SHORT COMMUNICATION

RECORDS OF PHARMACEUTICAL AND BIOMEDICAL SCIENCES

Gender dependent shifts in gut microbiome of obese Egyptian individuals

Mohammed Salah[a], Marwa Azab[b], Ahmed Ramadan[c] and Amro Hanora[b*]

[a]Department of Microbiology and Immunology, Faculty of Pharmacy, Port Said University, Egypt,
[b]Department of Microbiology and Immunology, Faculty of Pharmacy, Suez Canal University. Ismailia, Egypt,
[c]department of internal medicine, Faculty of Medicine, Al-Azhar University, Cairo, Egypt.

Received on: 20.03. 2019

Revised on: 25. 04. 2019

Accepted on: 01. 05. 2019

Correspondence Author:

Tel:+ 201000323406

E-mail address:

ahanora@yahoo.com

Abstract

The majority of human microbiota resides in the GIT approximately 3.6 x 10^{13}. Identification of gut microbiota composition in obese individuals and defining bacterial community differences between men and females help in the treatment of certain metabolic disorders. Gut microbiome analysis of men and females was performed with 16s rRNA genes using Illumina MiSeq sequencing. 5 stool samples for each group were collected from obese men and women. In our study, we found that bacterial communities of men were more diverse in comparison to women. *Firmicutes* /*Bacteroidetes* ratio was higher in men than females due to the overrepresentation of *Firmicutes* in men and overrepresentation of *Bacteroidetes* in case of females. Finally, Illumina MiSeq sequencing of 16S rRNA V4 region was allowing cheap and efficient studying of gut microbiota.

Keywords: Gender, Gut, Microbiome, Obesity, 16S rRNA.

1. Introduction:

Microbial communities that colonize or inhabit the GIT has been identified to play an important role in core functions, like the digestion and degradation of otherwise inedible nutrients, and therefore the development and stimulation of the alimentary tract of the host (Costello et al., 2012, Nicholson et al., 2012, Hooper et al., 2012, Abrams and Bishop, 1967, Rajilić-Stojanović and de Vos, 2014).

Obesity is a great problem across the world. The main cause of obesity is imbalances in energy production and storage which directly affected by environmental and host-associated factors including genetic, diet, and exercise (Pitsavos et al., 2006, Loos et al., 2012). The incidence of metabolic diseases is sexually dimorphic and varies depending on gonadal status; e.g., increases after menopause (Rao et al., 2013). Gut microbiota directly affects our health or disease status, it has been implicated to cause obesity (Baothman et al., 2016).

The 16S rRNA gene is characterized by large length providing sufficient sequence variability among bacteria, thereby enabling comparisons at different taxonomic levels. It is extremely valuable for rapid investigation of the microbial constituents in an environmental sample using the PCR (Spratt, 2004, Nossa et al., 2010). Studying of gut microbiota in men and females could help in identification of differences in bacterial community composition, and also aid in prevention and treatment of obesity. The current study was conducted to assess the differences in the gut bacterial composition between both genders in obese Egyptian population.

