

Alteration of the gut microbiome in normal and overweight school children from Selangor with Lactobacillus fermented milk administration

ABSTRACT

Childhood obesity is a serious public health problem worldwide. Perturbations in the gut microbiota composition have been associated with the development of obesity in both children and adults. Probiotics, on the other hand, are proven to restore the composition of the gut microbiome which helps reduce the development of obesity. However, data on the effect of probiotics on gut microbiota and its association with childhood obesity is limited. This study aims to determine the effect of probiotics supplement intervention on gut microbiota profiles in obese and normal-weight children. A total of 37 children, 17 normal weight, and 20 overweight school children from a government school in Selangor were selected to participate in this study. Participants were further divided into intervention and control groups. The intervention groups received daily probiotic drinks while the control groups continued eating their typical diet. Fecal samples were collected from the participants for DNA extraction. The hypervariable V3 and V4 regions of 16S rRNA gene were amplified and sequenced using the Illumina MiSeq platform. No significant differences in alpha diversity were observed between normal weight and obese children in terms of the Shannon Index for evenness or species richness. However, a higher intervention effect on alpha diversity was observed among normal-weight participants compared to obese. The participants' microbiome was found to fluctuate throughout the study. Analysis of the taxa at species level showed an increase in *Bacteroides ovatus* among the normal weight cohort. Genus-level comparison revealed a rise in genus *Lachnospira* and *Ruminococcus* in the overweight participants after intervention, compared to the normal-weight participants. The probiotics intervention causes an alteration in gut microbiota composition in both normal and overweight children. Though the association could not be defined statistically, this study has provided an improved understanding of the intervention effect of probiotics on gut microbiome dysbiosis in an underrepresented population.

Keyword: Probiotics; Gastrointestinal microbiome; Metagenomics; Obesity