



Range-wide phylogeography and conservation genetics of a narrowly endemic stream salamander, *Pachyhynobius shangchengensis* (Caudata, Hynobiidae): implications for conservation

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ABSTRACT. The Shangcheng stout salamander (*Pachyhynobius shangchengensis*) is an endangered amphibian endemic to the Dabie Mountains, southeast China, and is currently threatened by habitat loss and illegal poaching. Here we used the mitochondrial DNA control region sequence (768 bp) to conduct a comprehensive investigation of genetic diversity, phylogeographic pattern, and demographic history of the species across its geographic distribution to assist its conservation. We concluded that the levels of genetic variation are relatively low in all four populations. Analysis of molecular variance indicated that the most likely phylogeographic pattern is [JGT] [KHJ] [TM, BYM]. Two distinct clades were identified in the phylogenetic tree of 28 haplotypes, corresponding to the two southern populations (TM, BYM) and two

northern populations (JGT, KHJ). Significant population differentiation (F_{ST}) was detected among all populations. Among the four populations, historical demographic analyses (e.g., the g parameter, the Tajima D test, and the Fu Fs test) did not reveal definite information on population expansion except for the BYM population, which had undergone a strong population expansion event. Based on the analysis of a Bayesian skyline plot, the total population underwent a significant population fluctuation around 20 kya. This may have been triggered by the end of the last glacial maximum. In conclusion, the existence of three evolutionarily significant units (BMY-TM, KHJ, and JGT) and four management units (BMY, TM, KHJ, and JGT) is supported by our study.

Key words: *Pachyhynobius shangchengensis*; Genetic structure; Mitochondrial DNA control region; Phylogeography; Population demography