



OPEN ACCESS

EDITED AND REVIEWED BY
Akio Adachi,
Tokushima University, Japan

*CORRESPONDENCE
Hung-Yao Ho
✉ hoh01@mail.cgu.edu.tw

RECEIVED 30 November 2024
ACCEPTED 03 December 2024
PUBLISHED 13 December 2024

CITATION
Ho H-Y (2024) Editorial: Unraveling
enteroviral pathogenesis: host interactions
and antiviral strategies in Asia.
Front. Virol. 4:1537430.
doi: 10.3389/fviro.2024.1537430

COPYRIGHT
© 2024 Ho. This is an open-access article
distributed under the terms of the [Creative
Commons Attribution License \(CC BY\)](#). The
use, distribution or reproduction in other
forums is permitted, provided the original
author(s) and the copyright owner(s) are
credited and that the original publication in
this journal is cited, in accordance with
accepted academic practice. No use,
distribution or reproduction is permitted
which does not comply with these terms.

Editorial: Unraveling enteroviral pathogenesis: host interactions and antiviral strategies in Asia

Hung-Yao Ho^{1,2,3,4,5*}

¹Graduate Institute of Biomedical Sciences, College of Medicine, Chang Gung University, Taoyuan, Taiwan, ²Metabolomics Core Laboratory, Healthy Aging Research Center, Chang Gung University, Taoyuan, Taiwan, ³Clinical Metabolomics Core Laboratory, Chang Gung Memorial Hospital at Linkou, Taoyuan, Taiwan, ⁴Department of Medical Biotechnology and Laboratory Science, College of Medicine, Chang Gung University, Taoyuan, Taiwan, ⁵Research Center for Emerging Viral Infections, Chang Gung University, Taoyuan, Taiwan

KEYWORDS

enterovirus, rhinovirus, pathogenesis, host factors, virus detection, vaccine, antivirals

Editorial on the Research Topic

Unraveling enteroviral pathogenesis: host interactions and antiviral strategies in Asia

Enteroviruses are disease-causing pathogens. The genus *Enterovirus* consists of 15 species including *Enterovirus A-L* and *Rhinovirus A-C*. Enterovirus A71 (EV-A71) and coxsackievirus A16 (CV-A16) are predominant infectious agents causing hand, foot and mouth disease (HFMD). Most HFMD outbreaks have occurred in the Asia-Pacific regions that include Malaysia, Vietnam, China, and India. To date, most HFMD cases have occurred in China (1). HFMD poses persistent public health challenge, particularly in China, where its epidemiology is influenced by a multitude of factors, including environmental, social, and policy-related elements. Four articles included in this Research Topic provide an insight into the dynamics of HFMD transmission, its response to non-pharmaceutical interventions (NPIs), and broader spatiotemporal patterns. These provide valuable perspectives to our understanding and management of this disease.

The outbreak of coronavirus disease 2019 (COVID-19) occurred in China in early 2020. Non-pharmaceutical interventions (NPIs) were implemented to deter viral transmission. Ding et al. and Zhang et al. examined the indirect effect of COVID-19 NPIs on the HFMD incidence. In the former study, the data of HFMD cases in Zhejiang province of China were collected in a period between 2014 and 2023, which comprises a pre-COVID stage, strict control stage, regular control stage and reopening stage. In the latter study, the data of HFMD cases in Guangdong province were collected during 2012-2021. Both studies revealed that stringent measures, such as school closures, travel restrictions, regional lockdown and mask-wearing, led to a dramatic reduction in HFMD cases during the early phases of the COVID-19 pandemic. Ding et al. emphasized that while these interventions significantly disrupted HFMD transmission, the cessation of NPIs saw a rebound to historical levels, highlighting the transitory nature of such measures. Likewise, Zhang et al. quantified such decline in Guangdong Province, estimating that up to 455,000

HFMD cases were averted between 2020 and 2021. These findings underscore the benefits of NPIs in curbing multiple infectious diseases simultaneously. However, they also raise questions about the sustainability of such approaches.

Wei et al. focused on broader spatial and temporal patterns of HFMD across China during a period from 2014 to 2017. There were cyclical and seasonal changes in temporal relative risk of HFMD across different regions of mainland China. Their analysis identified southern and eastern provinces, such as Guangdong, Guangxi, and Hainan, as persistent high-risk areas, possibly owing to the favorable climatic conditions for viral transmission. Meteorological factors, like temperature, air pressure, relative humidity, and sunlight duration, increase the risk of HFMD, while higher wind speed negatively correlated with the risk. Integration of socioeconomic data revealed additional layers of complexity. Higher GDP per capita of a region was associated with lower HFMD risk, possibly indicative of allocation of more budget to disease control. High birth rate was associated with an elevated risk. This spatial heterogeneity highlights the need for the region-specific interventions tailored to local epidemiological contexts.

Yuan et al. applied molecular epidemiological approach to study the HFMD distribution in Jiashan region of Zhejiang province. Among the enterovirus-positive specimens, the most frequently identified strains were coxsackievirus (CA) 6 (52.86%), CA16 (18.21%), EV71 (2.86%), CA10 (2.50%). Further phylogenetic analysis assigned CA16 VP1 sequences to the B1a and B1b genogroups and those of CA6 to the D3a genogroup.

These studies provide critical insights into HFMD management. The marked decline in HFMD cases during COVID-19 underscores the potential of coordinated public health strategies to mitigate disease transmission. The spatial patterns and contributing factors detailed by Wei et al. emphasize the multifaceted nature of HFMD epidemiology. Control of HFMD necessitates an integrated approach that combines environmental management, socioeconomic improvements, and public health initiatives. The resurgence of HFMD following the lifting of NPIs, as demonstrated by Ding et al., calls for robust surveillance and ongoing preventive measures, such as vaccination and public education on hygiene. Emergence of CA6 and CA16 as predominant serotypes poses a need for development of multivalent vaccines against other human enteroviruses in addition to EV71.

Reference

1. Puenpa J, Wanlapakorn N, Vongpunsawad S, Poovorawan Y. The history of enterovirus A71 outbreaks and molecular epidemiology in the Asia-Pacific region. *J Biomed Sci.* (2019) 26:75. doi: 10.1186/s12929-019-0573-2

Author contributions

H-YH: Conceptualization, Writing – original draft, Writing – review & editing.

Funding

The author(s) declare that financial support was received for the research, authorship, and/or publication of this article. This work was supported by Chang Gung Memorial Hospital [grant number: BMRP819, BMRP564, CMRPD1L0161, CMRPD1L0162, CMRPD1M0351, CMRPD1J0263, CMRPD1M0341, CLRP3K0023, CMRPD1M0352, CMRPD1N0151, CMRPD1M0342, CMRPD1N0071, CMRPD1P0171, CORPD1P0011 and CORPD1P0021], National Science and Technology Council (NSTC) [grant number: 110-2320-B-182-017-MY3, 111-2320-B-182-011, 112-2320-B-182-020-MY3 and 113-2320-B-182-018-MY3], and Ministry of Education in Taiwan (MOE) [EMRPD1K0441, EMRPD1K0481, and EMRPD1L0421]. This work was also supported by the Research Center for Emerging Viral Infections from The Featured Areas Research Center Program within the framework of the Higher Education Sprout Project by the Ministry of Education (MOE) in Taiwan and the National Science and Technology Council (NSTC), Taiwan [MOST 111-2634-F-182-001].

Conflict of interest

The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.