



Morphological variation of Persian oak (*Quercus brantii* Lindl.) in Kohgiluyeh-va-Boyerahmad province, Iran

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Abstract

Key message The studied populations of Persian oak (*Quercus brantii* Lindl.) showed high phenotypic variation that is very necessary for the planning, design, and implementation of genetic protection programs for oaks.

Abstract Persian oak (*Quercus brantii* Lindl.) the most important tree species in the Zagros region includes more than 50% of the forests in this region. In the present study, 53 morphological traits were used to evaluate phenotypic variation among 100 trees belonging to *Q. brantii* collected from 10 areas of Kohgiluyeh-va-Boyerahmad province, Iran. Considerable variability was exhibited among the trees collected based on the traits measured (ANOVA, $P < 0.01$). The coefficient of variation (CV) ranged from 12.73 (in nut diameter) to 76.06% (in the transparency of leaf upper color). Leaf margin was highly variable, including doubly serrate, serrate, broadly spiny, spiny, and narrowly spiny. Leaf blade length ranged from 59.41 to 122.53 mm, nut weight ranged from 1.39 to 17.24 g, and kernel weight varied from 0.63 to 13.09 g. Principal component analysis (PCA) showed 15 main components, which contributed 76.60% of the total variance. Cluster analysis based on Ward's method showed two different major clusters among all the trees studied. Besides, the studied 10 populations were placed into four groups in the bi-plot generated with PCA of population analysis. The studied populations of *Q. brantii* showed high phenotypic variation that is very necessary for the planning, design, and implementation of genetic protection programs for oaks.

Keywords *Quercus brantii* · Variation · Conservation · Zagros · Management

Introduction

Attention has been paid to understanding the control mechanisms of the diversity and distribution of plant species. Human interventions and global climate changes have important effects on the distribution of the habitat of a region, which can threaten biodiversity. Therefore, understanding the mechanisms of biodiversity to reduce the risks of destroying valuable genetic resources, especially in sensitive areas, such as the forest ecosystem of Zagros in the west of Iran, is essential. Zagros forests, the largest forest area in Iran, are about 5 million hectares, which include 40% of

the country's forests (FAO 2002; Sagheb-Talebi 2005). The Zagros region in Iran has a sub-Mediterranean and temperate semi-arid climate. Most of the plants growing in this region are deciduous and broad-leaved trees. The dominated trees in this region are species of the genus *Quercus* (Zohary 1973; Olfat and Pourtahmasi 2010). Some of these species are xerophytic and have a high tolerance to cold (Sagheb-Talebi 2005). *Quercus brantii* Lindl. the most important tree species in the Zagros region includes more than 50% of the forests in this region, growing at an altitude of 1000–2000 m (Sagheb-Talebi et al. 2004).

Q. brantii, known as Persian oak, West oak, and Zagros oak, is native to temperate regions in Western Asia, including Iran, Syria, Iraq, and Turkey. Its border is in the Irano-Turanian vegetation area (Panahi et al. 2012). This plant is big and its height reaches up to 20 m. Its fruits have been used as food and medicine since ancient times. This plant grows at high altitudes and has high resistance to harsh environmental and ecological conditions such as cold, heat, drought, and stony soils (Olfat and Pourtahmasi 2010).

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Genetic diversity is an important indicator for explaining the differences between different regions (Barnes et al. 1998). Various factors, such as human manipulation and environmental condition can cause the genetic diversity of living organisms to fluctuate and face danger (Austin and Smith 1989). There is a close relationship between soil and vegetation, and changes in each can have a great impact on ecosystem functions (Beno 1998). Assessment of vegetation and forest habitat and the effects of environmental factors on them are important steps toward sustainable forest management (Zahedi-Amiri and Lust 1999). Oak forests, especially the *Q. brantii* species, are the most important components of the Zagros region in Iran, which play a decisive role in soil protection, water protection and regulation, and recreational and health functions. The protection and evaluation of *Q. brantii* is most important because it is subjected to genetic erosion. Given the fact that the habitats of *Q. brantii* have been both destroyed and fragmented due to exploitation in recent decades, habitat protection is the top priority. There are few studies about these plants, especially in terms of phenotypic variation. Therefore, the present study aimed to estimate the phenotypic variation of some populations of *Q. brantii* species located in Kohgiluyeh-va-Boyerahmad province, Iran. The populations examined here are not located in protected areas, but they need attention to conservation. The obtained information can be used for better management, protection, and use of this important species.

Materials and methods

Plant material

Morphological variability of 100 trees belonging to Persian oak (*Q. brantii*) collected from 10 areas of Kohgiluyeh-va-Boyerahmad province, Iran, was evaluated for two consecutive years (2021 and 2022). The areas studied includes Kata, Meimand, Banestan, Lama, Badengan, Chitab, Telgah, Mazdak, Ghelyani, and Dashtak. Ten individual trees were selected for each area. Geographical coordinates and altitude corresponding to collection sites are shown in Table 1 and Fig. 1. For correct sampling, a proper distance of at least 200 m between the trees of each area was regarded so that the clone samples were not collected.

The characteristics evaluated

In total, 53 morphological traits (Table 2) were used to evaluate phenotypic variation among the trees. For this, 50 adult leaves and 50 mature fruits per tree were randomly selected and harvested. The dimensions of leaf, fruit, and kernel were measured using a digital caliper with 0.005 mm resolution. A digital scale with an accuracy of 0.01 g was used to

Table 1 Geographical description for collection sites of *Q. brantii* trees studied in Kohgiluyeh-va-Boyerahmad province, Iran

No	Area	Longitude (E)	Latitude (N)	Altitude (m)
1	Kata	51° 15' 28"	31° 10' 39"	1609
2	Meimand	51° 15' 45"	31° 08' 10"	1985
3	Banestan	51° 13' 11"	31° 01' 16"	1887
4	Lama	51° 12' 44"	31° 02' 59"	1545
5	Badengan	51° 14' 50"	30° 59' 41"	1470
6	Chitab	51° 19' 14"	30° 47' 22"	1757
7	Telgah	51° 21' 02"	30° 50' 04"	1613
8	Mazdak	51° 31' 27"	30° 44' 30"	1908
9	Ghelyani	51° 28' 49"	30° 47' 57"	2044
10	Dashtak	51° 25' 15"	30° 53' 32"	2405

measure the weight of fruit and kernel. The qualitative traits (Table 3) were visually examined and coded according to the previous studies on the genus *Quercus*.

Statistical analysis

Analysis of variance (ANOVA) was done using SAS software (SAS® Procedures 1990). Descriptive statistics, simple correlation between traits, and principal component analysis (PCA) were performed using SPSS (Version 16.0) software (Norusis 1998). The coefficient of variation (CV) was calculated by dividing the standard deviation of each trait by the mean of that trait. Ward's method and Euclidean distance coefficient using PAST software were applied to perform cluster analysis (Hammer et al. 2001). Also, a bi-plot was created using the first two main components (PC1/PC2) using PAST software.

Results and discussion

Considerable variability was exhibited among the trees collected based on the traits measured (ANOVA, $P < 0.01$). The coefficient of variation (CV) ranged from 12.73 (in nut diameter) to 76.06% (in transparency of leaf upper color) (Table 2). The CV in 41 out of 53 traits was higher than 20.00%, indicating strong variation among the individuals studied.

