

## CHARACTERIZATION OF FIBROPAPILLOMA-ASSOCIATED TURTLE HERPESVIRUS IN GREEN TURTLES FROM BRAZIL

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The fibropapillomatosis is an emerging disease with high prevalence in turtles and characterized by multiple papillomas, fibromas and fibropapillomas in the skin or viscera. This disease is called "green turtle fibropapillomatosis" (GTFP) because it was first recorded in green turtles. In the Brazil, the first record of GTFP was in 1986 in the state of Espírito Santo (ES), and during the period of 2000-2004, 14.96% of the 4471 green turtles examined had tumors. The etiologic agent of GTFP is still uncertain, but the patterns of disease spread during outbreaks among captive green turtles have shown a pattern of infectious etiology. A herpesvirus has been isolated from fibropapillomas and is present in 95% of natural infections and in 100% of experimentally induced tumors. The aim of this work was to detect the fibropapilloma-associated turtle herpesvirus in marine turtles from Brazil by PCR, to characterize the virus by DNA sequencing and characterize tumors according to their location, appearance and pigmentation. A total of 122 tumors from green turtles from Bahia (BA), Ceará (CE) and ES states were analyzed; the green turtle was the only species of sea turtle captured; all turtles were juveniles and sexually immature. On the basis of the number and size of tumors, each animal was assigned a tumors severity score: mild (36.9%); moderate (31.2%) and heavy (32%). As for location 82% were in the anterior part of the animal, 14.8% on the back and 3.2% in the carapace or plastron. The tumors were collected from healthy (70.5%), 9.8% from weakened and 19.7% from dead turtles. As for the appearance of the tumor, 73.8% were papillary and 40.1% were pigmented. When analyzed by PCR, 69.7% (85/122) were positive, with 21/38, 44/60 and 20/24, respectively, for BA, CE and ES. Three samples of ES were sequenced and aligned with the five virus variants described in the literature. The three sequences are distinct from each other and more closely related to the variant HA.

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