

Subtropical Forages Differentially Influenced the Ruminal Fermentation and Microbial Community of Jersey Cow In Vitro

Bo Lin

College of Animal Science and Technology, Guangxi University, Nanning, Chin

Abstract

Oven dried cassava residues, corn straw silage, elephant grass and sugarcane tail silage were used as substrates to do a 24 h of incubation with a 100 ml glass syringe at 39°C. Gas production was recorded at the end of incubation and ruminal fluid was harvested to determine volatile fatty acids (VFA) using gas chromatograph, quantify microbial populations using real time PCR, and analyze microbial community using high throughput sequencing. Results showed in vitro incubation not only decreased population of bacteria, fungi, methanogen and some cellulolytic bacteria ($P < 0.05$), but also increased diversity of bacteria, reversed Firmicutes to Bacteroidetes ratio, and decreased abundance of *Prevotella*, *M. gottschalkii* and *Entodinium*. Gas production, acetate/propionate ratio and abundances of *Succiniclasticum*, *Entodinium* and *Diploplastron* were the highest, while total VFA concentration, fungal and cellulolytic bacterial populations, and abundances of *Methanomassiliicoccales* and *Ostracodinium* were the lowest with cassava residues ($P < 0.05$). Influence on fermentation pattern and microbiota of three gramineous substrates was similar, but inoculum incubated with sugarcane tail silage had higher abundance of *Methanomassiliicoccales* and *Diplodinium*. In conclusion, cassava residues which is a low neutral detergent fiber forage showed a completely different fermentation pattern and influence on microbe community indicated NDF was the most crucial factor to determine microbial community in vitro.

Forage usually makes up half or more of the ruminants' diet, influencing dry matter intake and microbial community composition both in vivo and in vitro. On account of distinct nutritive profile, different forages have discrete impacts on ruminal fermentation and microbiota. Changes in the ruminal microbial community induced by forage can provide a clear understanding of interaction between forage and microbes. Due to high biodiversity in tropical and subtropical areas, a variety of roughages is available for the ruminants. However, sustainably available roughage sources used for the ruminants on commercial scale are still the by-products of agricultural cultivations. Among those, cassava starch residues, corn straw silage, sugarcane tail

silage and elephant grass are the typical representatives and widely used in the southern China. Cassava starch residue is a source of non-forage fiber which has potential to be used as both beef and dairy cattle diet, as its dry matter contains low fiber but high soluble carbohydrates. Corn straw is a by-product of edible corn produced in the subtropical areas and intensively used as forage. Sugarcane is the most productive crop in the tropical areas, and its tail that contains most of leaves is a nutritious forage for the ruminants. Elephant grass is a fast-growing plant and famous for its higher production in the subtropical areas. It is extensively used as a stable forage source for the ruminants. The microbes inhabiting the gut/rumen are known to impose protective effects and

nutritional benefits to the host and due to their superior metabolic potentials compared to the host they are rightly considered equivalent to an organ [12,13]. Composition of the microbial community in the rumen and the end products of fermentation depend on the diet fed to the animals [14,15]. To study the impacts of forage source on ruminal fermentation, the in vitro techniques are widely used to realize more controlled and reproducible conditions, compared to in vivo experiments [16]. On the other hand, the advancement in latest microbial molecular techniques, in particular, high throughput sequencing technology have enabled to explore the rumen microbial consortium with higher precision.

Although, nutritional values and digestibility of these typical subtropical forages have been highly explored previously in both in vitro and in vivo studies, but their differential impacts on the ruminal microbial community are poorly researched due to limitations of microbial molecular research techniques in the past. Thus, the primary objective of this study was to examine the impacts of four typical subtropical forages on the ruminal fermentation, microbial population and community composition. Secondly, this study also compared the changes in microbial community composition before and after the incubation to elucidate the effect of fiber structure on ruminal microbiota and fermentation.

Keywords: Subtropical forages; In vitro fermentation; Microbial community; Microbial population

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E-mail: linbo@gxu.edu.cn