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Morphological Study of *Hemidactylus* Geckos (Squamata:Gekkonidae) from Iran

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The four species of *Hemidactylus* have been reported in Iran as follows: *H. persicus, H. robustus, H. flaviviridis* and *H. romeshkanicus* which is endemic to Lorestan province of Iran. In this study, 108 specimens belonging to these species of *Hemidactylus* were examined morphologically, using 19 metric and six meristic characters. The pairwise analysis of variance showed separation between *H. persicus* and *H. robustus*, *H. flavivirids* and *H. robustus* is more obvious rather than *H. persicus* and *H. flaviviridis* which have a similar body size. Multivariate analyses showed morphological differences among these three species with exception *H. romeshkanicus* which was found to be indistinguishable from the specimens of *H. persicus,* especially in the Canonical variates analysis. Additionally, previous study showed presences of high intraspecific variation among populations of *H. persicus* complex and therefore we could not definitely decide about the taxonomic status of *H. romeshkanicus* with only one specimen. But we suggest that latter species probably belongs to a local populations inside *H. persicus* complex.

Keywords: Gekkonidae, Iranian plateau, metric characters, meristic characters.

INTRODUCTION

The genus *Hemidactylus* Oken, 1817 is one of the most species-rich genera of the family Gekkonidae in the world which is widely distributed in the tropical and subtropical regions of the world and hundreds of continental and oceanic islands (Carranza and Arnold, 2006; Sindaco and Jeremčenko, 2008). This genus contains 132 species which is ranked as top ten species-rich genera of reptiles (Carranza and Arnold, 2012, Šmíd et al., 2013b, Utez and Hellerman, 2015). The genus has been witnessing a highly species description during the last decade, about twenty-two in the last three years, most from Arabian Peninsula and surroundings areas (Busais and Joger, 2011; Moravec et al*.,* 2011; Torki et al., 2011; Carranza and Arnold, 2012; Šmíd et al., 2013b; Vasconcelos and Carranza, 2014). Four species of *Hemidactylus* have been reported from south to southwestern Iran. The Persian gecko *H. persicus* J. Anderson, 1872 with continues distribution pattern along the Persian Gulf coast in Ilam, Lorestan, Khuzestan, Fars, Bushehr, Hormozgan, and Sistan and Baluchistan Provinces and the yellow-bellied house gecko *H. flaviviridis* Rüppell, 1840 mostly along the Persian Gulf coast; a more inland record recently reported from Fars Province; the Heyden's house gecko *H. robustus* Heyden, 1827 with distribution in coastal areas by the Persian Gulf in Hormozgan and Sistan and Baluchistan Provinces, including Qeshm and Larak islands and the Romeshkan house gecko *H. romeshkanicus* Torki, 2011 with a restricted distribution to Lorestan province; *H. romeshkanicus* is an endemic species to Iran and there is only one single record for its type locality from Romeshkan area in Lorestan province (Anderson, 1999; Bauer et al., 2006; Rastegar-Pouyani et al., 2008; Torki et al., 2011; Šmíd et al., 2014). However, *H. turcicus* and *H. robustus* formerly were

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considered synonyms. *H. turcicus* was believed to inhabit in large territory from the western Mediterranean across the Arabian Peninsula and Mesopotamian Plain to Iran and Pakistan for long time, but when *H. robustus* was revalidated as a full species, the eastern parts of the formerly large range of *H. turcicus* were assigned to *H. robustus* (Lanza, 1990; Moravec and Böhme, 1997; Anderson, 1999; Sindaco and Jeremčenko, 2008; Gholamifard et al., 2012; Šmíd et al., 2014). Therefore, all records of *H. turcicus* in Iran are referred to *H. robustus* in this study (Sindaco and Jeremčenko, 2008; Šmíd et al., 2014).

Morphologically, many external features of *Hemidactylus* species appear quite plastic, often varying within species or among similar species (Carranza and Arnold, 2006). Contrary to the high amount of morphological similarity within the genus *Hemidactylus* and occurrence of cryptic species, some species are geographically quite variable and may be easily confused in making identification keys, especially as some are known from only a few specimens (Carranza and Arnold, 2006; Busais and Joger, 2011). In some cases, description of new species and subspecies were based on only morphological characters and some species of *Hemidactylus* has been identified already using external traits (e.g. Moravec and Böhme, 1997; Sindaco et al., 2007; Giri and Bauer, 2008). Although, there are many cryptic species in the genus with a little morphological difference, the most described species have been based on morphological and morphmetrical studies along molecular approaches (Vences et al., 2004; Busais and Joger, 2011; Carranza and Arnold, 2012; Šmíd et al., 2013b; Vasconcelos and Carranza, 2014).

