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Biosystematics of three-toed Jerboas, Genus *Jaculus* (Erxleben, 1777) from Iran (Dipodidae, Rodentia)

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The genus *Jaculus*is distributed in Palearctic desert and semi-desert areas, extending from Central Asia to the Western Sahara in the North Africa. In Iran three species of three-toed Jerboa have been reported: *Jaculus jaculus* from the south west and west of Iran, *Jaculus blanfordi* from the northeast, east and central part of Iran and *Jaculus thaleri* from the east of Iran. In present study, the phylogenetic and taxonomic relationships in the genus *Jaculus* from Iran were examined using molecular, geometric morphometric and morphologic data. Our molecular analyses indicated two monophyletic clades which contain *J. jaculus* and *J. blanfordi*. There is a high amount of genetic interspecific distance (12.7%) between *J. jaculus* and *J.blanfordi*, while the intraspecific divergence within these two species is low. Analysis of Variance (ANOVA) of morphometric variables were significant ($P<0.05$) and shows that *J. jaculus* is significantly smaller than *J. blanfordi*. Statistical Analysis on outline data shows that there is an intraspecific geographic variation in 2nd lower molar shape in *J.blanfordi* so that northern populations are determinable from the south ones ($P_{value}= 0.016$). Although the findings strengthen an idea of presence of two subspecies in northeast and southeast of Iran, it would require further studies. In this study, expansion of *J. jaculus* to the center of Iran, suggests that it is sympatric with *J. blanfordi* in Esfahan province.

Key words: *Jaculus*, Morphometry, Cytochrome Oxidase subunit I, Iran.

INTRODUCTION

Jerboas of the genus *Jaculus* (Erxleben, 1777) are rodents belong to the family Dipodidae. They are desert dweller and their bipedal locomotion making them adapted to dried and salty regions (Harrison and Bates, 1991). First appearance of the genus related to the late Miocene from Asia and North Africa (Zazhigin and Lopatin, 2001; Holden and Musser, 2005; Shenbrotet al, 2008). In fact, different genera of Dipodines comprising the genus *Jaculus*, diversified following the formation of the Tibetian Plateau and consequent aridity of the central Asia between 5 to 8 Mya (Shenbrotet al., 1999; Zhang et al., 2012). Current distribution of this genus includes desert and semi-arid regions across northern Africa, the Sahara, and the horn of Africa, Arabia, Middle East and Central Asia (Musser and Carleton, 2005). Corbet (1978) described five extant species of this genus including Lesser Egyptian jerboa, *J. jaculus* (Linnaeus, 1758), Blanford's jerboa, *J. blanfordi* (Murray, 1884), Lichtensteini's jerboa, *J. lichtensteini* (Vinogradov, 1927), Greater Egyptian jerboa, *J. orientalis* (Erxleben, 1777) and *J. turcmenicus* (Vinogradov and Bondar, 1949). *J. jaculus* without style on glans

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penis (Didier and Petter, 1960) from the southwest of Iran and *J. blanfordi* with two styles on glans penis (Shenbrotet al., 1995) from the South and East of Iran were studied previously (Ellerman and Morrison-Scott, 1951; Lay, 1968; Corbet, 1978; Qumsieh and Mazin, 1996; Panteleyev, 1998). Darvish and Hosseinie (2005) added *J. thaleri* with the clear black color of tail flag and the too large style on the glans penis, from deserts of Khorasan Province in the east of Iran. There are two subspecies of *J. blanfordi* in Russian Central Asia: *J. b. turcomenicus* (Vinogradov and Bondar, 1949) in northern and western Turkmenia, kyzylkums and *J. b. margianus* (Shenbrot, 1989) in southern Turkmenia, ancient deltas of Tendzhen and Murgab but *J. b. blanfordi* (Murray, 1884) lives in Central, eastern and southern Iran, sometimes Afghanistan and western Pakistan (Shenbrot et al., 1995). Didier and Petter (1960) based on presence of spines on the bacula of *J. blanfordi* and *J. orientalis* considered them monophyletic and separated *J. jaculus*. Moreover, genetic divergence and variability of proteins between *J. jaculus* and *J. orientalis* were investigated based on 25 protein loci and the divergence time was estimated to be about 9.6 million years ago between these two taxa (Shahin, 2003). Karyological differences between *J. jaculus* and *J. orientalis* from Tunisia (Ben Falehet al., 2010a) and *J.jaculus* and *J.blanfordi* from Iran (Mohammadi et al., 2013) were reported. Ranck (1968) recognized two cryptic species in the complex species, *J. jaculus* (Linnaeus, 1758) and proposed *J. deserti* Loche, 1867as a separate cryptic species based on coloration and skull characters, which was rejected by Harrison (1978). Ben Falehet al (2012a) addressed phylogeographical analyses of mitochondrial Cytochrome b gene for reconstructing of phylogenetic history of *J.orientalis* in Mediterranean North Africa. Moreover, Ben Falehet al (2010 b & c), based on phylogenetic analysis of 23 allozymic loci and *Cyt b* gene beside multivariate analysis of morphological traits, recognized two distinct sympatric populations of *J. jaculus* and *J. deserti* in Tunisia and validated the taxonomic rank of species for *J. deserti.* Additionally, the Middle Pleistocene climatic change (1.65–4.92 Mya) was suggested to be the cause of diversification between *J.jaculus* and *J. deserti* in the North Africa and the status of the third clade from the Middle East remained questionable (Ben Falehet al., 2012b). Reconstruction of geographical history based on mitochondrial and nuclear markers suggested recent North-West expansion of *J. deserti* in Africa and proposed Mid-Upper Pliocene aridity of the North Africa as a result of diversification of these two cryptic species (Boratynski et al., 2012).

