

GUT MICROBIOME PROFILE IN ROTAVIRUS A AND NON-ROTAVIRUS A GASTROENTERITIS PATIENTS



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Abstract.

Gut microbiome could potentially be utilized as indicator of human health status due to increasing evidence of its characteristic associated with certain health conditions. This study aimed to investigate the intestinal microbiome profiles of pediatric patients under 5 years old with rotavirus A (RVA) diarrhea comparing to

Results.

1. Gut microbiome profile in phylum level





diarrhea from the other causes. The result showed that all study groups possessed similar major microbiota community at phylum level i.e. Proteobacteria, Firmicutes, Bacteroidetes, and Actinobacteria. However, statistically significant difference between RVA-positive and RVA-negative samples were detected in the relative frequency of Bacteroidetes (p = 0.019) and Proteobacteria (p = 0.034). RVA-positive and control were detected in Proteobacteria (p = 0.047) while there was no difference, between RVA-negative and control, and between two genders.

Introduction.



In 2016, the cause of deaths related to diarrhea accounted for 8% and 0.3% among children aged 1-59 months and period, neonatal respectively (1) (figure 1). Among them, rotavirus is the most common causative agent. It accounts for 25% of





D_0_Bacteria;D_1_Proteobacteria D 0 Bacteria; D 1 Firmicutes D 0 Bacteria; D 1 Bacteroidetes D_0_Bacteria;D_1_Actinobacteria D_0_Bacteria;D_1_Verrucomicrob D_0_Bacteria;D_1_Fusobacteria D_0_Bacteria;D_1_Spirochaetes D_0_Bacteria;D_1_Epsilonbactera

D_0_Bacteria;

%Average relative frequency (RVA-negative)



cases compared with other causative

Figure1: The cause of children death

Although the pathogenesis of rotavirus was extensively studied, the information on the gut microbiome of rotavirus diarrheal patients were few. Intestinal microbiome in children with viral gastroenteritis caused by rotavirus or norovirus was previously studied in Taiwan (3) showing reduced gut microbial diversity in diarrheal patients.

Materials and methods.



1. Ethic approval Siriraj Institutional Review Board (approval No. Si 148/2016).

agents (2).





Figure2: V3/4 region rRNA gene

Figure3: Gut microbiome profile in phylum level Non-diarrheal control (A), RVA-positive (B), and RVA-negative (C)

2. Microbial composition compared between gender



Figure 4: Gut microbial composition in Male (A) and Female (B)



 \leq 5 years old 14 Non-diarrheal control 146 RVA-positive 150 RVA-negative



3. DNA extraction

QIAamp[®] Fast DNA Stool Mini Kit

4. Next generation sequencing

Illumina MiSeq platform

5. Bioinformatic analysis

Quantitative Insights into Microbial Ecology meZ

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Predominant intestinal microbiota phylum in every samples are similar and the differences among study groups are minimal, possibly due to the acute nature of disease. There was also no significant difference between genders likely because the hormones at these ages still have less effect to microbiome. However, subtle differences in Bacteroides and Proteobacteria could be detected between RVApositive and RVA-negative, which are the subjects of further investigation.

References.

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- 3. Chen S-Y, Tsai C-N, Lee Y-S, Lin C-Y, Huang K-Y, Chao H-C, et al. Intestinal microbiome in children with severe and complicated acute viral gastroenteritis. Scientific Reports. 2017; 7: 46130.