outgroup comparison and ontogenetic study. Ontogenetic (growth) series of several representative cottoids will be examined to illuminate neotenic features and phylogenetic independence of serially homologous structures of the lateralis system. Significant findings potentially resulting from the proposed research include: 1) A comprehensive examination of cottoid phylogeny that will fill in many gaps of our current knowledge of these fishes interrelationships. 2) The lateralis system will be examined for independence of serially homologous structures, an important issue in theoretical phylogenetics and in rigorously interpreting phylogeny. 3) The variation and evolution of the cottoid lateralis system will be examined, modeling the evolution of this system in many different taxa. 4) Cottoid biogeography will be examined with a phylogenetic perspective, answering some general questions on the biogeography of antitropical fishes.

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PHYLOGENETIC RELATIONSHIPS OF GASTEROSTEIFORMES

The taxonomic status of Gasterosteiformes is obscure. Recently, Johnson and Patterson (1993) proposed a new taxon, Smegmamorpha, which includes Gasterosteiformes. The main objective of this study is to test the monophyly of Johnson and Pattersons Smegmamorpha. I will examine the osteology of the representatives of about 100 families to hypothesize their systematic relationship within Acanthopterygii. I will use outgroup comparison method for polarizing characters and cladistic method using the MacClade and Paup computer programs for reconstructing systematic relationships in this group. This study not only will increase our knowledge of the systematics of Gasterosteiformes, but also that of Percomorpha and Acanthopterygii that comprise the largest group of fishes. Evolution of some osteological characters especially caudal peduncle, pectoral skeleton, and visceral skeleton will be studied.

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DIMINISHED MISMATCH REPAIR DURING ADAPTIVE MUTATION

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Two mechanistic features distinguish adaptive reversion from normal, spontaneous growth-dependent reversion of a *lac*-frameshift mutation in *Escherichia coli*. The adaptive mutations require homologous recombination proteins, and have a different sequence spectrum. Adaptive mutations are mostly -1 deletions in mononucleotide repeats and growth-dependent reversion of the same *lac*-frameshift aleele are heterogeneous. The unique mutation spectrum suggests an absence of mismatch repair (MMR) function. In support of this idea, cells lacking MMR re-create the same *lac*-reversion sequence spectrum during growth.

To test the hypothesis that a decrease in proteins is required for adaptive mutation, we overproduced MutS and MutL, two key components of the system. We find that overproduction of MutS and MutL or MutL alone decreases levels of recombination-dependent adaptive mutation as much as 10-fold. Western analyses show that overproduction of MutL actually stabilizes the MutH protein, which is required for and which becomes less abundant during starvation. These results indicate, first, that MutH appears to be limiting during adaptive