Morphometric analyses increasingly use in conjunction with analyses of molecular data (Dryden and Mardia, 1998; Ben Falehet al., 2013). Few studies have been done on the genus *Jaculus* in Iranian Plateau (Darvish and Hosseinie, 2005; Darvish and Rastegar-Pouyani, 2012). According to Musser and Carleton, 2005, there had only been two species of this genus, *J.jaculus* and *J. blanfordi*, in Iran until Darvish and Hosseinie (2005) introduced *J. thaleri* in the north east. Most researches had been done on the basis of morphological and morphometrical studies in this region (Darvish and Hosseinie, 2005; Darvish and Rastegar, 2013). In order to consider species status of this genus in the Iranian Plateau, we analyzed the mitochondrial DNA, Cytochrome Oxidase subunit I (CoxI) of different species by molecular method, morphometric characters and geometric morphometric on different populations.

MATERIAL AND METHODS

The sample studied consisted of 73 three-toed Jerboas trapped in desert and semi desert of the Iranian Plateau for morphometric, 68 for geometric morphometric analysis and 32 samples for molecular analysis (Table 1 and Fig. 1).All specimens are deposited in the Zoology Museum of Ferdowsi University of Mashhad (ZMFUM), Iran.

TABLE 1. Number and locality of the samples.

Number of specimens for morphometry analysis	Number of specimens for outline analysis	Number of specimens for Sequencing	locality
1	1	1	Bojnord
2	1	2	Gonabad
3	4	3	Yazd
2	1	1	SistanBaluchestan
6	6	3	Esfahan
12	8	-	Nehbandan
7	9	-	DaghalZabol
2	-	3	Saravan
1	-	-	Afghanistan
9	13	2	Kashmar
5	3	3	Bajestan
6	5	-	Bushehr
7	7	6	Khuzestan (MahShahr)
7	7	7	Ilam
1	1	1	Kavire-Mesr
1	2	-	Ferdows
1	-	-	Tabas
73	68	32	Total

MORPHOMETRIC METHOD

11 cranial and 12 dental morphometric variables were measured by digital caliper and a Nikon measuring microscope MM-40 to the nearest 0.01 mm and 0.001 mm, respectively. These characters include: Condylo-basal length (LCB), Rostrum length (LR), Zygomatic length (LZ), Mastoid breadth (BM), Zygomatic breadth (BZ), Braincase breadth (BB), Inter-orbital breadth (BI), Rostrum base breadth (BR), Braincase height (HB), Tympanic bulla width (WB) as cranial characters and Upper tooth row length (UR), Length of first molar (upper) (ML1), Width of first molar (upper) (MW1), Length of second molar (upper) (ML2), Width of second molar (upper) (MW2), Length of third molar (upper) (ML3), Width of third molar (upper) (MW3), Length of first molar (lower) (M1L), Width of first molar (lower) (M1W), Length of second molar (lower) (M2L), Width of second molar (lower) (M2W), Length of third molar (lower) (M3L) and Width of third molar (lower) (M3W) as dental characters (Shenbrot, 2009) (Fig. 2). Comparison of Means was carried out using single and multiple analyses of variance. ANOVAs were conducted for comparison of each of the 23 parameters. To normalize distribution, all measurements were log-transformed. Canonical Variate Analysis (CVA) was conducted using PAST 2.06 (Hammer et al., 2011) to maximize the variance among groups relative to that within groups. To comparing both species, a pictogram and a ration chart have plotted based on the length of LCB and M1L and also whole measured morphometric characters, respectively.

GEOMETRIC MORPHOMETRIC ANALYSIS

- Digitizing

The outline of the occlusal surface of second lower molar teeth (m2) performed on 47 examined specimens from 17 sites spread across Iran. Images were captured using a digital camera (DP71) connected to a stereomicroscope (Olympus SZH10) with magnification of 10x. Molar outlines were

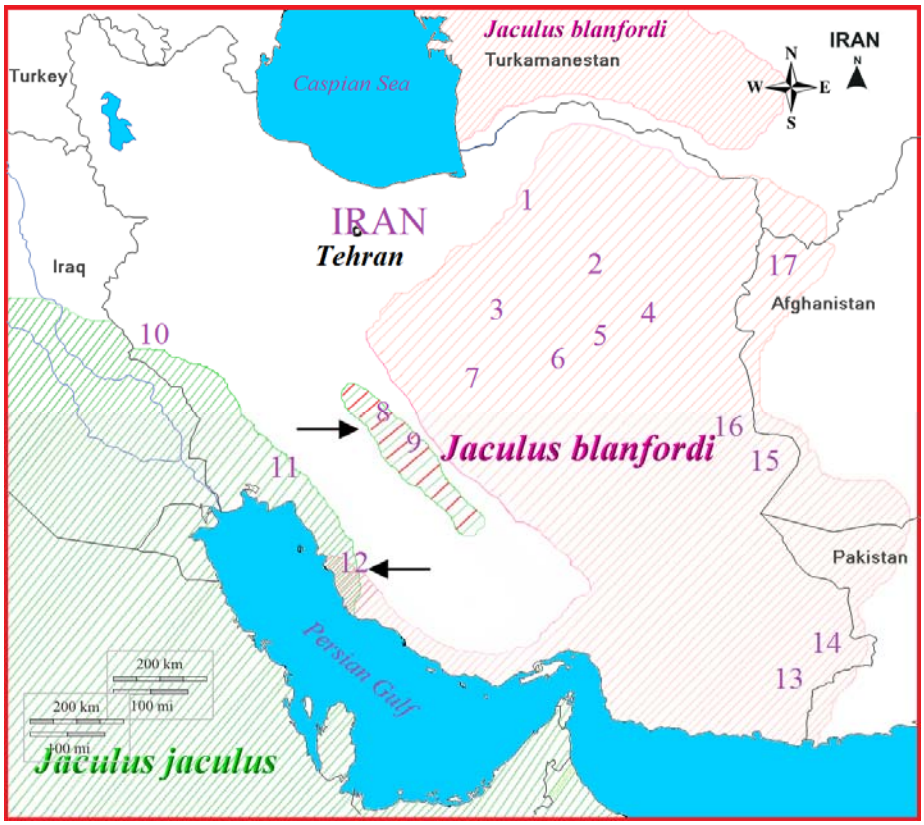

FIGURE 1. The map of the locality that samples were captured (1-Jajaram, 2-Kashmar, 3-Bajestan, 4-Gonbad, 5-Ferdows, 6-Tabas, 7-Yazd, 8-Esfahan, 9-Kavire-Mesr, 10-Ilam, 11-Khuzestan, 12-Bushehr, 13-Saravan, 14-Khash, 15-Daghal, Zabol, 16-Nehbandan, 17- Harat, Afghanistan) and the distribution areas of *J. jaculus* and *J. blanfordi* in Iran. Arrows indicate locations of presence of both species.

