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Preserving Pure Siamese Crocodile Populations: A Comprehensive Approach Using Multi-Genetic Tools

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Simple Summary: Hybrids between the critically endangered Siamese crocodile (*Crocodylus siamensis*) and least-concern saltwater crocodile (*C. porosus*) pose a significant challenge to conservation efforts due to human activities. Previous studies used microsatellite and mitochondrial DNA data to identify these hybrids, but potential biases and genetic drift within the populations could influence the results. To address these limitations and gain a clearer understanding of the genetic dynamics, we employed DArT sequencing to identify genome-wide single nucleotide polymorphisms (SNPs) in both species and confirm hybrid scenarios. We compared a population of Australian saltwater crocodiles to assess species-specific SNP distribution. Various analytical approaches were used to diagnose hybridization levels, especially in cases with potential backcrossing. Approximately 17.00–26.00% of loci were shared between Siamese and saltwater crocodile genomes. We identified 8051 species-specific SNP loci for Siamese crocodiles and 1288 for saltwater crocodiles. Using a PCR-based approach, three SNP loci were developed as markers, successfully enabling the distinction between species and various levels of hybridization. By combining mitochondrial and nuclear genetic information with species-diagnostic DNA markers, we developed a novel method for conservation prioritization, aiding long-term species survival through reintroduction and management programs.

Abstract: Hybrids between the critically endangered Siamese crocodile (*Crocodylus siamensis*) and least-concern saltwater crocodile (*C. porosus*) in captive populations represent a serious challenge for conservation and reintroduction programs due to the impact of anthropogenic activities. A previous study used microsatellite and mitochondrial DNA data to establish the criteria for identifying species and their hybrids; however, the results may have been influenced by biased allelic frequencies and genetic drift within the examined population. To overcome these limitations and identify the true signals of selection, alternative DNA markers and a diverse set of populations should be employed.

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