

Diversity and development of human gut microbiota in ICU patients suffering from acute or long standing illness

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Abstract

The entire genetic content of the human gut microbiota is commonly referred to as the gut microbiome which enormous genetic potential can contribute to host physiology, the human gastrointestinal tract (GIT) is considered one of the most densely populated with microbiota ecosystems, whose activities have significant consequences for the host in terms of health and disease. Indeed, the dysbiotic microbiota, which has deviated from the 'healthy' status in terms of diversity and functionality, has been implicated in a range of inflammatory or chronic diseases. Thus, a growing number of studies have reported on how the early human gut microbiota composition/development may affect risk factors related to adult health conditions. This concept has fueled that the gut microbiota is a reservoir of opportunistic pathogens that can cause life-threatening infections in critically ill patients during their stay in an intensive care unit (ICU). The study of the gut microbiome has been revolutionised over the last years by advances in genetic methods and sophisticated bioinformatic tools. Next generation sequencing is a low-cost, high-throughput sequencing platform that enables analysis of all the genomes within an ecosystem sample (shotgun metagenomics), or a description of the taxa within a given community by sequencing conserved marker genes, such as the 16srRNA gene of bacteria (marker gene metagenomics) Rectal swabs from ICU patients demonstrated differences from healthy stool similar to those from the same healthy controls.



Biography:

Amera Ibrahim Elkhailifa Ahmed has completed her Master degree at the age 28 years in Medical Microbiology from Khartoum University, Faculty of Medical Laboratory Sciences. She is the head department of Microbiology and Molecular biology at Universal Hospital Group since 2/9/2019 up to date.

She was former a senior Microbiology Specialist at Royal Care International Hospital from 17/9/2014 to 10/9/2019, during this period she was assigned as Quality Control & Safety Officer from 1/4/2019 till 10/9/2019.

Speaker Publications:

1. "Detection of carbapenem resistance genes among selected Gram negative bacteria isolated from patients in Khartoum stata, Sudan, 2015"
- 2 "Pulmonary nocardiosis caused by nocardia Otitidiscaviarum in an adult asthmatic female patient: The presence of acid-fast branching filaments is always significant. SAMJ January 2017"

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