

Mitochondrial markers as a tool for the management and conservation of American crocodiles (*Crocodylus acutus*) in Colombia

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Abstract: The American crocodile is the most widely distributed crocodile species in the neotropics, and it is essential in aquatic ecosystems given the ecological roles it plays. In recent decades, unsustainable exploitation along with different types of anthropic intervention, led to the decimation and local extinction of many of this species' populations. In Colombia, this situation gave rise to a legislative framework for its protection, including a hunting ban and the establishment of breeding programs intended to promote sustainable use and contribute to its conservation. However, to fully comply with these programs, it is essential to obtain information about genetic diversity, integrity, and distribution, in wild and captive populations, considering the impact these variables have for the species survival. This study evaluated the genetic diversity and phylogeographic patterns of the American crocodile in Colombia based on 3 mitochondrial markers (*COI*, *CytB* and *TrnP/trnF/D-Loop*), analyzing potential actions for management and conservation. To this end, 33 individuals belonging to natural and captive populations in the Caribbean and Andean regions of Colombia were genetically characterized, assessing their genetic variability, phylogenetic and phylogeographic patterns as well as performing neutrality tests. Our analyses included sequences that had been previously reported in Colombia and across the species' distribution. Consequently, we found evidence of a high genetic variability in Colombian populations from nucleotide diversity values (0,001 to 0,004) and haplotype diversity values (0,710 to 0,900), the existence of phylogenetic clades that might represent evidence for evolutionarily significant units (ESUs) in Colombia supported by genetic distance values (0,040 to 0,630 between haplogroups), phylogenetic reconstructions and haplotype networks (3 to 11 mutational steps between haplogroups), and events of demographic variation. Based on these results, dispersal events along the Caribbean and in the Magdalena River basin were evidenced. We establish a genetic baseline to propose management recommendations when releasing individuals into the wild. Finally, we suggest the assignment of Management Units (MUs) to Colombian populations and the identification of research priorities in the species.

Keywords: Crocodylians, Phylogeography, Genetics, Breeding

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