

ORIGINAL ARTICLE

rRNA-based analysis to monitor succession of faecal bacterial communities in Holstein calvesY. Uyeno^{1,2}, Y. Sekiguchi² and Y. Kamagata^{2,3}

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Keywords

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Abstract

Aims: To quantitatively analyse the faecal bacterial communities of Holstein calves and track their succession up to 12 weeks of age.

Methods and Results: Faecal samples obtained from four female Holstein calves were analysed by the RNA-based, sequence-specific rRNA cleavage method. Twelve scissor probes covering major rumen bacterial groups were used, detecting c. 60–90% of the total 16S rRNAs. At 1 week of age, 16S rRNAs from members of the *Bacteroides-Prevotella* group (40.0% of the total 16S rRNAs), *Faecalibacterium* (21.7%), the *Clostridium coccoides-Eubacterium rectale* group (16.7%) and the *Atopobium* cluster (10.9%) were detected at high levels. Throughout the 12-week period, rRNAs of the *Bacteroides-Prevotella* and the *Cl. coccoides-Eu. rectale* groups constituted the major fraction of microbiota (c. 50–70% of the total). The relative abundances of the *Atopobium* cluster, *Faecalibacterium*, and some probiotic bacteria (such as those of the genera *Lactobacillus* and *Bifidobacterium*) decreased as the animal aged. Instead, an uncultivated rumen bacterial group, as well as *Ruminococcus flavefaciens* and *Fibrobacter* emerged at the detectable levels (1–2%) in the faeces sampled at a postweaning age. In addition, certain bacterial groups that were not covered by the probe suite increased as the animals aged.

Conclusions: Young calves undergo dynamic changes in their intestinal bacterial community during the first 12 weeks of life. As young ruminants undergo metabolic and physiological development in their digestive tracts in the transition from a monogastric to a ruminant animal at an early age, the intestinal bacterial community may reflect such development.

Significance and Impact of the Study: The succession of the bacterial communities in the faeces of calves was quantitatively monitored in the present study for the first time. The approach used here was demonstrated to be a useful means for determining the populations of predominant faecal bacterial groups in a variety of calf experiments in response to diet, stress and disease.

Introduction

The period from birth to complete weaning at 6–8 weeks of age represents the period of greatest stress and metabolic challenge to young calves. During this critical stage, calves make the metabolic, nutritional, and behavioral changes to become a functional ruminant (Davis and

Drackley 1998). The indigenous intestinal microflora of mammals is involved in host nutrition, mucosal defense and host immunity and hence influences the performance of the animal (Van Loo *et al.* 2004; Zoetendal *et al.* 2004). The intestines of newly born animals and humans are sterile, but colonization of the gastrointestinal (GI) tract starts immediately at birth (Favier *et al.* 2002).