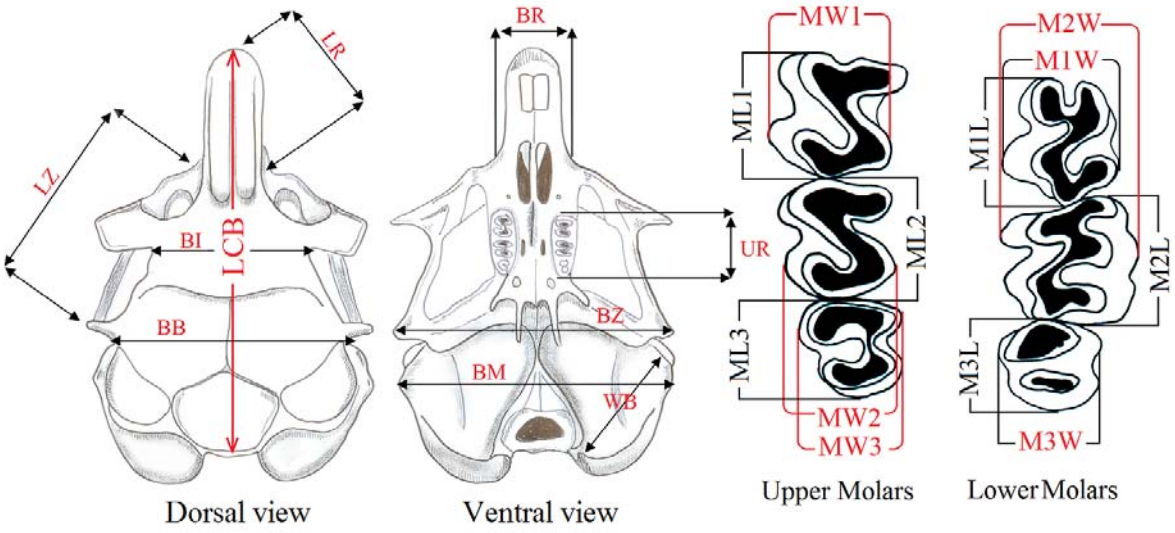

FIGURE 2. Cranial and dentalmeasured characters.

digitized clockwise by hand using TPS.DIG 2.10 (Rohlf, 2006). Since outline is sensitive to started point, all outlines conducted at the apex point of second molar tooth i.e. the most anterior point of the molar. The EFAWIN software (Rohlf and Ferson, 1992) was used to conduct an EFA. The program GMTP (Taravati and Darvish, 2010) was used to adjust the tpsDig output file format directly opened in EFAWIN.

- Elliptic Fourier and statistical Analyses

The first 15 harmonics were included in shape analysis. The 57 coefficients were used as variables in SPSS 16 and PAST. The centroid size was calculated for each individual. The size of the teeth was estimated by the square root of the outlined area, and size variation was analyzed with an ANOVA test. For visualizing the size variation among groups, a 95% confidence interval error bar graph was plotted. In addition, sexual dimorphism was tested for both molar size and shape. A Canonical Variates Analysis (CVA) was conducted to identify the main axes of differentiation between populations and a multivariate regression between size and shape was used to test for allometry effects on shape (Cucchi, 2008).

MOLECULAR METHOD

Genomic DNA of 32 specimens was extracted from muscle and heart by Salt method (Bruford et al., 1992). Complete *Cox1*gene was performed using the universal primer VF1d: 5 ' -TTC TCA ACC AAC CAC AAR GAY ATY GG-3 'and VR1d: 5 ' -TAG ACT TCT GGG TGG CCR AAR AAY CA-3 ' (Ivanova et al., 2006). Amplification of *Cox1* was carried out (Aliabadian et al., 2007). The amplified DNA fragments were sequenced commercially using the automated sequencer ABI prism 3700 at Macrogen Inc. (South Korea). In addition to specimens from Iran, one *Dipus sagitta* (JX962300) and one *Allactaga elater* (JQ954899) were retrieved from GenBank as outgroups (Table 1).

PHYLOGENETIC ANALYSES

The nucleotide sequences were aligned using the ClustalW program (Thompson et al., 1994) as implemented in the program Bioedit sequence alignment editor, ver. 7.0.9 (Hall, 1999). Genetic distance was calculated with MEGA v4.0 (Tamura et al., 2007) with the Kimura 2-parameter (K2P) model (Kimura, 1980). The final aligned dataset included 626bp for each taxon.

Maximum likelihood (ML), Maximum parsimony (MP) and Bayesian phylogenetic analysis were carried out. ML and MP were performed using PAUP* 4.0b10 (Swofford, 2002), with 500 and 5000 bootstrap replicates under ML and MP, respectively. Maximum likelihood carried out under heuristic tree search with 10 random addition sequence replicates, and tree bisection reconnection (TBR) branch swapping. Maximum parsimony analyses were performed using heuristic searches with tree-bisection-reconnection (TBR) branch swapping and random addition sequence with 1000 replicates. Bayesian analysis was conducted with MrBayes 3.1.1 (Huelsenbeck and Ronquist, 2001). Four simultaneous Markov chain Monte Carlo (MCMC) with incremental heating temperature 0.2 run 6000,000 generations and sampled every 100 generations. The burn-in size was determined by checking the convergence of −log likelihood (−InL) values, and the first 10% generations were discarded.

A minimum spanning network was constructed for *Cox1* using the TCS software package (Clement et al., 2000). It calculates the number of mutational steps by which pairwise haplotypes differ and computes the probability of parsimony for pairwise differences until the probability exceeds 0.95 (Templeton et al., 1992).

TABLE 2 Comparison of 23 morphometric variables among the specimens of *Jaculus*using ANOVA means with standard error (SE) and significance.

