Identification of the Rare Recombination Event of Torque Teno Virus in Taiwan

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Background/Objective

Torque Teno Virus (TTV) is a single-stranded DNA virus with high prevalence worldwide. Despite of being a DNA virus, TTVs have an unusual high genetic diversity and new genotypes are identified constantly. TTV is currently classified into 6 major phylogenetic groups, and is generally mixed-infected in individual. Therefore we attempt to identify what genotypes are mix-infected in Han Chinese individuals and to clarify if any recombinant event has occurred.

Method

TTV positive plasma samples: VC16, VC99, and VC288, were obtained from blood donor from our previous epidemiology study. The coding region sequence of TTV was obtained by PCR and Sanger sequencing. Phylogenetic analysis was performed with all known TTVs in the GenBank. The Maximum-Likelihood (ML) tree was constructed based on aligned nucleotide sequences of viral open reading frame 1 with best fitting GTR+G+I model, and statistically evaluated by bootstrap analysis. Potential recombination signal was evaluated by BootScan approach by using Simplot software package.

Result

In this study, 7, 9, and 11 TTV sequences were isolated from VC16, VC99, and VC288 respectively. Isolates from merely 3 individuals belongs to all 6 phylogenetic groups except group 2. Putative recombination breakpoint was identified at two group 4 isolates of VC99 at around the position of ORF1 gene at 1780 nt. The parents strains are from the consensus of yonban strains (yon-KC009, yon-KC011, yon-KC186, and yon-KC197) and JT41F, both parent strains are from Japan.

Conclusion

We cloned and sequenced 27 new TTV isolates from Taiwan, which belongs to 5 groups and recombination signal was found in ORF1 region. It is relatively rare event since single-stranded DNA virus recombination usually occurred in untranslated region.