

# Chromosomal diversity in the genus *Microtus* at its southern distributional margin in Iran

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**Abstract.** We karyotyped six species of *Microtus* voles collected along the southern edge of their range in northern and western Iran. Diploid and fundamental numbers were as follows: *M. socialis* and *M. paradoxus* 2n = 62, FNa = 60, *M. qazvinensis* 2n = 54, FNa = 54, *M. transcaspicus* 2n = 52, FNa = 52, and *M. mystacinus* (= *M. rossiaemeridionalis*) 2n = 54, FNa = 54. Two cytotypes were retrieved in *M. irani* from its type locality: 2n = 48, FNa = 46 and 2n = 64, FNa = 62. While our results confirmed an early report of 2n = 64 for this vole, the 2n = 48 cytotype remains unexplained. Karyological variability is relatively low in social voles and chromosomal data contribute little to individual species recognition. We argue that *Arvicola mystacinus* De Filippi, 1865, described from Lar Valley (north-east of Tehran) is the oldest available name for 2n = 54 voles with the following synonyms: *M. subarvalis* Meyer, Orlov & Skholl, 1969, *M. epiroticus* Ondrias, 1966, and *M. rossiaemeridionalis* Ognev, 1924.

**Key words:** karyotype, *Microtus irani*, *Microtus mystacinus*, zoological nomenclature

## Introduction

Latitudinal diversity gradient with species richness decreasing from the equator towards the poles is one of the most general patterns in biogeography (Brown 1995). Voles and lemmings (subfamily Arvicolinae) contradict the generality of this rule by attaining peak numbers of species per area in temperate and boreal latitudes (Shenbrot & Krasnov 2005). The genus *Microtus*, which accounts for about one half of arvicoline species, appears to have ongoing speciation (Jaarola et al. 2004) and the centres of diversification in two of its lineages coincide with south-western Palearctic. Pine voles (subgenus *Terricola*) speciated in the Mediterranean glacial refugia and the Caucasus area (Jaarola et al. 2004) and the social voles (subgenus *Sumeriomys*) diversified in south-western Asia (Kryštufek et al. 2009). Both groups contain evolutionary young species, therefore taxonomic uncertainties aggregate along the southern margin of the range of arvicolines (Musser & Carleton 2005). Delimitation of species in *Microtus* is traditionally

based on dental morphology (Hinton 1926, Gromov & Polyakov 1992). Because cryptic species are omnipresent in the group, the understanding of taxonomic relationships benefited tremendously from karyological studies (Zima & Král 1984) and utilization of molecular markers (Jaarola et al. 2004). In this paper we provide new evidence on karyotypes of six out of nine *Microtus* species reported so far for Iran (Karami et al. 2008). The investigated species belong to two lineages, which are either classified as subgenera (*Microtus* and *Sumeriomys*; Gromov & Polyakov 1992, Shenbrot & Krasnov 2005) or species groups (*arvalis* and *socialis* species groups; Jaarola et al. 2004, Martínková & Moravec 2012).

Although karyological data on voles have been reported for south-western Asia (e.g. Matthey 1952, 1954, Golenishchev et al. 2002, 2003, Arslan & Zima 2014) many uncertainties are left open. Firstly, several species still need to be defined chromosomally and the most notable example is the enigmatic *Microtus irani* Thomas, 1912 (Zima et al. 2013). Secondly,

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