

## Morphologic, Morphometric and Molecular Comparison of Two Sister Species of Rodents as Potential Reservoir Hosts of Zoonotic Cutaneous Leishmaniasis in the Southwest of Iran

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### ABSTRACT

**Introduction:** Rodents are reservoir hosts of various infectious diseases. Many species and subspecies of genus *Rattus* play a significant role as potential reservoir hosts of different emerging and re-emerging diseases, including leishmaniasis. **Methods:** Rodents were captured using live wooden traps from different localities of Khuzestan Province, southwest of Iran. To precise identification of two sister species of rats, including *Rattus rattus* and *Rattus norvegicus*, morphological, molecular, and biosystematics characters were examined using amplification of mitochondrial Cytochrome *b* (*Cytb*) gene fragment. **Results:** Out of 119 captured rodents, 44 were *R. rattus*, 12 were *R. norvegicus*, and 63 belonged to other species (*Tatera indica*, *Nesokia indica*, *Mus musculus*). Partial *Cyt b* gene ( $\leq 624$  bp) was amplified to characterize *R. rattus* and *R. norvegicus*, accurately. Three haplotypes of *R. rattus* (six samples) and a unique haplotype of *R. norvegicus* (three samples) were identified with some nucleotide variations. **Conclusion:** Mitochondrial results confirmed morphological disparity between the two *Rattus* species in Khuzestan Province. Therefore, we recommend applying an integrative approach to identify host reservoirs for infectious diseases, especially those suspected as reservoirs of cutaneous Leishmaniasis.

### INTRODUCTION

Rodents are reservoir hosts of at least 60 zoonotic diseases [1-2]. Asian rodents of the genus *Rattus* are reservoir hosts of several significant infectious diseases such as plague, murine typhus, scrub typhus, leptospirosis, and Hantavirus hemorrhagic fever [2-3]. Leishmaniasis is an emerging infectious disease caused by the protozoan parasites of the genus *Leishmania*. This disease is endemic in 98 countries in the world; about 90% of new cases occurs in 13 countries, including Iran and different rodent species serve as reservoir hosts of the pathogenic agents [4-5]. Leishmaniasis presents in three primary forms: visceral, cutaneous, and mucocutaneous, with the last mostly confined to the new world.

Some rodents, as proven or potential reservoir hosts of diseases, have similar or close morphologic characters and are indistinguishable from each other. Accurate morphologic, morphometric, and molecular characterization of different rodent species is essential in the strategic planning for disease control [6].

Many reports on detection, isolation, and molecular identification of *Leishmania* parasites from different rodent species are available [7-11], but there is not much data on

molecular identity and systematics of the two closely related rodent species [12] *Rattus rattus*, and *Rattus norvegicus* (also called sister species).

Recently, following the detection of *Leishmania major*, the causative agent of zoonotic cutaneous leishmaniasis, in *R. norvegicus*, the species was considered as a potential reservoir of ZCL in Fars Province of Iran [13]. Genus *Rattus* from the subfamily Murinae is a taxonomically mixed group, comprising many species and subspecies worldwide [14]. The brown rat, *R. norvegicus*, and the black rat, *R. rattus*, share some similar morphological features and may co-occur in some geographical areas. In the present, to examine the morphological disparity between these two sympatric species in Khuzestan Province, we examined the morphological characteristics, along with molecular characterization based on the mitochondrial *cytb* marker.

### MATERIAL AND METHODS

**Ethics Statement.** The animals were treated in accordance with the guidelines of the ethics committee of the Pasteur Institute of Iran (approval reference: 91/0201/4558).

**Rodent sampling.** Regarding the prevalence of cutaneous leishmaniasis disease in the area, the rodents were collected from 16 localities in North, South, East, West, and center of Khuzestan Province. The area is about 18 m above

mean sea level (MAMSL) and is within the geographical coordinates 30° 19' 40" N to 32° 22' 59" N and 47° 55' 59" E to 50° 13' 8" E (Fig. 1).