Herewith, we used multivariate analyses of metric and meristic characters to quantify morphological differences and their validity to identify the four *Hemidactylus* species in the Iranian plateau. Furthermore, the distinct taxonomic status of *H. romeshkanicus* was assessed.

MATERIAL AND METHODS

Sampling Data

During two years of field work in 2012-2013, a total of 108 specimens of the genus *Hemidactylus* were examined, including 54 males and 54 females. The studied specimens were deposited in Sabzevar University Herpetological Collection (SUHC), Collection of the Biology Department of Shiraz University (CBSU), Zoological Museum of University of Tehran (ZUTC), Department of the Environment of Hormozgan Zoological Collection (DHZC), Zoological Museum of Razi University (RUZM) and Zoological Museum of Ferdowsi University of Mashhad (ZMFUM). The morphological characters of the holotype of *H. romeshkanicus* have been measured by Frank Tillack from Zoologisches Museum of Berlin (ZMB). All specimens were studied for 19 metric and six meristic characters following Kluge 1969, Vences et al. (2004), Busais and Joger 2011, Carranza and Arnold 2012 (Table 1). Because the main sexual dimorphism in the *Hemidactylus* genus due to lack of number of preanofemoral pores in the female samples (Vences et al., 2004; Baha el Din, 2005), then this trait was excluded from data set in order to combine the morphological traits and run the same analyses for male and female. All metric and meristic characters were taken using digital calipers to the nearest 0.01 mm accuracy and the dissecting microscope, respectively. A list of collected species and their localities along with their voucher numbers are shown in Table 2; the localities are also mentioned within the map of Iran (Figure 1).

Statistical Analyses

A Multivariate Analysis of Variance (MANOVA) was performed with SPSS 16.0 and PAST v. 2.17c (Hammer, Harper& Ryan, 2001) to assess the significance of sexual dimorphism for each species using all morphological characters. To evaluate significance of differences among taxa we performed univariate analyses of variance (ANOVA).

Then principal component analysis (PCA) and canonical variates analysis (CVA) were conducted on the transformed matrix using meaningful characters. The PCA based on a correlation matrix of meaningful characters was used to determine when populations were morphologically clustered

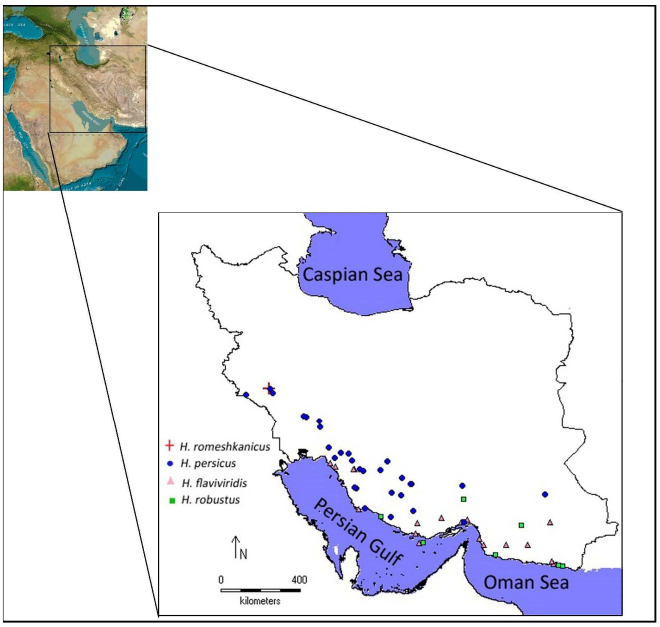

FIGURE 1. Map of the study area for the collected samples (*Hemidactylus).*

TABLE 1. The metric and meristic characters used in this study.

