

Mumps outbreak in university students: first detection of mumps virus genotype F in Borneo

ABSTRACT

Background: In October 2016, a mumps outbreak occurred among the students living in the on-campus dormitory of a public university located in Kota Kinabalu, Sabah, Malaysia. This study aimed to investigate the outbreak and identify the genotype of the mumps virus (MuV) strain that was involved in the outbreak. Main body: During the outbreak, one 21-year-old and four 20-year-old males staying in the same dormitory building were reported to have developed symptoms of mumps. Of these, two students were available during the investigation for sample collection to detect MuV by reverse transcription polymerase chain reaction (RT-PCR) of the 639- bp fragment encompassing the entire small hydrophobic (SH) gene. Nucleotide sequencing of the amplicon and phylogenetic analysis using the neighbor-joining method was performed to determine the MuV genotype. Of the two buccal swab samples, one was positive for MuV. The MuV strain in this sample belonged to genotype F and it was clustered together with genotype F strains from China with 96.84–99.68% nucleotide identity. Conclusions: Genotype F has limited circulation and is endemic in mainland China. Genotype F strains occasionally reported from other countries were epidemiologically linked to China. This study is the first to report a case of genotype F MuV in Malaysia and no epidemiological link could be established with mainland China. The results provide important information that can assist in strategic planning to improve the prevention and control of mumps infection in Malaysia.