

Section 2

Executive Summary of the Project:

Freshwater fish Genus *Puntius* constitute sixteen species and contributes as the major component of the freshwater fish fauna of Sri Lanka. This Genus is important in aquarium trade, food chains and freshwater biodiversity. Eight species are endemic and many have become endangered and threatened due to overexploitation for aquarium trade and habitat degradation. Genetic make up and relationships of these species are important in adopting conservation strategies. Present study focused on identification of the morphological and molecular relationships of the 16 *Puntius* species and in order to elucidate the phylogenetic relationships of these species.

Fish were collected from five major rivers of Sri Lanka representing different altitude ranges. Length measurements and meristic characters of individuals of each species were recorded and analysed by discriminant analysis and hierarchical cluster analysis. DNA was extracted from each individual and a fragment of 12S rRNA was amplified using specific primers. Amplified fragments were subjected to restriction digestion by four restriction enzymes to identify intraspecific polymorphism and inter specific polymorphism. Eight samples were sequenced initially to determine the phylogenetic relationships among species.

Morphological analysis revealed that 16 *Puntius* species could be grouped into four clusters according to the similarities found in their morphologies. Cluster 1 consists of *P. srilankensis*, *P. sinhala*, *P. ticto*, *P. dorsalis*, *P. chola*, *P. amphibious*, *P. sarana*, *P. pleurotaenia* and *P. martynstyne*. Second cluster includes *P. bimaculatus*, *P. vitatus* and *P. tittaya*. Single species; *P. asoka* forms a separate third cluster and the fourth cluster contains *P. bandula*, *P. nigrofasciatus* and *P. cumingii*. Selected individuals of *P. dorsalis* show intraspecific molecular variations among rivers, which also show intraspecific morphological plasticity. Analysis of limited molecular data showed that morphologically closely related species had different restriction patterns. Sequences obtained were not in a reliable form to do the phylogenetic study and sequencing will be continued and results of the phylogenetic analysis will be submitted to the NSF in future.