

Fish in virome fisheries pathology's impact on next-generation sequencing

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AUTHORS' CONTRIBUTION: (A) Study Design · (B) Data Collection · (C) Statistical Analysis · (D) Data Interpretation · (E) Manuscript Preparation · (F) Literature Search · (G) No Fund Collection

SUMMARY

The viruses that can be propagated in cell cultures or that can infect humans or economically important animals and plants are the focus of much of the research on viruses. However, only a small portion of the virosphere is represented here. As a result, we investigate the virome differences between Atlantic horse mackerels and gilthead seabreams from fisheries and aquaculture in the center and south of Portugal using targeted next-generation sequencing in this study. The Astroviridae, Nodaviridae, Hepadnaviridae, Birnaviridae, Caliciviridae, and Picornaviridae families were found to have viral genomes that could be harmful to humans as well as fish and crustaceans.

Keywords: Virome diversity; Metagenomics; Atlantic horse mackerel; Gilthead sea bream; Health-threat

INTRODUCTION

It was estimated that 179 million tons of fish were produced globally in 2018, with 87% of those tons being used directly for human consumption, making fish an important source of food and income for millions of people worldwide. Viral diseases are a major constraint on fish trade and aquaculture production, affecting the development of the fish industry and causing significant economic losses worldwide, despite the fact that demand for fish is rising [1]. In addition, the impact of climate change and the rising demand for seafood, which has led to the expansion of aquaculture systems, present new opportunities for the transmission of viruses, both novel and previously characterized pathogens [2]. The variety and abundance of viruses found in marine environments are well-known. As one of the most abundant fish-associated organisms, bacteriophages—common in freshwater and marine systems—prey on bacteria and contribute significantly to the equilibrium of aquatic ecosystems [3]. Notwithstanding the presence of bacteriophages, ongoing investigations propose that fish harbor a more prominent number of infections than some other class of vertebrates, including numerous groups of RNA infections recently remembered to contaminate just warm blooded creatures [4]. For example, the revelation of hepadnaviruses and filoviruses in fish suggests that these infections have old vertebrate starting points, and that their development perhaps required more host hopping than recently understood, including a potential move from sea-going to earthbound vertebrates [5].

Bioinformatic pipeline

Genome Detective, a web-based program, was used to examine the bioinformatic processing and taxonomical assignment of the pair-end reads obtained in the above manner [6]. Trimmomatic was used to filter low-quality reads and trim adapters. The DIAMOND protein-based alignment was used to select viral reads, and non-viral sequences were discarded. MetaSPAdes was used to assemble the viral reads from Genome Detective and the NCBI-BLASTn and BLASTx tools were used to taxonomically classify the viral reads and look for potential reference sequences in the NCBI RefSeq virus database [7]. Using Python scripts, the assembled unused viral contigs and discovery viral contigs from Genome Detective software were also compared to the NCBI RefSeq viral databases using the NCBI-BLASTn and tBLASTx tools. In this study, only viral contigs with 85% identity and an e-value below 10⁻³ (used as a cutoff) [8].

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DISCUSSION

Viruses can be found in every environment on Earth, but oceans, where they are known to store the majority of the genetic variety, are more important. Using a metagenomics approach, we analyzed viral sequences obtained from liver, gills, and skin tissue samples to investigate the viral diversity of two important commercially available fish species. As these species included shoaling Atlantic horse mackerel and solitary Gilthead seabream, the data we obtained allowed us to speculate on how virus composition might be affected by fish population density [9].

Viral fraction (i.e., lacking homology to any sequence in the databases) could be substantial, ranging from 20% to 99%, the presence of unknown virus genomes in fish samples was anticipated. In point of fact, the analysis of virus open reading frames (ORFs) revealed that a significant portion of them were orphans. These unclassified ORFs were found more frequently in viruses than in bacteria (30 percent versus 9%, respectively) [10].

CONCLUSION

Viruses can be found in every environment on Earth, but oceans, where they are known to store the majority of the genetic variety, are more important. Using a metagenomic approach, we analyzed viral sequences obtained from liver, gills, and skin tissue samples to investigate the viral diversity of two important commercially available fish species. As these species included shoaling Atlantic horse mackerel and solitary Gilthead seabream, the data we obtained allowed us to speculate on how virus composition might be affected by fish population density. Viral fraction (i.e., lacking homology to any sequence in the databases) could be substantial, ranging from 20% to 99%, the presence of unknown virus genomes in fish samples was anticipated. In point of fact, the analysis of virus open reading frames (ORFs) revealed that a significant portion of them were orphans. These unclassified ORFs were found more frequently in viruses than in bacteria (30 percent versus 9%, respectively).

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