



Category: Metagenomics

Next Generation sequencing as a tool in gut microbiota to discriminate between wellness and obese

Gifty Sara Mathew, Sribal Selvarajan, M. Padmini, Shriram Mahadevan and Padma Srikanth*

Sri Ramachandra Medical College & Research Institute, Chennai, INDIA

*Corresponding author: srikanth_padma@rediffmail.com

Abstract

Around 13% of the world's adult population are obese and its incidence has doubled in past 3 decades [1]. This study aims to discern the differences in gut microbial composition among healthy and obese individuals. A cross sectional study was conducted in a tertiary care centre. Human faecal and blood samples from healthy (n= 5) and obese (n=10) were collected after obtaining IEC and informed consent. Ultra-sonogram abdomen was also done to detect fatty liver changes. DNA was extracted using Qiagen DNA stool mini kit (Qiagen, Germany) and PCR was performed using Qiagen multiplex PCR master mix and fusion primers. Metagenomics analysis was performed using Ion torrent (PGM). The sequencing reads were in FASTA format and were clustered and reported as operational taxonomic units [2]. Statistical Analysis: Chi square test of significance and student 't' test was done using Quick Calcs, version 5 (Graph Pad Software Inc., La Jolly, CA, USA). Gut microbial composition among healthy lean participants (BMI 18-23) had predominantly gram positive bacteria like Ruminococcus, Bifidobacterium, Peanibacillus. Similarly, gram positive bacteria such as Bifidobacterium, Dialister, Clostridales were predominant in mild risk obese (BMI 30-35) whereas gram negative bacteria like Enterobacter, Vibrio and Escherichia were higher among moderate to severe risk obese participants (BMI >35). A clear shift of gram positive to gram negative bacteria was observed among study groups. Analysis by phyla showed a five-fold reduction in counts of Firmicutes in mild obese to moderate and severe obese and in contrast Proteobacteria doubled in moderate and severe obese category. The mean fasting blood sugar (FBS) was higher among obese (101.9 ± 10.9) in contrast to healthy participants (89.6 ± 7.1) with a statistical significance ($P=0.04$). Fatty liver was significantly higher among obese, n=10 (100%) when compared to healthy participants, n=1 (20%) ($P=0.007$). Gram negative bacteria is predominant in moderate to severe obese and from this it is evident that lipopolysaccharides found in GNB could be well associated with severe obesity and related consequences. Faecal transplant could possibly be used as an intervention among severe obese and other related metabolic disorders to revert to a lean phenotype.

References

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