

CHARACTERIZATION OF THE METAVIROME OBTAINED FROM THE NEUROTRANSCRIPTOME OF THE FISH SPECIES *Colossoma macropomum*

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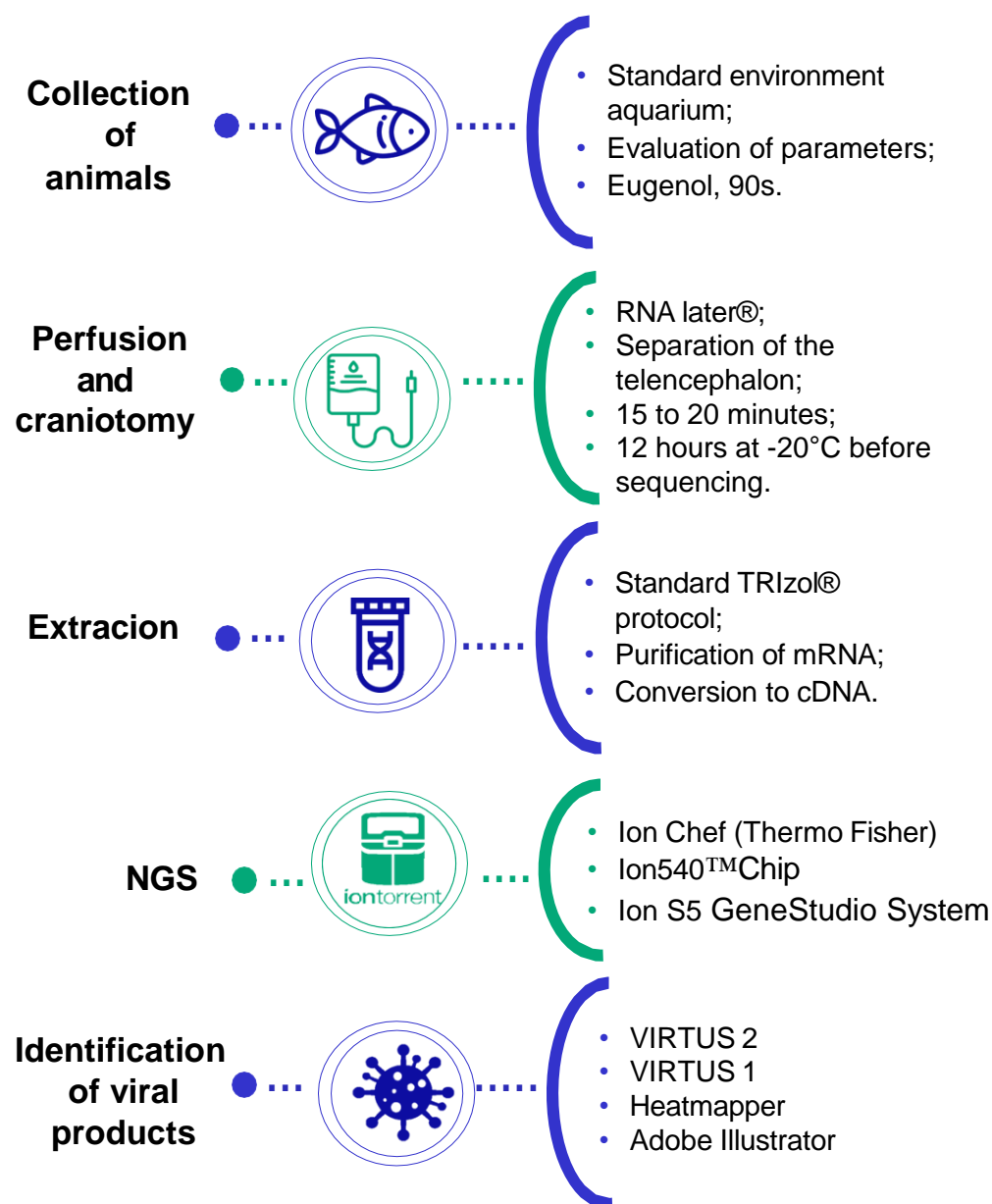
Thematic Area and ODS

