Accepted Manuscript

FVD: The fish-associated virus database

Yaxin Chen, Mijuan Shi, Yingyin Cheng, Wanting Zhang, Qin Tang, Xiao-Qin Xia

PII: S1567-1348(17)30384-2

DOI: doi:10.1016/j.meegid.2017.11.004

Reference: MEEGID 3319

To appear in: Infection, Genetics and Evolution

Received date: 1 August 2017 Revised date: 12 October 2017 Accepted date: 6 November 2017

Please cite this article as: Yaxin Chen, Mijuan Shi, Yingyin Cheng, Wanting Zhang, Qin Tang, Xiao-Qin Xia, FVD: The fish-associated virus database. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Meegid(2017), doi:10.1016/j.meegid.2017.11.004

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



ACCEPTED MANUSCRIPT

FVD: the fish-associated virus database

Yaxin Chen^{1,2†}, Mijuan Shi ^{1†}, Yingyin Cheng¹, Wanting Zhang¹, Qin Tang^{1,2*}, Xiao-Qin Xia^{1*}

¹Center for Molecular and Cellular Biology of Aquatic Organisms, Institute of
Hydrobiology, the Chinese Academy of Sciences, Wuhan 430072, China

²University of Chinese Academy of Sciences, Beijing 100049, China

*Corresponding author.

Mailing address: No. 7 Donghu South Road, Wuchang District, Wuhan, Hubei Province, 430072, China. Phone & Fax: 86-027-68780915. E-mail: xqxia@ihb.ac.cn

†These authors contributed equally to this work.

Abstract

With the expanding of marine and freshwater aquaculture, the outbreaks of aquatic animal diseases have increasingly become the major threats to the healthy development of aquaculture industries. Notably, viral infections lead to massive fish deaths and result in great economic loss every year across the world. Hence, it is meaningful to clarify the biodiversity, geographical distribution and host specificity of fish-associated viruses. In this study, viral sequences detected in fish samples were manually collected from public resources, along with the related metadata, such as sampling time, location, specimen type and fish species. Moreover, the information regarding the host fish, including aliases, diet type and geographic distribution were also integrated into a database (FVD). To date,

Download English Version:

https://daneshyari.com/en/article/8646999

Download Persian Version:

https://daneshyari.com/article/8646999

<u>Daneshyari.com</u>