The value of mitochondrial gene sequences in species conservation: case studies from the National Aquatic Resources Research and Development Agency (NARA)

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The research on molecular biodiversity at NARA tries to lay the scientific foundation of a logical conservation strategy that has its roots in various disciplines including molecular phylogenetics, diversity of ecological systems and genetic diversity. Mitochondrial DNA (mtDNA) has proved to be a valuable marker because of its fast evolutionary rate and the maternal mode of inheritance. DNA sequence analysis of mtDNA was carried out for assigning species identities for individual specimens of commercially exploited sharks, stranded marine mammals, marine turtles, jellyfish and determining the stock structure of giant tiger prawns (P. monodon), marine turtles and barramundi (Lates calcarifer). Two regions of the mtDNA: the control region and Cytochrome c oxidase 1(CO1) have been the focus of genetic studies. While Mitochondrial DNA CO1 region proved to be valuable for assigning species identities of sharks and jellyfish, it did not give a good resolution of the stock structure of giant tiger prawns but was able to differentiate the wild and the cultured species of barramundi. The control (D loop) region of the mitochondrial DNA (mtDNA) proved to be an efficient and accurate marker for identification of stranded marine mammals and determining the stock structure as well as the origin of marine turtles.

The results of ongoing projects and the achievements may allow us not only to quantify the diversity of the present biota of marine turtles, sharks, stranded marine mammals, jellyfish, barramundi and giant tiger prawns but also to extrapolate to their diversification in the future. A link between biodiversity and molecular genetics will create a platform, which may facilitate sustainable management strategies for conservation.

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