



Genetic diversity analysis of oriental river prawn, *Macrobrachium nipponense*, in Yellow River using microsatellite marker

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ABSTRACT. To assess the genetic status of this species, the genetic diversity of wild *Macrobrachium nipponense* from seven geographic locations in the Yellow River basin were investigated using 20 polymorphic microsatellite DNA loci. The genetic diversity between populations was indicated by the mean number of alleles per locus and mean observed heterozygosity (H) and the expected H, which was arranged from 2 to 10, from 0.4705 to 0.5731, and from 0.5174 to 0.6146, respectively. Hardy-Weinberg equilibrium analysis indicated that a deficiency of heterozygotes existed in all seven populations. Both the F_{ST} and AMOVA analyses showed that there is significant difference on population differentiation among populations. The UPGMA clustering tree demonstrated that their close relationship is consistent with their geographic proximity. The

data suggest that this Yellow River population has a wide genetic base that is suitable for breeding.

Key words: *Macrobrachium nipponense*; Genetic diversity; Yellow river; Microsatellite marker