

Analysis of the Bat Virome (*Carollia perspicillata*) in Bragança, Pará

Myrceya Odelly Assunção da Conceição (IFPA); Patrick Douglas Corrêa Pereira (McGill University); Mauro André Damasceno de Melo (IFPA); Nara Gyzely de Moraes Magalhães (IFPA), Cristovam Guerreiro Diniz (IFPA)

Author: myrceyaodelly09@gmail.com

THEMATIC AREA AND ODS

FIELD OF KNOWLEDGE/SUBFIELD: Area 02 - Genetics

Related ODS 03: Good Health and Well-being - Ensure healthy lives and promote well-being for all at all ages.

INTRODUCTION

Bats, belonging to the order Chiroptera, account for 22% of all mammal species (Burgin et al. 2018) and exhibit unique adaptations that make them significant reservoirs for viruses. Their ability to fly and diverse feeding strategies facilitate the acquisition and dispersion of viruses, while their complex social structures promote viral transmission and persistence (Olival et al. 2015). Previous studies have identified over 200 viruses in bats, representing a remarkable diversity (Moratelli & Calisher 2015). Along with rodents, bats are considered the groups hosting the greatest diversity of viral species with zoonotic potential (Mollentze & Streicker 2020), including Nipah viruses (Rahman et al. 2010; Antony et al. 2013), Marburg (Toet et al. 2009), and coronaviruses responsible for severe acute respiratory syndrome (SARS-CoV) (Zhu et al. 2020), Middle East respiratory syndrome (MERS-CoV) (Wang et al. 2014), as well as Ebola and Hendra viruses (Drexler et al. 2009).

This study focused on the analysis of the virome of *Carollia perspicillata*, belonging to the family Phyllostomidae, a bat species predominant in the mangroves and non-flooded forest areas of the Bragança region (Andrade et al. 2008). Using metagenomic techniques, this research aimed to better understand the viral diversity and identify viruses with zoonotic potential

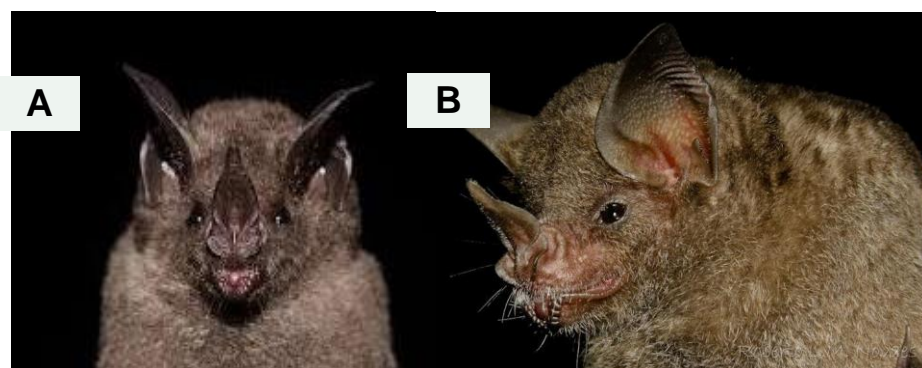


Figure 1 : (A) *Carollia perspicillata* in frontal view and (B) *Carollia perspicillata* in lateral view.

MATERIALS AND METHODS



Collection and Perfusion

At the selection site, a 12m x 2.5m mist net was deployed prior to nightfall. The animals were anesthetized with isoflurane and perfused using saline solution and RNA Later®.



Craniotomy

The brain was removed and stored in RNA Later®. Subsequently, the telencephalon was separated for subsequent sequencing. RNA extraction from telencephalic tissues was performed using the standard TRIzol™ protocol.



Sequencing

After the preparation of the templates, sequencing is initiated. At the end of the procedure, FASTQ format files are generated, which undergo quality assessment and filtering.



Viral Identification

The VIRTUS2 pipeline is utilized to scan the generated files. Subsequently, viruses with a high number of reads are identified by VIRTUS1.

RESULTS AND DISCUSSION

The analysis of the neurotranscriptome of the bat species *Carollia perspicillata* revealed the presence of viral particles (Table 1). The predominance of phages among the sequences suggests that this bat species may have high rates of bacterial infections. Phages can modulate the innate and adaptive immunity of mammals. Viruses from the Myoviridae and Siphoviridae families, once present in the bloodstream, can interact with immune system cells in humans (Bellegheem et al. 2018). The virus also identified with a high number of reads in the neurotranscriptome of *Carollia perspicillata*, *Desmodus rotundus* is an endogenous retrovirus, meaning its genetic material is integrated into the host genome. The presence of this virus may suggest that these bats carry viral sequences inherited from their ancestors (Zamudio et al. 2015).

Table 1. Characterization Table of Significant Viruses Found in *Carollia perspicillata*.

Family	Genus	Virus	Number of Reads	Host Lineage
Menderaviridae	Menderavirus	<i>Stenotrophomonas phage Medera</i>	451	Bacteria
Siphoviridae	Gorganvirus	UNVERIFIED: <i>Proteus phage VB_PsmiS-Isfahan</i>	354	Bacteria
Myoviridae	Ludhianavirus	<i>Aeromonas phage D3</i>	246	Bacteria
Retroviridae	Betaretrovirus	<i>Desmodus rotundus endogenous retrovirus isolate 824</i>	245	Vertebrate
Steitzviridae	Gihfavirus	<i>SsRNA phage SRR5466369_2</i>	170	Bacteria
Peduvoviridae	Tigvirus	<i>Burkholderia phage phiE094</i>	126	Bacteria

FINAL CONSIDERATIONS

The detection of high numbers of bacteriophages suggests the possibility of active bacterial infections in the species *Carollia perspicillata*. These phages may play a crucial role in regulating bacterial populations within the host organism, potentially influencing the health and behavior of these bats. Additionally, the identification of the endogenous retrovirus *Desmodus rotundus* as a virus associated with vertebrates provides new avenues for investigating viral evolution and the horizontal gene transfer in bats.

REFERENCES



Selo ODS



Organização:



INSTITUTO FEDERAL
Pará