

**CHARACTERIZATION OF THE METAVIROME IN THE NEUROTRANSCRIPTOME OF THE MARINE MIGRATORY BIRD SPECIES *Calidris pusilla*

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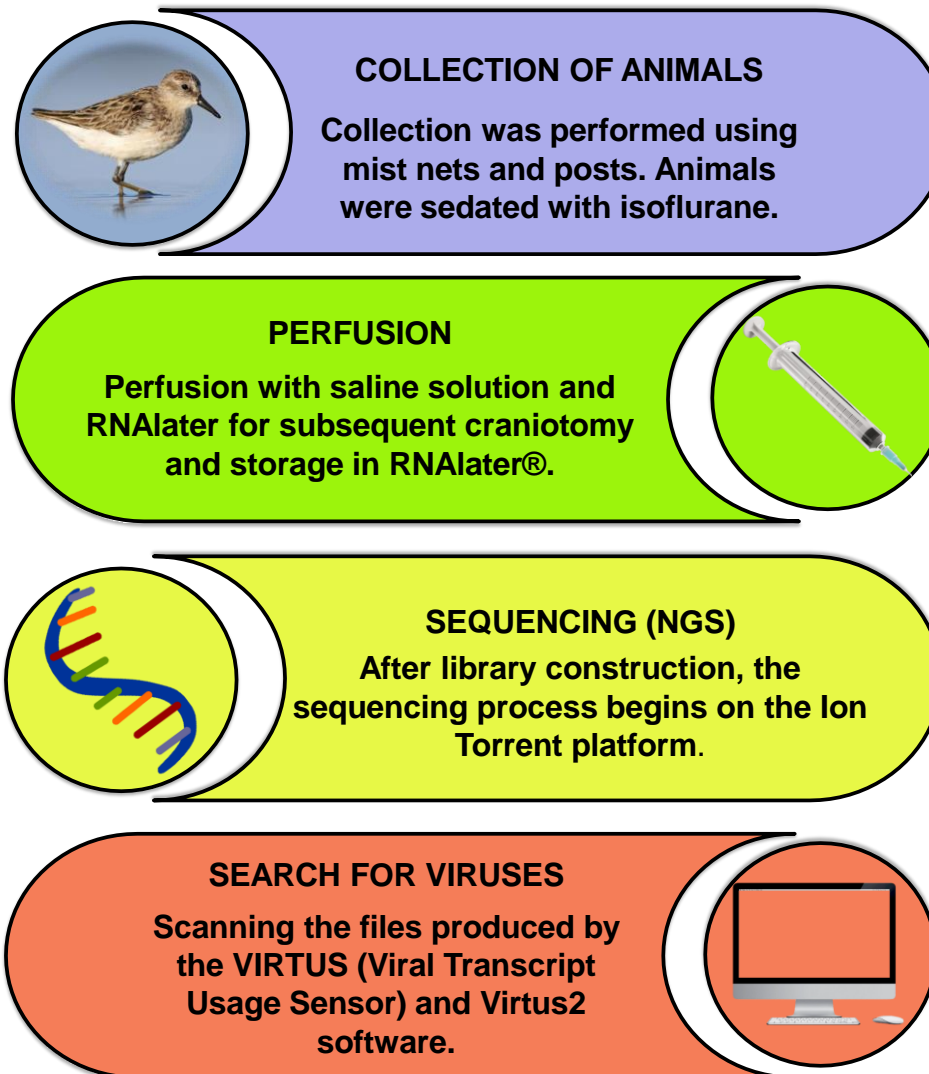
THEMATIC AREA AND ODS

FIELD OF KNOWLEDGE:
Biological Science/Genetics
RELATED ODS:
ODS03

INTRODUCTION

The animal migration process, essential for the survival of many species, is especially important in migratory birds, as it may contribute to significant public health concerns due to the transport of zoonotic pathogens. Birds such as the Semipalmated Sandpiper (**Calidris pusilla**), which migrate from Canada to South America, can, to some extent, aid in the transcontinental dispersal of viruses (Rolland et al., 2014; Reed op cit., 2003). The study of viral metagenomes in migratory birds through next-generation sequencing (NGS) analysis can provide insights into the diversity and prevalence of viruses, which is crucial for predicting and mitigating epidemics (Brown et al., 2014; Moraes et al., 2017). In Brazil, migratory birds are potential vectors for viruses such as influenza, highlighting the importance of monitoring these pathogens to protect the population by developing effective preventive strategies (Araujo et al., 2018; Reed et al., 2003). Therefore, in order to enable effective monitoring of diversity and potential interspecific spillovers, the characterization of the virome of key host species and vectors becomes essential (Fawaz et al., 2020). Moreover, the results obtained will contribute to the promotion of public health by providing relevant information for decision-making and the development of effective intervention strategies.

MATERIALS AND METHODS



RESULTS AND DISCUSSION

A total of 370 viral sequences were found/annotated after using the VIRTUS software. Of these, 5 species are known to be pathogenic to humans, primarily those from the Herpesviridae family (Figure 1).

Família	Gênero	Espécie	Hospedeiro
Herpesviridae	Mardivirus	Meleagrid herpesvirus 1	Gallus gallus domesticus
	Granulovirus	Choristoneura fumiferana	Choristoneura fumiferana
Baculoviridae	Chlorovirus	Acanthocystis turficaca virus 1	Chlorella heliozoae
	Ichnovirus	Glypta fumiferanae ichnovirus	Glypta fumiferanae
Phycodnaviridae		Shamonda virus	Bos taurus
Polydnaviridae	Orthobunyavirus	Sinbu virus RdRp	Bos taurus, Ovis aries
Peribunyaviridae	Pandoravirus	Pandoravirus incipitum	Acanthamoeba sp.
		Spodoptera frugiperda	Spodoptera frugiperda
Pandoraviridae	Betabaculovirus	Heterosigma akashiwo 01	Heterosigma akashiwo
	Rhabdovirus	Rakutama virus	Ixodes uriae, Ixodes signatus
Pheniviridae	Uukavirus	Pandoravirus salinus	Amoeba

Figure 1 – Alluvial graph of the viral species found that are pathogenic to humans.

Other viruses belonging to different families of interest were also found, such as: Poxviridae, Orthoherpesviridae, Adenoviridae, Retroviridae, and Baculoviridae.

The Herpesviridae family (DNA viruses) has been associated with infections in a wide range of animal species and in humans (Carter et al., 2006; Sehrawat et al., 2018). Studies on avian viruses are particularly important for public health, as these viruses primarily host in poultry, which is theoretically subject to potential viral spillover processes and outbreaks of infection in humans (Thomas, N. J., Hunter, D. B., & Atkinson, C. T., 2020). Similarly, bovine infections can have negative impacts on protein and milk production in Brazil (Brito et al., 2010), highlighting the importance of obtaining data on viruses that are circulating "naturally" in coastal regions of South America.

CONCLUSION

The findings presented here clearly indicate that birds of the species *C. pusilla* act as hosts and potential vectors of various viral pathogens capable of infecting humans and domestic animals. This leads us to believe that monitoring target species through the tools presented here is an effective alternative in the process of controlling future outbreaks, epidemics, and pandemics.

REFERÊNCIAS

