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NEW MTDNA DLOOP PRIMERS WHICH WORK FOR A VARIETY OF MARINE TURTLE SPECIES MAY INCREASE THE RESOLUTION OF MIXED STOCK ANALYSES

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Identification and monitoring of population units in marine turtle populations using molecular markers, particularly in foraging habitats where multiple stocks aggregate, has become one of the most critical aspects of conservation management at a regional level. In some regions such as the Wider Caribbean, where more than 30 countries share management responsibilities for multiple marine turtle stocks, the distinction of populations is even more crucial. The current, widely used mtDNA dloop PCR primers generate segments of about 380 to 510 bp´s in length and, although effective in distinguishing major rookeries in the earlier genetic surveys, they have become too limited in their resolution as the number of candidate source rookeries increases and the amount of haplotype frequency overlap more widespread. We have increased the number of dloop bases produced by PCR with two new sets of primers (LCM15382/H950 and LTEi9/H950) which amplify about 880 bp's and have been found by various laboratories to successfully amplify hawksbill, olive ridley, loggerhead and green turtle DNA. For hawksbills, so far, we have found a significant number of additional variable sites in the extended region which may aid in resolving some of the ambiguities in mixed stock analyses. Suitability of the primers across species and the extent of variability across the entire amplified segment are presented as well as a discussion of differences among species.

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