



Population genetic structure and historical demography of the ground beetle *Chlaenius costiger* in the Tsinling-Dabashan Mountains of central China

L.-N. Su^{1,2}, X.-C. Li¹, H.-Z. Meng¹, X.-Y. Gao¹, H. Yin³ and K. Li³

¹College of Life Sciences, Shaanxi Normal University, Xi'an, China

²Shaanxi Institute of Zoology,

Northwest Institute of Endangered Zoological Species, X'ian, China

³College of Life Sciences, Shanxi Normal University, Linfen, China

Corresponding author: X.-C. Li

E-mail: xiaochen@snnu.edu.cn

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ABSTRACT. Population genetic structure and demographic history of the ground beetle *Chlaenius costiger* (Coleoptera: Carabidae) in the Tsinling-Dabashan Mountains of central China were estimated using mitochondrial DNA sequences (Cox1-tRNA^{Leu}-Cox2) of 144 individuals from 16 local populations. The high haplotype diversity was accompanied by low nucleotide diversity. Phylogenetic analysis (Bayesian inference) of the 43 haplotypes revealed no phylogeographic structure. Analysis of molecular variance suggested that most of the variation was attributed to within population variation (79.26%). Mantel test results showed a significant correlation between the genetic distance and geographical distance of the populations with a correlation coefficient equal to 0.216964 ($P = 0.0471 < 0.05$), indicating the presence of isolation by distance. Spatial AMOVA and PERMUT analyses showed no phylogeographic structure. Gene flow calculated

through the number of migrants was high between many pairs of populations. The results of a neutrality test, mismatch distribution analyses, and Bayesian skyline plot analysis together showed a demographic expansion. The estimated expansion time of the whole sampled population was 0.125 million years. The complex topography in the Tsinling-Dabashan Mountains area led to the high level of genetic diversity, and migratory flight resulted in the high level of gene flow, leading to the lack of a phylogeographic structure.

Key words: Population genetic structure; Historical demography; *Chlaenius costiger*; Mitochondrial DNA; China