
Microbiome analysis in children hospitalized with pneumonia in low income countries: a proof of concept

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Résumé

The human upper respiratory tract is an ecological niche heavily exposed to microorganisms and such as considered as an important route of pathogens infection and transmission. The viruses and bacteria that are commonly found in a child's nose or throat can infect the lungs and lead to acute respiratory infections. Pneumonia is a severe acute respiratory infection and represents the main cause of death in children under five years old worldwide (estimated 1.3 million*).

Fondation Mérieux carried out an extensive multicenter pneumonia study (cases/controls) in eight low income countries, nine sites and three continents (GABRIEL network) with focus on the identification of etiological in pneumonia. Interestingly, we found around 30% of cases (n=900) without viral or atypical bacteria agents as well as a large portion of viral asymptomatic carriers in controls (n=900).

The growing power and reducing cost sparked an enormous range of applications of Next Generation Sequencing (NGS) technology such as marine ecology or clinical virology. In recent years, metagenomics has become an established method for both identifying known viruses and virus discovery in nature. NGS is now a standard technology for studying the human microbiome.

We hypothesized that a disturbance of balanced nasopharyngeal microbiome might be involved in the onset of symptomatic infections. Since human upper respiratory microbiome is not precisely known in pneumonia context, we therefore performed a proof of concept metagenomic study on the detailed composition and variability in nasopharyngeal microbiome in young children sampled worldwide.

Although NGS make genome sequences handy, the followed data analysis is still the bottleneck in understanding genomes. Here, we present the algorithm of the study with focus on the analysis pipeline datasets as shown by a limited number of analyzed samples.

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