Characters	State definition
SVL	Maximum Snout to Vent Length (from tip of snout to cloacal aperture)
HW	Head Width (at the widest point of head)
HH	Head Height (from occiput to underside of jaws)
HL	Head Length(from tip of snout to the reteroarticular process of jaw)
CL	Caudal Length (from posterior edge of cloaca to tip of tail)
IO1	Anterior Inter Orbital distance (distance between left and right supracilary scale rows at anteriormost point of eyes)
IO2	Posterior Inter Orbital distance (distance between left and right supracilary scale rows at posteriormost point of eyes)
SL	Supra Labial scales (right)
IL	Infra Labial scales (right)
4^{th} SC	Scansors under 4^{th} toe (Counts the subdigital lamellae in a single row of scales from the base of toe to the tip of the 4^{th} toe)
1^{st} SC	Scansors under 1^{st} toe (Counts the subdigital lamellae in a single row of scales from the base of toe to the tip of the 1^{st} toe)
OD	Orbital Diameter (from greatest diameter of orbit)
EED	Eye to Ear Distance (from anterior edge of ear opening to posterior corner of eye)
SED	Snout to Eye Distance (from anterior point of eye to tip of snout)
DS	No. of Dorsal Scales (Counts the sales mid-way between the fore and hind limbs)
VS	No. of Ventral Scales (Counts the transverse row across the belly that includes the greatest number)
CS	CL/SVL
HLS	HL/SVL
HWS	HW/SVL
HHS	HH/SVL
OS	OD/SVL
O1S	IO1/SVL
O2S	102/SVL
ES	EED/SVL
SS	SED/SVL

(Sneath and Sokal, 1973). The CVA was used to determine if individuals could be assigned and correct population group based on morphological measurements (Sneath and Sokal, 1973). A hierarchical cluster analysis was performed with PAST v. 2.17c to determine which individuals were the most morphologically similar based on the unweighted pair group method with arithmetic mean (UPGMA). The *H. romeshkanicus* were included in CVA and UPGMA analysis as there was only one specimen available for morphological analysis. However, the position of *H. romeshkanicus* was only checked in the PCA morphospace compare to other species.

RESULTS

Based on MANOVA, sexual dimorphism was not significant. Therefore, both sexes were pooled together in the analyses. The results of morphological data are summarized in Table 3. According to the ANOVA, all characters except of head height, anterior inter orbital distance , snout to eye distance , head length/maximum snout to vent length and posterior inter orbital distance /maximum snout to vent length were significantly different among species for metric and meristic characters (Table 4).

The PCA for metric characters indicated that the first and second principal axes explained 30.12%, 23.28% of the total variance, respectively. The first PC is primarily orbital diameter, maximum snout to vent length and the second PC is heavily weighted by eye to ear distance, head width. The scatter plot of PC1 against PC2 showed distinctions among *H. robustus* and *H. flaviviridis*, *H. robustus* and *H. persicus,* and slight differences between *H. persicus* and *H. flaviviridis* (Figure 2A). The PCA for metristic characters implied that the first and second principal axes explained 32.37%, 20.72% of the total variance, respectively. The first PC is supra labial scales, scansors under 1st toe and the second pc is heavily weighted by scansors under 1st toe, infera labial scales. A plot of PC1 against PC2 did not completely separate the four species of *Hemidactylus* (Figure 2B). In addition, the PCA approach for meristic characters showed that the *H. romeshkanicus* was placed close to population of *H. flaviviridis*.

