{ns}	0.042^{ns}	0.582**	0.369**	0.616**	0.577**	0.482**	0.227^{ns}	0.014^{ns}	0.916**

*, ** significant at 0.05 and 0.01 levels, respectively; ^{ns} not significance.

Table 5. Means comparison of 15 traits of five crown vetch groups produced in figure 2

Groups	Day to sprout	Days to 50%	Days to seed	Seed length	Seed width	Seed index	Plant height	Canopy diameter	Internode length	Stem number	Pod length	Pod width	Pod index	Biomass yield	Dry weight

		flowering	ripening	(mm)	(mm)		(cm)	(cm)	(cm)		(cm)	(cm)		(g)	(g)
G1	15.33b	500.7a	518.5a	3.924a	1.47a	2.69bc	94.88a	88.35a	9.39a	8.65a	5.28a	0.200a	26.41c	219.79a	47.40a
G2	18.00c	468.9b	486.9b	4.13b	1.44a	2.89a	78.65b	82.87a	7.35c	7.48b	5.26a	0.200a	26.32c	149.72b	32.41c
G3	22.16a	126.66e	143.3e	3.82b	1.32b	2.92a	71.02c	44.23b	8.27b	6.54c	4.44c	0.207a	21.61d	144.57b	37.80b
G4	22.33b	282.6d	300.8d	4.12a	1.48a	2.81ab	50.83d	47.64b	7.18c	6.35c	4.13d	0.103c	40.55a	108.69c	28.10d
G5	22.73b	426.7c	445.1c	3.87b	1.47a	2.66c	51.38d	50.09b	7.01c	6.19c	4.79b	0.177b	28.56b	103.64c	21.28e

Different letters indicate significant differences among different populations for the same species. P <0.05.

Table 6. Eigenvalues, the proportion of variance, and morphological traits that contributed to the first six PCs

Variable	PC1	PC2	PC3	PC4	PC5	PC6
Plant height	**0.353**	0.119	-0.002	-0.033	0.267	0.038
Stem number	**0.360**	0.048	0.017	0.104	-0.144	0.139
Pod length	**0.335**	0.008	-0.136	-0.166	0.067	0.13
Biomass yield	**0.347**	0.196	-0.031	0.17	-0.159	-0.052
Dry weight	**0.307**	0.325	-0.078	0.218	-0.001	-0.034
Canopy diameter	**0.310**	-0.151	-0.052	0.035	0.09	0.253
Days to 50% flowering	0.262	**-0.449**	-0.033	0.011	-0.148	0.048
Days to seed ripening	0.261	**-0.446**	-0.035	0.007	-0.153	0.049
Seed width	0.018	-0.168	**-0.552**	-0.226	**0.427**	-0.064
Seed index	0.017	-0.091	**0.542**	**0.461**	0.109	0.047
Pod index	-0.084	-0.063	**-0.476**	**0.466**	-0.189	0.073
Pod width	0.233	0.074	0.337	**-0.470**	0.212	0.003
Seed length	0.04	-0.328	0.096	**0.370**	**0.620**	-0.041
Day to sprout	-0.219	0.026	0.018	-0.059	0.043	**0.928**
Internode length	0.268	0.274	-0.058	0.057	-0.106	0.114
Eigenvalue	5.383	2.469	1.921	1.823	1.120	0.807
Proportion	0.336	0.154	0.12	0.114	0.07	0.05
Cumulative	0.336	0.491	0.611	0.725	0.795	0.845

