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Dermacentor (Acari: Ixodidae) species that we deal with in Iran: Polymorphic *D. marginatus* or more distinct species

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Ornate ticks of the genus *Dermacentor* are distributed in the Nearctic, Palearctic, Asian and Afrotropical region (Estrada-Peña *et al.* 2017). This genus was erected by Koch (1844) with *D. reticulatus* (Fabricius, 1794) as the type species (Camicas *et al.* 1998). Arthur (1960) classified American, Eurasiatic and African *Dermacentor* species throughout the world. About half of 35 recognized species (ca. 14) are found in the Palearctic region (Guglielmone *et al.* 2014; Estrada-Peña *et al.* 2017). The greatest species diversity of the genus *Dermacentor* (10 species) is characteristic of Central Asia and the adjacent territories (Filippova and Panova 1989). Seven *Dermacentor* species are commonly found on humans exposed to infested vegetation (Estrada-Peña and Jongejan 1999). *Dermacentor marginatus* (Sulzer, 1776) Brumpt, 1913 is a three-host species parasitizing cattle, sheep and goats as usual hosts of adult stages. Larvae and nymphs infest small mammals such as rodents, medium-sized carnivores and also birds (Estrada-Peña *et al.* 2004). This species is a highly polymorphic (multi-shaped) tick with big scutal pattern variability (Estrada-Peña and Estrada-Peña 1991). Morphological differentiation of closely related *D. marginatus*, *D. niveus* Neumann, 1897, *D. daghestanicus* Olenev, 1928 and *D. reticulatus* is debatable. Estrada-Peña and Estrada-Peña (1991) concluded that *D. niveus* and *D. daghestanicus* are junior synonyms of *D. marginatus*. However, Zahler *et al.* (1995) showed that the two closely related *D. marginatus* and *D. reticulatus* are distinct species according to *ITS2* gene analysis. Filippova and Panova (1989) examined various closely related species under the subgenus *Serdjukovia* including *D. raskemensis* Pomerantzev, 1946, *D. niveus*, *D. ushakovae* Filippova & Panova, 1987, *D. marginatus*, *D. silvarum* Olenev, 1931, *D. pomerantzevi* Serdyukova, 1951 and *D. nuttalli* Olenev, 1928. The taxonomic validity of some of these species has been discussed; *D. ushakovae* is a synonym of *D. marginatus* (Guglielmone *et al.* 2014), *D. niveus* a synonym of *D. marginatus* (Moshaverinia *et al.* 2009), *D. niveus*, *D. daghestanicus* synonyms of *D. marginatus* (Estrada-Peña and Estrada-Peña 1991). *Dermacentor* species including *D. marginatus*, *D. niveus*, *D. daghestanicus* and *D. raskemensis* were reported from Iran (Abbasian-Lintzen 1960; Mazlum 1971; Hoogstraal and Valdez 1980; Rahbari *et al.* 2007). According to morphological variability of scutal pattern (Fig. 1), this doubt was found that all of them may be polymorphic *D. marginatus*. So it was decided reanalyzing closely related *Dermacentor* species occurring in Iran and other countries based on GenBank sequence database. Sequences of internal transcribe spacer 2 (*ITS2*) gene were selected as

