



Invasion of *Procambarus Clarkii* in China: Genetic analysis



In this project, we aim to clarify the issues including: (i) whether the *P. clarkii* populations in China have relatively high genetic diversity, which would likely facilitate its invasion success to some extent, (ii) whether Nanjing was the initial point of entry of *P. clarkii* in China, (iii) whether the introduction of *P. clarkii* in China was derived from a single or multiple event(s).

Current situation of *P. clarkii* in China

P. clarkii invaded China in the early of 20th century, and now has been found in almost all forms of fresh water bodies including lakes, rivers and even paddyfields in most provinces of China.

Because of its high commercial value, this species has become one of the most important aquatic products in China. However, it threatened local freshwater ecosystems.

Presently less attention is being given to the invasive issue of *P. clarkii* in China



Genetic diversity of *P. clarkii*

Number of alleles (N_a) = 6.4-11.8, and expected heterozygosity (H_e) = 0.7002-0.8214;
 The haplotype diversity of the partial COI sequence (H_d) was 0.403;
 The haplotype diversity (H_d) of 16S rRNA was 0.390.

Analyses of population structure

A neighbour-joining tree based on the Nei's standard genetic distances for *P. clarkii* populations was constructed.

