



Genetic diversity among red swamp crayfish (*Procambarus clarkii*) populations in the middle and lower reaches of the Yangtze River based on AFLP markers

B.F. Zhu¹, Y. Huang², Y.G. Dai³, C.W. Bi² and C.Y. Hu²

¹Henry Fok School of Life Science, Shaoguan University, Shaoguan, Guangdong Province, China

²College of Life Science and Food Engineering, Nanchang University, Nanchang, China

³Fishery Technical Extension Station, Jiangxi Province, Nanchang, China

Corresponding author: C.Y. Hu

E-mail: hucy2008@163.com

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ABSTRACT. The red swamp crayfish has become one of the most important freshwater aquaculture species in China. At present, although it is widely distributed in the middle and lower reaches of the Yangtze River basin, little is known about its population genetics and geographic distribution in China. We estimated the genetic diversity among 6 crayfish populations from 4 lakes (Hongze Lake, Poyang Lake, Dongting Lake, and Yue Lake) using AFLPs. A total of 129 loci were generated with 5 *EcoRI-MseI* primer combinations and scored as binary data in 139 individuals. These data were analyzed by cluster methods with the NTSYSpc software package. The 6 populations were separated into 3 major clusters by principal coordinate analysis and cluster analysis. Among the 6 populations, the highest gene diversity was found within the Nanjing population. Analysis of molecular variance demonstrated that most variation occurred within populations (91.20%). The estimated

average G_{ST} value across all loci was 0.4186, suggesting (very) low gene flow among the different localities. We conclude that there is high genetic differentiation among crayfish in the middle and lower reaches of the Yangze River. This information will help in the selection of high-quality individuals for artificial reproduction.

Key words: *Procambarus clarkii*; AFLP; Genetic diversity; Yangtze River