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## Early gut microbiota response to infectious diarrhea in Vietnamese infants

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iarrheal diseases result in approximately 1.7 billion new infections and 0.75 million deaths in children under 5 years of age annually, making it the second most common cause of mortality in young children in developing countries. Repeated diarrheal episodes cumulatively increase the risk of malnutrition and stunting, which is associated with cognitive impairment and development of cardiovascular diseases and glucose intolerance in adulthood. These greatly exhaust societal resources, especially in impoverished regions and create vicious cycles of poverty demanding effective and effortful interventions. The human gastrointestinal tract is populated with immensely diverse microbial community with the large intestine harboring the greatest density. Research on gut microbiota has revealed the essential impacts that it may exert on human health, in relation to nutrition, metabolic diseases and cancer. Metagenomic techniques have been employed to investigate the microbial disturbances in persistent Clostridium difficile infection and inflammatory bowel diseases but such dysbiosis remains insufficiently characterized for infectious diarrhea in endemic setting. The highly dynamic succession of microbial colonization in young children further complicates analysis in this target group. Nevertheless, several 16S rRNA profiling studies have reached consistent findings on how gut microbiota initially responses following diarrhea, showing a transition toward facultative anaerobic Proteobacteria or Streptococcus in a more oxygenated environment. This is coupled with the significant reduction in several Firmicutes and Bacteroidetes colonizers and their abundances are restored to that resembling a healthy individual in post-diarrhea recovery state. However, these studies either focus only on cholera induced diarrhea or do not offer detailed granularity in understanding the microbiome alternation. In this study, we aim to characterize how gut microbiota changes in the early phase of secretory diarrhea in Vietnamese young children by examining their bacterial 16S rRNA composition. We utilized samples and associated metadata collected during a hospital based diarrheal surveillance study in Ho Chi Minh city, Vietnam from 2009 to 2010.

## Biography

Paola Florez de Sessions has completed her PhD from Duke University and Postdoctoral studies at the Novartis Institute for Tropical Diseases in Singapore. She is the currently the GIS Efficient Rapid Microbial Sequencing (GERMS) Platform Leader.

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