	J. jaculus N=25		*J. blanfordi* N=47		*P*-value
variables	Mean	S.D	Mean	S.D	
LCB	1.482	0.020	1.541	0.015	0.000
LR	1.005	0.024	1.043	0.018	0.000
LZ	1.184	0.030	1.244	0.019	0.000
BM	1.359	0.229	1.406	0.015	0.000
BZ	1.346	0.033	1.391	0.020	0.000
BB	1.276	0.024	1.328	0.012	0.000
BI	1.083	0.020	1.134	0.020	0.000
BR	0.879	0.022	0.924	0.023	0.000
HB	1.140	0.012	1.175	0.011	0.000
WB	1.005	0.023	1.055	0.019	0.000
UR	0.753	0.011	0.789	0.016	0.000
M1L	0.408	0.023	0.440	0.019	0.000
M2L	0.404	0.011	0.425	0.010	0.000
M3L	0.338	0.021	0.361	0.015	0.000
M1W	0.381	0.032	0.399	0.037	0.037
M2W	0.366	0.036	0.389	0.042	0.048
M3W	0.302	0.029	0.329	0.026	0.002
ML1	0.423	0.013	0.457	0.013	0.000
ML2	0.420	0.015	0.449	0.013	0.000
ML3	0.339	0.026	0.367	0.023	0.000
MW1	0.362	0.035	0.386	0.039	0.083
MW2	0.377	0.035	0.401	0.038	0.088
MW3	0.314	0.031	0.343	0.346	0.001

RESULTS

MORPHOMETRIC DATA

Analysis of Variance (ANOVA) of the data showed that 21 of 23 morphometric variables were significant (P<0.05) (Table 2). Standard descriptive statistics including the mean and standard deviation for 23 cranial and dental measurements of *Jaculus* are given in Table 2. The CVA scatter-plot showed that the two species are separated clearly (P=0.000 and Wilks Lambda = 0.072) across the CV1 (100% of all variances) (Fig. 3). According to a pictogram that has plotted in figure 4, *J.blanfordi* is characterized by bigger length of LCB and M1L than *J. jaculus*. Moreover, *J. jaculus* is smaller among all of measured morphometric characters (Fig. 5).

GEOMETRIC MORPHOMETRIC DATA

The centroid size (CS) data was checked for normality (P=0.252 for *J. jaculus* and P=0.006 for *J. blanfordi*) and homogeneity of variances by Levene`s test (P=0.32). The results of Mann-Whitney for CS was significant (P=0.001). Therefore, the null hypothesis was rejected. Sexual dimorphism was tested on centroid size and Fourier coefficients, the results showed differences between sexes were not significant (P=0.439 for size and P=0.138 for shape).So the male and female specimens were pooled. Mean and 95% confidence interval for CS are presented in figure 6. According to the plot, *J. blanfordi* is characterized by broad molar while *J. jaculus* is characterized by slender one.

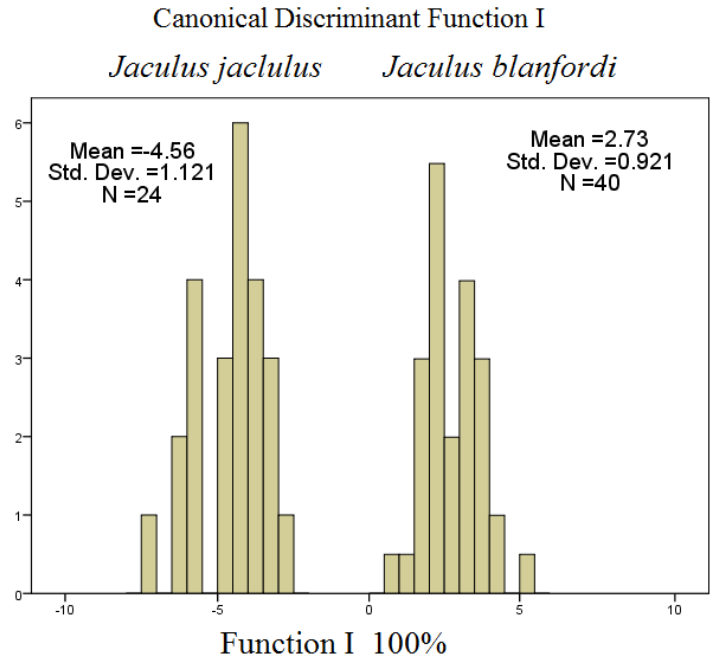

FIGURE 3. Scatter plot of CVA analysis, based on all measured morphometric variables of *Jaculus*.

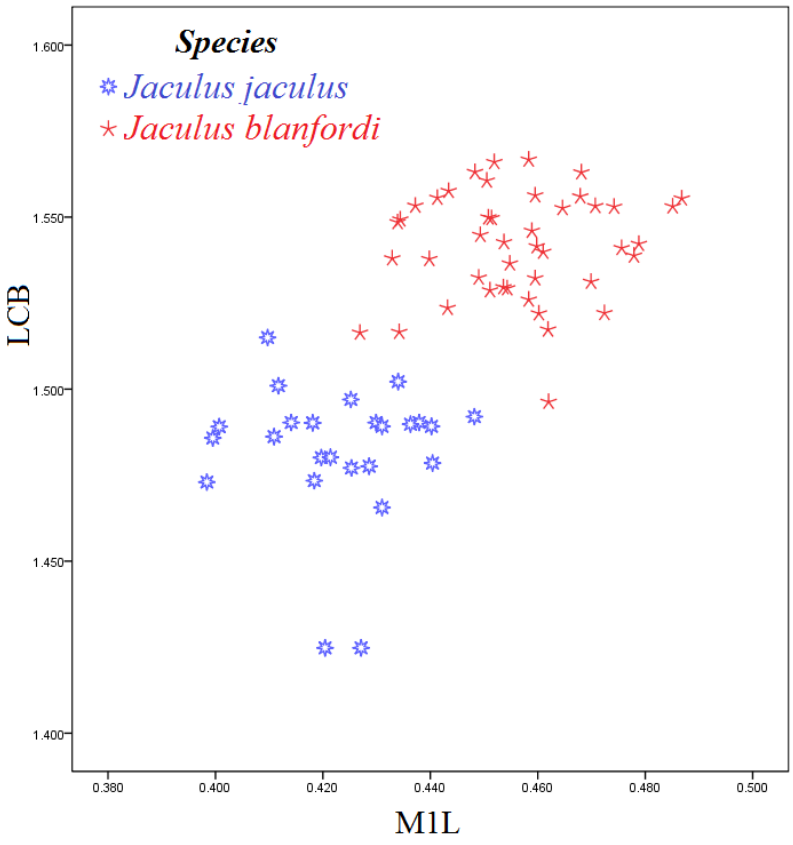

FIGURE 4. Projection specimens belonging to two species on pictogram of two morphometric characters LCB (length of condilobasal) and M1L (length of first upper molar).

