

Characterization of Gut Microbiome in Type-1 Diabetic Children in Qatar

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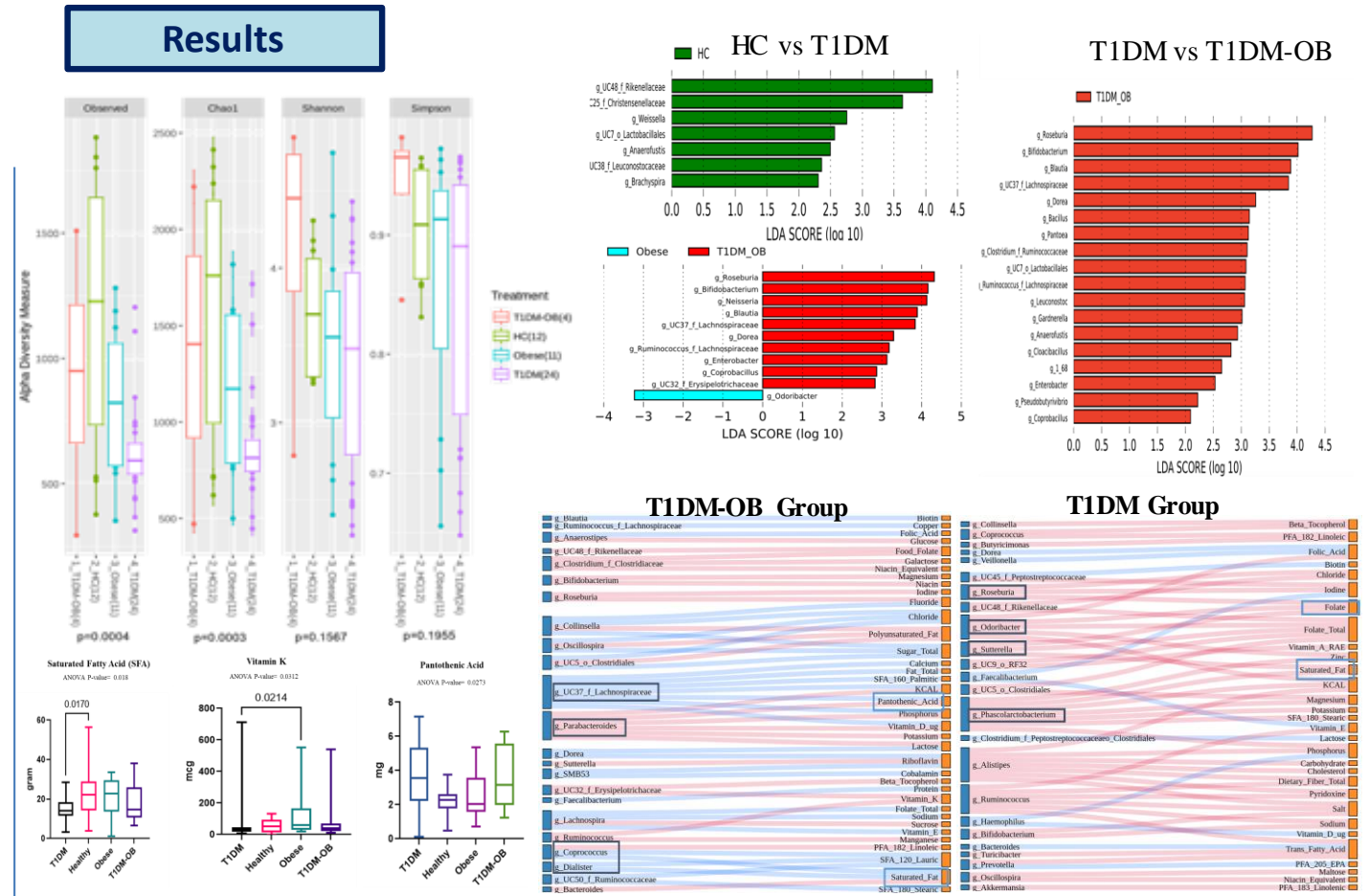
Introduction

The prevalence rates of type 1 diabetes mellitus (T1DM) and obesity in Qatar are among the highest rates worldwide. Interestingly, microbiome is a potential factor in the pathogenesis of non-communicable diseases including T1DM. This study aims to characterize the gut microbiome compositions in T1DM and T1DM-obese (T1DM-OB) children in Qatar and correlate the peculiar microbiota to dietary patterns.

Methods

- 16S rDNA library preparation was done with Illumina Nextera XT library preparation kit that targets V3-V4 region and sequenced using Illumina Miseq V3 kit (600 cycle).
- The raw data was obtained using QIIME 1.9.0 pipeline and matched with the Greengenes database.
- The biomarker analysis was done using LEfSe analysis.
- The alpha diversity estimation was done using R package.
- Dietary data was collected by 24-hrs recall & analyzed by Nutritionist Pro Axxya System.
- Statistical significance is considered when p -value < 0.05 .

Results



-Alpha diversity (Observed, Chao1) is significant ($p < 0.001$) between the 4 groups.
 -LefSe shows peculiar microbial signature for T1DM-OB vs T1DM & T1DM-OB vs Obese
 -Significant differences in 3 main nutrients: SFA, vitamin K and Pantothenic acid which had positive & negative correlations with microbiome as shown by Network analysis.
Conclusions: the microbial profiles of T1DM and T1DM-OB significantly differ & the dietary intakes seems to contribute to the bacterial signature.