

Investigating the intraspecific biodiversity of the threatened rodent

***Leopoldamys neilli* in Southeast Asia**

Alice Latinne¹, Surachit Waengsothorn², Vincent Herbreteau³, Johan R. Michaux^{1,4}

¹Institut de Botanique (Bat. 22), Université de Liège, 4000 Liège (Sart Tilman), Belgique

²Thailand Institute of Scientific and Technological Research, Bangkok, Thailand

³CIRAD, UR AGIRs (Animal et Gestion Intégrée des Risques), Campus International de Baillarguet, CS 30016 , 34988 Montferrier-sur-Lez cedex France

⁴CBGP (Centre de Biologie et de Gestion des Populations), UMR INRA/IRD/Cirad/Montpellier SupAgro, Campus international de Baillarguet, CS 30016 , 34988 Montferrier-sur-Lez cedex France

E-mail: alice.latinne@ulg.ac.be

We study the phylogeography of *Leopoldamys neilli*, a threatened murine rodent species endemic to limestone karsts of Thailand, in order to assess the influence of its endemism to karstic habitat on its intraspecific biodiversity and phylogeographic pattern.

Samples of *L. neilli* were collected in limestone karsts from 20 localities in seven provinces of Thailand.

Two mitochondrial markers, the cytochrome *b* gene (cytb) and the cytochrome c oxydase subunit I gene (COI), were sequenced for 115 *L. neilli* individuals. A nuclear fragment, the β -fibrinogen intron 7 (bfibr), was amplified in a subset of 65 samples. Phylogenetic reconstructions and median joining networks were used to explore relationships between haplotypes of the studied populations. Haplotype and nucleotide diversities of the main lineages were estimated for each locus. Divergence times of the main lineages of *L. neilli* were estimated using Bayesian inference. The demographic histories of the main lineages of *L. neilli* were also examined.

Our study gave evidence of a strong geographic structure of the genetic diversity for *L. neilli*. Six highly differentiated genetic lineages were observed in the phylogenetic and phylogeographic analyses. These lineages are allopatric and correspond to particular regions of Thailand. They exhibit very high degree of genetic divergence and gene flows between them are extremely low. Within each lineage, the levels of haplotype and nucleotide diversities are very low for each gene. These results suggest a severe fragmentation of *L. neilli*'s populations, correlated to the fragmented distribution of its habitat and highlight its high endemism to limestone karsts. The strong phylogeographic pattern of *L. neilli* and the very ancient separation of some lineages could be explained by the geological history of Thailand during Tertiary and Quaternary era.

In conclusion, this study revealed an unexpectedly high level of intraspecific biodiversity within the species *L. neilli*. These results consolidate the importance to strengthen the protection of limestone habitats and to preserve not only their huge interspecific but also intraspecific biodiversity.