Four types of tree growth habits were observed, including spreading (19 trees), open (54), semi-erect (22), and erect (5). Moderate status was predominant in tree growth vigor, tree height, trunk diameter, canopy density, and leaf density. Trunk type was predominantly single (63 trees). Hair density on upper and lower surfaces of leaves was predominantly low (73 and 59 trees, respectively) (Table 3). Leaf shape showed strong variation, including oblong (20 trees), broadly oblong (13), oval (35), ovate (26), and obovate (6)

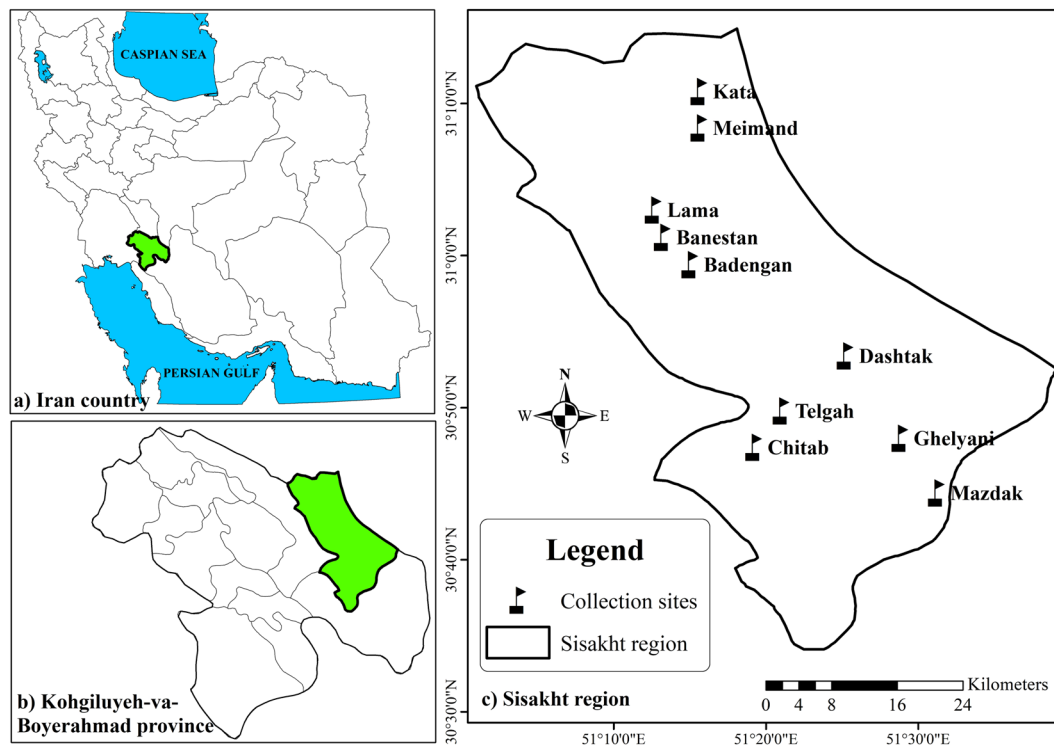


Fig. 1 Geographic locations of collection sites of the studied the studied *Q. brantii* individuals in Kohgiluyeh-va-Boyerahmad province, Iran

(Figs. 2 and 3). Leaf apex shape was rounded (22 trees), broadly acute (13), and narrowly acute (65), and leaf base shape was rounded (3), cordate (74), and truncate (23) (Fig. 3). Leaf margin was highly variable, including doubly serrate (6), serrate (21), broadly spiny (13), spiny (55), and narrowly spiny (5) (Fig. 3). Leaf fall time ranged from Early-November to Late-December (Table 3). The importance of leaf margin as a tool to study phenotypic variation between and within oak populations has been proven (Taleshi and Maasoumi Babarabi 2013; Rafezi et al. 2023). Considerable variation in leaf-related traits has been reported in *Q. brantii* populations in Iran from Ilam (Rafezi et al. 2023) and Fars (Taleshi and Maasoumi Babarabi 2013) provinces. It has also been reported that leaf-related traits are important and reliable indicators for distinguishing *Q. robur* and *Q. petraea* species from each other (Kremer et al. 2002).

The number of teeth on the right side of leaf ranged from 6 to 16, and number of teeth on the left side of leaf varied from 6 to 18, while total number of teeth varied from 13 to 34. Tooth length (for the widest tooth) ranged from 0.63 to 11.57 mm, and tooth base width (for the widest tooth) varied from 2.67 to 17.30 mm. The number of secondary veins on the right side of leaf ranged from 6 to 15, and the number of secondary veins on the left side of leaf varied from 7 to 15. The value of quantitative traits of leaf was as follows: leaf blade length: 59.41–122.53 mm, leaf blade width (the widest point): 34.17–95.30 mm, leaf petiole length:

8.24–27.03 mm, and leaf petiole width: 0.67–3.12 mm (Table 2). Rafezi et al. (2023) reported the highest values of leaf length as 98.75 mm and leaf teeth length as 6.84 mm in *Q. brantii* populations from Ilam province, Iran. As one of the most important plant organs, leaves are highly adaptable due to their response to environmental conditions such as temperature and light. Leaf structure in trees is very important for carbon sequestration because it can maintain the balance between photosynthesis and respiration (Bruschi et al. 2003).

Nut shape was predominantly ellipsoid (78 trees), and also ovoid (9 trees) and cylindric (13 trees) shapes were also observed (Figs. 2 and 4). Nut apex shape was rounded (55 trees), broadly acute (14), and acute (31), and nut base shape was truncate (38 trees), rounded (48), and acute (14) (Fig. 4). Nut color was highly variable, including yellow (21 trees), light brown (56), brown (16), and dark brown (7) (Table 3).

The value of quantitative traits of nut was as follows: nut length: 0.55–64.10 mm, nut diameter (in the middle): 11.11–21.73 mm, nut maximum transverse diameter: 11.23–21.80 mm, nut cover length (in cupule): 7.20–31.00 mm, nut weight: 1.39–17.24 g, and nut skin thickness: 0.27–1.87 mm (Table 2).

Cupule shape showed strong variation, including cylindric (24 trees), campanulate (33), cupulate (11), funnellform (8), and bowl-shaped (24) (Fig. 4). The value of quantitative

Table 2 Statistical descriptive parameters for morphological traits used to study *Q. brantii* trees

No	Trait	Unit	Min	Max	Mean	SD	CV (%)
V1	Tree growth habit	Code	1	7	3.26	1.55	47.48
V2	Tree growth vigor	Code	1	5	3.00	1.27	42.37
V3	Tree height	Code	1	5	3.08	1.48	47.89
V4	Trunk type	Code	1	3	1.74	0.97	55.75
V5	Trunk diameter	Code	1	5	3.04	1.50	49.47
V6	Trunk color	Code	1	5	3.98	1.60	40.08
V7	Canopy density	Code	1	5	3.32	1.50	45.09
V8	Leaf density	Code	1	5	3.50	1.35	38.43
V9	Leaf blade length	mm	59.41	122.53	95.50	13.38	14.01
V10	Leaf blade width (widest point)	mm	34.17	95.30	56.72	10.89	19.20
V11	Leaf petiole length	mm	8.24	27.03	15.54	4.30	27.70
V12	Leaf petiole width	mm	0.67	3.12	1.82	0.58	32.00
V13	Leaf color	Code	1	5	3.60	1.74	48.36
V14	Transparency of leaf upper color	Code	1	5	1.88	1.43	76.06
V15	Hair density on leaf upper surface	Code	1	5	1.68	1.21	72.20
V16	Hair density on leaf lower surface	Code	1	5	1.96	1.26	64.03
V17	Leaf shape	Code	1	9	4.70	2.39	50.74
V18	Leaf apex shape	Code	1	5	3.86	1.66	43.11
V19	Leaf base shape	Code	1	5	3.40	0.94	27.74
V20	Leaf margin	Code	1	9	5.64	2.02	35.82
V21	Number of teeth on the right side of leaf	Number	6.00	16.00	10.07	2.41	23.88
V22	Number of teeth on the left side of leaf	Number	6.00	18.00	10.32	2.18	21.10
V23	Total number of tooth	Number	13.00	34.00	20.39	4.32	21.18
V24	Tooth length (for widest Tooth)	mm	0.63	11.57	3.24	2.03	62.59
V25	Tooth base width (for widest Tooth)	mm	2.67	17.30	9.91	2.69	27.16
V26	Number of secondary veins on the right side of leaf	Number	6.00	15.00	10.91	1.84	16.89
V27	Number of secondary veins on the left side of leaf	Number	7.00	15.00	10.84	1.81	16.73
V28	Leaf fall time	Code	1	11	6.60	3.09	46.79
V29	Fruit stalk length	mm	2.40	11.83	5.71	2.16	37.74
V30	Fruit stalk diameter	mm	1.73	8.04	4.35	1.27	29.14
V31	Nut shape	Code	1	5	3.08	0.94	30.49
V32	Nut Symmetry	Code	1	5	2.12	1.40	66.13
V33	Nut apex shape	Code	1	5	2.52	1.80	71.47
V34	Nut base shape	Code	1	5	2.52	1.37	54.25
V35	Nut length	mm	20.55	64.10	46.36	7.04	15.19
V36	Nut diameter (in the middle)	mm	11.11	21.73	16.06	2.04	12.73
V37	Position of maximum transverse diameter	Code	1	5	1.90	1.40	73.84
V38	Nut maximum transverse diameter	mm	11.23	21.80	16.16	2.09	12.92
V39	Nut cover length (in cupule)	mm	7.20	31.00	15.93	4.41	27.71
V40	Scar diameter	mm	3.07	11.86	6.59	1.29	19.53
V41	Cupule shape	Code	1	9	4.50	3.03	67.27
V42	Cupule height	mm	8.44	28.12	18.67	4.57	24.50
V43	Cupule outer diameter	mm	11.80	25.05	18.99	2.95	15.53
V44	Cupule inner diameter	mm	10.33	20.94	15.37	2.05	13.35
V45	Cupule scale length	Code	1	5	3.20	1.57	49.06
V46	Nut color	Code	1	7	3.18	1.61	50.63
V47	Nut weight	g	1.39	17.24	7.28	3.51	48.18
V48	Nut skin thickness	mm	0.27	1.87	1.04	0.33	31.32
V49	Kernel length	mm	15.33	61.72	42.17	7.77	18.43
V50	Kernel diameter	mm	7.30	19.74	13.91	2.20	15.82

