

compared to those didn't have NSAIDS. Hence, NSAIDS should not be used in fever patients when Dengue is a possibility.

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Clinical features and virology of hand foot mouth disease in Southern Vietnam, July 2013 - March 2015



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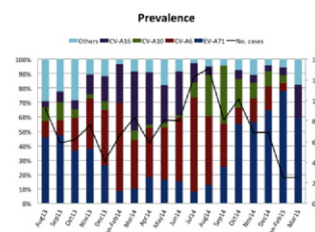
Background: In Asia, hand, foot and mouth disease (HFMD) is associated with large and sometimes severe outbreaks since 1997, and is caused by enterovirus A (EV-A), in particular EV-A71. Monitoring the pattern of replacement between EV-A serotypes, the associated clinical profiles and pathogen evolution are essential for understanding the progress of outbreak/epidemics and development of intervention strategies.

Methods & Materials: A large prospective study was conducted at three referral hospitals in southern Vietnam since July 2013: Children's Hospital 1, Children's Hospital 2 and Hospital for Tropical Diseases in Ho Chi Minh City. Clinical data, throat and rectal swabs were collected and analysed using multiplex real-time and nested RT-PCRs to detect and identify specific EV serotypes. Selected positive swabs were then subjected to VP1 or whole-genome deep sequencing.

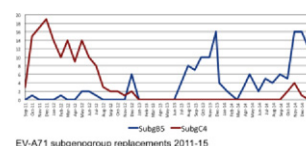
Results: Over 18 months, 1350 HFMD patients were enrolled. The most common detected pathogens included CV-A6 (24%), EV-A71 (23%), CV-A16 (11%) and CV-A10 (9%), followed by CV-A2/A4/A12 and EV-Bs. A total of 295 genome sequences were obtained. B5 (n = 156) was the predominant EV-A71 subgenogroup. Phylogenetic analysis further showed that all CV-A16 (n = 25), CV-A2 (n = 7), CV-A5 (n = 3), CV-A8 (n = 4), CV-A12 (n = 10) and CV-A14 (n = 1) were closely related to those from China and the region, while CV-A4 (n = 10), CV-A6 (n = 26) and CV-A10 (n = 43) clustered with viruses belonging to genogroups collected in other parts of the world. Two separate introductions were observed for CV-A4.

Clinically, there was no significant difference between CV-A6, CV-A16 and CV-A10 groups. Patients with EV-A71 infection were

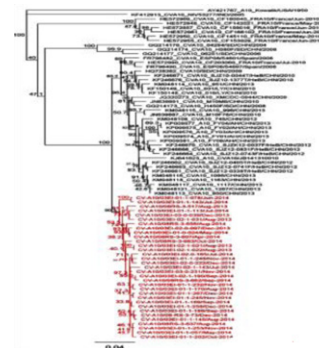
older than those with non-EV-A71 infection (21.7 vs. 17.3 months old, $p < 0.001$). Other differences included myoclonus (21% vs. 13%, $p = 0.001$), irritability (17% vs. 70%, $p < 0.001$) and location of erythema. There was a trend toward EV-A71 detection and clinical severity: 23% grade 1, 17% (2A), 39% (2B group 1), 71% (2B group 2), 64% (3) and 67% (4).



Enteroviruses sequence result within 18 months



EV-A71 subgenogroup replacement 2011–2015



Phylogenetic tree of CV-A10

Conclusion: Our study represents the most comprehensive descriptive HFMD study from Vietnam to date. The analysis of 1350 patients revealed important insights into the epidemic patterns of this multi-pathogen disease, including pathogen associated phenotypes and viral evolution, which are essential for public health strategies and of clinical significance.

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