FIELD OF KNOWLEDGE: Area 02
BIOLOGICAL SCIENCE/GENETICS
RELATED ODS: ODS03

INTRODUCTION

A large portion of our current knowledge about viruses that infect fish is based on the study of pathogenic viruses in symptomatic hosts. However, the recent rise of next-generation metagenomic sequencing (mNGS) has led to the discovery that fish harbor a greater number of viruses than any other class of vertebrates (Geoghegan et al., 2018; Silva et al., 2020; Perry et al., 2022). Most RNA virus families previously thought to infect only mammals have now been described in bony fish (Geoghegan et al., 2018). For instance, research on dead or moribund Chinook salmon (*Oncorhynchus tshawytscha*) revealed the first coronavirus (Coronaviridae) associated with fish, the Pacific salmon nidovirus (Mordecai et al., 2019). Although these viruses retain several key characteristics of other filoviruses, they are genetically distinct from ebolaviruses and marburgviruses (which are known to cause lethal diseases in humans) (Hume et al., 2019). Similarly, hepadnaviruses, previously known only in mammals and birds, infect amphibians and fish (Dill et al., 2016). The viromes found in wild freshwater fish are comparatively less studied than those of their marine counterparts. In most cases, these studies have been conducted in response to mortality events (Sibley et al., 2016) or in aquaculture environments (Hierweiger et al., 2021). The lack of data on the viromes of wild freshwater fish represents a potentially significant gap in knowledge. Lundberg et al. (2000) estimated that 10,000 species of fish reside in freshwater bodies, constituting 40% of all fish species (Lundberg et al., 2000). Based on this information, it will be possible to direct resources and implement appropriate preventive measures in cases of zoonotic or interspecific spillover, aiming to minimize the impact of potential epidemics and protect public health. In this context, the objective was to construct a database containing the molecular information of the different viruses found in the neurotranscriptome of *Colossoma macropomum*, identifying and characterizing the main families present in the metavirome.

MATERIALS AND METHODS



RESULTS AND DISCUSSION

A total of 303 viruses were found in the metavirome of the species *C. macropomum*, including bacteriophages. Eleven viruses of interest were detected, distributed across six families, namely: *Poxviridae*, *Orthoherpesviridae*, *Alloherpesviridae*, *Polydnaviriformidae*, *Pandoraviridae*, and *Picornaviridae*.

Família	Gênero	Vírus	Hospedeiro
Poxviridae	Orthopoxvirus	BeAn 58058 virus	Chlorocebus aethiops & Oryzomys sp.
Orthoherpesviridae	Vancellovirus	Bubaline alphaherpesvirus 1	Bos taurus & Bubalus bubalis
	Batrachovirus	Bufo herpesvirus 1	Bufo bufo, Lithobates pipiens & Terrapene carolina
Alloherpesviridae	Cyrtus	Cyprinid herpesvirus 3	Cyprinus carpio
	Ichnoviriform	Glypta fumiferanae ichnovirus	Choristoneura fumiferana & Glypta fumiferanae
Polydnaviriformidae		Hyposoter fugitivus ichnovirus	Malacosoma disstria & Hyposoter fugitivus
	Ictaluvirus	Ictalud herpesvirus 1	Ictaludae & Ictalurus punctatus
Pandoraviridae	Pandoravirus	Pandoravirus dulcis	Acanthamoeba castellanii
		Pandoravirus macleodensis	
		Pandoravirus salinus	Acanthamoeba sp.
Não classificado	Não classificado	Picornavirales Bu-3	Sus scrofa domesticus

Figure 1 – RAWGraphs 2.0: Alluvial Diagram. Correlation and proportion.

Six families were detected, among which is Poxviridae, a well-known family of viruses that can cause severe diseases in both vertebrates and invertebrates. This family includes hosts that are part of human consumption, such as cattle. Viruses of the genus Orthopoxvirus are responsible for transmitting bovinepox, which can infect humans (Silva et al., 2008), while viruses from the genus Parapoxvirus infect agricultural and wild animals across various regions of the world, potentially causing mild zoonotic infections in humans (Delhon, 2022; Espinoza, 2022).

CONCLUSION

This research has highlighted that delving into the characteristics and focused studies of each virus is of utmost importance for understanding their nature. In addition to having effective knowledge regarding viruses of interest, learning about the species belonging to the same family and genus, as well as those that should be of concern regarding infection in humans or even domestic animals, is crucial. The study of hosts also helps us understand how viruses may have infected other animals. Therefore, new investigations into the viruses considered significant could provide strategies and approaches for better comprehension and prevention of potential epidemics.

REFERENCES

