

Epidemiological assessment and Motif Fingerprint-based Genomic Characterization of Tilapia Lake Virus (TiLV) infection and co-infections in Colombia

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Abstract

Tilapia Lake Virus (TiLV) infection is one of the most challenging diseases of farmed tilapia (*Oreochromis* sp.) production systems globally, however, few studies have described the epidemiology of TiLV. Here, we assessed the TiLV infection's status in Colombia Departments by RT-PCR amplification of a pool of tissues (liver, spleen, eye, and brain) collected from units of five to ten tilapias per lot/pond. From June 2016 to March 2018, epidemiological assessments of TiLV infection found positive cases of TiLV from 109 out of 463 submitted samples (23%) representing 25 TiLV positive farms, 21 districts, and 13 departments. Spatial distribution of cases indicate that the disease is widespread in Colombia including 21 TiLV positive municipalities out of 29 sampled (72,4%). Segment 6 of Colombian TiLV showed 98 to 100% of sequence identity to the viruses previously reported from Ecuador, Israel, and Peru. Almost all cases of TiLV (103/109; 94.5%) were associated to mortalities and clinical signs attributed to the disease and were reported at any life stages of tilapia. Six additional cases (5,5%) were reported from apparently healthy alevins at three Epidemiological Units (EU). Among the 109 cases, 44 cases (40.4%) had concomitant TiLV infection with other bacterial and/or parasitic diseases, highlighting the complex interactions between the virus and other pathogens. Grouping tests such as histopathology and molecular techniques, may be able to improve the detection of moribund and apparently healthy TiLV cases. This study, TiLV was reported throughout Colombia as the first comprehensive epidemiological investigation of TiLV status in South America.

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