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Coxsackievirus A16 in Viet Nam

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Background: Hand, foot and mouth disease (HFMD), a common childhood illness recognized as endemic in Asia-Pacific countries, poses major public health concerns in this region. Most of HFMD outbreaks have been caused by Enterovirus A, predominantly enterovirus A71 (EV-A71), coxsackievirus A16 (CVA16), CVA10 and CVA6. In Vietnam, CVA16, together with EV-A71 and CVA6, is the most common causes of HFMD. Nevertheless, there has been limited data available regarding CVA16 epidemiology and genetic diversity in Vietnamese population.

Methods and materials: From 2011 to 2017, clinical samples were collected from in- and out-patients enrolled in an HFMD research program conducted at three referral hospitals in Ho Chi Minh City, Vietnam. Throat or rectal swabs positive for enterovirus real-time RT-PCR were subtyped and CVA16 positive specimens, viral load Cp $\leq$ 30, were selected for whole genome sequencing using an Illumina MiSeq platform.

Results: Throughout the study period, 320 CVA16 samples were detected in 2808 HFMD patients (11.43%). Male and female percentages were 59.4% and 40.6%, respectively. Age median of the study population was 20.82 months. 55.3% of patients resided in Ho Chi Minh City, the rest from Mekong Delta (22.2%) and South East Vietnam (22.5%). 11.2% CVA16 infected patients had moderately severe or severe (grade 2b2 and above) HFMD.

153 CVA16 samples were selected for whole genome sequencing and 66 complete genomes were obtained. Phylogenetic analysis demonstrated that Vietnamese isolates belong to genogroup B1a and cluster together with isolates from China, Japan, Thailand, Malaysia, France and Australia.

Conclusion: We report for the first time detailed investigation into the epidemiology and molecular evolution of CVA16 in Vietnam. These results, combining with epidemiological data of other common enteroviruses (EV-A71, CVA6 and CVA10) obtained from the same study, revealed that they replaced each other during the study period. Intriguingly, unlike EV-A71, which showed a frequent replacement between subgenogroups B5 and C4 every 2–3 years in Vietnam, CVA16 displays a less pronounced genetic alternation with only subgenogroup B1a circulating in Vietnam since 2011. Further examinations are needed for better understanding of pathogen emergence and evolution, which is crucial for development and implementation of intervention strategies (including vaccine).

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Outbreak of highly pathogenic avian influenza A (H5) clade 2.3.2.1a in a backyard pig-rearing village in Rajshahi, January, 2017

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Background: On January 9th, 2017 a community health worker notified of increased number of deaths in backyard poultry in a pig rearing village of Rajshahi district, Bangladesh. We investigated the reported morbidity and mortality among backyard poultry in Rajshahi to confirm there was an ongoing outbreak of avian influenza, determine the etiology, and identify possible associated illnesses in humans and pigs.

Methods and materials: On January 10th, 2017, we discussed with villager's residents and village leaders, to verify a high number of avian influenza like illness cases occurred among poultry in the villages compared to the same time period the previous year. We conducted a survey of households to identify all households that reared poultry and any morbidity or mortality events in their poultry. In the affected households of the village, we inquired about influenza-like illness among household members. We also searched for pigs with signs of acute respiratory illness in the village. We collected conveniently oropharyngeal and cloacal swab samples from six ill and five dead poultry. We performed one-step rRT-PCR to screen for influenza A virus by targeting the matrix (M) gene and subtype influenza A-positive samples for H5, H7, and H9 virus. We also performed phylogenetic analyses of six of the hemagglutinin genes of H5 virus.

Results: We surveyed 63 households that raised backyard poultry and pigs in the affected village. Thirty-six (57%) of the 63 households reported poultry illnesses or deaths within 14 days of our investigation. Approximately half (484 of 956 [51%]) of their poultry were ill with diarrhea, ataxia, cyanotic comb and wattle, and most of those that became symptomatic subsequently died (467 of 484 [96%]). All poultry sampled tested positive for avian influenza A(H5) virus. Phylogenetic analyses of six of the hemagglutinin genes of these samples identified that they were clade 2.3.2.1a A (H5) viruses and shared 97.3–98.9% nucleotide identity with previously circulating A(H5) strains in Bangladesh. No pigs and humans were infected with A(H5) in the village.