

Research Highlight

GENETIC VARIATIONS IN PARADISE THREADFIN (POLYNEMUS PARADISEUS)

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Paradise threadfin (*Polynemus paradiseus*) belongs to the family Perciformes¹ and it is found in Bangladesh, India, Malaysia, Myanmar, Thailand, Pakistan and Combodia², but it is widely distributed in the Indo-pacific Ocean such as the Bay of Bengal³. This species is globally known as Paradise threadfin but it has different common names in different countries like; in Bangladesh it is commonly known as Tapasi⁴.⁵, in India it is known as Tapsee-mahh⁶.⁷, in Malaysia its common names are striped threadfin and Tassel fish® and in Philippines its common names are Buka-dulce and Kulampiros°.

It is reported that a few years ago, it was available approximately all round the year in coastal waters. Consumers preferred this fish because of its good taste and palatability, but unfortunately, at present, this fish is not accessible in those water bodies and almost at the verge of extinction because of apparent decline of the habitat, over-exploitation as well as lack of proper management.

Moreover, amplified water pollution as well as devastation of breeding grounds has limited the natural breeding of *P. paradiseus*. As a

result of which, the wild populations of this species have become genetically poor. Therefore, it's the need of hour to understand the genetic status of the wild stocks of the species.

Accordingly, Allozyme electro-phoresis is a useful molecular marker that is employed as an efficient tool for fish population studies as well as fishery management¹². Therefore, a new research was done in order to investigate the genetic status of the three river populations of *P. paradiseus* i.e., Tentulia, Paira and Kirtonkhola by means of horizontal starch gel electrophoresis method¹³.

During this study, on the basis of genetic distance, UPGMA dendrogram exhibited that the three river populations of this fish species constructed two clusters. Paira and Kirtonkhola populations made one cluster and separated from Tentulia population by the genetic distance of 0.014.

Conclusively, despite of the significant genetic variation is present among the wild populations of *P. paradiseus*, special care should be taken when taking management options. In this regard, detailed investigation

regarding *P. paradiseus* population differentiation would be helpful in order to examine the population structure of this species. The existing differentiation appears to be weak; therefore, application of molecular markers has become vital with a higher polymorphism, like microsatellites, which have been able to detect a greater degree of population diversity as compared to allozymes.

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