**Fig. 1.** Map of Khuzestan Province, Iran. Sixteen localities in ten cities in which the rodents were collected

First, the active colonies of rodents were identified, and then 50 live traps for each location were put near the rodent burrows [15]. The specimens were captured using live wooden traps baited with cucumber, butter, cheese, or bread from June 12th to July 12th, 2014.

**Morphological identification.** Specimens were identified first based on morphological characters using external criteria according to the standard reference for the rodents in Iran [16]. In all animals, the head and body length, tail length, ear length, hindfoot length were measured (Table 1). After preparing the skulls, 15 cranial variables were measured as described by others [14, 17] using a digital caliper with a 0.1 mm precision [12] (Table 2).

**DNA extraction and PCR.** Whole genomic DNA was extracted from a piece of an ear of animals using ISH-Horovize and DynaBio kit. A partial sequence of mitochondrial cytochrome *b* gene was amplified using a pair primers UNFOR403-(5'-TGAGGACAAATATCATTCTGAGG-3') and UNREV1025-(5'-GGTTGTCCTCCAATTCATGTTA-3') [18] using *Taq* polymerase enzyme (TakapooZist, Iran) and 50 ng DNA.

The amplification was performed in a thermocycler (Eppendorf, Hamburg, Germany) programmed for an initial denaturation of 5 min at 95°C, followed by 35 cycles, each consisting 95°C for 1 min, 58°C for 1 min, and 72°C for 1 min and a final extension at 72°C for 7 min [18]. PCR products were visualized on 2% agarose gel along with a premix DNA ladder (Parstous Biotechnology, Iran). The PCR products were sequenced in both directions by a commercial company (Bioneer company, South Korea) using the Sanger method.

**Alignment and phylogenetic analysis.** DNA sequences were edited and aligned using Sequencher™ v.4.1.4 software (Gene Codes Corporation). The final alignment was checked for unexpected stop codons using MEGA6, and a 601 bp was used to construct a phylogenetic tree with Maximum Likelihood (ML) procedure using parsimony criteria in MEGA6 software [19].

## RESULTS

**Morphology and morphometry.** We captured 44 *R. rattus* and 12 *R. norvegicus*. The external morphological features and cranial criteria were used to identify the two species (Tables 1 and 2, Figs. 2 and 3). Unlike *R. rattus*, the length of the tail in *R. norvegicus* was less than the head-body. In *R. norvegicus*, the ear was shorter and, when laid forward, did not reach the eye, while in *R. rattus* specimens, the ears reached the eyes when laid forward (Fig. 2). Some morphological characters are summarized in Tables 1 and 2.

**Molecular characterization and DNA analysis of *R. rattus* and *R. norvegicus*.** From 56 examined *Rattus* specimens, only nine were used for molecular characterization. Our study revealed three unique haplotypes within six *R. rattus* sequences (Accession Nos. MH311782, MH345733, MH345734) and one haplotype within three *R. norvegicus* sequences (Accession No. MH281952).

A phylogenetic tree was constructed using the sequences obtained in this study and those of other species available in the GenBank database (AB033702, *R. rattus* from Japan; AF295545, *R. norvegicus* from China; KP001566, *Tatera indica* from Khuzestan, Iran; KF783119 and KF783118, *Erinaceus europaeus* from Russia), (Fig. 4)

