

ANALYSIS OF HEPATITIS C VIRUS PROPAGATION AMONG SPOTTED SANDPIPER (*Actitis macularius*) POPULATIONS

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THEMATIC AREA AND ODS

FIELD OF KNOWLEDGE/SUBFIELD: 04

Biological Sciences | Immunology.

RELATED ODS: ODS03 Good Health and Well-being - Ensure healthy lives and promote well-being for all at all ages.

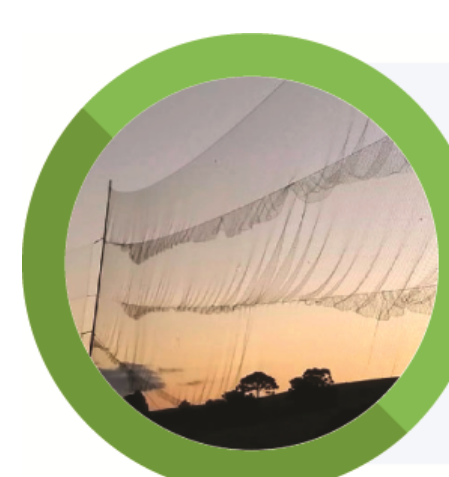
INTRODUCTION

Seasonally, birds migrate due to prolonged droughts and harsh winters (Nunes; Tomas, 2008). Annually, around 40 species of Scolopacidae migrate to coastal regions of the Southern Hemisphere in search of food, shelter, and rest. The Bragantina region in northeastern Pará hosts a great diversity of these birds, including the Spotted Sandpiper (*Actitis macularius*) (Campos; Naiff; Araújo, 2008). During migration, some birds may become infected and spread viruses (Araújo et al., 2018), acting as zoonotic reservoirs (Hubálek, 2004) and propagating serious diseases (Verhagen et al., 2014). To prevent viral epidemics, research on viral populations in hosts and their environments is essential (Bexfield; Kellam, 2011). Hepatitis C is a public health issue, with around 170 million people infected worldwide (Lauer et al., 2001). Studying the presence of HCV in migratory birds is crucial, especially in Brazil, which holds 18% of the world's avian diversity (Rahman et al., 2021). We investigated the presence of HCV in the transcriptome of the Spotted Sandpiper (*Actitis macularius*).



Figure 1: Spotted Sandpiper (*Actitis macularius*). On the left, non-breeding plumage; on the right, breeding plumage.

MATERIALS AND METHODS



Bird Collection

The birds were collected on Otelina Island, in the Amazon estuary in Bragança-PA, using mist nets.



Perfusion

The animals were anesthetized and perfused with saline solution and RNA later, followed by craniotomy.



Sequencing

The sequencing and chip reading were performed using the Ion 540 Chip and the Ion S5 GeneStudio System.



Virus Search

The virus search was conducted using the VIRTUS2 pipeline, with the genome of *Calidris pugnax* as a reference.



Virus Identification

The NCBI Viral Genomes RefSeq database was used as the viral sequence repository.



RESULTS AND DISCUSSION

In the present study, a total of 627 viral species were identified in the telencephalon of *Actitis macularius*, including a virus from the genus Hepacivirus. This finding is significant considering that the hepatitis C virus (HCV), the most well-known hepacivirus, has been predominantly associated with mammals, but recent studies have revealed its presence in a surprisingly wide variety of species, including marine animals, fish, reptiles, and birds (Chu et al., 2019). The metatranscriptomic approach used by Porter et al. (2020) also identified hepaciviruses in Australian marsupials, birds, and reptiles, broadening our understanding of the distribution of these viruses in nature.

The discovery of these hepaciviruses in birds such as *Actitis macularius* opens new perspectives for research, especially concerning the understanding of viral spread dynamics among different animal populations and potentially to humans. Although the discovery phase of these viruses is ongoing, significant advancements in genomic technologies allow for the exploration of the evolution and transmission patterns of these pathogens beyond what is known about human HCV.

It is crucial to emphasize that while initial HCV infection in humans is generally asymptomatic, the absence of appropriate treatment can lead to serious complications such as acute and chronic hepatitis, liver cirrhosis, and even hepatocellular carcinoma (Bletsa et al., 2020). Therefore, a comprehensive characterization of these hepaciviruses, both

Name	Numreads	Covbases	Coverage	Rate_hit
NC_009823.1 Hepatitis C virus genotype 2, Complete genome	1	48	0.494285	1.22978E-08
NC_038882.1 Hepatitis C virus (Isolate H77) genotype 1, Complete cds	2	41	0.427128	2.45957E-08
NC_005950.1 Snow goose hepatitis B virus, Complete genome	2	87	2.876998	2.45957E-08

Table 1: Hepacivirus Viral Species Found in the Telencephalon of *Actitis macularius*.

CONCLUSIONS

Our findings suggest that the autumn migration of the migratory bird *Actitis macularius* contributes to the spread of Hepacivirus. To prevent potential pandemics, it is crucial to understand the dissemination of pathogens across different ecosystems through the transcriptome analysis of various species.

REFERENCES



Selo ODS

