

2016年度森基金研究活動報告書

個々人の腸内環境に合わせたプロバイオティクスの開発

政策・メディア研究科 修士1年

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Abstract

Gut microbiota plays important roles in human homeostasis, such as food digestion, nutrient absorption, and immunostimulation. In particular, *Bifidobacterium longum* have beneficial effects on the amelioration of colonic inflammation and protection from infectious diseases through acetate production. Although *B. longum* strains are present in the human intestine, the mechanism of Bifidobacterial colonization is yet to be understood. Previous studies have suggested each individual harbors an indigenous *B. longum* strain and external probiotic strains are not able to colonize for prolonged periods. In this study, the final goal is to clarify the mechanism of intestinal colonization of *B. longum*. As a first step, we aimed to identify whether there is the bacterial gene content specific to a host by comparative genomic analysis of dominant *B. longum* in each individual. Therefore, we first targeted two individuals, and determined that a unique *B. longum* strain colonizes for long periods. In this term, we analyzed each individual strain for antibiotic resistance genes. Furthermore, to conduct a more comprehensive analysis, we further identified 6 individuals that harbored *B. longum* from 9 individuals, and determined that the ratio of *B. longum* were unique in each individual. We are planning to conduct whole genome shotgun sequencing of these *B. longum* strains.

※ 国際論文を執筆中のため、詳細は割愛させていただきます。

Oral presentation

“Draft genome sequences of *Bifidobacterium longum* strains from two healthy Japanese adults”

Watabe T., Yoshida Y., Suzuki H., Arakawa K., Tomita M., Fukuda S., 2016, MetaSUB conference, Shanghai, China