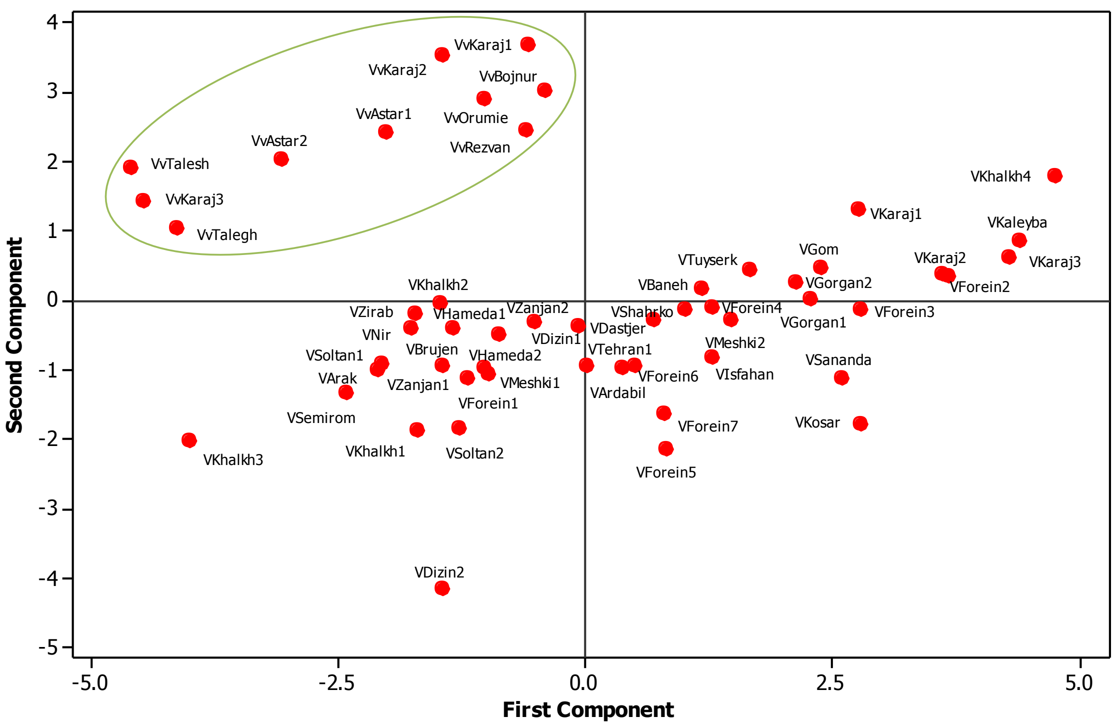

Fig. 1. Two principal components showing the relationship among 15 traits of 52 populations of *C. varia* (with prefix V) and *C. varia* v. *varia* (with prefix Vv)