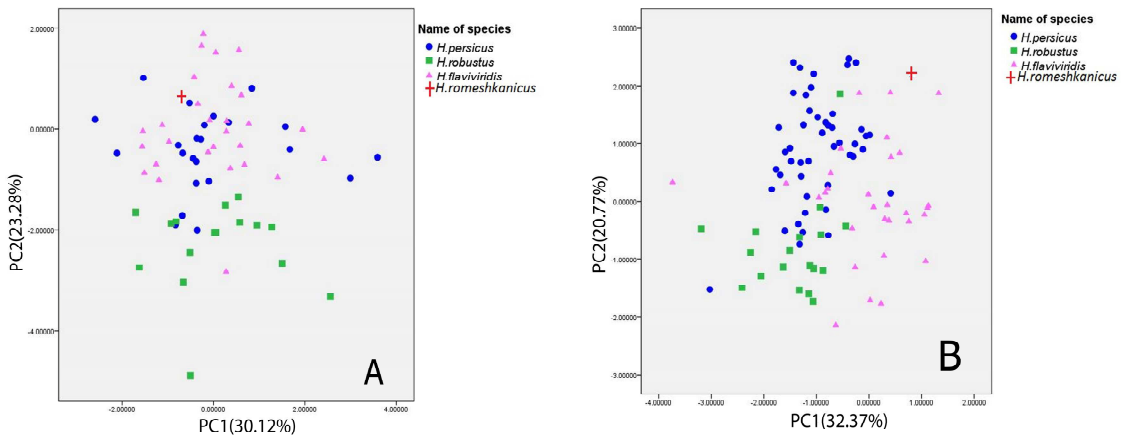

FIGURE 2. The principal components of 14 metric and six meristic characters of *Hemidactylus*. Graphs A and B parts belong to metric and meristic characters, respectively.

TABLE 2. Locality and the voucher numbers of studied specimens of *Hemidactylus*.

Species	Voucher N.	Longitude	Latitude	Locality	Num.
H. persicus	SUHC 1153-1156	49° 51' 19"	31° 31' 16"	40 Km east of Haftgel, Khuzestan Province	4
H. persicus	SUHC1222,1223	51° 52' 10"	27° 50' 49"	5Km west of Dayyer, Bushehr Province	2
H. persicus	SUHC1425,1433	51° 17' 27"	29° 59' 49"	Nourabad, Fars Province	2
H. persicus	SUHC 3623,3624	49° 14'	31° 58'	Masjed solyeman, Khuzestan Province	2
H. persicus	SUHC 3643-3645	51° 28' 45"	28° 45' 17"	Ahram mountain, Bushehr Province	3
H. persicus	SUHC 3693,3694,3696	56° 17' 34"	28° 51' 48"	Khabr national park, KermanProvince	3
H. persicus	ZMFUM 10005	49° 51' 19"	30° 18' 44"	Gakal Cave, Gachsaran,Iran	1
H. persicus	ZMFUM10001-10003	51° 09' 28"	31° 46' 26"	Izeh, Khuzestan Province	3
H. persicus	CBSU R081-R083	53° 03	27° 28'	25km NW of Lamerd, Fars Province	3
H. persicus	ZMFUM10007-10009	53° 03'	27° 28'	Varavi, Fars Province	3
H. persicus	ZMFUM10010-10011	50° 14' 30"	30° 35' 45"	Behbahan, Khuzestan Province	2
H. persicus	CBSU 8071, 8068, 8091, 8083	53° 6'	28° 33'	Gooh Gorm Jahrum, , Fars Province	4
H. persicus	CBSU 4217	53° 57'	28° 57'	Jahrum, Fars Province	1
H. persicus	CBSU 8055	51° 39' 15"	29° 37' 12"	Kazeron, Fars Province	1
H. persicus	CBSU 5395,8056	52° 34' 58"	29° 35' 19"	Shiraz, Fars Province	1
H. persicus	CBSU R111	50° 47' 37"	30° 21' 11"	Gachsaran, Fars Province	1
H. persicus	RUZM-GH 10.4	49° 7' 25"	32° 0' 25"	Masjed soleman, , Khuzestan	1
H. persicus	RUZM–GH 10.8	46° 30' 7"	32° 59' 52"	Mehran, , Ilam Province	1
H. persicus	SUHC 1558	53° 30' 30"	28° 27' 13"	Jahrom, Fars Province	1
H. persicus	SUHC 1974	52° 53' 11"	29°56' 34"	Marvdasht,Iran	1
H. persicus	DHZCH132	55° 20'	26° 55'	Qeshm island, Hormozgan Province	1
H. persicus	ZMFUM10004	54° 30' 41"	26° 17' 20"	Faro island, Hormozgan Province	1
H. persicus	ZUTC R.1222, R.1234	50° 30' 01"	30° 07' 22"	Bibi Hakemieh, Kohgiloyeh va Boyerahmad	2
