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Title: Population Genetic Structure and Post-Establishment Dispersal Patterns of the Red Swamp Crayfish *Procambarus Clarkii* in China

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Abstract: The red swamp crayfish (*Procambarus clarkii*) was introduced to China in the early 20th century. It has been spread to almost all forms of fresh water bodies including lakes, rivers and even paddyfields in most provinces of China. To clarify issues such as the initial entry point(s), dispersal pattern, genetic diversity and genetic structure of *Procambarus clarkii* in China, the genetic structure and diversity of *P. clarkii* populations at 37 sampling sites (35 from China, one from the USA and one from Japan) were analyzed using both mitochondrial gene sequences (COI and 16S rRNA) and 12 nuclear microsatellites. Multiple tests including phylogenetic analyses, Bayesian assignment and analysis of isolation by distance showed that (i) the population from Japan and those collected from China, particularly from Nanjing (BGt and XG) and its some neighboring sites (CJr, NT and NB), have similar genetic composition, (ii) relatively high genetic diversity was detected in Chinese populations, (iii) the *P. clarkii* populations in China did not experience significant population expansions. Taken together, Nanjing, Jiangsu province is the presumed initial entry point, and human-mediated dispersal and adaptive variation are likely responsible for the observed genetic pattern of *P. clarkii* in China.

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