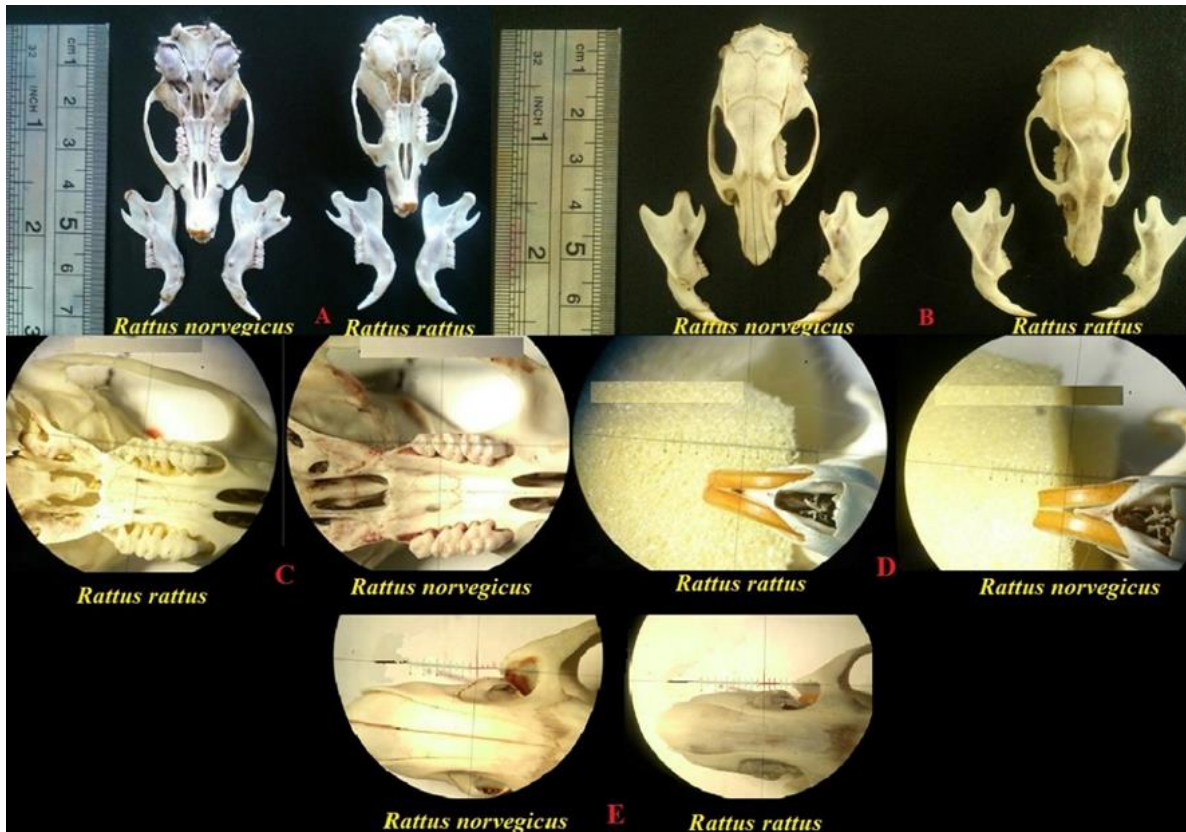
**Table 1.** Morphological and morphometric characters of *R. rattus* (R.r) and *R. norvegicus* (R.n) collected in Khuzestan province.