H. persicus	ZUTC R.1476	58° 57'	28° 4'	Jod Village, Sistan and Baluchistan	1
H. persicus	SUHC 451, 1787	54° 04' 01"	27° 45' 18"	10 Km East of Evaz, Fars Province	2
H. persicus	CBSU B636	51° 39' 30"	29° 37' 6"	Kazeron, Fars Province	1
H. persicus	RUZM –GH 10.5,10.6,10.7	47° 43' 34"	33° 04' 20"	Pole-e-dokhtar, Lorestan Province	3
H. persicus	ZMFUM 10024	47° 37' 14"	33° 14' 59"	Romeshkan, Lorestan Province	1
H. romeshkanicus	ZMB 75020	47° 35'	33° 16'	Romeshkan, Lorestan Province	1
H. robustus	SUHC1231-1234	52° 37' 27"	27° 21' 47"	Nayband region, Asalooye, Bushehr Province	4
H. robustus	SUHC1263	57° 46' 48"	25° 39' 03"	Jask city, Hormozgan Province	1
H. robustus	ZUTC Rep.1479	58° 57'	28° 04'	Chabahar region, Sistan and Baluchistan	4
H. robustus	ZUTC Rep.1475	60° 38' 35"	25° 17' 31"	Chabahar region, Sistan and Baluchistan	1
H. robustus	ZUTC Rep.1474	60° 50' 10"	25° 15' 06"	Lipar,Chabahar region, Sistan and Baluchistan	1
H. robustus	ZMFUM10012-10020	56° 21' 57"	27° 14' 32"	Bandar abbas, Hormozgan Province	6
H. robustus	ZMFUM 10006	54° 30' 41"	26° 17' 20"	Faro island, Hormozgan Province	1
H. faliviridis	ZMFUM10022	54° 30' 41"	26° 17' 20"	Faro island, Hormozgan Province	1
H. faliviridis	SUHC1159,1160, 1163, 1164, 1165	50° 30' 23"	29° 33' 55"	Genave city, Bushehr Province	5
H. faliviridis	SUHC1185,1201-1203	50° 49' 02"	28° 54' 51"	Bushehr city	4
H. faliviridis	SUHC1206-1207	51° 56' 02"	27° 49' 57"	Dayyer City, Bushehr Province	2
H. faliviridis	SUHC1250-1252	57° 06' 13"	26° 31' 03"	Sirik city, Hormozgan Province	3
H. faliviridis	SUHC1254	56° 45' 05"	27° 21' 54"	45 Km west of Minab , Hormozgan Province	1
H. faliviridis	SUHC1255,1256,1258,1259	54° 16' 02"	26° 43' 40	Charak seaport, Hormozgan Province	4
H. faliviridis	SUHC1264-1267	60° 36' 35"	25° 21' 57"	Chabahar region, Sistan and Baluchistan	4
H. faliviridis	SUHC 1947,1948,1950	51° 38' 30"	29° 37' 15"	Kazeron city, Fars province	3
H. faliviridis	ZMFUM10023,10013,10016,10018,10021	56° 21' 57"	27° 14' 32"	Bandar abbas, Hormozgan Province	5
H. faliviridis	CBSU 8002-8004	54° 22'	27° 11' 56"	Bastak city, Fars province	3
H. faliviridis	CBSU 5310	55° 28' 50"	27° 25' 19"	Bandar abbas, Hormozgan Province	1

