



Microsatellite markers reveal genetic divergence among wild and cultured populations of Chinese sucker *Myxocyprinus asiaticus*

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ABSTRACT. Studies of genetic diversity and genetic population structure are critical for the conservation and management of endangered species. The Chinese sucker *Myxocyprinus asiaticus* is a vulnerable monotypic species in China, which is at a risk of decline owing to fluctuations in effective population size and other demographic and environmental factors. We screened 11 microsatellite loci in 214 individuals to assess genetic differentiation in both wild and cultured populations. The single extant wild population had a higher number of alleles (13) than the cultured populations (average 7.3). High levels of genetic diversity, expressed as observed and expected heterozygosity ($H_O = 0.771$, $H_E = 0.748$, respectively), were found in both wild and cultured populations. We also report significant differentiation among

wild and cultured populations (global $F_{ST} = 0.023$, $P < 0.001$). Both STRUCTURE analysis and neighbor-joining tree revealed three moderately divergent primary genetic clusters: the wild Yangtze population and the Sichuan population were each identified as an individual cluster, with the remaining populations clustered together. Twenty-two samples collected from the Yangtze River were assigned to the cultured population, demonstrating the efficacy of artificial propagation to avoid drastic reduction in the population size of *M. asiaticus*. These genetic data support the endangered status of the *M. asiaticus* and have implications for conservation management planning.

Key words: Chinese sucker; Microsatellite; Genetic differentiation; Population structure; Conservation