Table 2 (continued)

No	Trait	Unit	Min	Max	Mean	SD	CV (%)
V51	Kernel color	Code	1	5	4.40	1.16	26.25
V52	Kernel weight	g	0.63	13.09	5.57	2.96	53.17
V53	Nut cover/kernel	Ratio	0.13	1.50	0.38	0.25	66.46

Table 3 Frequency distribution for the measured qualitative morphological characteristics in the studied *Q. brantii* trees

Trait	Frequency (No. of accessions)						
	1	3	5	7	9	11	
Tree growth habit	Spreading (19)	Open (54)	Semi-erect (22)	Erect (5)	–	–	–
Tree growth vigor	Low (20)	Moderate (60)	High (20)	–	–	–	–
Tree height	Low (25)	Moderate (46)	High (29)	–	–	–	–
Trunk type	Single trunk (63)	Multi-trunk (37)	–	–	–	–	–
Trunk diameter	Low (27)	Moderate (44)	High (29)	–	–	–	–
Trunk color	Dark brown (19)	Gray (13)	Dark gray (68)	–	–	–	–
Canopy density	Low (21)	Moderate (42)	High (37)	–	–	–	–
Leaf density	Low (13)	Moderate (49)	High (38)	–	–	–	–
Leaf color	Light green (27)	Green (16)	Dark green (57)	–	–	–	–
Transparency of leaf upper color	Transparent (69)	Relatively transparent (18)	Matt (13)	–	–	–	–
Hair density on leaf upper surface	Low (73)	Moderate (20)	High (7)	–	–	–	–
Hair density on leaf lower surface	Low (59)	Moderate (34)	High (7)	–	–	–	–
Leaf shape	Oblong (20)	Broadly oblong (13)	Oval (35)	Ovate (26)	Obovate (6)	–	–
Leaf apex shape	Rounded (22)	Broadly acute (13)	Narrowly acute (65)	–	–	–	–
Leaf base shape	Rounded (3)	Cordate (74)	Truncate (23)	–	–	–	–
Leaf margin	Doubly serrate (6)	Serrate (21)	Broadly spiny (13)	Spiny (55)	Narrowly spiny (5)	–	–
Leaf fall time	Early-November (11)	Mid-November (11)	Late-November (16)	Early-December (26)	Mid-December (21)	Late-December (15)	–
Nut shape	Ovoid (9)	Ellipsoid (78)	Cylindric (13)	–	–	–	–
Nut Symmetry	Symmetric (56)	Slightly asymmetric (32)	Asymmetric (12)	–	–	–	–
Nut apex shape	Rounded (55)	Broadly acute (14)	Acute (31)	–	–	–	–
Nut base shape	Truncate (38)	Rounded (48)	Acute (14)	–	–	–	–
Position of maximum transverse diameter	Towards base (67)	Central (21)	All over (12)	–	–	–	–
Cupule shape	Cylindric (24)	Campanulate (33)	Cupulate (11)	Funnelform (8)	Bowl-shaped (24)	–	–
Cupule scale length	Low (26)	Moderate (38)	High (36)	–	–	–	–
Nut color	Yellow (21)	Light brown (56)	Brown (16)	Dark brown (7)	–	–	–
Kernel color	Light brown (6)	Brown (18)	Dark brown (76)	–	–	–	–

traits of cupule was as follows: cupule scar diameter: 3.07–11.86 mm, cupule height: 8.44–28.12 mm, cupule outer diameter: 11.80–25.05 mm, and cupule inner diameter: 10.33–20.94 mm.

Kernel color showed high variation, including light brown (6 trees), brown (18), and dark brown (76). The

value of quantitative traits of kernel was as follows: kernel length: 15.33–61.72 mm, kernel diameter: 7.30–19.74 mm, and kernel weight: 0.63–13.09 g. Rafezi et al. (2023) reported the highest value of kernel width as 19.53 mm in *Q. brantii* populations from Ilam province, Iran.

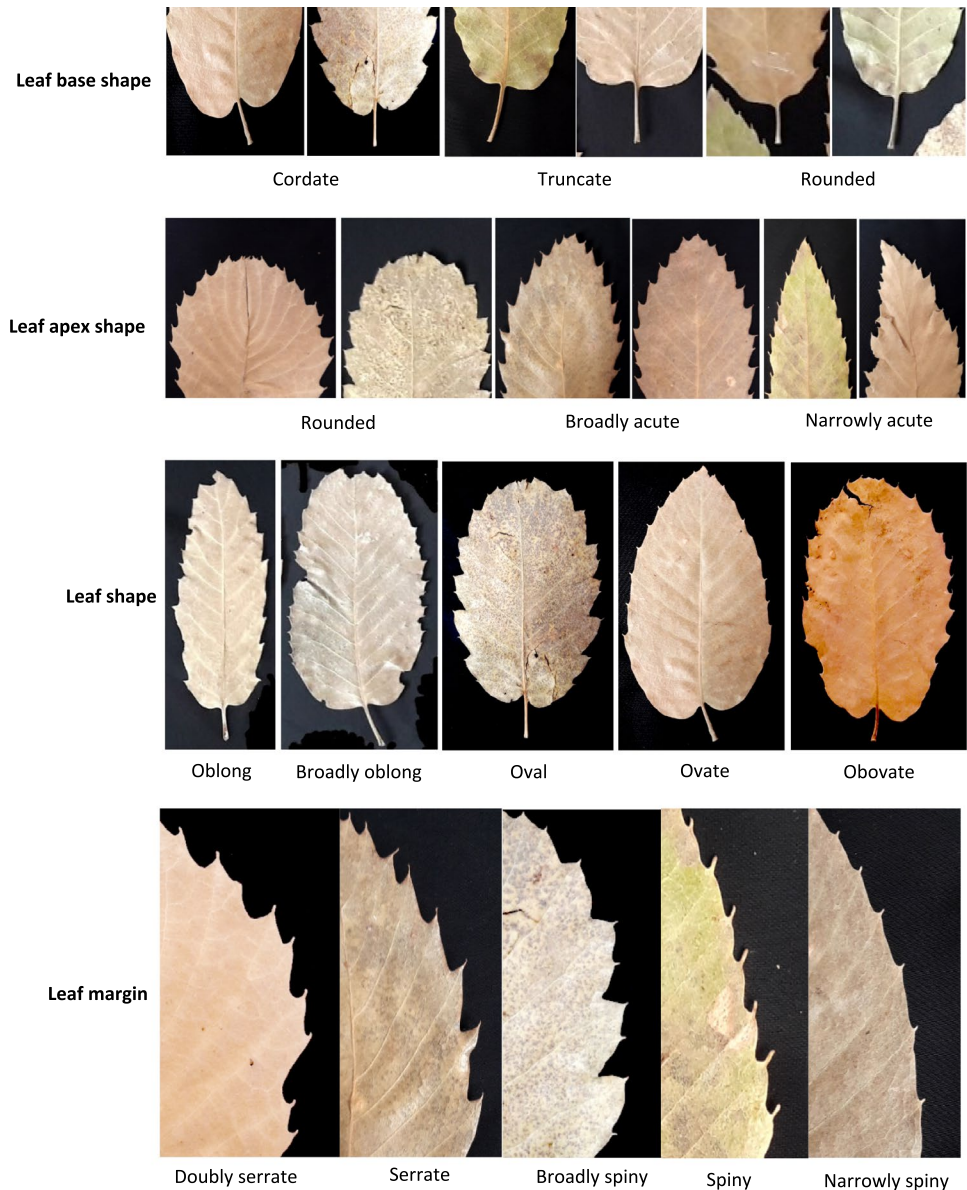
Fig. 2 Tree, leaves, nut, cupule, and kernel of the studied *Q. brantii* individuals



