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The taxonomic position of *Tonkinomys daovantieni* (Rodentia: Muridae) based on karyological and molecular data

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Abstract

Tonkinomys daovantieni was recently described from Northern Vietnam, but very sparse information exists for the taxon. We report for the first time the karyotype of this species and investigate its phylogenetic position in the *Dacnomys* division using both mitochondrial and nuclear genetic data. The diploid chromosome number of the species is 2n=44. This chromosomal set consists of one submetacentric pair, one metacentric pair, and nineteen pairs of subtelocentric/acrocentric autosomes progressively decreasing in size. The X chromosome is submetacentric and approximately equal in size to the largest subtelocentric autosome. The Y chromosome is metacentric and equal in size to the smallest pair of autosomes. The phylogenetic reconstruction based on the Cyt *b* COI and GHR genes reveals that *Saxotilomys paulinae*, a species distributed in the karst formations of the Lao PDR, is the closest relative to *T. daovantieni*. These two taxa are similar not only in a number of morphological characters, but also in their major ecological preferences (both are petrophylic species associated with limestone karst formations). Based on our data, we can conclude that the similarities among the ecological adaptations, natural conditions and habitat preferences of these species are a reflection of their phylogenetic relationship.

Key words: limestone rats, Southeast Asia, Vietnam, taxonomy, molecular phylogeny, karyotype

Introduction

The monotypic genus *Tonkinomys* Musser, Lunde & Nguyen 2006, comprising the species *Tonkinomys daovantieni* Musser, Lunde & Nguyen 2006, was first described from the forested tower karst formations of the Huu Lien Nature Reserve of north-eastern Vietnam (Musser *et al.* 2006). Based on its morphological peculiarities, this species was classified as a member of this *Dacnomys* division of the tribe Rattini. According to Musser & Carleton (2005), the division includes four Indo-Sundaic genera (*Dacnomys* Thomas, *Niviventer* Marshall, *Leopoldamys* Ellerman, and *Chiromyscus* Thomas), the Sri Lankan endemic *Srilankamys* Musser, and the Philippine genus *Anonymomys* Musser. The composition of the *Dacnomys* division was recently subjected to a taxonomic revision based on molecular data (Balakirev *et al.* 2011, 2012, 2013**)** and it was demonstrated that the genus *Saxatilomys* Musser (Musser *et al.* 2005) should be considered an additional member of the *Dacnomys* division. It was also discovered that *Srilankamys* should be excluded from the *Dacnomys* division and placed instead in the *Rattus* division (Buzan *et al*. 2011, Balakirev *et al.* 2012). Until the present study, no molecular or chromosomal data have been available for *Tonkinomys*, and the species was known only from its original morphological description.

Musser *et al.* (2006), when describing the new taxon, stated that the phylogenetic position of *Tonkinomys* with respect to *Leopoldamys, Niviventer*, and *Saxatilomys*, the three extant genera with morphologies most similar to that of *Tonkinomys* was unresolved; the differences between *Tonkinomys daovantieni* and the species of *Leopoldamys* and *Niviventer* reflected a combination of primitive and derived features. The pelage coloration, as well as the tail shape and its length relative to the length of head and the body in *Leopoldamys* and *Niviventer*, are in contrast with those of *Tonkinomys. Tonkinomys* and *Saxatilomys* display a series of common morphological

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The monophyly for the *Saxatilomys/Tonkinomys* clade, along with its clear morphological distinctiveness, provide strong support for its phylogenetic relationship, and the intergroup genetic distances of 0.1363–0.1455 for *Cytb* and 0.1130–0.1179 for *COI* are high enough to indicate generic specificity in agreement with the genetic species conception (Breadly & Baker, 2001, Baker & Breadly, 2006). These genera undoubtedly belong to an original phylogenetic clade within the *Dacnomys* division (comprising the *Dacnomys*, *Leopoldamys* and *Niviventer/Chiromyscus* genera). Although, the basal tree topology of the *Dacnomys* division remains unresolved, the data reported into present study and in Balakirev *et al.* (2012, 2013) indicate that *Saxatilomys* and *Tonkinomys* genera are more closely related to each other than to other members of the division. Similarly, the *Leopoldamys* and *Dacnomys* genara as well as the *Chiromyscus* and *Niviventer* genera (Balakirev *et al,* 2012, 2013) compose another pairs of most closely related taxa. It should also be noted also that the position of *Maxomys* clade, which is usually regarded as an outgroup to the *Dacnomys* division (as a member of a separate *Maxomys* division, Musser & Carleton 1993, 2005) may be in need of revision. A special survey is needed to investigate this question in details, because of the complex composition of the genus *Maxomys*.

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APPENDIX 1. List of *Tonkinomys daovantieni* samples and its localities.

ZMMU S-190817 (LD3), Ad. M. 21º41’26.95”N; 106º19’52.70”E (GeneBank IDs; KC209558, KC209569, KF154058)
ZMMU S-191155 (HL17), Ad. M. 21º40’N; 106º22’22.32”E (GeneBank IDs; KC209559, KC209564, KF154059)
ZMMU S-191155 (HL22), Ad. F. 21º40’29”N; 106º22’51”E (GeneBank IDs; KC209560, KC209565, KF154060)
ZMMU, S-191156 (HL23), Ad. F. 21º39’37”N; 106º23’15”E
ZMMU S-191157 (HL24), Ad. M. 21º40’N; 106º22’22.32”E (GeneBank IDs; KC209561, KC209566, KF154061)
ZMMU S-191158 (HL25), Sad. M. 21º40’N; 106º22’22.32”E (GeneBank IDs; KC209562, KC209567, KF154062)
ZMMU S-191159 (HL26), Sad. M. 21º40’N; 106º22’22.32”E (GeneBank IDs; KC209563, KC209568, KF154063)
ZMMU S-191160 (HL27), Ad. M. 21º37’32”N; 106º20’49”E (GeneBank IDs; KC209558)
ZMMU S-191161 (HL28), Ad. M. 21º37’32”N; 106º20’49”E, **karyotyped**. (GeneBank IDs; KC209558)
ZMMU S-191162 (HL30), near 21º40’N; 106º22’22E, no precise locality available (GeneBank IDs; KC209558)
ZMMU S-191163 (HL31), near 21º40’N; 106º22’22E, no precise locality available (GeneBank IDs; KC209558)
ZMMU S-191164 (HL32), near 21º40’N; 106º22’22E, no precise locality available (GeneBank IDs; KC209558)
ZMMU S-191165 (HL33), near 21º40’N; 106º22’22E, no precise locality available (GeneBank IDs; KC209558)
ZMMU S-191166 (HL34), near 21º40’N; 106º22’22E, no precise locality available (GeneBank IDs; KC209558)