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Elucidation of bacterial species during childhood diarrhea through 16S rRNA Illumina Miseq approach.

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Abstract

Diarrhea causes a debilitating infectious illness among children, especially in developing countries with higher mortality and morbidity rates. Gastrointestinal (GI) tract is occupied by complex microbial-communities structures and the composition of indigenous microbial-consortia gets altered during diseases associated with GI tract. However, effect of microbial imbalance and proliferation in childhood diarrhea severity is less understood. Therefore, present study is focused to compare composition and diversity of bacterial communities in healthy and diarrhea infants using metagenomic approach.

Stool specimens were collected from two acute and one persistent diarrhea infected infants. A stool sample from a healthy infant of same geographical region was taken as reference for comparative analysis. All four fecal specimens were subjected to 16S rRNA V3 region metagenomic profiling.

Metagenomic analysis of healthy control revealed enrichment with higher proportion of *Firmicutes*, *Bacteroides* and *Proteobacteria* phyla. In case of acute and persistent diarrhea infected infants, collapse of indigenous anaerobic microbial-communities like *Firmicutes*, *Bacteroides*) and aberrant proliferation of facultative anaerobes (*Proteobacteria*) was observed. Moreover, *Klebsiella*, *Haemophilus*, *Rothia*, *Granulicatella*, *Chelonobacter* and *Vibrio* species were identified as key pathogenic lineages in diarrheal samples.

Our findings reveal significant imbalance between intestinal bacteria of healthy and diarrhea subjects and witnessed occurrence of pathogenic bacteria which may be responsible for diarrheal illness.