Significant correlations were observed between some quantitative characters (Table 4). Leaf blade length showed significant and positive correlations with leaf blade width ($r=0.41$), number of teeth on the right side of leaf ($r=0.23$), number of teeth on the left side of leaf ($r=0.20$), total number of tooth ($r=0.23$), number of secondary veins on the right side of leaf ($r=0.28$), and number of secondary veins on the left side of leaf ($r=0.29$), in agreement with previous findings in *Q. brantii* in some cases (Rafezi et al. 2023). Cupule height showed significant and positive correlations with leaf blade length ($r=0.24$), fruit stalk diameter ($r=0.35$), nut length ($r=0.43$), nut diameter (in the middle)

($r=0.29$), nut maximum transverse diameter ($r=0.31$), nut cover length (in cupule) ($r=0.72$), cupule outer diameter ($r=0.56$), and cupule inner diameter ($r=0.54$). Nut weight was significantly and positively correlated with leaf blade length ($r=0.28$), nut length ($r=0.28$), nut diameter (in the middle) ($r=0.73$), nut maximum transverse diameter ($r=0.74$), nut cover length (in cupule) ($r=0.72$), cupule height ($r=0.41$), cupule outer diameter ($r=0.40$), cupule inner diameter ($r=0.60$), and nut skin thickness ($r=0.47$), in agreement with previous findings in *Q. brantii* in some cases (Rafezi et al. 2023). Kernel weight showed significant and positive correlations with leaf blade length ($r=0.22$), nut

Fig. 3 Variation in leaf shape and margin of the studied *Q. brantii* individuals



length ($r=0.70$), nut diameter (in the middle) ($r=0.75$), nut maximum transverse diameter ($r=0.72$), nut cover length (in cupule) ($r=0.36$), cupule height ($r=0.32$), cupule outer diameter ($r=0.59$), cupule inner diameter ($r=0.47$), nut weight ($r=0.98$), kernel length ($r=0.71$), and kernel diameter ($r=0.77$), and in contracts, it was negatively and significantly correlated with nut skin thickness ($r=-0.40$), in agreement with previous findings in *Q. brantii* in some cases (Rafezi et al. 2023).

For the PCA, components with eigenvalues of more than 1.00 were retained to uphold the reliability of the final output. Thus, 15 PCs were observed which contributed 76.60% of the total variance (Table 5). The values above 0.53 were considered to be significant for the studied traits. The PC1 explained 13.83% of the total variance and it was represented

by nut length, nut diameter (in the middle), nut maximum transverse diameter, cupule outer diameter, cupule inner diameter, nut weight, kernel length, kernel diameter, and kernel weight. The PC2 was constituted by number of teeth on the right side of leaf, number of teeth on the left side of leaf, total number of teeth, number of secondary veins on the right side of leaf, and number of secondary veins on the left side of leaf, accounting for 8.21% of the total variance. The PC3 was constituted by leaf petiole width, fruit stalk diameter, cupule shape, and kernel color, accounting for 6.10% of the total variance. The above characters were the most effective traits for separating and identifying the studied trees, in agreement with previous findings in *Q. brantii* from Iran (Rafezi et al. 2023). Di Pietro et al. (2020) also obtained similar results while examining the morphological PCA of

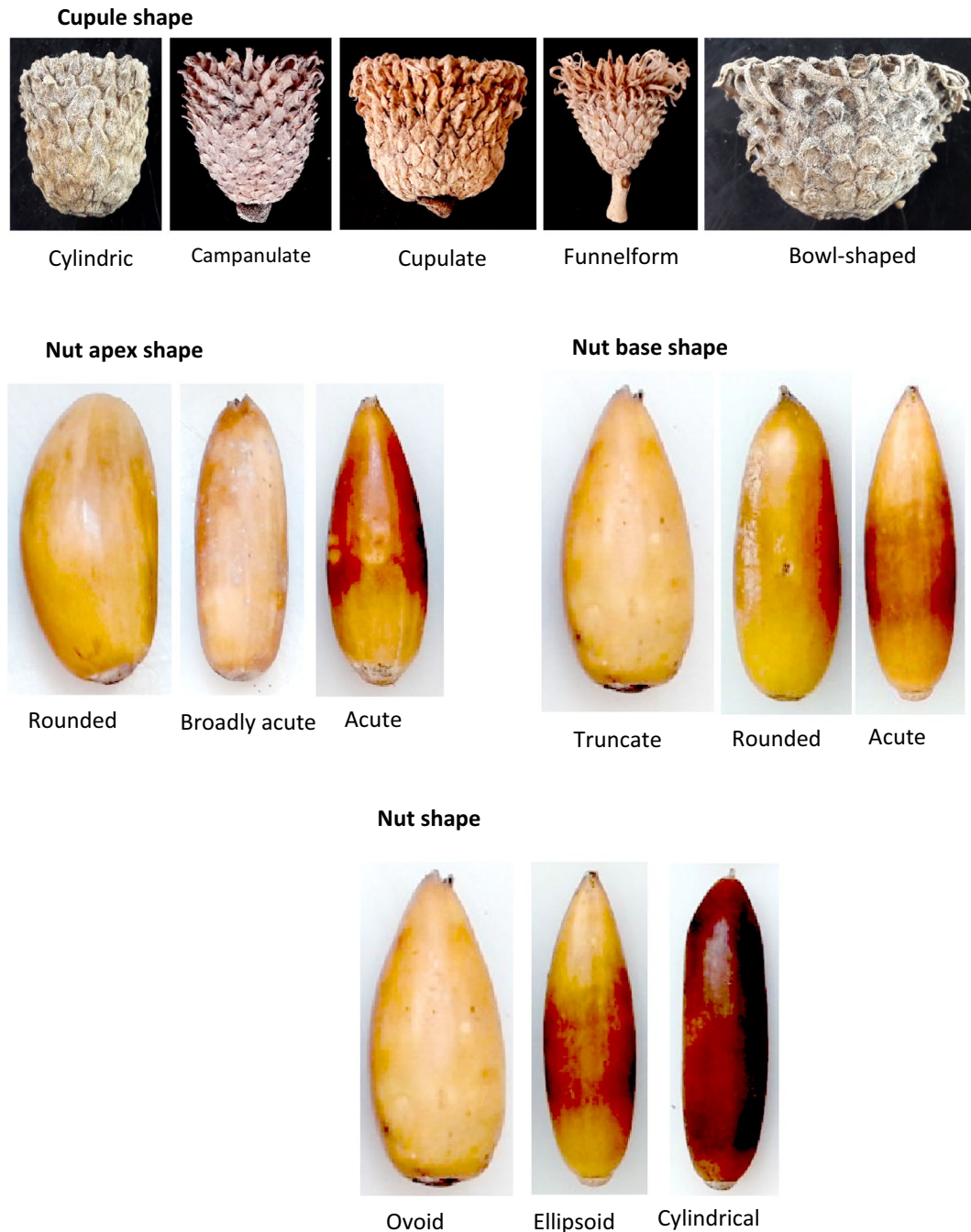


Fig. 4 Variation in cupule and nut shapes of the studied *Q. brantii* individuals

