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Nucleotide and Amino Acid Sequence Diversity of the RNA Dependent RNA Polymerase of Human Caliciviruses (HuCVs) Isolated from Sporadic Cases of Pediatric Gastroenteritis in Korea.

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HuCVs cause sporadic cases and out breaks of acute gastroenteritis (AGE). Three major genogroups of HuCVs have been described including the Norwalk virus (NV), the Snow Mountain virus (SMV), and the Sapporo-genogroups. This study describes the detection and genetic variation of HuCVs obtained from stools of hospitalized infants with AGE in Korea. The cDNA fragments of 206 to 470bp corresponding to the region of 3 primer pairs (36/35, 36/51 or 3/51) in the polymerase region of NV were generated by RT-PCR and their nucleotide sequences were determined. Of 185 stools screened, 8% were HuCV positive and their deduced amino acid sequences showed that all isolates contained the GLPSG and YGDD motifs which are conserved in other HuCV isolates. Comparative amino acid (aa) sequence analysis showed that these isolates can be divided into 2 major genogroups corresponding to the NV and SMV genogroups. High conservation was observed in the one strain shares 98% of aa sequence with Southampton virus, and 2 strains share 94% with Hawaii virus. However, significant sequence variation was also found in other strains. This studies indicates that HuCVS are a common cause of AGE in Korean infants, and at least 2 of the 3 major genogroups of HuCVs are circulating in Korea.

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Molercular cloning of *trp*D, *trp*A and *trp*B genes from *Corynebacterium glutamicum*

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Complementation cloning of the *trp*D, *trp*B, *trp*A genes in *Corynebacterium glutamicum* was performed by transforming DNA library into the corresponding tryptophan auxotrophs of *Escherichia coli*. The recombinant plasmids containig 4kb and 8.4kb fragment complement the *E.coli trp*D mutant. This insert DNA of the recombinant plasmid termed pTD2 and pTD23 were physically mapped with several restriction enzymes. The recombinant plasmids were also able to complement the *E.coli trp*A, *trp*B mutants indicating the clusterd organization of the three genes within the DNA fragment. We also cloned other trp genes including *trp*E, *trp*C gene in *C. glutsmicum*. We want to determine the moleculer structure and organization of the clusterd trp genes. Our long term goal is to genetically engeneer *C. glutamicum* which produces more tryptophan than a typical strain.