

Effect of *Clostridium butyricum* MIYAIRI 588 supplementation on the intestinal microbiota and meat quality of fattening pigs

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Objectives: Pork production accounts for approximately one-third of the total meat production worldwide and is one of the most crucial livestock production systems. Efficient meat production is required to meet the increasing demand for livestock products due to human population growth. Recently, probiotics have attracted increasing attention since antibiotic use as growth promoter was banned in the European Union. Furthermore, the relationship between gut microbiota and livestock growth performance has also received considerable attention. Although there are several studies on the effects of *Clostridium butyricum* administration on the gut microbiota in piglets after weaning, similar studies in growing pigs are limited. Therefore, this study aimed to investigate the effect of *C. butyricum* MIYAIRI 588 (CBM588) on the intestinal microbiota composition and meat quality of fattening pigs.

Materials and Methods: This study comprised 20 pigs housed in a pig experimental facility at Tokushima University. They were divided into two groups (n=10 each): one group was fed a basic diet (control group), and the other was fed a basic diet supplemented with CBM588 (2.5×10^8 colony-forming units/kg; treatment group). The experimental period was from 88 days of age until slaughter. Fecal samples were collected at the end of the study, and the contents of the ileum, cecum, and colon were collected after slaughter. All samples were used for 16S rRNA gene sequence analysis. Meat quality was determined by chemical composition and physical characteristic analyses of the longissimus dorsi muscles.

Results and Discussion: The α -diversity of microbiota in the ileal contents was lower than that in the cecal and colonic contents and fecal samples ($p < 0.05$). A significant shift in β diversity was detected among the intestinal segments from which the digesta had been collected. However, CBM588 administration did not significantly affect the α - and β -diversity of microbiota in the fecal samples and intestinal contents, regardless of the collection site. Noteworthy, at the phylum level, the relative abundance of Actinobacteria in the cecal and colonic contents and fecal samples was higher in the treatment group than in the control group ($p < 0.05$). Moreover, at the genus level, the relative abundance of *Lactobacillus* and *Bifidobacterium* in the cecal and colonic contents and fecal samples was higher in the treatment group than in the control group ($p < 0.05$). Meat quality analysis did not show significant differences in the physical properties and chemical composition between the groups, except for pliability, which was lower in the treatment group than in the control group.

Conclusions: These results indicate that CBM588 administration does not affect the diversity of the intestinal bacterial microbiota but induces the growth of specific bacteria including some genera reported as beneficial. Our results also confirm that CBM588-related intestinal microbiota changes extend throughout the large intestine below the cecum. Hence, even in relatively stable gut microbiota ecosystems, CBM588 administration may contribute to the growth of beneficial bacteria in the host.

Key words: Pig, Gut microbiota, Microbiome, Probiotics, *Clostridium butyricum*