The Phylogenetic Analysis of Enterovirus 68 in Taiwan

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Background/Objective

Human enterovirus D68 (EV-D68), an enterovirus D species in the Picornaviridae family, has been reported to cause emerging diseases in recent years. In 2014, the first pandemic of EV-D68 was reported in USA which caused several deaths and more than a thousand infected. In Taiwan, some cases of EV-D68 were identified recently. In this research, we studied the genetic evolution of EV-D68 strain in Taiwan.

Method

12 EV-D68 isolates from viral culture were collected and identified by CODEHOP assay between 2011 and 2014. All strains were amplified by using 6 sets of primer pairs and sequenced for full genome sequence analysis, with approximately 7500 nucleotides using Sanger sequencing method. The sequence analysis was performed with BioEdit and MEGA6 software.

Result

The result showed that 12 EV-D68 strains were consist of approximately 7,270-7,350 bases and included genome sequence as follow: 5' UTR, VP4, VP2, VP3, VP1, 2A, 2B, 2C, 3A, 3B, 3C, 3D, 3' UTR. Among the strains, nucleotide and amino acid sequences were highly conserved (nt identity 95%-99% and aa identity 96%-99%). However, Taiwan strains had lower similarities to the Fermon reference strain (nt identity <90% and aa identity <95%) than to the USA strains (nt identity 90%-95% and aa identity 90%-95%). More interestingly, we found that genome deletion occurred within two blocks of the 5’ UTR (position 681-704 and 717-727) comparing to the Fermon reference strain. For evolution study based on the VP1 region, the data showed that all of the EV-D68 strains in Taiwan belonged to clade A.

Conclusion

EV-D68 is rarely detected in Taiwan, and there was no epidemics reported. We carefully studied the full-genome sequence and found that deletions and evolution occurred in the genomes of EV-D68 strains in Taiwan. The significance of this variation and its mechanism should be further studied.