Morphological and Genetic Characterization of Intestinal Flukes of the Caribbean Hawksbill Sea Turtle, *Eretmochelys imbricata*

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Abstract:
Objective: The main objective of this study is to identify trematodes found within the gastrointestinal tract of five hawksbill sea turtles collected off the coast of Grenada. Using morphological characterization and genetic sequencing, the species of the flukes will be determined and compared to those known to parasitize hawksbill sea turtles in the Caribbean.

Design & Methods: Five adult male hawksbill sea turtles were presented to St. George’s University for post-mortem examination. The post-mortem examination followed the guidelines set forth by the sea turtle stranding and salvage network gross necropsy report. Upon post-mortem examination, adult flukes were found in the gastrointestinal tract of all turtles. Flukes were preserved in 10% formalin before being stained. Flukes were stained with Semichon’s acetocarmine or Van Cleave’s hematoxylin for 8 hours, destained, and dehydrated in ethanol. They were cleared and mounted longitudinally for examination. PCR was performed targeting ribosomal genes, 18S-ITS1-5.8S-ITS2-28S, and the mitochondrial gene, cytochrome c oxidase subunit 1. Genetic sequencing was completed using Sanger sequencing.

Results: Morphological examination suggests that the species of fluke is *Diaschistorchis pandus*, which was originally described from the hawksbill sea turtle in 1913. Genetic sequencing is pending.

Conclusions: Flukes identified in Grenadian Hawksbill sea turtles are consistent with those previously reported in the Caribbean. No genetic information for *Diaschistorchis pandus* is currently available. Genetic sequences gathered will be submitted to Genbank to proliferate the information.

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