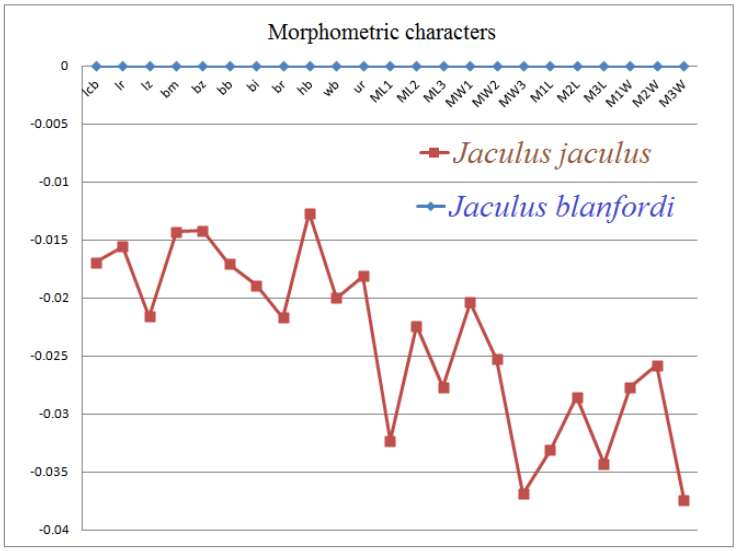

FIGURE 5. The ratio chart of whole morphometric characters which indicate all of measured variable in *J.jaculus* are smaller than *J.blanfordi*.

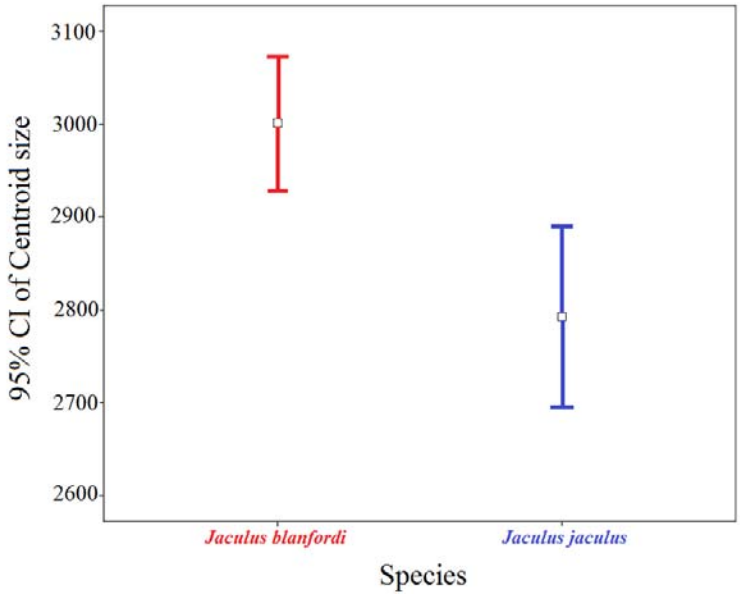

FIGURE 6. 95% confident interval for centroid size of second lower molar in two species of *Jaculus*. The circle on each line is mean. Same results were achieved by traditional morphometric and also landmark technique (Not shown).

In discriminant function analysis, the first component was responsible for 100% of variance. The Wilk`s lambda value confirmed the significance of this function (P=0.008).Projection of the species on the discriminant function is shown in figure 7. *J. jaculus* was separated with positive scores on DF1 while *J. blanfordi*, with negative one.The regression between centroid size and shape variables was not significant ($P_{regress}$=0.4167 and Wilk`s lambda = 0.06415). Therefore, differences in m2 shape were not related to the allometry. The correlation among centroid size, the first three PCA axes and CV axis was conducted by PAST and the highest correlation (0.44318) was observed between centroid size and CV axis (Fig. 8). According to the plot, *J. blanfordi* was separated by positive scores on CV axis and bigger centroid size in comparison with *J. jaculus*.

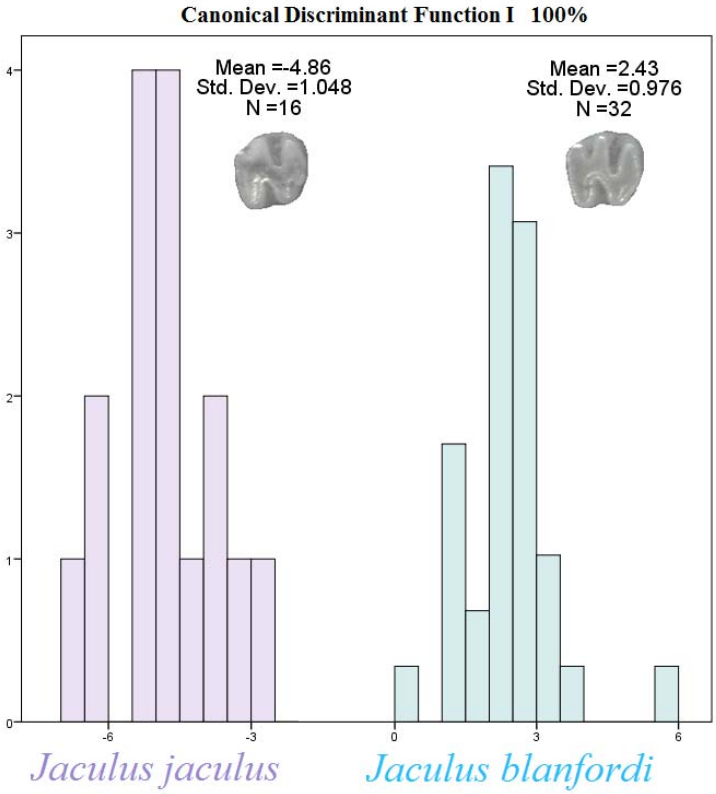

FIGURE 7. The projection of two species on function of CDA according to the shape of 2nd lower molar. Horizontal axis explains 100 % of whole variance.