We used CVA to estimate the group membership of all specimens to the group which they shared the greatest morphological similarity. The CVA predicted the originally grouped samples almost correctly, including more than 78.4% and 89.4% for metric and meristic characters, respectively. Exceptionally, the single specimen of *H. romeshkanicus* evaluated 0% group membership for metric characters and it was grouped with individuals of *H. persicus* (Table 5). The CVA for metric and meristic characters indicated that the first two canonical axes explained 100% of the total variance. For metric characters, the first and second canonical functions are heavily weighted by head width, maximum snout to vent length and anterior inter orbital distance /maximum snout to vent length, eye to ear distance, respectively. For meristic characters, the first and second canonical functions are

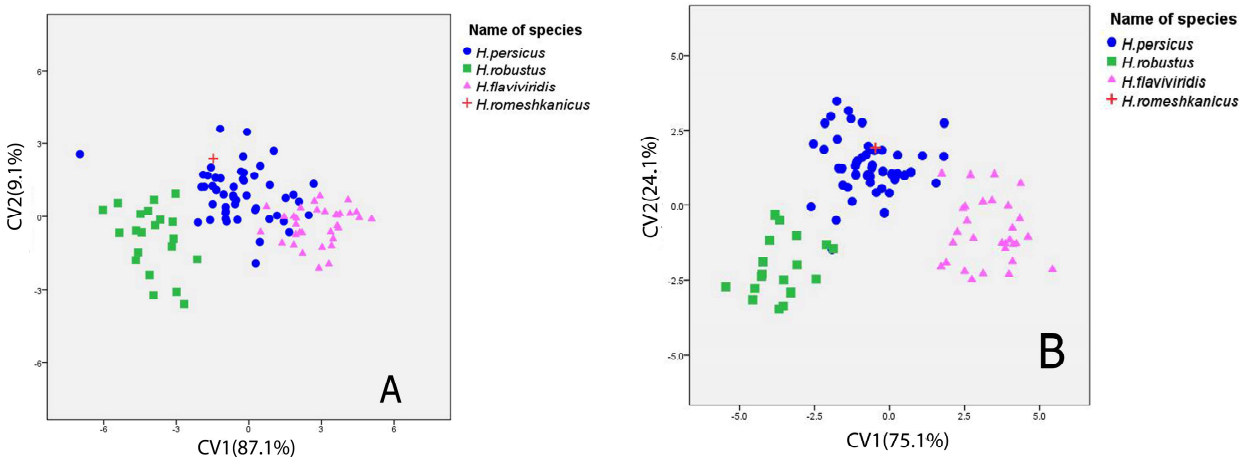

FIGURE 3. Canonical variates analysis of 14 metric and six meristic characters of *Hemidactylus*. Graph A and B parts belong to metric and meristic characters, respectively.

TABLE 3. Descriptive parameters of meaningful 14 metric and six meristic characters in the studied species of the genus of *Hemidactylus*.

Species	*H. persicus*		*H. robustus*		*H. flaviviridis*		*H. romeshkanicus*	
Characters	Mean ± SE	Range	Mean ± SE	Range	Mean ± SE	Range	Mean ± SE	Range
SVL	58.228±1.077	35.72-73.06	36.306±1.841	18.59-51.98	70.105±1.279	53.22-82.70	71.0	71.0
HW	11.496±0.2198	6.78-14.27	6.523±0.294	3.90-9.31	14.356±0.301	10.68-17.84	14.49	14.49
HL	17.104±0.286	11.77-21.59	10.789±0.427	7.06-13.89	21.733±1.458	16.40-71.57	22.47	22.47
CL	65.850±2.775	43.21-90.14	38.7825±2.96973	13.39-54.84	72.431±2.334	34.41-100.6	86.0	86.0
SL	11.500±.1646	9.00-15.00	9.333±0.1594	8.00-10.00	13.676±0.1875	11.00-16.00	11.0	11.0
IL	8.944±0.113	8.00-11.00	7.619±0.109	7.00-8.00	10.829±0.190	8.00-14.00	9.0	9.0
IO2	6.480± 0.160	8.73-3.20	3.991± 0.17	5.71- 2.87	7.804± 0.136	9.54- 6.51	8.63	8.63
OD	3.837±0.105	2.60-6.49	2.226±.115	1.18-3.04	4.01±0.0698	3.31-4.89	4.78	4.78
EED	4.421±0.101	2.41-6.03	2.918±.1203	1.81-3.96	5.547±0.145	3.87-7.82	5.08	5.08
DS	43.708±1.124	30-78	39.833±1.284	28-49	69.559±1.849	45-88	49	49
VS	43.077±0.659	31-53	35.611±0.871	30-44	41.364±1.109	31-65	36	36
1 st SC	8.537±0.139	5-11	5.952±0.129	5-7	8.171±0.190	6-10	11	11
4 th SC	12.426±0.126	10-14	10.143±0.232	9-14	12.057±0.169	10-14	14	14
CL/SVL	1.159 ±0 .030	0.83-1.35	1.030 ± 0.049	0.42-1.19	1.039 ± 0.027	0.63-1.26	1.21	1.21
HL/SVL	0.295±0.002	0.25-0.33	0.301±0.005	0.27-0.38	0.307±0.026	0.02-1.16	0.32	0.32
HW/SVL	0.198±0.003	0.12-0.34	0.181±0.002	0.17-0.21	0.199±0.006	0.01-0.23	0.20	0.20
HH/SVL	0.096±.002	0.07-0.13	0.091±0.003	0.07-0.12	0.099±0.003	0.01-0.13	0.13	0.13
OD/SVL	0.066±0.0017	0.05-0.12	0.062±0.001	0.04-0.08	0.057±0.001	0.05-0.07	0.07	0.07
IO1/SVL	0.076±0.001	0.06-0.10	0.083±0.003	0.06-0.11	0.469±0.385	0.01-0.1	0.072	0.072
IO2/SVL	0.110 ±0.0017	0.08- 0.13	0.112 ±0.004	0.09-0.16	0.112 ± 0.002	0.09 - 0.14	0.12	0.12
EED/SVL	0.076±0.0009	0.06-0.09	0.082±0.002	0.07-0.10	0.267±0.008	0.07-0.38	0.07	0.07
SED/SVL	0.1078±0.002	0.01-0.16	0.103±0.001	0.09-0.12	0.109±0.003	0.01-0.13	0.07	0.07