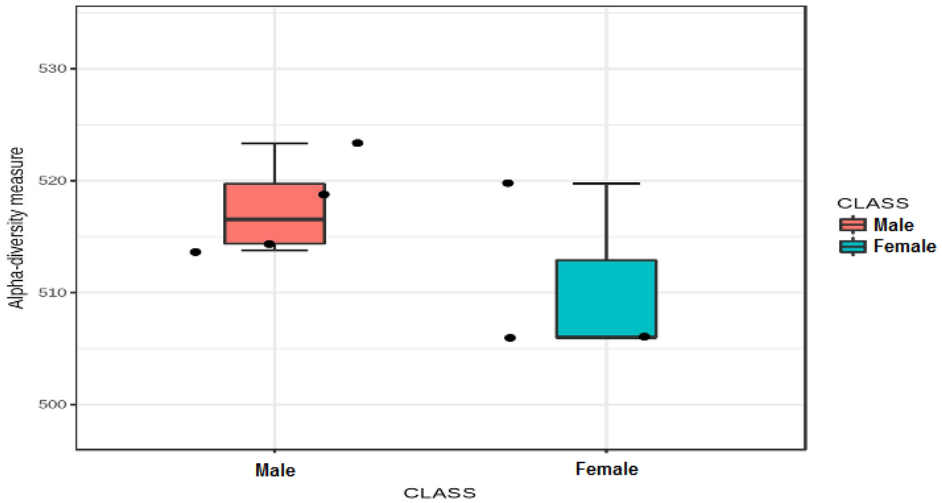

Figure 1. Group-wise Boxplot showing alpha diversity at OUT level by Chao index

2. Results

2.1 characteristics of study cohort

In total, stool samples were collected from ten obese subjects representing both genders (5men and 5 females). Inclusion criteria included adults with Body Mass Index (BMI) between 31-35 kg/m^2. Subjects with BMI were less than 31 kg/m^2, taking systemic antibiotics, immunosuppressive cytotoxic agents and with history of cancer, were excluded.

2.2 Alpha diversity analysis

Amplified 16S rRNA V4 region sequenced using Illumina MiSeq platform. The sequences obtained were analyzed using Mothur software (V 1.33.2). OTU (operational taxonomic units) were picked against green genes (V 13_8) database. Alpha diversity analysis using Chao index, which combining richness and evenness of communities, was ranged from 505 to 525 (*P* value = 0.001). The gut microbiota of men was more diverse than women (**Fig. 1**).

2.3 Taxonomic profiling of gut microbiota

At phylum level, we found 27 phyla and the ratio of *Firmicutes/ Bacteroidetes* phylum is higher in men (1.66) than females (0.44). Furthermore, relative abundance of *Proteobacteria* and *Actinobacteria* in females is higher than those of males. The main predominant phyla were *Firmicutes* (61.4%), *Bacteroidetes* (36.8%) and *Proteobacteria* (1.5 %) in men while *Bacteroidetes* (67.7 %) were the most predominant phylum followed by *Firmicutes* (30.5%) and *Proteobacteria* (1.7%) in females (**Fig. 2**).

At genus level, we observed differences (Wilcoxon rank test; *P* value $\leq$ 0.05) in relative abundance between male and female gut microbiota (Table 1).

Table 1. Genera that distinguish between men and female gut microbiota

Genera	**Male (%)**	**Female (%)**
Prevotella	33.7	48.4
Clostridium	19.6	0.45
Faecalibacterium	8.4	3.3
Dialister	8.4	2.5
Lactobacillus	4.9	0.31
Blautia	3.8	0.8
Dorea	1.8	0.23
Roseburia	1.6	0.7
Ruminococcus	1.	1.2

3. Discussion

Identifying the composition of gut microbiota in obese individuals and defining bacterial community differences between men and women seems to help in the treatment of certain metabolic disorders. In our study, we observed that, the Alpha diversity was enriched in obese men than obese females this could be linked to hormonal variation between genders such as; gherline hormone which attributed to increased food intake, change in richness and diversity of gut microbiota composition (Rao et al., 2013, Markle et al., 2013). Ghrelin hormone plays an

