



Title	Effects of yacon ( <i>Smallanthus sonchifolius</i> ) tuber on physiology, fermentation products, and intestinal microbial communities in rats [an abstract of dissertation and a summary of dissertation review]
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## 学位論文内容の要旨

博士の専攻分野の名称：博士（農学）

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### 学位論文題目

Effects of yacon (*Smallanthus sonchifolius*) tuber on physiology, fermentation products, and intestinal microbial communities in rats

(ヤーコン(*Smallanthus sonchifolius*) の根がもたらす効果

－生理機能、発酵生産物、ラットの腸内微生物叢の変化－)

The beneficial health effects of prebiotics has led to increasing studies of microbial ecology in human and animal guts in order to better understand the links between food, gut microbiota and overall health. Two approaches being used are to include prebiotics in the diet; one is to add prebiotic compounds to commonly consumed foods and the other is to include functional foods, food naturally containing high concentrations of prebiotics, in the diet. Yacon (*Smallanthus sonchifolius*) is a plant originally from the Andean region of South America and has been cultivated in Japan. Yacon tuber contains oligofructose, soluble fibers, resistant starch and polyphenols. There have been some studies on the potential use of yacon tuber as a prebiotic using *in vitro* and *in vivo* rat and guinea pig model systems and human studies. They have shown beneficial effects of eating yacon tubers including accelerated colonic transit time in healthy individuals, hypolipidemic, hypoglycemic, immunomodulatory, and improvement of iron bioavailability. These effects may be either directly or indirectly related to the prebiotic stimulation of the growth of beneficial bacteria and production of short chain fatty acid (SCFA). We added 10% of yacon tuber which contain FOS equivalent to 5% commercialized FOS to the rat's conventional diet. The objective of our study are to investigate the effects of yacon tuber in comparison with fructooligosaccharides (FOS), a well known prebiotic, on rat's physiology, fermentation products and intestinal microbial communities in rats.

### **1. Fermentation of yacon tuber in rat's cecum enhanced short chain fatty acid (SCFA) production and affected rat's physiology**

Oligofructose contained in yacon tuber resists to absorption and degradation by the intestinal enzymes, thus they were reached cecum and were fermented by specific bacteria. Fermentation of yacon tuber increased SCFA concentration in cecum. We found significantly increased of acetate, propionate and butyrate 1.5- to 2-fold higher in the cecum of rats fed yacon tuber compared to rats fed FOS and control. This higher

SCFA caused decreased cecum pH. On the rat's physiology, we investigated increasing of cecum size compared to control and blood triglycerides compared to FOS and control. The change of cecum size; the elevation noted in cecum total weight and wall weight was indirectly affected by SCFA. Butyrate providing the energy source for increasing crypt depth and cell density, resulting in higher intestinal wall weight compared with the control. Furthermore, increased of blood triglyceride was also related to SCFA. The possible hypolipidemic was propionate inhibits cholesterol synthesis by inhibiting both 3-hydroxy-3-methyl-glutaryl-CoA (HMG-CoA) synthase and HMG-CoA reductase. This effect showed that yacon tuber can be used as compromising substrate for antilipidemic effects.

## **2. Different impact of yacon tuber diets on the rat's microbial communities**

However, studies of yacon tuber effects on intestinal microbiota have relied mainly on culture dependent-methods that targeted only a few bacterial groups in the cecum. We compared the microbial communities between rats fed yacon tuber, rats fed FOS and rats fed control diet with a molecular biological techniques based on 16S rRNA gene sequences. PCR-DGGE analysis indicates differences in the compositions of microbiota in feces and cecum between rats fed yacon tuber and rats fed FOS and control diet. Lower number of DGGE bands in experimental groups showed the substrates increased the growth of specific intestinal bacteria. A UPGMA dendrogram based on the Dice similarity coefficients of samples taken from cecum at week 4 generated two robust clusters, a group of rats fed control and group rats fed two experimental diets. Temporal transition of fecal microbial community was clearly shown by MDS scatter plot, changes of community in FOS diet occurred sooner than on yacon diet. From the sequencing analysis; *B. pseudolongum*, and *Barnesiella* spp. were found predominantly in rats fed yacon tuber while *B. animalis* and *L. acidophilus* were found both in FOS and yacon diet. The genus *Barnesiella*, up to now has not been reported to be associated with yacon or FOS fermentation.

## **3. Conclusion**

Our result demonstrated that the gut microenvironment of rats fed yacon tuber were clearly differed from that of FOS and control diet. Yacon tuber exhibited a prebiotic effect by promoting the growth of *Lactobacilli* and *Bifidobacteria* in the rat cecum; resulting in greater concentration of SCFA and lower pH. We obtained a band with sequence most closely related to *Barnesiella* spp., this genus has not been reported to be involved in yacon or FOS fermentation using the conventional cultivation technique.