Location	Species	Head and body length					Tail length					Ear length			Hindfoot length				Gender		Total			
		10.5-23		11-22			1-2.3		3-4.5			M	F	N (%)										
		10.5-12.5	13-15	16-18	18.5-20	20.5-23	11-13	13.5-15	16-18.5	19-20	20.5-22				1-1.5	1.7-2.3	3	3.5	4	4.5				
Shadegan	R.r	7	17	11	3	0	4	9	9	9	7	22	16				21	17	0	0	23	15	38 (67.9)	
Abadan	R.r	0	0	0	0	0	0	0	0	0	0	0	0				0	0	0	0	0	0	0 (0)	
Khoramshahr	R.r	0	0	0	0	0	0.51	0	0	0	0	0	0	0.48	-0.43	0.11	0	0	0	0	0.48	0	0	0 (0)
Shushtar	R.r	1	2	0	0	0		0	1	2	0	0					1	2	0	0	2	1	3 (5.4)	
Dezful	R.r	0	3	0	0	0		0	1	2	0	0					0	2	0	1	2	1	3 (5.4)	
Shadegan	R.n	0	0	0	0	0		0	0	0	0	0					0	0	0	0	0	0	0 (0)	
Abadan	R.n	2	2	0	0	2		4	0	1	0	1					0	5	1	0	0	6	6 (10.7)	
Khoramshahr	R.n	0	0	0	4	0	0.55	0	0	3	1	0	0.34				0	0	1	3	0.41	3	1	4 (7.1)
Shushtar	R.n	0	0	0	0	0		0	0	0	0	0					0	0	0	0	0	0	0 (0)	
Dezful	R.n	2	0	0	0	0		2	0	0	0	0					0	2	0	0	0	2	2 (3.6)	
<b>Total No. of R.r Species</b>		8	22	11	3	0		4	11	13	9	7					22	21	0	1		27	17	44 (78.5)
<b>Total No. of R.n Species</b>		4	2	0	4	2		6	0	4	1	1					0	7	2	3		3	9	12 (21.4)
<b>Total</b>		12	24	11	7	2		10	11	17	10	8					22	28	2	4		30	26	56 (100)

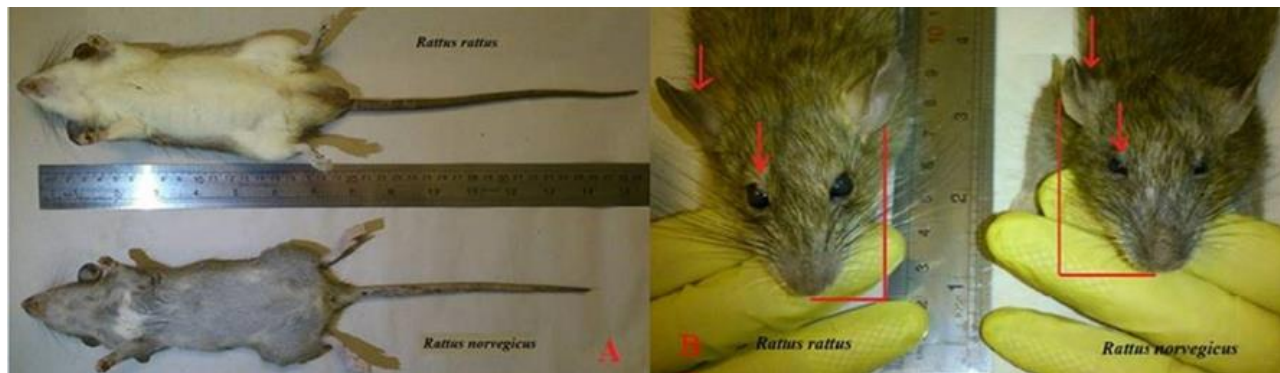
\* P-value is generated using the ANOVA test. § P-value is generated using Tajima's D index. £ Correlation coefficient. ¥ P-value is generated using Tajima's D index. M, Male; F, Female; R.r, *Rattus rattus*; R.n, *Rattus norvegicus*

**Table 2.** Morphological characters of *R. rattus* and *R. norvegicus* based on the skulls in the study areas (Student's paired t-test: one-tailed p-values was derived from the two-tailed p-values)

