Extraordinary mtDNA Substitution Rates within Pygmy Sunfishes (Elassomatidae): A Multi-scale Analysis of Molecular Divergence within North America's Most Ambiguous Fishes

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ABSTRACT

Nucleotide substitution is the fundamental component of the adaptive processes responsible for the maintenance of biodiversity. Lineage specific substitution rate is a pervasive concept in evolutionary biology, having been shown to correlate (to varying degrees) with population size, body size, metabolic rate, and generation time. A trade-off is hypothesized for the mitochondrial genome, whereby an increased substitution rate improves the adaptive potential of proteins involved in the electron transport chain, but is perhaps inescapably tied to increased random mutation via oxidative damage. Random nonsynonymous mutation could result in maladaptive metabolic rate and reduced longevity. On the other hand, species that exhibit highly efficient mtDNA repair mechanisms may forfeit the potential to adapt to novel physiological stressors. Within pygmy sunfishes, an extraordinarily high degree of mtDNA polymorphism is the suspected result of a relatively rapid substitution rate within the family. Among vertebrates, the banded pygmy sunfish exhibits the highest degree of intraspecific mtDNA divergence recorded to date (>16% Cytochrome-*b*). This study uses molecular phylogenetics to test the hypothesis that mtDNA substitution rate is uniquely elevated in this species, as well as within the family Elassomatidae. Since no fossil record exists for Elassomatidae, biogeographic vicariance patterns are used to calibrate divergence times among mtDNA haplotypes. Pairwise comparison of nuclear and mitochondrial gene sequences among Elassomatidae and their closest relatives suggest that mtDNA substitution rates are indeed elevated (*c.a.* 400%) within the species and the family. A replicated pattern of domain specific rate variation is uncovered for a subset of mitochondrial genes, and the functional significance of this variation is discussed. Additional research is required to elucidate the compounding effects drawn from natural history variables, *e.g.* coincident reduction of generation time, dispersal ability, and body size exhibited by the pygmy fishes. Further exploration of mtDNA substitution rate variation in nonmodel organisms is poised to serve as a resource for investigation of metabolically induced oxidative stress, intergenomic conflict, and mitochondrial disease in humans (*e.g.* Alhzheimer's disease, deafness dystonia syndrome, Kearns-Sayre Syndrome, Leber's hereditary optic neuropathy, etc.).