MOLAR MORPHOLOGY

In general the length of M1and m2 in genus *Jaculus* is nearly equal in size, while m2 is larger than m1 (Fig. 9).The molars are brachyodont with distinguishable crown and roots parts (Shahin, 1999). M1, M2 and M3are tetra cuspidate, the cusps are: Protocon and Hypocon in labial side, Paracon and Metacon in lingual side, the cusps form a Z-shaped pattern (Fig. 9).m1and m3 are tetra cuspidate with Protoconide and Hypoconide in labial side, Metaconide and Entoconide in lingual side.M2 is panta cuspidate with a mesolophide in labial side between Protconide and Hypoconide (Fig. 9).

During morphogenesis, the molars erupt into four separate cusps or cuspids except m2 which arises by five cuspids. In the molars morphogenesis process, these cusps and cuspids gradually become confluent together and the whole structure becomes either tetra cuspidate in M1, M2, M3, m1 and m3 or penta cuspidate in m2 (Fig.9). For dental morphology, *J. jaculus* is characterized by smaller molars and an anterior fine notch (AN) in some specimens. On the contrary, *J. blanfordi* has larger molars with interaspecific variations in the shapes and the places of cusps and cuspids and presence of labial and lingual conules in the first lower molars. In addition, the anterior notch is remarkable in *J.blanfordi*. Due to wear of cusps and cuspids during life, the structure of molars is variable.

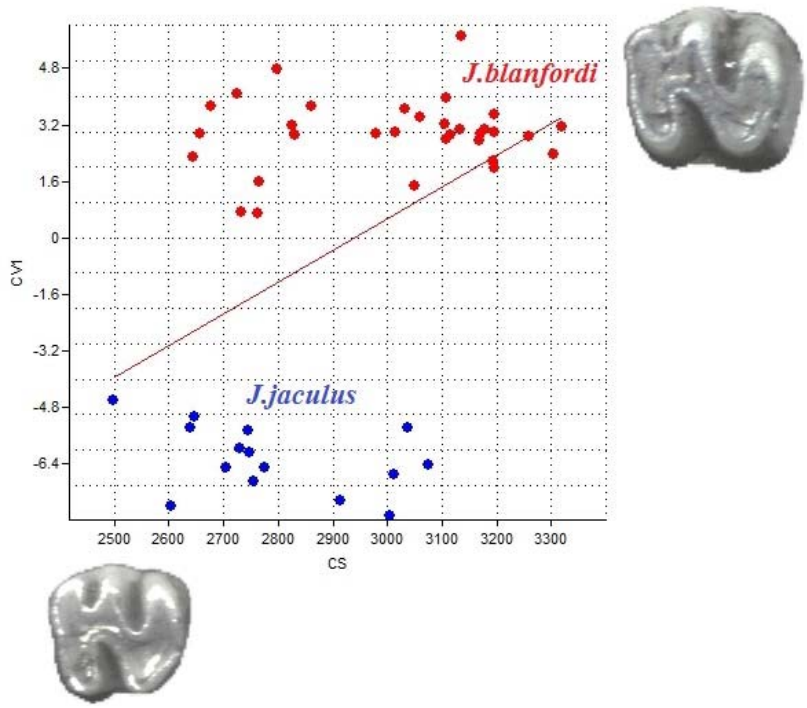

FIGURE 8. Projection of examined specimens belonging to two species based on correlation centroid size and CV axis. Heterogeneity in *J.blanfordi* is visible.

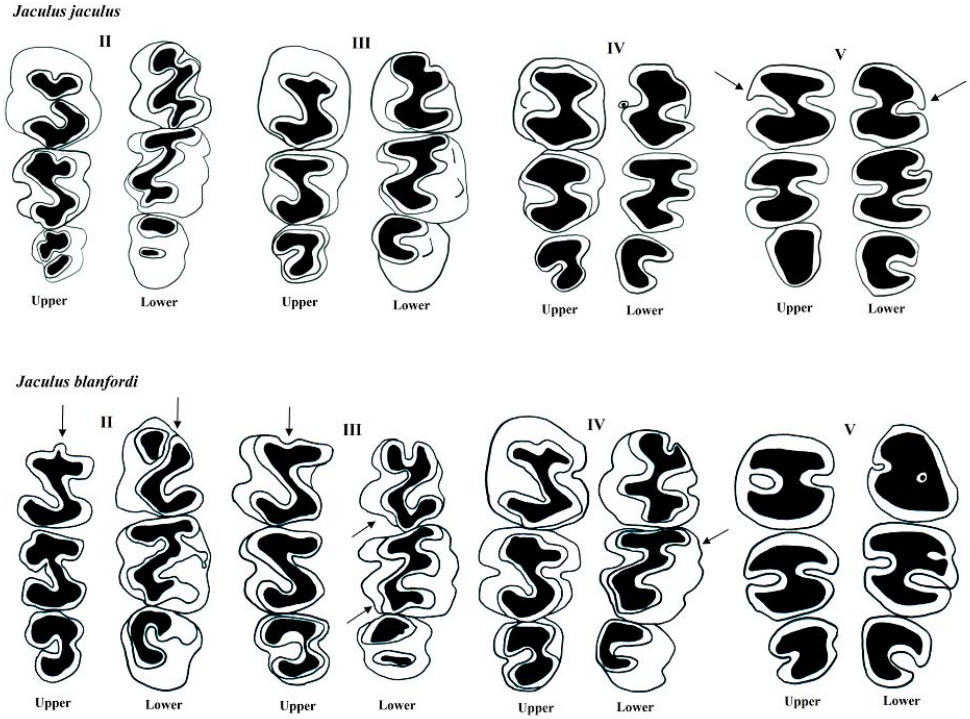

FIGURE 9. Different age sets in upper and lower molars in *Jaculus*. Above: *J.jaculus* and Bottom: *J.blanfordi*. The first age set not shown.