oak trees in Italy. By using PCA, the individuals and even the traits could be categorized into groups, thereby saving time and effort when screening for germplasm and populations that are worthy of breeding, as well as parent selection (Khadivi-Khub and Anjam 2014).

A dispersion bi-plot prepared according to PC1 and PC2 reflected the relationship among the trees in terms of phenotypic similarity. The trees were distributed on four sides of the plot and showed significant variations (Fig. 5). By

starting from negative toward positive values of PC1, trees showed gradual increases in nut length, nut diameter (in the middle), nut maximum transverse diameter, cupule outer diameter, cupule inner diameter, nut weight, kernel length, kernel diameter, and kernel weight. Furthermore, by starting from negative to positive values of PC2, the trees indicated gradual increases in number of teeth on the right side of leaf, number of teeth on the left side of leaf, total number of teeth, number of secondary veins on the right side of

Table 4 Simple correlations among the quantitative morphological variables utilized in the studied *Q. brantii* trees

Trait	V9	V10	V11	V12	V21	V22	V23	V24	V25	V26	V27	V29	V30	V35	V36	V38	V39	V40	V42	V43	V44	V47	V48	V49	V50	V52	
V9	1																										
V10	0.41**	1																									
V11	-0.11	0.05	1																								
V12	0.05	0.19	0.08	1																							
V21	0.23*	-0.07	-0.10	0.07	1																						
V22	0.20*	-0.13	-0.14	0.00	0.77**	1																					
V23	0.23*	-0.10	-0.13	0.04	0.94**	0.93**	1																				
V24	0.08	0.33**	0.11	0.11	-0.03	0.01	-0.01	1																			
V25	0.07	0.27**	-0.05	0.34**	-0.43**	-0.36**	-0.42**	0.21*	1																		
V26	0.28**	-0.19	0.05	-0.06	0.51**	0.43**	0.50**	-0.18	-0.35**	1																	
V27	0.29**	-0.18	0.00	-0.05	0.50**	0.49**	0.53**	-0.15	-0.36**	0.83**	1																
V29	0.11	-0.04	-0.18	0.17	0.05	-0.02	0.02	-0.13	0.13	-0.02	-0.10	1															
V30	-0.08	0.01	-0.20*	0.40**	0.13	0.17	0.16	-0.11	0.11	-0.12	-0.14	0.32**	1														
V35	0.22*	0.12	-0.17	-0.14	-0.12	-0.19	-0.16	-0.01	0.05	0.11	0.12	-0.19	-0.04	1													
V36	0.15	0.10	0.10	-0.07	0.17	0.08	0.14	0.25*	-0.02	0.11	0.12	-0.10	-0.08	0.52**	1												
V38	0.14	0.05	0.03	-0.15	0.17	0.08	0.14	0.26**	-0.03	0.07	0.09	-0.11	-0.05	0.53**	0.92**	1											
V39	0.20	0.21*	-0.07	0.01	0.04	-0.05	0.00	0.21*	-0.02	0.07	0.06	-0.13	0.24*	0.44**	0.34**	0.35**	1										
V40	-0.01	-0.05	0.09	0.29**	0.20*	0.17	0.19	0.12	0.04	0.05	0.00	0.23*	0.28**	-0.14	0.38**	0.32**	-0.02	1									
V42	0.24*	0.19	-0.07	0.01	0.04	0.04	0.04	0.10	0.04	0.06	0.06	-0.12	0.35**	0.43**	0.29**	0.31**	0.72**	-0.02	1								
V43	0.07	-0.04	-0.03	-0.12	0.11	0.12	0.13	0.15	-0.10	0.16	0.21*	-0.24*	0.03	0.44**	0.62**	0.60**	0.47**	0.20	0.56**	1							
V44	0.00	-0.11	-0.03	0.01	0.25*	0.21*	0.25*	0.11	-0.07	0.15	0.17	-0.08	0.23*	0.29**	0.66**	0.65**	0.43**	0.37**	0.54**	0.84**	1						
V47	0.28**	0.18	0.01	-0.31**	0.09	0.02	0.06	0.13	-0.12	0.19	0.20*	-0.26**	0.73**	0.74**	0.72**	0.41**	0.02	0.40**	0.60**	0.47**	0.47**	1					
V48	-0.09	0.00	-0.04	0.33**	0.07	0.04	0.06	0.10	0.00	-0.22*	-0.22*	0.02	0.15	-0.26**	-0.12	-0.10	-0.10	0.14	-0.12	-0.28**	-0.13	-0.39**	1				
V49	0.21*	0.18	-0.10	-0.16	-0.10	-0.19	-0.15	-0.03	0.04	0.08	0.11	-0.16	-0.04	0.92**	0.54**	0.55**	0.41**	-0.16	0.42**	0.42**	0.32**	0.74**	-0.34**	1			
V50	0.18	0.15	0.08	-0.04	0.13	0.03	0.09	0.26**	-0.01	0.11	0.08	-0.10	-0.09	0.56**	0.92**	0.86**	0.36**	0.31**	0.27**	0.56**	0.57**	0.75**	-0.23*	0.59**	1		
V52	0.22*	0.13	0.06	-0.37**	0.05	-0.01	0.03	0.12	-0.15	0.17	0.18	-0.27**	-0.29**	0.70**	0.75**	0.72**	0.36**	0.05	0.32**	0.59**	0.47**	0.98**	-0.40**	0.71**	0.77**	1	

*, **, Correlation is significant at $P \leq 0.05$ and 0.01 levels, respectively

Table 5 Eigenvalues of the principal component axes from the PCA of the morphological characters in the studied *Q. brantii* trees