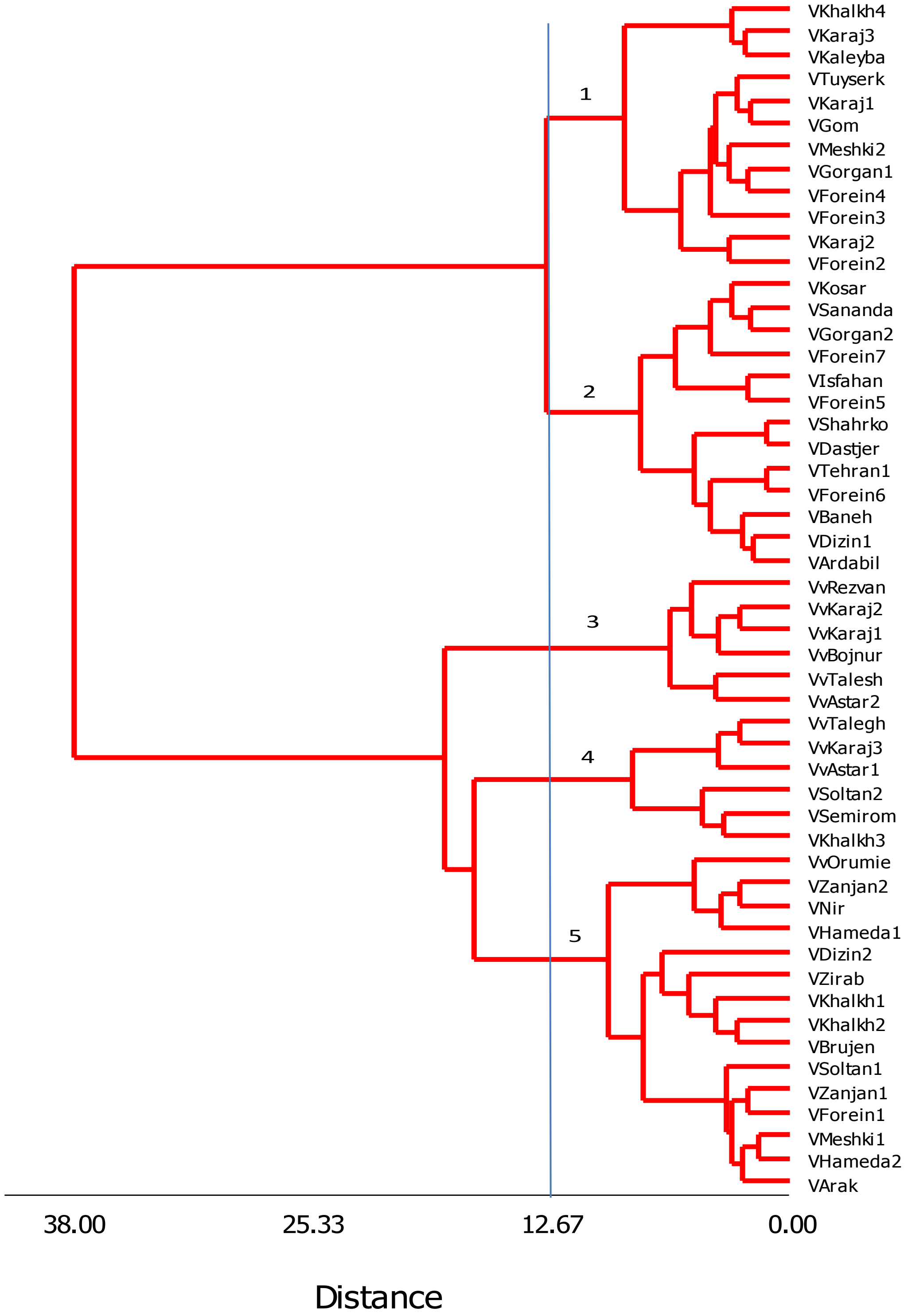

Fig. 2. Dendrogram of 52 populations of *C. varia* (with prefix V) and *C. varia* v. *varia* (with prefix Vv) explained by complete linkage clustering of 15 traits

Discussion

In this study, morphological traits of 52 wild crown vetch populations of the Natural Resources Gene Bank of Iran were compared. Germplasm collections from endemic forage species such as crown vetch can be an important step in breeding and rehabilitation of degraded pastureland (Nelson *et al.*, 2011; Andini *et al.*, 2013). Lauriault *et al.* (2005) by comparing the vegetation cover and dry matter yield of *Medicago sativa*, *Lotus corniculatus*, *Astragalus cicer*, *C. varia*, *Trifolium ambiguum*, *T. pratense*, *Onobrychis viciifolia*, *T. fragiferum* and *T. repens* indicated that with some limitations and lower yields, *A. cicer*, *C. varia*, and *O. viciifolia* offer alternatives during periods of alfalfa stand decline and re-establishment or as replacements altogether in the Southern High Plains of USA.

The *C. varia* populations under this study are morphologically very diverse by the multivariate analysis of the studied traits. The populations demonstrated high variation in plant height, plant canopy diameter, internode length, stem number, and biomass yield. Large variability among natural populations of *Medicago sativa* (Moawed, 2016), *M. truncatula* and *M. laciniata* (Chebouti *et al.*, 2019), *Onobrychis viciifolia* (Irani *et al.*, 2016), and *Trifolium repens* (Welham *et al.*, 2002) was observed for morphological traits. Variation in the traits is an important informative trait in differentiating populations, particularly those desirable for biomass production. The high variation detected among populations may be related to genetic structure, which is probably due to heterozygosis and cross-pollination. This indicated that improvement through simple selection for these traits is possible. In *C. varia* population VGorgan (for plant height), population VForein2 (for plant canopy diameter), population VKhalkh4 (for internode length and biomass yield), and population VKaleybar (for stem number) showed the highest values of the mentioned traits. Besides, populations VvBojnur (for plant height and canopy diameter), population VvRezvan (for internode length and stem number), and populations VvKaraj1 and -2 (for biomass yield) are the selected populations for ecotype introduction in *C. varia* var. *varia*. However, broadening the genetic base from diverse sources is recommended to include most of the genetic determinants of these traits (Laghetti *et al.*, 1998; Ghafoor *et al.*, 2002). This variability can be exploited in fodder breeding programs to select an adapted plant material for the arid and semi-arid areas (Chebouti *et al.*, 2019).

The analysis of simple correlations among the traits revealed that populations with high plant height, plant canopy, internode length, and stem number had high biomass yield. Positive correlations recorded among the populations suggest that these traits can be used as selection criteria for populations with high biomass yields. According to researches that biomass yield and plant height are discriminating traits among *Medicago sativa* L. (Basafa and Taherian, 2009; Bakheit *et al.*, 2011), *Onobrychis viciifolia* (Irani *et al.*, 2016), and *Trifolium repens* (Welham *et al.*, 2002) populations. In the breeding of forage plants, these materials can be used as parental stock. Plant height was also positively and significantly related to the number of days to 50% flowering. In each taxon, three categories including early, mid, and late 50% flowering were observed. Similar to this study, a significant correlation between days to 50% flowering and plant height was reported in lentil (Ojiewo *et al.*, 2012) and *Corchorus* spp. (Ngomuo *et al.*, 2017). The most limiting and significant factors to leaf production and yield are early and prolific flowering and seed production (Shukla *et al.*, 2010)

In PCA analysis, traits of plant height and stem number accounted for the variations recorded in the populations in PC1. On the other hand, the number of days to 50% flowering and seed ripening accounted for the variation observed in the populations in PC2. The total cumulative variance in the first two PC was 49.1%, indicating the high degree of diversity among the traits under study. Furthermore, the traits can be used as phenotypic traits in differentiating the populations.