TABLE 4. Results of pairwise ANOVA comparisons between three *Hemidactylus* species from Iran. Asterisks mark show significance difference ($P < 0.05$).

Characters	*H.persicus- H.robustus*	*H.persicus- H.flaviviridis*	*H.robustus- H.flaviviridis*
SVL	0.000*	0.000*	0.000*
HW	0.000*	0.005*	0.000*
HL	0.000*	0.020*	0.000*
CL	0.000*	0.201	0.000*
IO2	0.023*	0.041*	0.630
OD	0.526	0.000*	0.000*
EED	0.324	0.000*	0.000*
CL/SVL	0.016*	0.009*	0.856
HW/SVL	0.000*	0.008*	0.000*
HH/SVL	0.227	0.047*	0.007*
OD/SVL	0.100	0.000*	0.126
IO1/SVL	0.003*	0.000*	0.085
EED/SVL	0.009*	0.083	0.275
SED/SVL	0.161	0.118	0.012*
SL	0.000*	0.000*	0.000*
IL	0.000*	0.000*	0.000*
DS	0.050*	0.000*	0.000*
VS	0.000*	0.168	0.000*
1st SC	0.000*	0.099	0.000*
4th SC	0.000*	0.088	0.000*

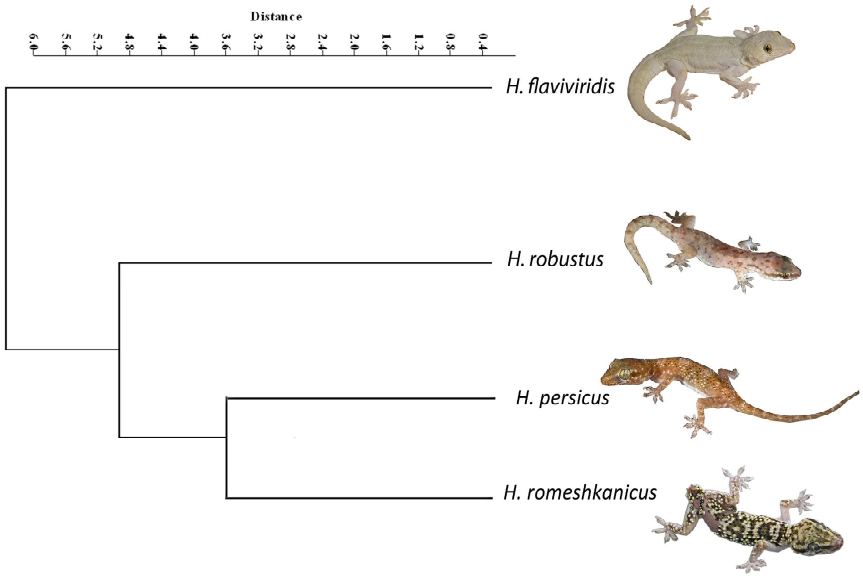

FIGURE 4. Dendrogram resulting from cluster analysis of the four studied species of *Hemidactylus* based on UPGMA.

heavily weighted by supra labial scales, infer labial scales and scansors under 4th toe and Scansors under 1st toe, respectively. The CVA for metric and meristic characters of *Hemidactylus* is given in figure 3. As is shown, there is a discernable pattern among the three species in metric characters but some overlapping was observed between *H. persicus* and *H. flaviviridis* in the metric characters. The CVA analysis showed clearly disjunction species of *Hemidactylus* in meristic rather than metric characters. In both analyses, the holotype of *H. romeshkanicus* (ZMB75020) is located within the individuals of *H. persicus* (Figure 3A, B). The cluster analysis found three major morphological clusters that correspond with close similarity of *H. persicus* with *H. robustus* and then *H. flaviviridis* grouped with them (Figure 4). Providing that all analyses of *H. romeshkanicus* were based on one specimen, suggesting they are not trustworthy.

