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## Microbiota in relation to obesity among healthy Saudi females

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**Background:** Obesity has been considered as one of the major modern global epidemics and a risk factor for both cardiovascular diseases (CVD) and diabetes. There is a rapid rise in the rate of overweight and obese people in the Kingdom of Saudi Arabia which has a tremendous impact on health and economic resources. Gut microbiota has lately been a major factor for many metabolic disorders and diseases, including obesity, diabetes, and CVD.

**Objective:** The aim of this research was to define those specific gut microbiota that are obesity-associated as determined based on mass index (BMI) among healthy Saudi females.

**Methodology:** 120 healthy females, below the age of 30, with different degrees of obesity were included in this study. All the participants had to fill out a questionnaire concerning their nutritional habits, health conditions and demographics. Their height, body weight, hip and waist circumference were measured and their BMI was determined accordingly. Stool samples were collected and genomic DNA was extracted from our study group. The DNA samples were sequenced using next generation sequencing (MiSeq), sequencing reads were trimmed, analyzed and filtered and assigned to taxonomic units.

**Results:** The results revealed the existence of different bacteriological groups including *Firmicutes*, *Actinomyces odontolyticus*, *Escherichia coli* and *Ruminococcus obeum* and others. Work is in progress to correlate the prevalence of those bacterial groups with BMI.

**Conclusion & Recommendations:** The data showed the presence of a variety of bacterial strains and microbiota populations among our study individuals. Bioinformatics data analysis will help to identify certain microbiota marker populations to be associated with different stages of obesity among the female Saudi population. Final goal is an early prediction of obesity and to target those patient groups to treat obesity.

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**Notes:**