Morphological Characters	Rodent species										Correlation coefficient (r)	T test (P value) (P < 0.05)
	<i>R. rattus</i>					<i>R. norvegicus</i>						
	Rodent code numbers											
	88	90	91	95	97	120	121	122	123	125		
Width of rostrum	0.64	0.61	0.59	0.62	0.60	0.73	0.54	0.54	0.54	0.54	0.82	0.0419*
Occipitonasal length	4.45	4.22	4.24	4.12	4.01	4.84	3.55	3.52	3.38	3.60	0.80	0.0490*
Condylbasal length	4.24	4.08	4.11	3.98	3.89	4.66	3.45	3.37	3.30	3.50	0.72	0.0842
Zygomatic width	2.07	1.95	2.00	1.99	1.91	2.21	1.77	1.76	1.70	1.78	0.73	0.0775
Least interorbital width	0.60	0.59	0.60	0.58	0.58	0.67	0.58	0.57	0.62	0.57	0.28	0.3186
Cranial width	1.40	1.30	1.33	1.35	1.30	1.44	1.28	1.26	1.34	1.26	0.93	0.0100*
Length of nasal	1.70	1.52	1.55	1.45	1.48	1.90	1.26	1.25	1.14	1.28	0.94	0.0070*
Length of diastema	1.21	1.11	1.17	1.09	1.01	1.32	0.94	0.93	0.89	0.93	0.67	0.1075
Length of anterior palatine foramina	0.81	0.73	0.78	0.70	0.71	0.82	0.64	0.63	0.60	0.62	0.82	0.0412*
Length of tympanic bullae	0.77	0.70	0.65	0.70	0.63	0.79	0.66	0.66	0.68	0.63	0.92	0.0129*
Width of tympanic bullae	0.65	0.64	0.47	0.67	0.51	0.67	0.49	0.45	0.47	0.50	0.41	0.2417
Upper cheekteeth	0.73	0.71	0.69	0.68	0.69	0.74	0.68	0.69	0.60	0.72	0.67	0.1054
Lower cheekteeth	0.66	0.65	0.61	0.61	0.60	0.72	0.68	0.59	0.69	0.59	0.76	0.0660
Height of skull	1.45	1.38	1.31	1.30	1.26	1.51	1.15	1.22	1.07	1.26	0.63	0.1235
Length of mandible	2.44	2.29	2.20	2.29	2.16	2.62	1.90	0.87	1.87	0.97	0.96	0.0036*



**Fig. 2.** The skulls of *R. rattus* and *R. norvegicus*. The ventral (A) and dorsal (B) surface of the skull of the two species with morphologic differences reflected in the zygomatic plate (C) upper molars (D) upper incisors (E).



**Fig. 3.** *Rattus rattus* and *R. norvegicus* external view, including morphologic differences in ventral surface (A) and skulls (B).

## DISCUSSION

Rodents are known as reservoir hosts for many infectious diseases [20-23]. These diseases can be transmitted through bites or direct contact with contaminated food, feces, and urine of the rodents or infective bites of arthropod vectors. Classification of rodents based on morphological criteria is the subject of numerous publications in the world [24]. However, the relationships among rodent families are confounded by the current morphological characters [25, 26]. The *R. norvegicus* and *R. rattus* are known as reservoir hosts of ZCL in Khuzestan Province and have a significant role in maintaining *Leishmania* parasites in this area, which highlights the importance of current research on these two

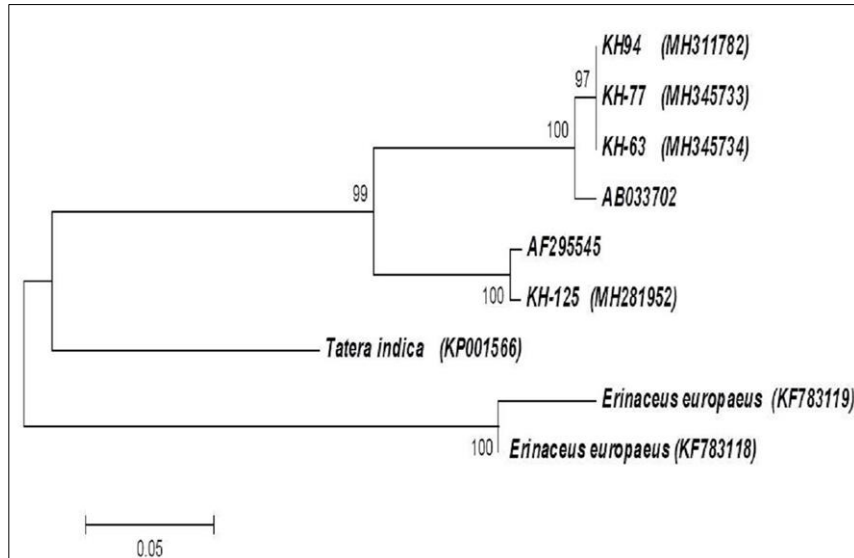
species. Since these species vary in preference habitat, behavior, and biology, accurate identification of host species is of high importance and is critical in adopting strategies for controlling programs.