Trait	Component														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Tree growth habit	-0.01	-0.18	0.21	0.00	-0.11	-0.02	0.04	0.01	-0.03	0.05	0.15	0.13	0.63**	0.32	-0.01
Tree growth vigor	0.03	0.09	0.09	-0.11	0.76**	0.08	-0.02	-0.03	-0.05	0.10	-0.02	-0.11	0.17	-0.16	0.05
Tree height	-0.06	0.01	0.10	0.16	0.54**	-0.06	-0.15	-0.03	0.05	0.25	0.52	-0.14	-0.03	-0.01	0.29
Trunk type	-0.15	-0.02	0.11	0.06	-0.10	0.12	-0.08	-0.18	-0.04	0.09	-0.80**	-0.09	0.08	0.03	0.04
Trunk diameter	-0.12	-0.02	-0.01	0.14	0.69**	-0.18	0.01	-0.01	0.06	0.12	0.36	-0.13	-0.20	0.03	0.19
Trunk color	-0.32	-0.11	-0.06	-0.15	-0.06	0.07	-0.41	0.27	0.25	-0.06	-0.07	0.05	-0.11	-0.04	0.30
Canopy density	0.10	-0.02	-0.22	0.02	0.74**	-0.03	0.08	-0.02	0.09	0.00	-0.07	0.13	-0.11	0.07	-0.27
Leaf density	0.12	0.06	-0.13	-0.02	0.77**	0.04	-0.08	0.09	-0.06	-0.03	0.01	0.19	-0.07	0.10	-0.09
Leaf blade length	0.17	0.31	0.02	0.00	-0.05	-0.07	0.03	0.66**	-0.02	0.14	0.07	-0.17	-0.11	0.17	-0.17
Leaf blade width (widest point)	0.11	-0.16	0.06	0.06	0.09	-0.08	0.03	0.75**	-0.12	0.16	0.16	0.11	0.08	-0.09	0.14
Leaf petiole length	-0.01	-0.13	-0.12	-0.20	0.04	0.23	0.17	0.04	0.27	0.27	-0.31	0.43	-0.08	0.07	0.19
Leaf petiole width	-0.15	0.03	0.67**	-0.18	-0.04	0.21	0.26	0.23	0.09	-0.19	-0.09	0.11	0.24	0.01	0.17
Leaf color	0.07	0.06	-0.03	-0.01	0.11	0.05	-0.05	0.21	0.05	0.80**	-0.05	0.06	0.00	-0.08	-0.04
Transparency of leaf upper color	0.25	0.00	-0.14	0.72**	-0.13	-0.06	-0.15	0.02	-0.16	-0.21	0.03	0.09	-0.04	-0.01	0.12
Hair density on leaf upper surface	0.25	0.16	-0.12	0.79**	0.01	0.10	0.15	0.14	0.17	-0.04	-0.01	0.02	0.11	0.09	-0.11
Hair density on leaf lower surface	0.08	0.12	0.05	0.85**	0.09	0.01	0.12	-0.01	0.04	0.14	-0.04	0.04	0.05	0.07	-0.05
Leaf shape	-0.10	0.07	-0.13	0.15	0.04	0.05	-0.12	0.00	0.12	0.09	0.13	0.75**	0.06	-0.01	-0.19
Leaf apex shape	-0.03	0.10	-0.05	0.04	0.05	0.09	-0.10	-0.02	-0.05	0.06	-0.01	0.14	-0.05	-0.09	-0.83**
Leaf base shape	-0.06	0.14	0.04	0.05	0.08	-0.01	-0.14	-0.31	0.22	-0.05	-0.21	0.38	0.34	0.08	-0.13
Leaf margin	0.29	-0.07	-0.14	-0.12	-0.07	-0.20	0.25	-0.20	0.17	0.32	0.27	0.12	0.11	0.40	-0.19
Number of teeth on the right side of leaf	0.03	0.89**	0.03	0.14	0.03	0.07	0.10	0.01	-0.01	0.03	0.08	-0.03	0.10	-0.13	0.01
Number of teeth on the left side of leaf	-0.06	0.87**	0.03	0.17	-0.01	0.07	-0.10	0.03	0.01	-0.11	0.07	0.08	0.04	-0.07	-0.06
Total number of tooth	-0.02	0.94**	0.03	0.17	0.01	0.07	0.01	0.02	0.00	-0.04	0.08	0.03	0.07	-0.11	-0.03
Tooth length (for widest Tooth)	0.13	-0.09	-0.14	0.21	-0.02	0.22	-0.02	0.54**	0.07	-0.13	-0.22	0.12	0.08	-0.37	0.14
Tooth base width (for widest Tooth)	-0.03	-0.52	0.26	-0.05	0.04	0.28	0.10	0.40	0.07	-0.33	0.11	-0.16	-0.04	0.11	-0.03
Number of secondary veins on the right side of leaf	0.13	0.72**	-0.02	-0.18	0.03	0.01	0.07	-0.03	0.15	0.14	-0.17	-0.08	-0.30	0.24	-0.03
Number of secondary veins on the left side of leaf	0.15	0.73**	0.02	-0.14	0.12	-0.08	0.06	0.01	0.10	0.15	-0.13	0.01	-0.26	0.25	-0.06
Leaf fall time	0.20	0.10	-0.34	-0.04	0.24	-0.02	0.15	-0.11	0.19	0.53**	0.16	0.14	-0.23	0.19	-0.05
Fruit stalk length	-0.21	-0.01	0.27	-0.05	-0.03	0.46	0.00	-0.01	-0.27	0.17	0.38	-0.31	-0.01	0.18	-0.14
Fruit stalk diameter	-0.10	0.06	0.71**	0.14	-0.19	0.04	-0.07	-0.14	0.02	0.07	0.13	-0.26	0.15	-0.14	0.01
Nut shape	-0.15	-0.03	-0.03	0.12	-0.08	-0.02	0.85**	0.14	-0.15	0.07	-0.02	-0.06	-0.07	-0.13	-0.02
Nut symmetry	-0.04	-0.01	-0.02	0.19	0.04	0.05	-0.17	-0.06	-0.15	-0.08	-0.06	0.01	0.12	0.75**	0.15
Nut apex shape	0.06	0.03	-0.35	-0.07	-0.15	-0.31	-0.22	-0.04	0.34	-0.10	0.03	-0.31	0.09	0.12	0.22
Nut base shape	-0.13	0.01	0.10	0.02	-0.02	-0.81**	0.05	-0.03	-0.06	0.07	0.14	-0.02	0.03	-0.07	0.13
Nut length	0.83**	-0.09	0.08	-0.12	0.01	-0.32	-0.05	0.09	0.01	-0.10	0.05	-0.17	-0.07	0.14	-0.02
Nut diameter (in the middle)	0.86**	0.09	-0.06	0.15	0.02	0.36	0.03	0.03	0.10	0.06	-0.01	0.01	0.10	-0.08	0.01

Table 5 (continued)

Trait	Component														
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Position of maximum transverse diameter	-0.13	0.09	0.25	-0.02	0.00	0.04	0.85**	-0.03	0.14	-0.08	0.06	-0.04	0.07	-0.02	0.15
Nut maximum transverse diameter	0.85**	0.08	-0.07	0.13	0.00	0.32	-0.05	0.00	0.05	0.03	-0.03	-0.06	0.13	-0.13	-0.03
Nut cover length (in cupule)	0.43	-0.03	0.27	0.28	-0.07	-0.22	-0.22	0.21	0.35	0.14	-0.22	-0.27	-0.02	-0.10	-0.02
Scar diameter	0.16	0.16	0.29	0.09	-0.12	0.65**	0.06	-0.10	-0.09	0.10	-0.05	0.13	0.14	-0.16	0.09
Cupule shape	0.06	0.16	-0.55**	0.00	0.11	0.31	0.03	-0.11	0.35	0.17	0.04	0.15	0.23	-0.26	0.11
Cupule height	0.39	-0.01	0.46	0.23	0.04	-0.25	-0.33	0.23	0.34	0.21	-0.02	-0.13	-0.04	-0.11	-0.18
Cupule outer diameter	0.62**	0.10	0.15	0.25	0.10	0.05	-0.15	-0.09	0.49	0.06	0.06	0.09	-0.14	-0.17	-0.07
Cupule inner diameter	0.56**	0.18	0.30	0.35	0.03	0.23	-0.11	-0.20	0.36	0.10	0.05	-0.01	-0.06	-0.25	-0.03
Cupule scale length	0.15	0.08	-0.12	0.02	0.00	-0.02	0.00	-0.10	0.83**	0.10	0.03	0.19	-0.08	-0.08	0.07
Nut color	0.28	-0.35	0.27	0.09	-0.10	-0.25	-0.19	0.13	0.01	0.24	-0.03	0.32	-0.20	-0.05	0.30
Nut weight	0.88**	0.07	-0.20	0.17	0.07	-0.09	-0.08	0.12	0.03	0.10	0.05	0.04	-0.19	0.05	0.01
Nut skin thickness	-0.28	0.02	0.10	0.11	-0.05	0.09	0.02	0.06	-0.11	-0.11	-0.25	-0.08	0.72**	-0.08	0.08
Kernel length	0.84**	-0.11	0.09	-0.13	0.05	-0.29	-0.05	0.08	-0.06	-0.02	0.08	-0.13	-0.13	0.10	0.01
Kernel diameter	0.88**	0.05	-0.05	0.11	-0.02	0.28	0.06	0.07	0.03	0.02	-0.01	0.06	0.05	-0.04	-0.01
Kernel color	-0.09	0.02	0.71**	-0.26	0.00	0.04	0.21	0.01	-0.10	-0.11	-0.10	0.03	0.10	0.08	0.06
Kernel weight	0.88**	0.04	-0.25	0.17	0.05	-0.04	-0.07	0.04	0.02	0.10	0.03	0.08	-0.20	0.06	0.04
Nut cover/kernel	-0.48	0.13	0.24	-0.01	-0.03	-0.05	0.04	0.44	-0.15	0.03	0.11	-0.14	0.13	-0.15	-0.22
Total	7.33	4.35	3.24	2.87	2.79	2.62	2.35	2.29	2.15	1.85	1.84	1.82	1.82	1.68	1.59
% of variance	13.83	8.21	6.10	5.41	5.27	4.94	4.44	4.32	4.05	3.49	3.48	3.44	3.44	3.17	3.01
Cumulative %	13.83	22.04	28.14	33.55	38.82	43.76	48.20	52.52	56.58	60.07	63.55	66.98	70.42	73.59	76.60

