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Genetic diversity and phylogenetic relationship of catfish order *siluriformes* inferred from mitochondrial gene sequence variationLashari Punhal¹, Muhammad Younis Laghari¹, Xiaowen Sun², Yan Zhang² and Yulin Deng³¹University of Sindh, Pakistan²Chinese Academy of Fishery Sciences, China³Beijing Institute of Technology, China

Order *Siluriformes* includes many commercially and economically important species throughout the world. Here, we investigated genetic relationships and diversity in this order. Sequence comparisons and phylogenetic analyses revealed considerable variations between mitochondrial *CO1* genes among twenty-four *siluriformes* species. The nucleotide frequencies are A=23.80%, T/U=29.62%, C=26.63%, and G=19.95%. For estimating ML values, a user-specified topology was used. The maximum Log likelihood for this computation was -9413.645. Estimates of average evolutionary divergence over all sequence and the numbers of base substitutions per site from averaging over all sequence pairs were 4.984. Our results suggest that *Batasio tranvancoria* formed a single clade; *R. Rita*, *W. Attu*, *M. Montanus* and *B. Bagarius* comprised a single separate family; and *M. Vittatus*, *M. Horai*, *B. Tengana*, *M. Malabaricus*, *M. Bacourti*, *M. Singaringan*, *M. Bleekeri*, *M. Gulio*, *M. Multiradiatus*, *M. Rhegma*, *M. Cavasius*, *M. Tengara*, *S. Aor*, *S. Seenghala*, *B. Bajad*, *B. Filamentosus*, *B. Macracanthus*, *P. Siamensis*, *E. Vacha* and *B. Travancoria* formed single subfamily.

Biography

Punhal Khan Lashari is working as an Associate Professor in the Department of Fresh Water Biology and Fisheries, University of Sindh, Pakistan. He is responsible to conduct research in the field of Fish genetics/Fisheries Biology/Aquaculture from various aspects. His research mainly focuses on aquaculture, aquatic ecology, fish biology, fish genetics, and fish health management.

lashari.punhal@usindh.edu.pk

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