TABLE 5. The predicted group membership of specimens belonging to one of the four a priori groups of *Hemidactylus* by the first two canonical varieties using Mahalanobis distances.

Predicted Group Membership	*H. persicus*		*H. robustus*		*H. flaviviridis*		*H. romeshkanicus*		Total		% correct	
Characters	metric	meristic	metric	meristic	metric	meristic	metric	meristic	metric	meristic	metric	meristic
Species												
H. persicus	40	42	0	2	9	0	2	3	51	47	78.4	89.4
H. robustus	0	0	21	18	0	0	0	0	21	18	100	100
H. flaviviridis	1	1	0	0	31	29	1	0	33	30	93.9	96.7
H. romeshkanicus	1	0	0	0	0	0	0	1	1	1	0	100

DISCUSSION

The results obtained based on the multivariate approach (PCA and CVA) confirmed distinctiveness of three species of *Hemidactylus* in Iran. According to pairwise ANOVA, differentiation between *H. persicus* and *H. robustus*, *H.flaviviridis* and *H. robustus* is more obvious than *H. persicus* and *H. flaviviridis*. Because of the significance of size characters in the first PC, some overlapping was specially observed between *H. persicus* and *H. flaviviridis* that are quite resemble in body size. Our finding confirmed previous studies which showed orbital diameter, head width, anterior inter orbital distance, posterior inter orbital distance and Scansors under 4th toe as informative characters for distinguishing *Hemidactylus* geckos species (Vences et al., 2004; Baha el Din, 2005; Busais and Joger, 2011; Vasconcelos and Carranza, 2014). Our data also showed that meristic characters are more powerful in separating species rather than metric characters.

According to the recently phylogenetic study on *Hemidactylus* (Carranza and Arnold, 2006), four phylogenetic lineages has been defined for this genus: (i) tropical Asian clade, (ii) *H. angulatus* clade, (iii) arid clade, and (iv) African – Atlantic clade. The *H. robustus* and *H. persicus* were clustered in the arid clade and *H. flaviviridis* was located in the tropical Asian clade. The UPGMA cluster analysis also showed compatible grouping, in which *H. romeshkanicus* grouped with *H. persicus* and then both with *H. robustus* and finally *H. flaviviridis* grouped with them. Therefore, our data suggested the position of *H. romeshkanicus* in the arid clade as previous authors mentioned (Carranza and Arnold, 2006; Torki et al., 2011; Šmíd et al., 2014). However, our morphological studies did not show precise distinctiveness among individual Persian gecko. It could be caused due plasticity in morphology and cryptic species of *Hemidactylus* gecko but molecular studies showed high intraspecific variation and are better regarded as species complex (Carranza and Arnold, 2006; Bauer et al. 2010; Šmíd et al., 2013a). Therefore, grouping the holotype of *H. romeshkanicus* within population of *H. persicus* probably implies that *H. romeshkanicus* is just a variation of local populations of *H. persicus*. However, this is also notable that we have conducted a field work in the type locality of *H. romeshkanicus,* where we collected a specimen of *H. romeshkanicus* but, after a careful and close check, it was identified as *H. persicus* and did not match with the description of *H. romeshkanicus*. In addition, we could not definitely decide about the taxonomic status of *H. romeshkanicus* with only one specimen and it needs further study.

Other studies on the morphology of the hemipenis and multiple chirp call (MC call) of *Hemidactylus* might provide more information on the Iranian *Hemidactylus* (Marcellini, 1977; Das and Purkayastha, 2012). However, some species of *Hemidactylus* geckos are ecologically separated so that they might probably occur at similar altitudes but replace each other geographically or if they are sympatric; there might be separated by altitude and/or humidity (Arnold 1980, Carranza and Arnold, 2012). Carrying out supplementary investigations would shed more light on taxonomic status of local population of the Iranian *Hemidactylus*.

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