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target phylogenetic marker; thus, *ITS2* sequences of *D. marginatus*, *D. reticulatus*, *D. niveus*, *D. silvarum*, and *D. nuttalli* were aligned using SeaView4 software (Gouy *et al.* 2010), and genetic distances among the sequences were calculated using maximum composite likelihood (MCL) in the MEGA7 software (Kumar *et al*. 2016, see Table 1). Phylogenetic relationships between taxa were inferred using Bayesian inference (BI) in BEAST v.2.5.1 (Bouckaert *et al.* 2014). For this purpose, 20, 12, 4, 4 and 4 sequences of *D. marginatus*, *D. reticulatus*, *D. niveus*, *D. silvarum*, and *D. nuttalli* were used, respectively. The clades in the phylogenetic tree were arranged and labeled based on more than 99% posterior probability values (except Clade I with 91%) and reasonable genetic distance differences within and between the clade members. *Dermacentor andersoni* Stiles, 1908 was examined as the outgroup taxon. The ITS2 phylogenetic tree (Fig. 2) shows various distinct *Dermacentor* clades including in-group taxa; *D. marginatus*, *D. reticulatus*, *D. niveus*, *D. silvarum*, *D. nuttalli,* and the outgroup taxon; *D. andersoni*. The GenBank *ITS2* sequences of Iran arise from two distinct clades with 5% genetic distance (Table 1). This can be a considerable *ITS2* genetic difference at species level. The MCL genetic distance for *ITS2* sequences of two closely related *D. reticulatus* and *D. marginatus* was 7% (Zahler *et al.* 1995); between other species it was as follows: 5% *D. variabilis* / *D. andersoni*, 13% *D. andersoni* / *D. marginatus*, 15% *D. reticulatus* / *D. variabilis*, 1–7% *D. marginatus* / *D. nuttalli*, 13% *D. reticulatus* / *D. nuttalli*, 7–9% *D. niveus* / *D. nuttalli* (according to GenBank database). The Iranian *Dermacentor ITS2* sequences belong to northern populations (*D. marginatus*: GQ144707, KJ004039, KJ004037, FJ416315-6; *D. niveus*: KJ004041, GQ144706) and southern populations (*D. marginatus*: KJ004032, *D. niveus*: KJ004042). According to these results, this was concluded that morphological variability in scutal pattern of Iranian *Dermacentor* specimens (Fig. 1) was not entirely narrated in *ITS2* phylogenetic tree. It does mean that there are not several separate species, but there are probably only two closely related species with 5% genetic distance including *D. marginatus* (northern population) and one of the three species, *D. raskcmensis* / *D. niveus* / *D. daghestanicus* (southern population).

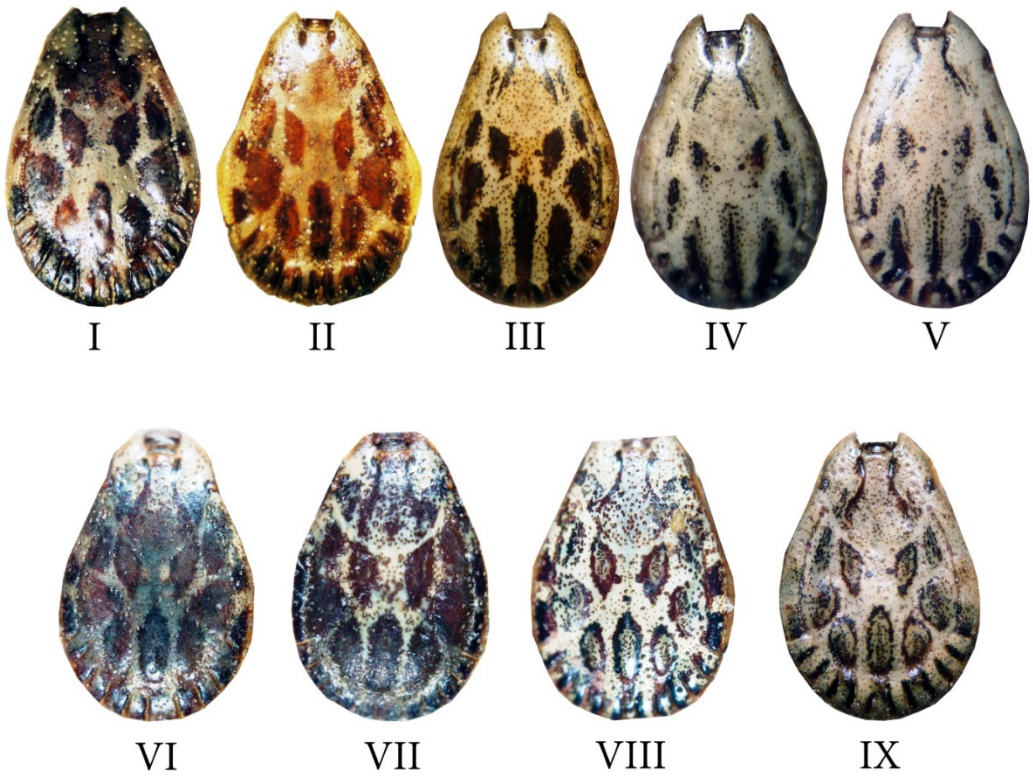

Figure 1. Morphological variability in scutal pattern of *Dermacentor* specimens collected from different parts of Iran.

