ABSTRACT

ANALYSIS OF ENTEROTOXIN REGION IN NSP4 GENE SEQUENCE AND ROTAVIRUS GENOTYPES BASED ON NSP4 AND VP4 GENES AMONG CHILDREN WITH ACUTE DIARRHEA IN BANDAR LAMPUNG IN 2016 AND 2018

Introduction: Rotavirus is the most common cause of diarrhea in children under 5 years old. Rotavirus has 11 genes coding 11 proteins. the NSP4 protein binds to VP4 protein during morphogenesis at amino acids 112–148. The protein interactions during morphogenesis influence rotavirus gene constellation. NSP4 protein is the first viral enterotoxin protein. Changes in amino acids from the enterotoxin region are likely to be related to rotavirus pathogenesis variations. Information on NSP4 and VP4 genetic variations and changes in amino acid sequences within the enterotoxin region of NSP4 gene is still limited in Indonesia, especially in Lampung.

Aims : This research was aimed to analyze the enterotoxin region in rotavirus NSP4 gene sequence and rotavirus genotypes based on NSP4 and VP4 genes in children with acute diarrhea in Bandar Lampung over the years 2016 and 2018.

Materials and methods: The subjects of the present study were children with acute diarrhea 0–60 months of age admitted to 2 hospitals and 2 primary health cares in Bandar Lampung, Indonesia in September–December 2016 and June–August 2018. Identification of rotavirus was performed by genetic material identification with the PCR method and sequencing.

Results: Rotavirus-positive cases were found in 47/74 children (63.5%). The severity diarrhea most common was the severe diarrhea (87.2%). This research found changes in the distribution of dominant NSP4 and VP4 genotypes between 2016 and 2018 in Bandar Lampung. An uncommon strain with VP4 genotype P[8] and E2 NSP4 genotype combination was encountered in 2016. An NSP4 genotype E2 amino acid substitution in the enterotoxin region, R129H, was obtained. A Significant relation between the sequence variance in the NSP4 enterotoxin region and the VP4 genotype P[4] was found ($p = 0.001$). However, no significant relationship was detected between the amino acid substitution in the sequence in the enterotoxin region and diarrhea severity ($p = 1.00$).

Conclusion: There were changes in the distribution of VP4 and NSP4 genes in 2016 and 2018. The results showed that no relationship between sequence variance in the enterotoxin region of NSP4 gene and acute diarrhea severity was detected, but there was a significant relationship between amino acid sequence variance in the enterotoxin region of NSP4 gene and VP4 genotype P[4].

Keyword : Rotavirus, NSP4, VP4, genotype, severity diarrhea