According to Montgelard *et al.* [27], mitochondrial genes, as well as nuclear exonic and intronic sequences, can help to classify mouse-related clades. Mitochondrial DNA markers are considered useful tools in identifying potential cryptic species [28]. Cytochrome *b* is a commonly used mitochondrial gene for species identification and determination of phylogenetic relationships [29].

There are many reports on using molecular approaches for the identification of rodents in Iran, while the data on the identity of rodents that serve as reservoirs of

leishmaniasis is not much [30, 31], and most studies focused on taxonomy, phylogeny, and phylogeography of the rodents [12, 16, 32, 33]. Recently, the *Cytb* gene revealed intraspecific variations among *Tatera indica* specimen, a reservoir host of cutaneous leishmaniasis in southern Iran (from the area where we collected *R. rattus* and *R. norvegicus* specimen) [12].

Our phylogenetic tree exhibited separation of two species, *R. norvegicus*, and *R. rattus* into two clades and confirmed the morphological disparity between these species. Our results indicated three haplotypes for *R. rattus* (MH311782, MH345733, MH345734) and one haplotype for *R. norvegicus* (MH281952) in the studied area, southwest of Iran.



**Fig. 4.** The ML tree constructed based on the partial sequence of the *cytb* gene. Only the bootstraps  $\geq 90$  are shown. The scale represents the number of base substitutions per site. KH-94, KH-77, and KH-63 represent *R. rattus* and KH-125 *R. norvegicus* investigated in this study. (AB033702, *R. rattus* from Japan; AF295545, *R. norvegicus* from China; KP001566, *Tatera indica* from Khuzestan, Iran; KF783119 and KF783118, *Erinaceus europaeus* from Russia).

Our study provided three haplotypes for *R. rattus*, which differed by 1 to 6 nucleotides, while the *R. norvegicus* rats, including those obtained from GenBank differed by 1–5 nucleotides. The variation between *R. rattus* and *R. norvegicus* sequences was high (14.17% or 34 among 240 bp). One-tailed and two-tailed tests revealed no significant differences among morphometric measurements and morphologic features ( $P > 0.05$ ) and confirmed the previous reports on these two species that showed similarity in morphological criteria [14]. The correlation coefficient ( $r$ ) was used to measure how strong a relationship between the ear length of two species (*R. rattus* and *R. norvegicus*) was and revealed no significant linear relationship ( $r = -0.4291$  correlation) between *R. rattus* and *R. norvegicus* in the population. In our study, molecular characterization of *R. rattus* and *R. norvegicus* species based on *cytb* sequence corroborated morphological and morphometric findings.

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#### CONFLICT OF INTEREST

The authors declare that there are no issues to be perceived as a conflict of interest.

