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Phylogeography and population structure of *Tenualosa toli* inferred from Cytochrome b mitochondrial DNA fragment



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Abstract

Aim : Shad fish of genus *Tenualosa* subfamily Alosinae (shads) family Clupeidae, are commercially and culturally important estuarine fish in many Asian countries, especially in Sarawak. In this study, the phylogenetics of three species from the genus *Tenualosa* (*Tenualosa toli*, *Tenualosa macrura* and *Tenualosa ilisha*) was determined.

Methodolgy : Sequence analysis of 910 base pairs of Cytochrome b gene were conducted on the samples of indigenous *T.toli* (N=111) and *T. macrura* (N=24), which were collected from Sarawak including the samples of non-native *T. ilisha* (N=4) obtained from Bangladesh.

Results : A total of 28 haplotypes were found with *T. toli* producing 15 haplotypes, where 13 haplotypes were unique haplotypes while 2 shared haplotypes among the 6 populations.

Interpretation : Phylogenetic analysis supported the monophyletic status between the three shad species. The highest intraspecific genetic divergences were recorded between imported samples and samples from other localities. There is evidence of overfishing and recently occurred bottleneck events which led to a population size expansion of *T. toli*, especially in Sebuyau, Daro and Mukah.

Collection of *Tenualosa toli* samples



DNA extraction
sequence analysis
(910 base pairs)

Phylogenetic analysis

- Monophyletic status of *T. toli*,
T. macrura and *T. ilisha*

DNA polymorphism analysis on *T. toli*

- Existence of overfishing
- Recently occurred bottleneck
- *T. toli* population size expansion