Research and Reports in Immunology

Study of the gut enterotypes in some Egyptian patients with Type 1 diabetes mellitus

Amany Ahmed Elbanna

Alexandria University, Egypt, E-mail: AMANI.ALBANA@alexmed.edu.eg

Abstract

Introduction: Gut microbiota cluster into three enterotypes named the Bacteroides, Prevotella and Ruminococcus. While each person???s microbial ???fingerprint??? is unique, there are specific patterns seen in those that are healthy and those that have specific illnesses.

Objective: The objective of the present study was to identify the enterotypes that are possibly associated with Type I Diabetes Mellitus (T1DM) Egyptian patients as well as their possible role in the course of the disease.

Subjects & Methods: The study included 40 T1DM patients as well as control group of 20 healthy subjects of matched age and sex. Stool specimens were taken from each. Quantitative SYBR Green Real-Time PCR was done for the identification and quantitation of Bacteroides, Prevotella and Ruminococcus which constitute the core of the three major enterotypes.

Results: Enterotype 1 was the most common enterotype detected in T1DM and control cases (75% versus 65% respectively) with no significant differences between the two groups (P=0.418). Regarding enterotype 2 no significant differences was noted between T1DM patients and control group (25% vs. 35% respectively P=0.324). For enterotype 3, it was detected neither in patients with T1DM nor in control cases.

Conclusion: There was no significant difference in the distribution of enterotypes in all study groups. Therefore, collapsing the whole microbiome variations into dominant enterotypes was not appropriate to identify disease association or to be used as a disease biomarker. Diabetes remains a growing public health concern in Egypt, as prevalence of Type II diabetes (TIID) has nearly tripled there in the last two decades. Egypt was ranked ninth worldwide in number of diabetes cases, with prevalence of 15.56% among adults. Recent studies have proposed that disturbance of gut microbiota could influence TIID development and indicated associations between a reduced diversity in microbiomes and Type I diabetes (TID). In the present study, we investigated the composition and abundance of the bacterial microbiome in disease state (TID and TIID) of Egyptian patients. Our goal in this study was to characterize features of the gut microbiota and possible differences associated with TID and TIID in this population. Diabetes mellitus (DM) is a diverse metabolic disorder characterized by elevated blood sugar levels as a result of deficiency of insulin secretion, defective insulin action or both. DM can cause complications if uncontrolled, including, stroke, cardiovascular disease and kidney failure. Globally, DM is the ninth major cause of death; one in eleven adults worldwide have DM.The International Diabetes Federation (IDF) ranked Egypt ninth worldwide in number of diabetes cases, with prevalence of 15.56% among adults

This work is partly presented at

14th Euro-Global Gastroenterology Conference on July 08-09, 2019, held in Zurich, Switzerland.