

SUMMARY

A study of population variability and inter-relationships using allozyme electrophoresis and RFLP's of mtDNA is presented. Populations of *Mugil cephalus*, *Mugil georgii*, *Liza argentea*, *Myxus elongatus* and *Aldrichetta forsteri* were considered in this analysis. Populations of *Mugil cephalus* from Burrum Heads in Queensland to Tathra in New South Wales showed no significant allozymic difference at 19 loci studied. The same allozymes for an outgroup population of *Mugil cephalus* from Negombo Lagoon in Sri Lanka also showed no significant difference to the east Australian populations of *Mugil cephalus*. This showed the conservative nature of the nuclear genome of this species. Among *Liza argentea*, *Myxus elongatus* and *Aldrichetta forsteri* the allozyme distribution conforms more towards that of panmixia along the eastern Australian coast. However, the inbreeding coefficient estimated for *Liza argentea* populations was higher compared to the other species. The average heterozygosity and proportion of polymorphic and variant loci estimated for *Mugil cephalus*, *Mugil georgii*, *Liza argentea* and *Myxus elongatus* were lower than the comparable data for Osteichthyes. However, *Aldrichetta forsteri* produced estimates comparable to those for other fishes. The genetic distance between populations of each species was low and showed no tendency towards genetic isolation. Phylogenetic trees and cladograms showed distinct clustering of populations that belonged to an individual species. Some degree of intra population variation was also shown on trees and cladograms.

The restriction fragment length polymorphism's (RFLP's) of mtDNA also showed that the east Australian populations of *Mugil cephalus* belong to a single panmictic group. However, the RFLP's of mtDNA distinctly showed that the Sri

Lankan and east Australian populations were different entities with a sequence divergence of 9.4%. This estimate is high for a within species assessment. Therefore, the taxonomic relationships of these two groups are discussed. The Sri Lankan population showed intra population variation while no variation was observed for the eastern Australian population with the mtDNA RFLP's study. This observation is also discussed together with variation observed in allozyme data. A single mtDNA RFLP's profile for *Mugil cephalus* populations from eastern Australia, Western Australia and Sri Lanka showed that the latter two have a closer resemblance. The possibility of this feature is also discussed.

An assessment of relationship between *Mugil cephalus* and *Mugil georgii* is also discussed using allozyme and mtDNA RFLP's data. The divergence time between the five species was also estimated. These estimates showed that this group has diverged within the last 7-16MY.

Recommendations were also made for the regulation and management of the *Mugil cephalus* population along the eastern Australian coast, which was proved to be a panmictic group both by allozyme and mtDNA RFLP's data.