

## Molecular Evolution of The Mitochondrial NADH Dehydrogenase Subunit 2 Gene in Populations of Arowana (*Scleropages formosus*, Osteoglossidae) in Peninsular Malaysia

S. Rahman<sup>1</sup>, M.Z. Ismail<sup>2</sup>, M.R. Iddid<sup>2</sup> and S. Muniandy<sup>3</sup>

<sup>1</sup> Institute of Postgraduate Studies, University of Malaya, 50603, Kuala Lumpur, Malaysia

<sup>2</sup> Institute of Biological Science, Faculty of Science, University of Malaya, 50603, Kuala Lumpur, Malaysia

<sup>3</sup> Department of Molecular Medicine, Faculty of medicine, University of Malaya, 50603, Kuala Lumpur, Malaysia

Molecular evolution of NADH dehydrogenase subunit 2 (ND2) was described to facilitate the phylogenetic analysis of arowana (*Scleropages formosus*) which belongs to the order of Osteoglossiformes. We determined the DNA sequence of the mitochondrial ND2 gene for 15 individuals of green arowana and a gold arowana. Among the fifteen collected green individuals, 10 were from Tasek Bera, Pahang and 5 were from Endau River, Johor, Malaysia. The gold arowana was a blue-based Malaysian golden arowana from Bukit Merah Reservoir.

Alignment of a total 16 sequences of NADH dehydrogenase subunit 2 (ND2) showed that populations in both Tasek Bera and Endau River shared similar haplotypes. ND2 sequences exhibited typical characteristic traits of vertebrate mtDNA: low frequency of guanine residue, a negative GC skew, minor AT skews and higher AT composition. The observed pattern of nucleotide substitution in these sequences showed a high transition bias. The majority of the variation was detected in the third codon, which accounted for 18 variable sites. First and second codon positions had 1 and 3 variable sites, respectively. Synonymous substitutions were higher than nonsynonymous substitutions at third position of the ND2 gene. Among 9 nonsynonymous substitutions of green arowana, 5 amino acid replacements were at 3<sup>rd</sup> positions, 3 were at 2<sup>nd</sup> position and one were at 1<sup>st</sup> position. The arowana ND2 sequences exhibited a highly biased amino acid composition (0.404) with high frequency of leucine (20.42%) which suggests functional constraint on the molecular evolution of the ND2 gene.

Phylogenetic analysis using the ND2 sequences showed that *S. formosus* is monophyletic and the green Malaysian arowana is genetically different from gold/red variety. The two populations cannot be distinguished genetically. There are no genetic differences between the two green arowana populations as same haplotypes were showed. Branching patterns also showed low resolution for these populations.