

CHAPTER VII

SUMMARY

The present study investigated the prevalence of NV, SV, and HAstV infections in children hospitalized with diarrhea during May 2000 to March 2002. The NV, SV, and HAstV were detected in 40 of 296 (13.5%) of fecal specimens tested. Among the viruses detected, NV was the most predominant virus with the prevalence of 58.5% (24 of 41), of which 17.1% were NVGI and 41.4% were NVGII. Interestingly, one specimen was positive for both NVGI and SV. The SV was detected at 24.4% (10 of 41), while HAstV was detected at 17.1% (7 of 41).

A total of 24 NV nucleotide sequences were analyzed and found that NVGII was more predominant than NVGI. The NVGI sequences were grouped into 5 distinct genotypes, NVGI/4, NVGI/6, NVGI/3, NVGI/7, and NVGI/13. In contrast, NVGII detected in this study was grouped into 7 distinct genotypes, NVGII/4, NVGII/3, NVGII/10, NVGII/1, NVGII/6, NVGII/8, and NVGII/15.

Analysis of 10 nucleotide sequences of SV could be classified the SV into 2 distinct genogroups, SVGI and SVGII, according to the recent SV capsid region classification scheme. The SVGI was more common than SVGII. Eight strains of SVGI were further classified into 3 genotypes, SVGI/1, SVGI/4, and SVGI/5. Two strains of SVGII, GII/1 and GII/2 genotypes, were also detected.

All 7 HAstV strains were classified into 4 distinct genotypes or serotypes, HAstV-1, HAstV-2, HAstV-3, and HAstV-5.