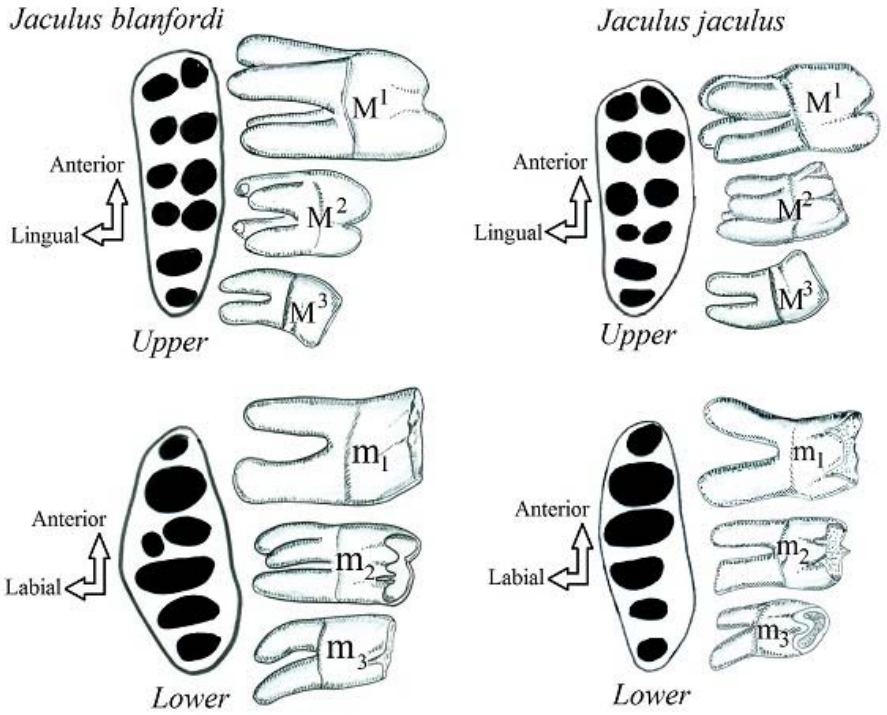

FIGURE 10. Variation of number of roots in upper and lower molars in *Jaculus*. Left: *J. blanfordi* and Right: *J. jaculus*.

In addition, morphological studies on upper and lower molars in randomly examined specimens indicated that there is a variation in the number of roots in second and third upper molars between two species so that the numbers vary between 2 to 4 roots in M3, 3 to 4 in M2 while M1 is always four-rooted. The variations of lower jaw were seen just for second molar that vary between 2 to 3 roots in both species whereas first and third lower molars are two-rooted (Fig. 10). Moreover, age variations in molars have been investigated in specimens. Five age sets were defined according to the amount of teeth wearing. The first set was defined for specimens with lacking of third molar and others sets have been shown in figure 10.

MOLECULAR DATA

626 bp for the *Cox1* gene were sequenced. The data file, comprising 32 individuals showed 422 invariable (monomorphic) sites and 171 variable (polymorphic) sites (73 singleton variable sites and 98 parsimony informative sites). A strict consensus tree indicated two clades which contain *J. jaculus* and *J. blanfordi*. Furthermore, it almost supports the separation of the samples of Bojnord, Yazd, Bajestan, Gonabad, Kash, Esfahan, Kashmar and Kavire Mesr of Esfahan from the Saravan specimens of *J. blanfordi*. Maximum likelihood analyses yielded a single tree (-lnL = 5260.9653), which agreed largely with the MP consensus tree (Fig.11).Kimura-2-parameter genetic distance showed a high genetic distance between *J.jaculus* and *J. blanfordi* (12.7%) and low distance within the species group of *J. jaculus* (0.05%) and *J. blanfordi* (0.03%).Using TCS, 15 haplotype networks were recovered based on *Cox1* sequences of 32 individuals (Fig.12). The samples of *J. blanfordi* and *J. jaculus* were grouped to two separate networks.

