

Detection and Analysis of VP1 regions of New Enterovirus Strains in Korea During 2006

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ABSTRACT

Genus Enterovirus is a member of the family Picornaviridae. In this study, clinical samples (n=1,174) were examined for enterovirus by using the VP1 seminested RT-PCR designed by US CDC (Nix, WA, et al.) and we detected 251 enteroviruses. Most strains belonged to HEV-8 (n=214) followed by HEV-A (n=36) and HEV-C (n=1). The most common enterovirus was E25 (n=54) followed by E30 (n=48) and E5 (n=27). We have isolated 7 enterovirus for the first time in Korea: CA2 (n=3), CA12 (n=1), E5 (n=27), E14 (n=1), E16 (n=1), E33 (n=2), and EV74 (n=1). CA2, CA12, and Echo 5 isolates had nucleotide identities (91-97%) and amino acid identities (100%) with CA2 10549 isolate, CA12 Kanagawa/2003, and Echo5 FR-07-2003-73, respectively. EV74 isolate showed sequence identities of 84% and 98% at the nucleotide and amino acid levels, respectively, with EV74 USA/CA75-10213. We are analyzing full VP1 gene sequences of these isolates and monitoring other newly emerging enteroviruses.

INTRODUCTION

Human enteroviruses are the major etiological agents of aseptic meningitis. A variety of clinical manifestations are associated with enteroviral infections, including respiratory illness, hand-foot-mouth diseases, acute hemorrhagic conjunctivitis, myocarditis, neonatal sepsis-like disease, encephalitis, and acute flaccid paralysis. Sixty-six human enterovirus serotypes have been classified into coxsackieviruses A and B, echoviruses, polioviruses, and enteroviruses 68 to 71. Recently, molecular methods have enabled the rapid identification of new enterovirus (EV) serotypes that are untypeable using existing neutralizing antisera. Sequencing of the gene that encodes the capsid protein VP1 has been used as surrogate for antigenic typing in order to distinguish enterovirus serotype. In this study, we have detected 251 enterovirus strains from samples collected from patients with aseptic meningitis, encephalitis, hand foot and mouth disease, etc. and analyzed the sequences of VP1 region of enteroviruses.

MATERIALS AND METHODS

Figure 1. Schemes for RT-PCR of the complete VP1 gene

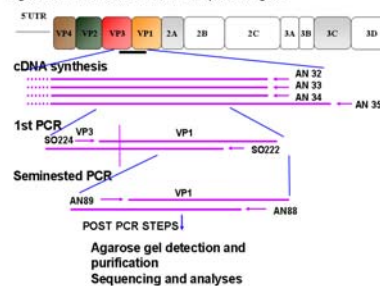


Table 1. Specimens collected for isolations of Enteroviruses in 2006

CSF	Stool	Conjunctival swab	Throat swab	Others	Total
342 (26%)	604 (46%)	11 (1%)	115 (9%)	234 (18%)	1306

CONCLUSION

- We have detected 251 enterovirus strains from samples collected from patients with aseptic meningitis, encephalitis, hand foot and mouth disease, etc. and analyzed the sequences of VP1 region of enteroviruses.
- Most strains belonged to HEV-8 (n=214) followed by HEV-A (n=36) and HEV-C (n=1). The most common enterovirus was E25 (n=54) followed by E30 (n=48) and E5 (n=27).
- CA2, CA12, and Echo 5 isolates had nucleotide identities (91-97%) and amino acid identities (100%) with CA2 10549 isolate, CA12 Kanagawa/2003, and Echo5 FR-07-2003-73, respectively.
- EV74 isolate showed sequence identities of 84% and 98% at the nucleotide and amino acid levels, respectively, with EV74 USA/CA75-10213.

RESULTS

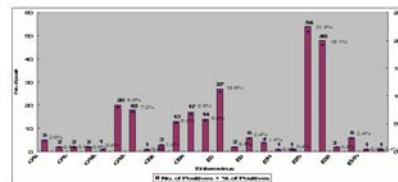


Figure 2. Distribution of the different enterovirus serotypes in 2006.

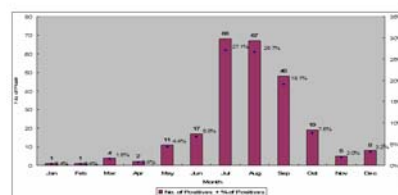


Figure 3. Monthly detected number of virus-positive samples in 2006

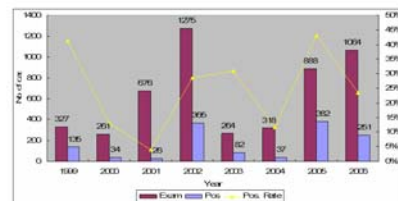


Figure 4. Enterovirus isolation during 1999-2006.

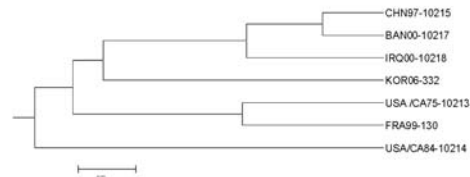


Figure 5. Phylogenetic relationships of EV 74 isolates based on the complete VP1 nucleotide sequences (858 nt).

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