** Eigenvalues ≥ 0.53 are significant

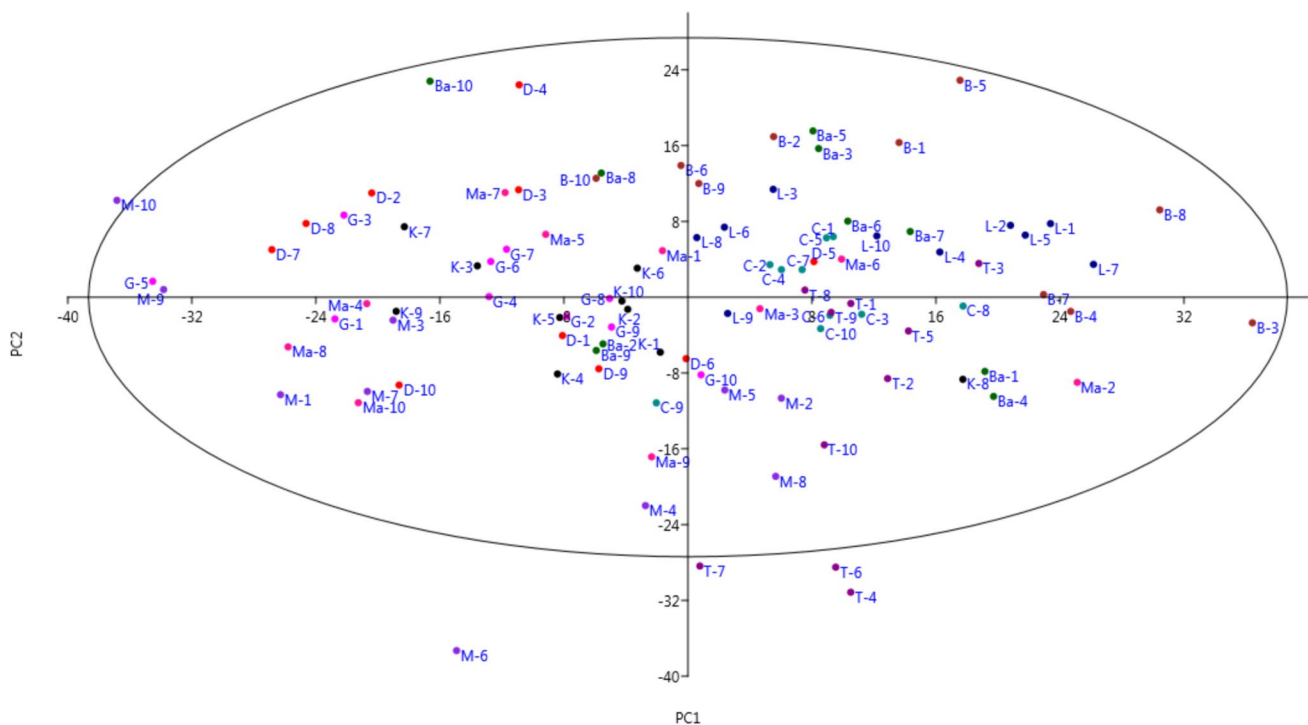


Fig. 5 Scatter plot for the studied *Q. brantii* trees based on PC1/PC2

leaf, and number of secondary veins on the left side of leaf. Meimand-6, Meimand-10, Telgah-4, Telgah-6, and Telgah-7 were placed outside of elliptic due to having the highest or lowest values for some characters. For instance, Meimand-6 was characterized by the highest values for number of teeth on the right side of leaf, number of teeth on the left side of leaf, and total number of teeth, and also the lowest values for nut length, kernel length, and kernel diameter. Meimand-10 was characterized by the lowest values for leaf blade length, leaf petiole width, and fruit stalk length. Telgah-4, Telgah-6, and Telgah-7 were characterized by the highest values for fruit stalk diameter and scar diameter and also the lowest values for nut weight and kernel weight.

Cluster analysis based on Ward's method showed two different major clusters among all the trees studied (Fig. 6). The first cluster (I) contained 50 trees, forming two sub-clusters. Sub-cluster I-A consisted of 17 trees, and sub-cluster I-B included the rest of 33 trees. Also, the second cluster (II) consisted of 50 trees studied, forming two sub-clusters. Sub-cluster II-A consisted of 8 trees, and sub-cluster II-B included the rest of 42 trees. In some cases, the trees of the same area were placed in another cluster. Nocchi et al. (2022) studied the diversity and genomic structure of oak populations using sequencing the whole genome of 360 trees from four regions in British Parkland. They reported the dispersion of Persian oak individuals from one area to other areas. Also, clear signs of differentiation were not observed among 360 samples of four populations of *Q. robur* oak in

the sampling regions (Nocchi et al. 2022). Besides, Rafezi et al. (2023) observed that all the ecotypes of only one location were clustered in the same group, while the ecotypes of the rest locations were distributed in different groups. Also, similar findings were recorded by Shabaniyan et al. (2016) and Taleshi and Maasoumi (2013) on oak populations. Zeng et al. (2011) suggested that some subspecies can exist in oak populations, indicating that the phenotypic variation obtained here may not be relevant in terms of species affinity to different subspecies. Besides, the hybrid nature of some samples of oak was proposed as a reason for genetic diversity by Pettenkofer et al. (2020). A main reason for the considerable variation observed in oak species is the natural occurrence of interbreeding within species populations. Therefore, the consistent genetic diversity among the studied individuals in the present study may be attributed to hybridization and the conserved, inherited polymorphism in *Q. brantii* and other species of oak (Rafezi et al. 2023).