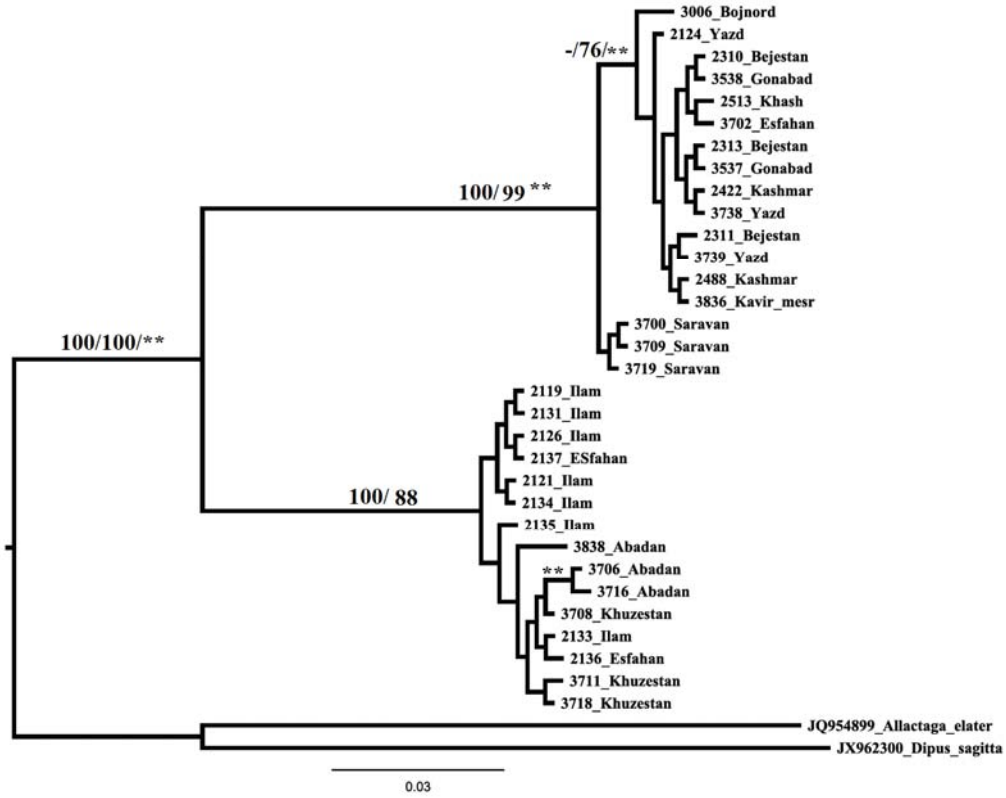

FIGURE 11. Ninety-percent majority-rule consensus tree sampled from the posterior distribution of the most-partitioned analysis. Posterior probability values from the Bayesian analysis are indicated at the >99% (**) >95% (*) significance levels. Numbers represent ML and MPbootstrap values (500/5000 replicates; given only if>50%).

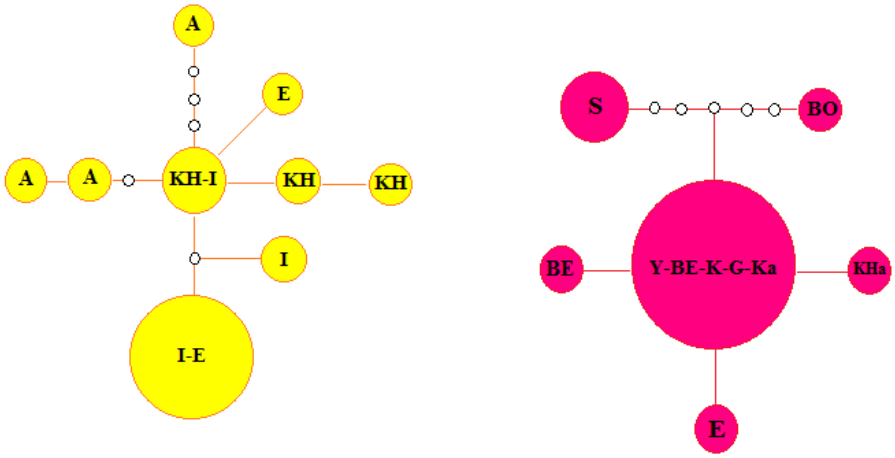

FIGURE 12. Haplotype network of *Jaculus* (32 individuals), based on 626 bp of the Cytochrome Oxidase subunit I gene (Cox1). Networks were not joined if haplotypes were separated by more than 9 mutations. Each circle represents one haplotype. (Yellow circles: *J. jaculus*: A: Abadan, I: Ilam, KH: Khuzestan, E: Esfahan. Violet circles: *J.blanfordi*: S: Saravan, BE: Bajestan, BO: Bojnord, KHa: Khaash, E: Esfahan, Y: Yazd, K: Kashmar, G: Gonabad, Ka: KavireMesr).The size of circles is related to the numbers of specimens.

DISCUSSION

Regarding to the considerable intraspecific variations in the morophological characters, molecular studies were used as an appropriate index to determinethe species boundaries.The results showed that the populations of *Jaculus* in Iran separate into two clades *J. jaculus* and *J. blanfordi* with high genetic distance between them (clade1-the populations of central and east of Iran: Bojnord, Gonabad, Yazd, Zabol, Afghanistan, Kavire Mesr, Bajestan, Ferdows, Tabas, one sample of Esfahan, Khaash, Saravan, Nehbandan and Kashmar which are belonging to *J. blanfordi*and clade2-the populations of south and west of Iran: Bushehr, Shush, Abadan, Ilam, Khuzestan(MahShahr) and Esfahan which are belonging to *J. jaculus* (Fig. 3) which is confirmed with the morphology, morphometric and geometric morphometric data. Morphometric results indicate that these two species are easily recognizable according to LCB and M1L that can be useful in the archeozoological studies and for distinguishing subfossil species. Cited differences in teeth size is related to the precipitation (Ben Faleh et al., 2013), so that in arid areas, selection pressure is on the bigger size due to water economy. *J. blanfordi* which inhabit in the arid regions such as Bafgh, Abarkooh, Khash, Zabol, Nehbandan as well as south Khorasan has bigger skull, body and tooth than *J. jaculus*. The mean annual of precipitation in these areas is 140.72 mm while *J. jaculus* which inhabit in the areas such as Khuzistan, Ilam, Bushehr and Esfahan has more precipitation (293.58 mm mean annually) (www.chaharmahalmet.ir/iranarchive.asp). In the current study the intraspeciefic morphological variations of *J. blanfordi* is influential as an innovation (refer to morphology results) which are significant in dental characters. Although the populations of *J. blanfordi* create one clade by molecular research, morphologic and morphometric studies show that the populations of South East of Iran are different from the other parts. There is an intraspecific geographic variation in 2nd lower molar shape (P=0.016). In other hand, it could be due to the distribution route of *J. blanfordi* from its origin region into the Central of Iran. To shed light the taxonomic status of the populations of *J.blanfordi*, further studies would be required.

In other side, by molecular researches, the distribution range of *J. jaculus* was reviewed and showed that in spite of expectation, this species has extended into the central Iran. Considering presence of *J. jaculus* near Esfahan, it seems that this species has penetrated into Gavkhuni basin from the Persian Gulf margin throughout Sirjan-Esfahan route which has located between Zagros and Kohrud mountains. Since Ilam is one of the lowland regions in the western margin of Zagros Mountains, so this region is a suitable habitat and it probably represents the continuous distribution of *J. j. loftusi* (Blanford, 1875) from Iraq into this region. According to the results *J. jaculus* in Iranian Plateau is different from the ones in the North of Africa by external and habitat characters. In fact, Iranian plateau may be the easternmost region of its distribution.

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