



Altered gut microbiota in Obese children: sex-associated signature

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Background: The incidence of obesity, especially in children, have dramatically increased over the last few decades. Recently, studies highlighted the involvement of gut microbiota in the pathophysiology of obesity. Gender-related differences have been reported in animal and adult. Nonetheless, reports related on the features of gut microbiota in children with obesity is limited and no one reported the different composition of gut microbiota at different sex of obese children.

Objective: This study is to analyze the differences of gut microbiota between obese and normal-weight children. In addition, to investigated the difference of gut microbiota in obese children with different sex.

Method: A cross-sectional study was performed between obese children and normal-weight children aged 6 to 14 years old who visited to Fuzhou Children's Hospital of Fujian Province from January 2018 to December 2018. The anthropometric and physiological parameters were obtained, and fecal samples were collected from all subjects. The relative abundance of gut bacteria was determined by 16S rRNA gene sequencing using Illumina MiSeq.

Result:

1) A total of 50 obese children (24 boys and 26 girls, mean age 9.67 ± 1.60 years, mean BMI 24.69 ± 1.96 kg/m²) and 24 normal-weight children (11 males and 13 females, mean age 9.08 ± 2.07 years, mean BMI 16.09 ± 1.91 kg/m²) were enrolled in this study. There was no significant difference in age between the two groups ($p > 0.05$).

2) There was no significant difference of alpha diversity between obese and normal-weight children ($P > 0.05$). Firmicutes and Bacteroidetes were the two predominant bacterial taxa in feces of the two groups. Linear discriminant analysis effect size (LEfSe) analysis showed that children with obesity were accompanied with a significant reduced abundance of Bacteroides (from phylum to genus), as well as an increased abundance of Enterococci (from order to family), Puccinia (from family to genus) and Escherichia compared to the normal-weight children ($P < 0.05$).

3) Characteristic microbiome in obese. Children with different sex showed that there was no significant difference in the alpha diversity of the gut microbiota between the two groups ($P > 0.05$); Also no significant difference at phylum level ($P > 0.05$) between the two groups. The genus level of Bilophila, Granulicatella, Lactobacillus, Megamonas, Paravotella and the species level of Bacteroides_ovatus and Bacteroides_uniformis in obese children with different sex were significant different between the two groups ($P < 0.05$).

Conclusion: Children with obesity exhibited a microbial flora which differed from those of normal weight and with a sex-specific responses.