In the present study, the studied 10 populations were placed into four groups in the bi-plot generated with PCA of population analysis (Fig. 7). Four populations, including Meimand, Banestan, Badengan, and Lama were placed into the first group. The Chitab and Kata populations were placed in the second group. Also, the Ghelyani and Telgah populations formed the third group. The fourth group consisted of the Mazdak and Dashtak populations. Morphological traits are effective in clustering oak populations based on environmental conditions and seasonal changes, leading to

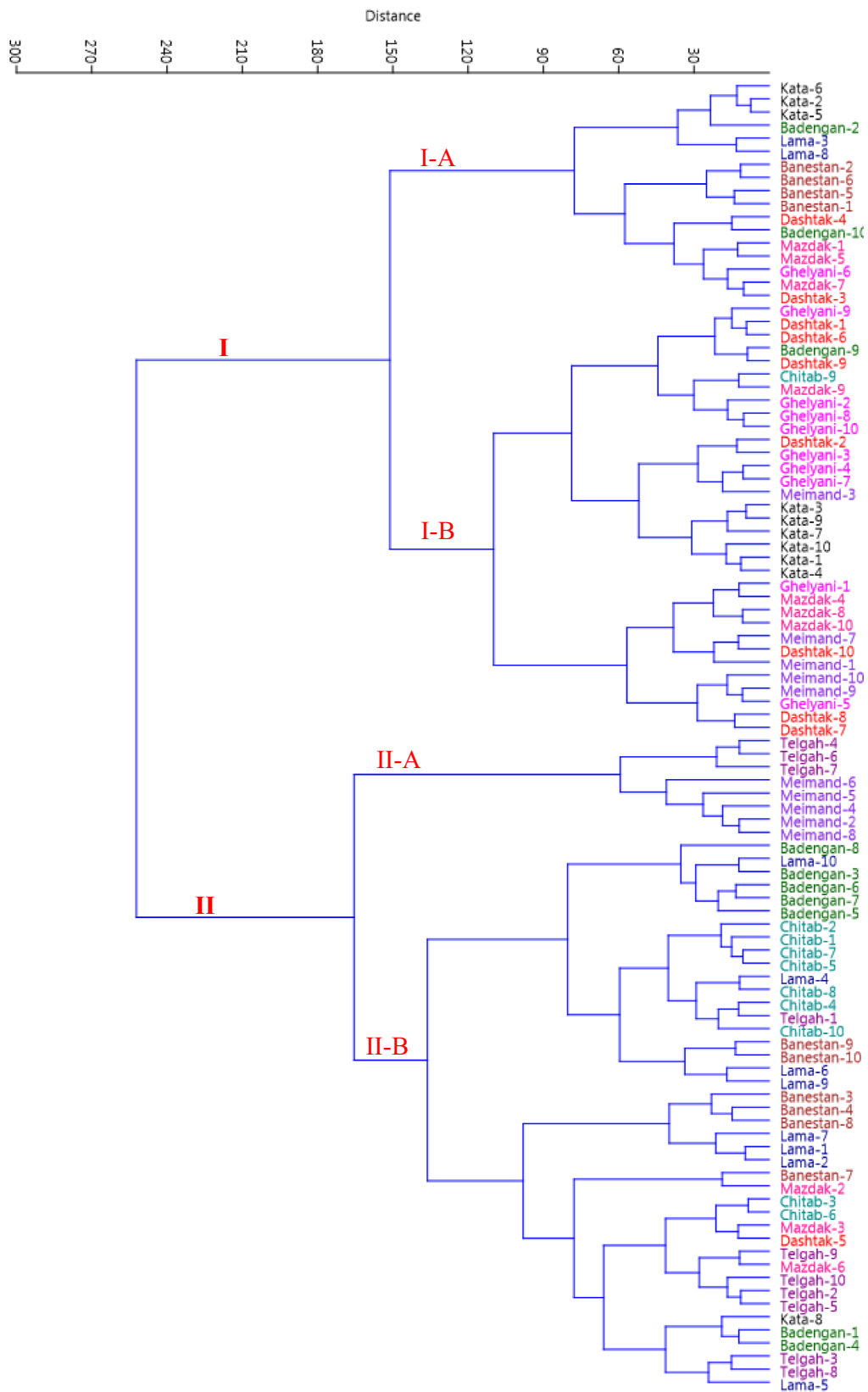


Fig. 6 Ward cluster analysis of the studied *Q. brantii* trees based on morphological traits using Euclidean distances

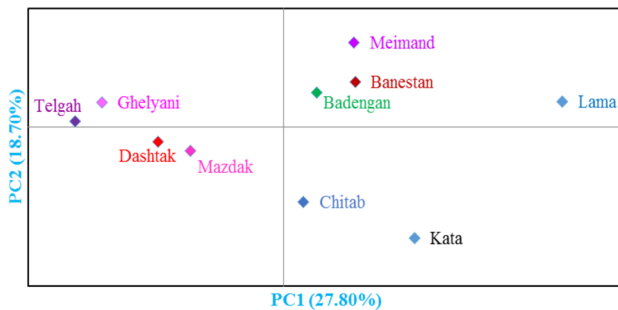


Fig. 7 Bi-plot for the studied populations of *Q. brantii* based on the morphological characters

variations from year to year (Martinik et al. 2014). The use of multiple morphological traits in statistical analysis can provide reliable results at both the intra- and inter-species level (Viscosi and Fortini 2011; Fortini et al. 2015), contrary to the previously held hypothesis that using too many traits may lead to errors.

The studied trees showed a high variation in terms of recorded characteristics. Rafezi et al. (2023) also reported that *Q. brantii* populations from Ilam province, Iran have considerable diversity in terms of morphological traits. Hybridization, genetic drift, and propagation methods contribute to the genetic diversity of plants (Conte et al. 2004; Ranker et al. 2004). Oak species have pollination self-incompatibility, and accordingly, cross-pollination is high in them, which increases the genetic diversity and gene flow within and between their populations (Hamrick and Godt (1996). Also, the amount and distribution distance of pollen have a significant effect on genetic diversity. Various studies have reported high genetic diversity of oak species (Gailing et al. 2012; Taleshi and Maasoumi Babarabi 2013; Alikhani et al. 2014; Khadivi-Khub et al. 2015; Rahmani et al. 2015; Ebrahimi et al. 2017; Mohammad-Panah et al. 2017; Rafezi et al. 2023). The main factors involved in the high diversity of morphological traits in many trees, including forest trees, are the type of pollination and intense gene flow (Bruschi et al. 2003).

A tendency for marked genetic variation and relatively limited genetic divergence is observed in abundance in tree species, such as oak. Some factors, such as longevity, high fertility, anemophilic pollination, and high seed propagation by animals probably cause this pattern. Such factors lead to a low-level differentiation among populations and thus increase homogeneity of allele frequency among adjacent local populations (Alfonso-Corrado et al. 2014; Wang et al. 2014). It has been suggested that *Q. brantii* seedlings are suitable choices for reforestation in the Zagros forests in Iran due to their high compatibility and high survival rates (Hemati 1996; Aminpour 2009; Alvani nezhad S, 2009). Persian oak is more adaptable to fluctuations in

soil fertility and available water compared with other oak species (Jazirehi and Rostaghi 2003). Furthermore, the decrease in leaf area is an adaptation mechanism in plants and plays a significant role to reduce the rate of photosynthesis leading to survival in limited water conditions (Larcher 2003; Royer et al. 2005; Xu et al. 2008). In the present study, the individuals of Ghelyani and Dashtak areas showed the lowest values of leaf blade length and leaf blade width, and they may be potentially proper for reforestation programs.

Conclusions

There is little about the phenotypic variation of *Q. brantii* in Kohgiluyeh-va-Boyerahmad province, Iran. The results showed that the studied populations of *Q. brantii* showed high phenotypic variation that is very necessary for the planning, design, and implementation of genetic protection programs for oaks. In any program for the protection of genetic reserves of plant species, the main goal should be focused on maintaining the highest possible genetic diversity in the target species in the natural ecosystems where that species grows. In addition, planting and enriching different populations of forest trees requires the expansion of genetic diversity in plant reserves to select the most suitable trees among them. Determining genetic regions based on the information obtained from morphological traits can be very useful and necessary for the production of high-quality seedlings, the production of seeds required for forestry programs, and reforestation to improve the production capacity in the forest by enhancing the ecological and economic characteristics of forest stands. Although in this study, all the populations of the habitat ecosystem of *Q. brantii* were not covered, the present results can be used to protect the genetic reserves of this species in Zagros forests, Iran.

Author contribution statement Farhad Mirheidari and Younes Moradi performed the experiment and collected data. Ali Khadivi guided all stages of the research, analyzed data, and wrote and edited the article. All authors approved the final manuscript.

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Data availability The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declarations

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

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