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Table 1. Estimates of MCL genetic distance (%) inferred from *ITS2* sequences of *Dermacentor* taxa deposited in GenBank database. Within-clade divergences are shown as diagonal (in **bold**).

Clades	Clade I	Clade II	Clade III	Clade IV	Clade V
Clade I	-				
Clade II	15	**0**			
Clade III	13	8	**2**		
Clade IV	15	10	5	**0**	
Clade V	27	26	24	27	**0**

Clade I: *D. niveus*; Clade II: *D. nuttalli*, *D. silvarum*, *D. marginatus*; Clade III: *D. marginatus*, *D. niveus*, *D. silvarum*; Clade IV: *D. marginatus*, *D. niveus*; Clade V: *D. reticulatus*.

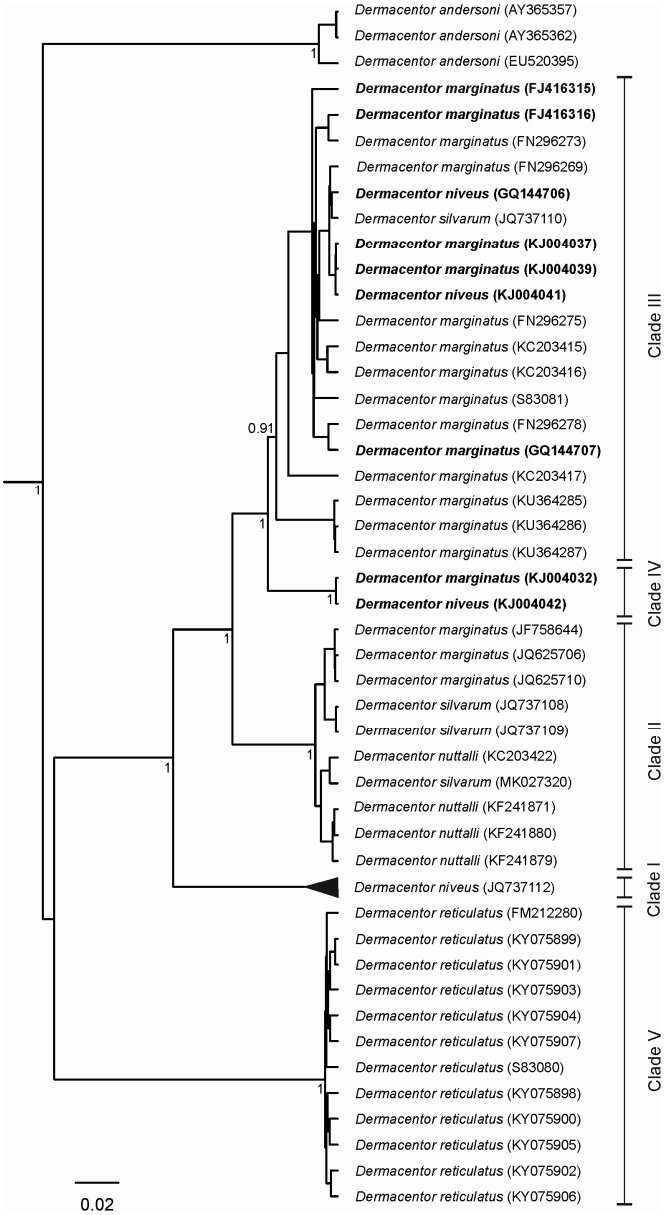

Figure 2. Phylogenetic relationships among *Dermacentor* taxa derived from Bayesian inference (BI) analysis of ITS2 sequence data; numbers below each node show posterior probability value in BI analysis (1,000 replicates). Taxon labels give the species name followed by (in turn) GenBank accession numbers in parentheses; taxa of Iran are highlighted in bold. The main clade of the tree is shown on the right side. Posterior probability values are inserted in the place of nodes. Branch lengths are proportional to the evolutionary changes. The phylogeny is rooted with *Dermacentor andersoni* as out-group.

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