

RESEARCH

Kyawt, Y.Y.; Aung, M.; Xu, Y.; Zhou, Y.; Li, Y.; Sun, Z.; Zhu, W.; Cheng, Y. **Methane production and lignocellulosic degradation of wastes from rice, corn and sugarcane by natural anaerobic fungi-methanogens co-culture.** *World Journal of Microbiology and Biotechnology* 2024, 40, 109, doi:10.1007/s11274-024-03938-8.

Abstract: Biomass from agriculture, forestry, and urban wastes is a potential renewable organic resource for energy generation. Many investigations have demonstrated that anaerobic fungi and methanogens could be co-cultured to degrade lignocellulose for methane generation. Thus, this study aimed to evaluate the effect of natural anaerobic fungi-methanogens co-culture on the methane production and lignocellulosic degradation of wastes from rice, corn and sugarcane. Hu sheep rumen digesta was used to develop a natural anaerobic fungi-methanogen co-culture. The substrates were rice straw (RS), rich husk (RH), corn stover (CS), corn cobs (CC), and sugarcane baggage (SB). Production of total gas and methane, metabolization rate of reducing sugar, glucose, and xylose, digestibility of hemicellulose and cellulose, activity of carboxymethylcellulase and xylanase, and concentrations of total acid and acetate were highest ($P < 0.05$) in CC, moderate ($P < 0.05$) in RS and CS, and lowest ($P < 0.05$) in SB and RH. The pH, lactate and ethanol were lowest ($P < 0.05$) in CC, moderate ($P < 0.05$) in RS and CS, and lowest ($P < 0.05$) SB and RH. Formate was lowest ($P < 0.05$) in CC, RS and CS, moderate ($P < 0.05$) in SB, and lowest ($P < 0.05$) in RH. Therefore, this study indicated that the potential of methane production and lignocellulosic degradation by natural anaerobic fungi-methanogens co-culture were highest in CC, moderate in RS and CS, and lowest in SB and RH.

Huuki, H.; Vilkki, J.; Vanhatalo, A.; Tapio, I. **Fecal microbiota colonization dynamics in dairy heifers associated with early-life rumen microbiota modulation and gut health.** *Frontiers in Microbiology* 2024, 15, doi:10.3389/fmicb.2024.1353874.

Abstract: Early-life modulation of rumen microbiota holds promise for enhancing calf growth, health, and long-term production in ruminants. However, limited attention has been given to the impact of rumen microbiota modulation on the establishment of hindgut microbiota. In this study, fecal microbiota development was examined in identical twin calves for 12 months. The treatment group (T-group) received adult cow fresh rumen liquid inoculum during the pre-weaning period, while the control group did not (C-group). The effects of inoculum were assessed on calf gut health and as microbial seeding route into the hindgut. The early rumen modulation had no effect on age-related fecal microbiota development. The fecal bacterial community evolved gradually following dietary changes and categorized into pre-weaning and post-weaning communities. Bacterial richness increased with age and stabilized at month 9, while between-sample variation reduced in post-weaning samples. Archaeal load in fecal samples increased after month 4, while archaeal richness increased and stabilized in both groups by month 9. Between-sample similarity was higher during the pre-weaning period, with increased dissimilarity from month 4 onward. Anaerobic fungi were detected in feces at month 4, with richness peaking at month 7. Before month 6, fungal community composition distinctly differed from mature communities. When colostrum, calf rumen, and donor inoculum were evaluated as seeding sources for hindgut colonization, the calf's own rumen was identified as the primary seeding source for fecal bacteria and fungi. Colostrum was a source for several bacteria detected in feces, but these were of temporary importance until weaning. The donor inoculum had limited impact on gut health as diarrhea rates were similar between the T-group and C-group. In conclusion, early-life microbiota modulation shows potential in ruminant development. However, a more targeted approach with bacteria adapted to the hindgut environment may be necessary to modulate hindgut effectively. This research contributes to our understanding of the complex relationship between gut microbiota and calf health and growth.