

Genetic diversity analysis in Malaysian giant prawns using expressed sequence tag microsatellite markers for stock improvement program

ABSTRACT

The Malaysian giant prawn is among the most commonly cultured species of the genus *Macrobrachium*. Stocks of giant prawns from four rivers in Peninsular Malaysia have been used for aquaculture over the past 25 years, which has led to repeated harvesting, restocking, and transplantation between rivers. Consequently, a stock improvement program is now important to avoid the depletion of wild stocks and the loss of genetic diversity. However, the success of such an improvement program depends on our knowledge of the genetic variation of these base populations. The aim of the current study was to estimate genetic variation and differentiation of these riverine sources using novel expressed sequence tag-microsatellite (EST-SSR) markers, which not only are informative on genetic diversity but also provide information on immune and metabolic traits. Our findings indicated that the tested stocks have inbreeding depression due to a significant deficiency in heterozygotes, and FIS was estimated as 0.15538 to 0.31938. An F-statistics analysis suggested that the stocks are composed of one large panmictic population. Among the four locations, stocks from Johor, in the southern region of the peninsular, showed higher allelic and genetic diversity than the other stocks. To overcome inbreeding problems, the Johor population could be used as a base population in a stock improvement program by crossing to the other populations. The study demonstrated that EST-SSR markers can be incorporated in future marker assisted breeding to aid the proper management of the stocks by breeders and stakeholders in Malaysia.

Keyword: *Macrobrachium rosenbergii*; Population genetics; EST microsatellites; Stock improvement program