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Identification of Coxsackievirus A20 as the recombinant counterpart of type 1 cVDPV in the Philippines

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Abstract

The genomic sequences of circulating vaccine-derived polioviruses (cVDPVs) are said to have been derived mostly from genomes of human enterovirus (HEV) species. In the Philippines, the last indigenous wild-type polio was detected in 1993 and the country was declared polio-free in 2000. But, a year after the country's polio-free declaration, type 1 cVDPV was reported. Genomic sequences showed that the capsid region is homologous to the parental Sabin 1 strain, however, the nonstructural sequences downstream at the 2ABC region were derived from an unidentified HEV- C. Here, we seek to identify the donor strain at the nonstructural region of type 1 cVDPVs among the identified HEV-C from acute flaccid paralysis cases (1992-2008) by using molecular methods to unravel their possible evolutionary origin. The sequences of cVDPVs were obtained in GenBank and were aligned with the NPEV strains detected. Sequence and recombination analyses were done using MEGA 4.0 and SimPlot software respectively.

Phylogenetic analysis showed that the near full-length sequence of sample 24-PHL-2000 is closely related to both CV A20a and PV 1. The polyprotein 1 (P1) which encodes for the structural region clearly categorized 24-PHL-2000 under the CV A20 cluster but diverged away and grouped with the cVDPV type 1 in nonstructural regions (P2 and P3). The high sequence similarities at the beginning of the P2 to P3 regions with the cVDPV were supported by prominent nucleotide sequence identities. Furthermore, the genome sequence of 24-PHL-2000 revealed a single intertypic recombination event with the type 1 cVDPVs in the Philippines at the nonstructural region.

Our results suggest that the nonstructural proteins of CV A20 may functionally interchange with the genomes of PVs, supporting recent studies that the nonstructural proteins of HEV-C are evolving independently of one another. The emergence of a confirmed recombinant type 1 cVDPV is of vital consideration in the global program for eradicating poliomyelitis. The results reveal that with high circulation of HEV-C adjunct with OPV vaccination campaigns may provide a great pool for genetic mix-up of EVs among the susceptible population and may give rise to cVDPV. In conclusion, we found sample 24-PHL-2000, which is CV A20 at P1 region, to be the recombination counterpart of the type 1 cVDPVs in the Philippines. Its identification may allow an understanding of the molecular evolution and genomic transfers of the nonstructural proteins among HEVs.

Biography:

LN Apostol has completed her PhD from Tohoku University Graduate School of Medicine, Sendai, Japan in 2012. She returned to her country and now serves as the laboratory manager of the Department of Virology, Research Institute for Tropical Medicine, the research arm of the Department of Health in the Philippines.