

Genetic divergence of two *Axis* species found in Sri Lanka revealed by two mitochondrial gene regions

D.R. Herath^{1,4}, H.A.C.C. Perera^{1,2}, C.D. Dangalle³ and G.H.C.M. Hettiarachchi^{4*}

¹National Aquatic Resources Research and Development Agency (NARA), Crow Island, Colombo 15, Sri Lanka

²Department of Zoology and Environmental Management, Faculty of Science, University of Kelaniya, Sri Lanka

³Department of Zoology and Environmental Science, Faculty of Science, University of Colombo, Sri Lanka

⁴Department of Chemistry, Faculty of Science, University of Colombo, Sri Lanka

The two *Axis* species found in Sri Lankan waters, *Axis thazard* (frigate tuna) and *Axis rochei* (bullet tuna), have very similar morphological features and are frequently misidentified. The present study was initiated to identify these *Axis* species accurately by molecular methods and to study their phylogenetic relationship. Samples of *A. thazard* and *A. rochei* were collected from the Western, Northwestern, Southern and Eastern provinces of Sri Lanka. The mitochondrial cytochrome oxidase I (COI) region was amplified and sequenced for 95 *A. thazard* samples and 56 *A. rochei* samples. The sequences were identified with 99.25% similarity for *A. thazard* and 98.9% similarity for *A. rochei*. DNA barcodes for *A. thazard* and *A. rochei* found in Sri Lanka were determined using the mt COI sequences (700 bp) obtained for the two species. In addition, partial mitochondrial D-loop sequences (500 bp) were also obtained for 84 *A. thazard* and 81 *A. rochei* samples for the phylogenetic study. The phylogenetic trees derived for the mt COI and mt D-loop sequences showed *A. thazard* samples in one clade and *A. rochei* samples in a separate clade, with the *A. rochei* clade being ancestor to the *A. thazard* clade. Tajima's D values, -1.88173 for mt COI and -1.39850 for mt D-loop sequences showed recent population expansions of both populations. The nucleotide diversity for the COI sequences of *A. thazard* was 0.02886 and for *A. rochei* it was 0.03541. As nucleotide diversity is higher in older populations, it can be suggested that *A. rochei* is the ancestral species out of the two *Axis* species, which is also confirmed by the branching pattern of the phylogenetic trees.

Keywords: *Axis thazard*, *Axis rochei*, mitochondrial, phylogenetic

*Corresponding author- email: chamarih@chem.cmb.ac.lk