D-38: Phylogenetic relationships of 15 species of Cyprinids based on morphology and protein electrophoresis

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Phylogenetic relationships of 15 species of cyprinids were studied based on 33 morphological characters and 20 biochemical characters. Morphological characters included 16 meristic characters and 17 morphometric characters. The biochemical characters were obtained by protein electrophoresis of skeletal muscles of fish. Protein electrophoresis was carried out using horizontal starch gel method and tested for 10 enzymes. Both morphological and biochemical characters were coded into discrete states. Character matrices were prepared for morphological, biochemical and combined morphological and biochemical characters. Phylogenetic analysis was done using the computer software packages, PAUP and MacClaid.

The phylogenetic tree, based on morphology is not totally congruent with the phylogenetic tree, based on biochemical characters, but they show some similarities. Both phylogenetic trees indicate that *Puntius* dorsalis and *P. filamentosus* were separated from the rest at an early stage of evolution. *P. nigrofasciatus* is very closely related to *P. cumingi*.

Analysis of combined biochemical data and morphological data produced 4 equally parsimonius cladograms each with a consistency index of 0.702 and a length of 238 steps. The separation of clusters is more clear in this analysis than in the analysis of morphological data and biochemical data. Analysis of combined data separate 15 species into 6 clusters. All types of consensus trees of combined data set indicate that *P. dorsalis*, *P. amphibius* and *P.chola* are distantly related to other species and originated from separate lines. The smaller

Puntius species *P. nigrofasciatus P. cumingi, P. titteya P. bimaculatus* and *P. vittatus* are very closely related to each other. *P.sarana* is closely related to *P. filamentosus*.