

# **A five-year retrospective study on the epidemiology of hand, foot and mouth disease in Sabah, Malaysia**

## **ABSTRACT**

Hand, foot, and mouth disease (HFMD) is endemic in Malaysia, with the number of cases increasing. Sabah has experienced several HFMD outbreaks, but information on the epidemiology and molecular characteristics of responsible viruses is scarce. In this study, data of 17,574 reports of HFMD cases in Sabah from 2015 to 2019 were extracted from a public health disease surveillance system and analyzed. Twenty-one swab samples from 13 children were collected from Beaufort, Sabah, during an outbreak in August 2018 for detection and serotyping of causative viruses by semi-nested reverse transcription-polymerase chain reaction (snRT-PCR) of the VP4–VP2 region and consensus degenerate hybrid oligonucleotide primer PCR of the VP1 region, respectively. Nucleotide sequencing and phylogenetic analysis were conducted by the neighbor-joining method. The average annual incidence of HFMD was 94.3 per 100,000 people, with the greatest yearly increase between 2017 and 2018. Swabs from six children were tested positive for enterovirus, of which five were positive for CVA16 and one for EV71. All CVA16 strains belonged to sub-genotype B1a, and the EV71 strain belonged to sub-genotype B5. Phylogenetic analyses indicate that enterovirus genotype shift might be responsible for the increasing trend of HFMD in Sabah, however, further study is needed.