



Population genetic structure and its implication in the conservation of *Schizopygopsis pylzovi* in Yellow River as inferred from mitochondrial DNA sequence analysis

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ABSTRACT. To assess the genetic diversity, structure, and population dynamics of *Schizopygopsis pylzovi*, we examined the changes in mitochondrial DNA sequences (the mtDNA control region and the Cyt b gene; 1835 bp) in 304 individuals from nine populations. The samples were segregated into 112 haplotypes, with high haplotype diversity and low nucleotide diversity. The haplotype diversity was highest in the Minhe (HS) range of Huangshui River and lowest in the Weiyuan (WY) range of Weihe River. Analysis of molecular variance showed that 69.64% of the total genetic variance was contributed by within-the-group variation and 30.36% was contributed by among-the-group variation. Pairwise F_{ST} revealed significant divergence between the populations. The F_{ST}

between the MT and WY was highest, and that between the YZ and YJ was lowest. The neighbor-joining phylogenetic tree demonstrated that all geographic populations were not monophyletic, but overlapped each other, indicating that the duration of geographical isolation was not long enough or the populations had not yet reached significant genetic isolation or differentiation at the monophyletic level. Tajima's D and Fu's Fs were negative and statistically significant, indicating that *S. pylzovi* had experienced certain population expansion events, which is consistent with the hypothesis that the headwater area of the Yellow River was dramatically affected by the geological and climatic upheaval during the Quaternary ice age. Our analysis indicated that the management units corresponding to the WY population should be managed and conserved first. *In situ* conservation is first recommended to protect the original habitat from further destruction.

Key words: *Schizopygopsis pylzovi*; Mitochondrial DNA; Genetic structure; Genetic diversity; Conservation strategy