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Metagenomic profiling of gut microbiota of diarrhoeic children in Southwest Nigeria

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Background: Globally, around 63% of all diarrhoea cases occur in children that are below five years of age. accurate and timely detection of the aetiology of these diseases is very crucial but some of the current methods apart from being laborious and time-consuming, often fail to identify difficult to culture pathogens. Here we investigated the impact of diarrhoea on the gut microbiome of children under 5 y of age in Southwest Nigeria using metagenomic approach.

Methods and materials: Amplicon-based metagenomics analysis was carried out on 8 human DNA samples obtained from stool samples of diarrhoeic children and a control group. Phylogenetic diversity, species richness and relative abundance of bacterial taxa were determined using the CLC Genomics Workbench v12.0 and the implemented Microbial Genomics Module version 4.0 (Qiagen).

Results: Six bacterial phyla comprising 78 genera were identified. The gut microbiome profile revealed Firmicutes (61%), Bacteroidetes (17%), Proteobacteria (15%), Actinobacteria (5%), Fusobacteria (1%) and Verrucomicrobia (1%). Among the diarrhoeic samples, the relative abundance of phyla shows decreasing order of Firmicutes, Proteobacteria, Actinobacteria, Bacteroidetes, and Fusobacteria, except phylum Verrucomicrobia which was not identified. There was a remarkably decreased abundance of Proteobacteria among the control samples when compared to the diarrhoeic samples (38%). *Escherichia coli*, *Shigella*, *Staphylococcus* and *Klebsiella* had increased species richness among the diarrhoeic samples, whereas, *Bifidobacterium*, *Faecalibacterium*, *Lactobacillus*, *Clostridium (sensu stricto)*, and *Bacteroides* were significantly increased among the control samples.

Conclusion: An understanding of the impact of diarrhoea on the gut microbiota may help elucidate the role of the gut microbiome in the health and disease status of children in a Sub-Saharan setting, however, this can only be made easy with the application of metagenomics techniques.


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