

Time Restricted Feeding are Associated with Changes in Human Gut Microbiota Related to Nutrients Intake

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Abstract

Objectives: Time restricted feeding (TRF) is a dietary therapeutic remedy for the prevention and treatment of metabolic diseases. Gut microbiota may contribute to influence the host metabolism and nutritional status of the individuals. Given the significance of TRF and gut microbiota in metabolic diseases, this study was conducted to explore the association between TRF and gut microbiota in healthy individuals, which is not clearly elucidated.

Methods: Thirty healthy males (age=18-30 years) were divided in to two groups (TRF, n=15 and Non-TRF, n=15). TRF group was instructed, to not use any food for 16 hours per day. Two days food diary was used for dietary data collection. Stool samples were collected from both groups after 25 days of TRF or Non-TRF. Gut microbiota profile was analyzed and quantified by using 16S rRNA gene sequencing.

Results: Cluster analysis revealed that *Prevotella_9*, *Faecalibacterium* and *Dialister* were the most abundant species in TRF, while *Prevotell_7*, *Alloprevotella* and *Prevotella_2* were less abundant in Non-TRF group. At genus level, gut microbiota of TRF group was significantly changed from Non-TRF. Moreover, bar plot analysis revealed that *Bacteroidetes* was the most abundant phylum in TRF group followed by *Firmicutes*. Heatmap correlation showed that PUFA and vitamin D were positively correlated with *Firmicutes*, while iodine, vitamin E, magnesium and carbohydrates intakes were negative correlated with microbial richness.

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