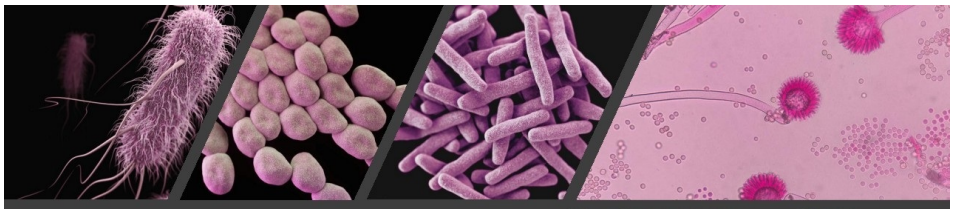

Abstract ID : **54**

Discovery of novel hepadnaviruses in passerine birds

Content

The Hepadnaviridae family comprises circular DNA viruses with hepatotropism [1]. The genome sequence of a novel avian hepadnavirus was serendipitously generated in a passerine ornamental bird while performing a sequence-independent enrichment protocol for circular DNA, based on rolling cycle amplification (RCA) [2]. An archival collection of samples was screened with a specific qPCR, with an overall prevalence of 7.9% (8/101). The presence of replicative covalently closed circular DNA (cccDNA), indicative of active viral replication, was confirmed in embryonated eggs, feather quills, and liver through RCA enrichment and inverse PCR [3]. By in-depth sequencing on Oxford Nanopore TechnologiesTM (ONT) platform, the whole genome sequence was obtained from 3 strains detected in Gouldian finch (Chloebia gouldiae), Society finch (Lonchura striata domestica) and Long-tailed finch (Poephila acuticauda). On phylogenetic analysis, the viruses were genetically distinct from other known avian hepadnaviruses, thereby forming a novel viral clade. These findings expand the known host range of hepadnaviruses to passerine birds. More importantly, they suggest potential vertical and feather-based transmission routes, as observed for other avian viruses [4,5]. The identification of hepadnavirus DNA in feather quills also represents a valuable, non-invasive method for future epidemiological surveillance in wild and domestic avian populations.

Keywords

hepadnavirus, RCA, finch

Registration ID

ECVM25-82

Professional Status of the submitter, who is also the speaker

Postdoc

Track Classification: Veterinary Bacteriology, Mycology and Virology

Contribution Type: Oral presentation

Comments:

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