Abstract

The disease acute gastroenteritis causes a big economic loss every year. The etiologic agents related to this disease are rotavirus, enteric adenovirus, calicivirus, and astrovirus. It is still not clear what is the role of these gastroenteritis viruses in Taiwan.

Fecal samples were collected from clinical laboratories distributed in different parts of Taiwan. Rotaviruses were detected by ELISA. The samples detected as rotavirus positive were further analyzed the G and P genotypes by RT-PCR, and the electropherotypes by RNA polyacrylamide gel electrophoresis. The VP7, VP4, and NSP4 genes of G9 rotaviruses were sequenced and analyzed phylogenetically.

In the fecal samples from the patients with acute gastroenteritis, the positive detection rates in Taipei and Kaoshiung for rotavirus were 14.7% and 17.8%, respectively.

Caliciviruses were detected by RT-PCR. About 5% of the rotavirus-negative samples from 2002 were detected as calivirus positive. About 70% of these calicivirus positive samples were collected from children under age 3. The calicivirus positive samples did not show distinct seasonal distribution. By sequence and phylogenetic analyses, these caliciviruses could be classified as Norwalk-like virus (NLV, Norovirus) and Saporo-like virus (SLV, Sapovirus). The number of NLV-positive samples was more than that of SLV-positive samples. In the NLV samples, majority belonged to genogroup II, one belonged to genogroup I, and 5 were distantly related. SLV strains could be differentiated as two groups, similar to reference strains, Hou7 and Lyon, respectively.

The rotavirus infections in 2003 did not show distinct seasonal distribution, though more cases were found in the cooler months. Calicivirus infections did not show seasonal distribution in 2002. More than 60% of the rotavirus infections were from children under the age of two, 10% were from the age group older than 5.

G9 rotavirus contributed about 20% of the rotavirus infection in Taipei, over 40% of the infection in Kaoshiung. G1, G2, and G3 rotaviruses were detected in these regions.

Analysis of the G and P genotypes, and RNA electropherotypes of rotavirus samples showed that some rotaviruses had unusual combinations of G and P types or incompatible RNA electropherotypes. These rotaviruses could have been formed from genetic reassortment. We must pay attention to their contribution in rotavirus epidemics in the future. Phylogenetic analysis of VP7 and NSP4

genes showed that the major prevalent G9 rotavirus strain was a newly emerged reassortant.

We need to keep the study of the virological agents related to acute gastroenteritis for understanding the role of each viral agent and the changes from year to year. These information will be important for future selection or development of vaccine for our needs.