#### REFERENCES

- Luis AD, Hayman DTS, O'Shea TJ, Cryan PM, Gilbert AT, Pulliam JR, et al. A comparison of bats and rodents as reservoirs of zoonotic viruses: are bats special? Proceedings of the Royal Society of London. Proc Biol Sci. 2013; 280: e20122753.
- Morand S, Jittapalpong S, Kosoy M. Rodents as hosts of infectious diseases: biological and ecological characteristics. Vector Borne Zoonotic Dis. 2015; 15 (1): 1-2.
- Kuo CC, Wang HC, Huang CL. The potential effect of exotic Pacific rats *Rattus exulans* on vectors of scrub typhus. J Appl Ecol. 2011; 48: 192-8.
- Parvizi P, Ready PD. Nested PCRs and sequencing of nuclear ITS-rDNA fragments detect three *Leishmania* species of gerbils in sandflies from Iranian foci of zoonotic cutaneous leishmaniasis. Trop Med Int Health. 2008; 13 (9): 1159-71.
- Amin M, Azizi K, Kalantari M, Motazedian MH, Asgari Q, Moemenbellah-Fard MD, et al. Laboratory-based diagnosis of leishmaniasis in rodents as the reservoir hosts in southern Iran, 2012. Asian Pac J Trop Biomed. 2014; 4 (2): S575-80.
- Mirshamsi O, Darvish J, Kayvanfar N. A preliminary study on Indian gerbils, *Tatera indica* Hardwicke, 1807 at population level in eastern and southern parts of Iran (Rodentia: Muridae). Iran J Anim Biosyst. 2007; 3 (1): 49-61.
- Yaghoobi-Ershadi MR, Akhavan AA, Mohebbali M. *Meriones libycus* and *Rhombomys opimus* (Rodentia: Gerbillidae) are the main reservoir hosts in a new focus of zoonotic cutaneous