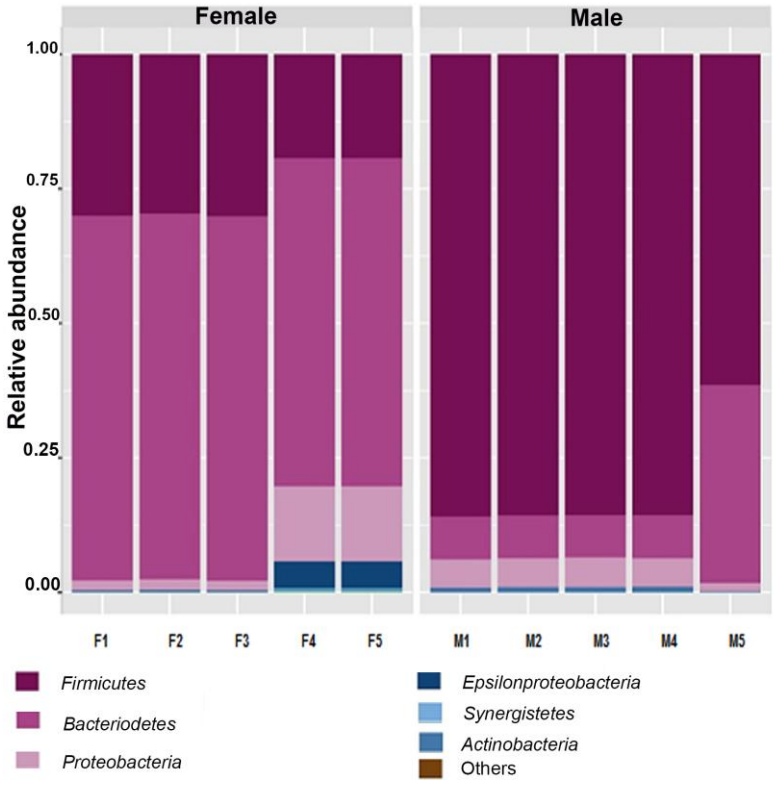

Figure 2. Phylum level analysis of gut microbiota

important role in the regulation of appetite and body adiposity, Women had higher plasma ghrelin levels than men (Makovey et al., 2007). *Firmicutes*/*Bacteroidetes* ratio was higher in males than females due to overrepresentation of *Firmicutes* in men and the overrepresentation of *Bacteroidetes* in case of obese women. According to BMI, men have higher *Firmicutes*/*Bacteroidetes* ratio under a BMI of 33 (Haro et al., 2016).

4. References

Abrams GD and Bishop JE (1967). Effect of the normal microbial flora on gastrointestinal motility. Experimental Biology and Medicine 126**,** 301-304.

Baothman OA, Zamzami MA, Taher I, Abubaker J and Abu-Farha M (2016). The role of gut microbiota in the development of obesity and diabetes. Lipids in health and disease 15**,** 108.

Costello EK, Stagaman K, Dethlefsen L, Bohannan BJ and Relman DA (2012). The application of ecological theory toward an understanding of the human microbiome. Science 336**,** 1255-1262.

Haro C, Rangel-Zúñiga OA, Alcalá-Díaz JF, et al. (2016). Intestinal microbiota is influenced by gender and body mass index. 11**,** e0154090.

Hooper LV, Littman DR and Macpherson AJ (2012). Interactions between the microbiota and the immune system. Science 336**,** 1268-1273.

Loos RJJBP, Endocrinology RC and Metabolism (2012). Genetic determinants of common obesity and their value in prediction. 26**,** 211-226.

Makovey J, Naganathan V, Seibel M and Sambrook P (2007). Gender differences in plasma ghrelin and its relations to body composition and bone–an opposite-sex twin study. Clinical endocrinology 66**,** 530-537.

Markle JGM, Frank DN, Mortin-Toth S, et al. (2013). Sex differences in the gut microbiome drive hormone-dependent regulation of autoimmunity. Science 339**,** 1084-1088.

Nicholson JK, Holmes E, Kinross J, et al. (2012). Host-gut microbiota metabolic interactions. Science 336**,** 1262-1267.

Nossa CW, Oberdorf WE, Yang L, et al. (2010). Design of 16S rRNA gene primers for 454 pyrosequencing of the human foregut microbiome. World journal of gastroenterology: WJG 16**,** 4135.

Pitsavos C, Panagiotakos D, Weinem M and Stefanadis CJTRODS (2006). Diet, exercise and the metabolic syndrome. 3**,** 118.

Rajilić-Stojanović M and De Vos WM (2014). The first 1000 cultured species of the human gastrointestinal microbiota. FEMS microbiology reviews 38**,** 996-1047.

Rao PM, Kelly DM and Jones THJNRE (2013). Testosterone and insulin resistance in the metabolic syndrome and T2DM in men. 9**,** 479.

Spratt DA (2004). Significance of bacterial identification by molecular biology methods. Endodontic Topics 9**,** 5-14.