



Genetic diversity and historical demography of the narrow-range endemic Alpine toad, *Scutiger liupanensis*, in the Liupan Mountains of central China

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ABSTRACT. The genetic diversity and historical demography of the narrow-range endemic Alpine toad, *Scutiger liupanensis*, in the Liupanshan National Forest Park of central China were estimated using cytochrome b and cytochrome c oxidase subunit I (COI) from 85 individuals from five local populations. Both the haplotype diversity (H_d) and the nucleotide diversity (P_i) were very high. Phylogenetic analysis of the 63 haplotypes revealed two major clades, and an analysis of molecular variance attributed most of the variation to within populations. Mantel tests did not reveal an isolation by distance pattern of genetic divergence between populations, and SAMOVA showed no phylogeographic structure. The results of neutrality tests,

mismatch distribution analyses, and allelic frequency spectra suggest that a sudden demographic expansion occurred, and that high genetic variation is beneficial to the survival and development of this species.

Key words: Alpine toad; Genetic diversity; Historical demography; China