- leishmaniasis in Iran. *Trans R Soc Trop Med Hyg.* 1996; 90: 503-4.
8. Momenbellah-Fard MD, Kalantari M, Rassi Y, Javadian E. The PCR based detection of *Leishmania major* infection in *Meriones libycus* (rodentia: Muridae) from southern Iran. *Ann Soc Belges Med Trop Parasitol Mycol.* 2003; 79: 811-16.
  9. Mohebbali M, Javadian E, Yaghoobi-Ershadi M, Akhavan A, Hajjaran H, Abaei M. Characterization of *Leishmania* infection in rodents from endemic areas of the Islamic Republic of Iran. *East Mediterr Health J.* 2004; 10: 591-99.
  10. Akhavan AA, Yaghoobi-Ershadi MR, Khamesipour A, Mirhendi H, Alimohammadian MH, Rassi Y, Arandian MH, et al. Dynamics of *Leishmania* infection rates in *Rhombomys opimus* (Rodentia: Gerbillinae) population of an endemic focus of zoonotic cutaneous leishmaniasis in Iran. *Bull Soc Pathol Exot.* 2010; 103: 84-9.
  11. Vazirianzadeh B, Saki J, Jahanifard E, Zarean M, Amraee K, Navid Pour S. Isolation and identification of *Leishmania* species from sand flies and rodents collected from Roffaye district, Khuzestan province, Southwest of Iran. *Jundishapur J Microbiol.* 2013; 6 (6): e10025.
  12. Mohammadi S, Parvizi P. Simultaneous morphological and molecular characterization of *Tatera indica* in Southwestern Iran. *J Arthropod Borne Dis.* 2016; 10 (1): 55-64.
  13. Motazedian MH, Parhizkari M, Mehrabani D, Hatam G, Asgari Q. First detection of *Leishmania major* in *Rattus norvegicus* from Fars province, southern Iran. *Vector Borne Zoonotic Dis.* 2010; 10 (10): 969-75.
  14. Yigit N, Colak E, Cözen H, Özkurt S. The taxonomy and karyology of *Rattus norvegicus* (Berkenhout, 1769) and *Rattus rattus* (Linnaeus, 1758) (Rodentia: Muridae) in Turkey. *Turk J Zool.* 1998; 22: 203-12.
  15. Mehrabani D, Motazedian MH, Asgari- Gholam Q, Hatam R, Owji SM, Oryan A. *Leishmania major* in *Tatera indica* in Estahban, southern Iran: microscopy, culture, isoenzyme, and PCR. *Pak J Med Sci.* 2011; 27 (4): 734-73.
  16. Etemad E. Mammals of Iran, rodents and identification key. Vol.1. Tehran: Natural resource protection and human environment association press; 1978 [In Persian].
  17. Etemad E. Mammals of Iran (Rodentia). 3th ed. Tehran: Natural resource protection and human environment association press; 1975 [In Persian].
  18. Kent RJ, Norris DE. Identification of mammalian blood meals in mosquitoes by a multiplexed polymerase chain reaction targeting cytochrome b. *Am J Trop Med Hyg.* 2005; 73 (2): 336-42.
  19. Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. MEGA6: Molecular evolutionary genetics analysis version 6.0. *Mol Biol Evol.* 2013; 30 (12): 2725- 9.
  20. Webster JP, Macdonald DW. Parasites of wild brown rats (*Rattus norvegicus*) on UK farms. *Parasitology.* 1995; 111 (3): 247-55.
  21. Ceruti R, Sonzogni O, Origgi F, Vezzoli F, Cammarata S, Giusti AM, et al. *Capillaria hepatica* infection in wild brown rats (*Rattus norvegicus*) from the urban area of Milan, Italy. *J Vet Med B Infect Dis Vet Public Health.* 2001; 48: 235-40.
  22. Di Bella C, Vitale F, Russo G, Greco A, Milazzo C, Aloise G, et al. Are rodents a potential reservoir for *Leishmania infantum* in Italy? *Methods Ecol Evol.* 2003; 7: 125-9.
  23. Gundi VAKB, Davoust B, Khamis A, Boni M, Raoult D, La Scola B. Isolation of *Bartonellatimmassiliensis* sp. nov. and *Bartonellaphoceensis* sp. nov. from European *Rattus norvegicus*. *J Clin Microbiol.* 2004; 42 (8): 3816-18.
  24. Lockett WP, Hartenberger JL. Evolutionary relationships among rodents a multidisciplinary analysis. New York and London: Plenum Press; 1985.
  25. Jaeger JJ. Rodent phylogeny: new data and old problems. In: Benton MJ, editor. The phylogeny and classification of the tetrapods. Vol.2. Oxford: Clarendon Press; 1988; 177-99.
  26. Blanga-Kanfi S, Miranda H, Penn O, Pupko T, DeBry RW, Huchon D. Rodent phylogeny revised: analysis of six nuclear genes from all major rodent clades. *BMC Evol Biol.* 2009; 9: 71.
  27. Montgelard C, Forty E, Arnal V, Matthee CA. Supra familial relationships among Rodentia and the phylogenetic effect of removing fast-evolving nucleotides in mitochondrial, exon and intron fragments. *BMC Evol Biol.* 2008; 8: 321-10.
  28. Blouin MS. Molecular prospecting for cryptic species of nematodes: mitochondrial DNA versus internal transcribed spacer. *Int J Parasitol.* 2002; 32: 527-531.
  29. Castresana J. Cytochrome b phylogeny and the taxonomy of great apes and mammals. *Mol Biol Evol.* 2001; 18: 465-71.
  30. Hajjaran H, Mohebbali M, Mamishi S, Vasigheh F, Oshaghi MA, Naddaf SR, et al. Molecular identification and polymorphism determination of cutaneous and visceral leishmaniasis agents isolated from human and animal hosts in Iran. *Biomed Res Int.* 2013; 7: e789326.
  31. Darvishi M, Jafari R, Darabi H, Zendehbodi I, Jahangard SA. Survey of rodents fauna regarding to their probabilistic contamination to *Leishmania*. *Iran South Med J.* 2017; 20 (4): 362-9.
  32. Seddon JM, Baverstock PR. Evolutionary lineages of RT1.Ba in the Australian *Rattus*. *Mol Biol Evol.* 2000, 17 (5): 768-72.
  33. Darvish J, Gholi Kami H, Mirshamsi O. Rodent fauna of the western Golestan province in Northeast Iran. *Iran J Anim Biosyst.* 2010; 6 (1): 37-48.

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