Genetic diversity analysis of germplasms using morphological traits is an initial step for crop improvement (Julia *et al.*, 2016; Peratoner *et al.*, 2016; Loumerem and Alercia, 2016; Shen *et al.*, 2019). The variations in morphological traits can be used to classify materials into different groups. Based on the days to 50% flowering, two taxa *C. varia* var. *varia* and *C. varia* were identified based on flowering date. However, a close relationship was found between local and exotic crown vetch populations. In the present study, the 52 populations were grouped into five clusters using 15 traits. Clusters 1 and 2 contained populations from *C. varia* species.

Six out of seven materials with uncertain origin appeared in clusters 1 and 2. The populations of cluster 1 are characterized by the highest values of seed size, plant height, and plant canopy diameter, internode length, stem number, pod size, biomass yield, and dry weight which are the candidate of further evaluations. Also, these populations had longer 50% flowering and seed ripening periods classified as late ripening populations. It is interesting that the population from different climates like Qom (hot and dry) clustered with populations from Tuyserkan (cold and semi-dry), Khalkhal (cold), and Gorgan (wet). This pattern of clustering indicates, on one hand, the diversity of population within these geographical areas and, on the other hand, the similarity of populations from different geographical areas. These results agree with the report of Alemayehu and Becker (2002) in *Brassica carinata*. This is due to some level of similarity in other quantitative traits, though the population belongs to *C. varia* species.

Cluster 3 contained six populations belong to *C. varia var. varia*. Cluster 4 contained mixed populations from *C. varia* and *C. varia* var. *varia*. These were classified with the lowest value of plant height and canopy and smallest pod size compared with other clusters. Cluster 5 contained mixed populations of *C. varia* from all over Iran indicating no relationship between studied traits and the origin of populations. These were classified as early 50% flowering and seed ripening populations.

No significant differences between the local and exotic populations revealed that geographic origin was not related to the similarity among populations. However, in controversial reports, Mengoni *et al.* (2000) and Yan *et al.* (2009) detected a significantly positive correlation between phenotypic and geographical distances in *Medicago sativea* and *M. lupulina* populations with different geographical origins. They found a general tendency that closely situated populations are morphologically more similar.

Results of this study showed that phenotypic diversity and geographic distribution in wild populations of crown vetch were independent of each other and no definite relationship existed between phenotypic and geographic diversity. Results suggested different ecological conditions from which plants were obtained may have caused the observed variations. The results of this work implied that the genetic diversity of crown vetch was not the result of the joint effects of one or several ecological factors, i.e., the ecological factors have not played an important role in influencing the morphological variation of crown vetch. The distribution of genetic diversity in a plant species depends on its evolution and breeding system, ecological and geographical factors, and often on human activities (Ramanatha and Hodgkin, 2002).

Cross-pollination may play a role, depending on the presence of suitable insects at flowering time (Lv *et al.*, 2009; Zhang *et al.*, 2006). Ecological and geographical factors have not played an important role in the evolution of crown vetch since we have not found any association between phenotypic diversity and population origin.

The diversity of populations within the geographical region might be due to the heterogeneity and genetic architecture of populations and developmental traits (Singh, 1991) that has been reported in different plant species (Alemayehu and Becker, 2002; Singh *et al*., 2004; Bhargava *et al*., 2007; Aryakia *et al*., 2016; Jafari *et al*., 2017). The populations of a particular cluster having desirable genes for a specific trait can be hybridized with the other populations of different clusters, which may facilitate the accumulation of favorable genes in hybrids. The hybrids thus obtained may be fixed by selecting transgressive segregants, followed by recurrent selections in advanced generations, which may lead to the development of high-yielding varieties with desirable components (Jafari *et al*., 2017).

Conclusion

The results from ANOVA, simple correlations, and multivariate analyses indicated high variation among the studied materials. Based on the number of days to 50% flowering, two taxa *C. varia* var. *varia* and *C. varia* were identified based on length of flowering date in the first and the second years, respectively. A significant and positive correlation between biomass yield and high plant height, plant canopy, internode length, and stem number indicates the potential of using these populations to improve new varieties for forage yield. On the other hand, the PCA showed that the variations observed in the populations are mainly caused by traits such as plant height and stem number, the number of days to 50% flowering and seed ripening, indicating that their contribution was important in discriminating the populations.

