BIOCHEMICAL GENETIC DIFFERENTIATION AMONG WILD POPULATIONS OF MILKFISH *(Chanos chanos)* IN INDONESIA

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ABSTRACT

Four populations of milkfish (*Chanos chanos*) were collected (N=100) from coastal water of Aceh, Bali, East Java and South Sulawesi and were examined electrophoretically at 29 loci to determine the genetic variability and the population structure. Twelve loci (Adh, Aat-1, Est-1, Est-2, -Gpd, Gpi-1, Gpi-2, Idh-1, Ldh-1, Mdh-1, 6-Pgd and Pgm-2) were polymorphic in at least one population. Six loci (Adh, Est-1, Est-2, Gpi-1, 6-Pgd and Pgm-2) were reliable genetic markers. The number of polymorphic loci, number of alleles per locus and heterozygosity were 0.336, 1.577 and 0.068 respectively. These values were slightly higher than other marine fishes. Significant differences in allele frequencies were observed at more than one locus except between Bali and East Java populations. The mean Nei s genetic distance between population pairs was 0.00155. This value is typical divergence between conspecific populations. The UPGMA cluster analysis of genetic distance revealed that the milkfish populations formed three geographical groups. The results suggest that the natural populations of milkfish in Indonesia could be devided into 3 geographical groups located in the west (Aceh), midle (Bali/ E. Java) and East (South Sulawesi) Indonesia.

KEYWORD: ***Chanos chanos*, genetic variability, population structure**

INTRODUCTION

The milkfish *(Chanos chanos)* is one of the most important species extensively cultured in brackish-water Indonesia ponds. Recently, this species has become more important as frozen and live bait for tuna long-line capture. The supply of milkfish fry comes mainly from the wild. High demands on the supply of fry emphasize the need for artificial propagation to supplement the supply. The technology for artificial seed production of milkfish has been developed in Gondol Research Station for Coastal Fisheries, Agency for Agriculture Research and Development, and the technology has been adopted by private hatcheries who mass produced egg and fry to supply brackishwater pond of milkfish culture (Sugama *et al.*, 1997).

The broodstocks for seed production have been collected from several regions in the country. An understanding of milkfish population structure particularly in this region is therefore a requirement for broodstock development since the existence of subpopulations or stock, heterogeneity will necessarily influence the formulation of stocking and/or conservation practices (Macaranas *et al.*, 1990; Taniguchi & Sugama, 1990).

Several authors have shown that proteins and enzymes are useful genetic markers for fish in culture and breeding studies (Taniguchi *et al.*, 1983; Sugama *et al.*, 1992; Agenese *et al.*, 1995; Goudie *et al.*,1995). Proteins and enzymes electrophoresis is also considered to be an extremely useful technique in population genetics and is particularly powerful in identifying of genetic differentiation between populations (Allendorf & Utter, 1979; Sumantadinata & Taniguchi, 1982; Taniguchi & Sugama, 1990).

Although various studies have been conducted on reproduction, larva rearing, nutrition and disease of milkfish, none study directed toward genetic improvement. Therefore, genetic studies of this species were conducted to obtain basic information on the amount of genetic variability and genetic differentiation among wild populations. Electrophoresis was used for allozyme analysis. The results may be important for the future development of milkfish breeding and proper management of natural populations.

MATERIALS AND METHODS

Electrophoresis

A total of 400 milkfish, (BW:10.0-35.8 g) were collected from the coastal waters of Aceh (sample size n=100), Tuban, East Java (n=100), Singaraja, Bali (n=100) and Takalar, South Sulawesi (n=100). Whole fish were freighted to Gondol Research Station for Coastal Fisheries, Bali, where they were held frozen at-20°C until electrophoresed.

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