

A new subspecies of the Iranian Vole, *Microtus irani* Thomas, 1921, from Turkey

(Mammalia: Rodentia)

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Abstract. *Microtus irani* Thomas, 1921, is known with certainty from two localities which are separated by a gap of almost 2000 km. In this paper we describe a population from Balkusan in Turkey as a new subspecies *Microtus irani karamani*. In a complete sequence for cytochrome *b* gene (1140 bp), the new subspecies has unique mutations when compared with a sequence of *M. i. irani* from the type locality (Shiraz, Iran) at 32 positions, and differs in 35 mutations and a mean nucleotide divergence of $3.19\% \pm 0.50$. It has 60 acrocentric chromosomes in the diploid complement. Morphologically, *M. i. karamani* ssp. n. is smaller than *M. i. irani*, with a shallower braincase, shallower rostrum, and shorter bullae. The new subspecies can be reliably separated from social voles occupying Turkey, Iran and adjacent regions of the Near East, by a combination of morphological, chromosomal and molecular data.

Key words. *Microtus irani karamani* subsp. n., taxonomy, cytochrome *b*, karyotype, baculum, Arvicolinae.

Introduction

Social voles form a monophyletic lineage within the genus *Microtus* and are either classified as a subgenus on their own (*Sumeriomys*; ARGYROPULO 1933, GOLENISHCHEV et al. 1999, SHENBROT & KRASNOV 2005) or as a species group (*socialis* (Pallas, 1773) group) within the subgenus *Microtus* (JAAROLA et al. 2004). While the taxonomy of the majority of western Palearctic species groups of *Microtus* has stabilized in the last decades (MUSSER & CARLETON 2005), taxonomic uncertainties still dominate in the *socialis* group. The number of species has therefore varied in taxonomic revisions between one (CORBET 1978) and eight (MUSSER & CARLETON 2005), but a tripartite taxonomy with *M. socialis*, *M. guentheri* (Danford & Alston, 1880) and *M. irani* Thomas, 1921 was most commonly applied in the interim period (MUSSER & CARLETON 1993). The taxonomic and geographic scope of *M. irani* was particularly ambiguous (KRYŠTUFEK & VOHRALÍK 2005) and a re-examination of the type restricted this species to its type locality in Bagh-i-Rezi near Shiraz, Iran (KRYŠTUFEK & KEFELIOĞLU 2001). Phylogenetic relations among social voles inhabiting south-western Asia have become better understood from molecular data. A study based on a *cyt b* gene therefore confirmed the species status of *M. irani* which differed from *M. socialis* in 58 mutations (mean nucleotide divergence = $5.65\% \pm 0.67$) and from *M. anatolicus* Kryštufek & Kefelioğlu, 2002 by 59 mutations (mean nucleotide divergence = $5.76\% \pm 0.67$). The mean nucleotide divergence between *M. irani* and three further social vole species (*M. guentheri*, *M. hartingi* Barrett-Hamilton, 1903, *M. dogramacii* (Kefelioğlu & Kryštufek, 1999)) was even higher ($>5.8\%$). Two supported lineages were retrieved within *M. irani*, separated by 35 mutations and a mean nucleotide divergence of $3.19\% \pm 0.50$ (KRYŠTUFEK et al. 2009). While one of *cyt b* haplotypes originated from the type locality of *M. irani* in Shiraz, Iran,