MOLECULAR CHARACTERIZATION OF HUMAN GROUP A ROTAVIRUS FROM STOOL SAMPLES IN YOUNG CHILDREN WITH DIARRHEA IN INDONESIA

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Abstract. Detection and genotyping of group A rotavirus strains from stool samples in young children with diarrhea in Indonesia were examined using reverse transcription-nested multiplex PCR. Of 421 stool specimens, 257 samples was rotavirus positive. G1 type was the most common G-type (54%), followed by G2 (6%) and G9 (3%). P[8] was the most common P-type (39%), followed by P[6] (19%), P[4] (10%) and P[11] 1%. Eighteen percent of the samples had mixed G genotype infection and 5% had mixed P genotype infection. The prevalence of G-P combination type was genotype G1P[8] (24%), followed by G1P[6] (7%), G2P[4] (3%), and G1P[4] (2%). A total of 118 specimens could not be assigned as a G and/or P type suggesting the presence of new circulating genotypes in Indonesia.

Key words: diarrhea, multiplex nested PCR, reverse transcription, rotavirus A, VP4, VP7

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