Direct selection can also be made for the populations with high biomass yield based on the recorded performance of these populations during the field experiments. Cluster analysis grouped the populations into five clusters that contained mixed populations from all over Iran indicating no relationship between studied traits and the origin of populations. A close genetic relationship between local and exotic crown vetch populations and that great variation exists among populations within local or exotic groups. The results indicate that comprehensive germplasm collection in major geographic regions is required to broaden the genetic base and sample the full extent of the available variation. Breeding strategies need to exploit the existing variation within the crown vetch germplasm. The results demonstrate that the divergence of microenvironments has an obvious effect on the diversity of crown vetch. Consequently, major attention should be paid to the sustainable conservation of crown vetch at different populations when strategies for breeding and germplasm conservation are being implemented in future programs.

The diversity and relationships of crown vetch can be used in the development of germplasm collection, breeding, and conservation. In *C. varia,* 12 populations classified in cluster 1 including VKaraj1, -2, -3, VForein2, -3, -4, VGorgan1, VKhalkh4, VKaleybar, VTuyserk, VQom, and VMeshki2 with the highest values for 12 out of 15 traits could be useful for including in future breeding programs. Besides, in *C. varia* var. *varia*, populations VvBojnur (for plant height and canopy diameter), population VvRezvan (for internode length and stem number), and populations VvKaraj1 and 2 (for biomass yield) are recommended for breeding programs. These issues warrant further study.

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ارزیابی صفات ریخت‌شناسی جمعیت‌های *Coronilla varia*

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چکیده..*Coronilla varia* L.، یونجه تاجی، به عنوان یک گیاه علوفه‌ای دارای سازگاری وسیع و ویژگی‌های مورفولوژیکی مطلوب بوده و دوره های کوتاه چرای بیش از حد را تحمل می‌کند. در این پژوهش، تنوع ریخت شناختی ۵۲ جمعیت *C. varia* با استفاده از تجزیه و تحلیل‌های تک متغیره و چند متغیره بررسی شد. بذرهای *C. varia* از بانک منابع طبیعی ژن ایران تهیه گردید و در مزرعه موسسه تحقیقات جنگل ها و مراتع کشور، استان البرز، طی سال‌های ۱۳۹۷-۱۳۹۹ کاشته شدند. بر اساس صفت زمان ۵۰ درصد گل‌دهی دو تاکسون *C. varia* var. *varia* (گیاه چندساله که در سال اول گل می‌دهد) و *C. varia* (گیاه چندساله که در سال دوم گل می‌دهد) تشخیص داده شد. نتایج نشان دادند که جمعیت‌ها در تمام صفات گوناگونی قابل توجهی داشته و تمایزی بین نمونه‌های بومی و خارجی نشان ندادند. از بین ۱۵ صفت مورد بررسی بیشترین گوناگونی در صفات ارتفاع بوته، قطر تاج پوشش، طول میانگره، تعداد ساقه و عملکرد زیست توده مشاهده شد. عملکرد زیست توده از نظر آماری همبستگی مثبت و معنی داری (p<۰/۰۵) با صفات ارتفاع بوته (r =۰/۶۳)، قطر تاج پوشش گیاه (r = ۰/۴۸)، طول میانگره (r = ۰/۵۷)، تعداد ساقه (r =۰/۶۶)، طول غلاف (r =۰/۵۲) نشان داد. بعلاوه این آزمون نشان داد که گوناگونی مشاهده شده در جمعیت‌ها عمدتاً توسط صفاتی مانند ارتفاع بوته، تعداد ساقه، زمان ۵۰ درصد گلدهی و رسیدن بذر ایجاد می‌شود، که نشان می‌دهد این صفات سهم بیشتری در تمایز جمعیت‌ها دارند. به این ترتیب می‌توان بر اساس بیشترین عملکرد زیست توده ثبت شده در آزمایش‌های مزرعه‌ای، نسبت به انتخاب مستقیم اقدام نمود. طبق نتایج حاصل از این پژوهش ۱۲ جمعیت *C. varia* گروه‌بندی شده در خوشه ۱ با بالاترین مقادیر برای ۱۲ از ۱۵ صفت، می‌توانند در برنامه‌های اصلاحی آینده توصیه شوند. بعلاوه، در *C. varia* var. *varia* جمعیت بجنورد (برای ارتفاع بوته و قطر تاج پوشش)، جمعیت رضوانشهر (برای طول میانگره و تعداد ساقه)، و جمعیت کرج۱ (در ویژگی عملکرد زیست توده) برای استفاده در برنامه‌های اصلاح‌نژاد پیشنهاد شدند.

کلمات کلیدی: تجزیه به مولفه‌های اصلی، رسیدگی بذر، عملکرد زیست توده، *Coronilla varia*