

**RESEARCH**

Scheftgen, A.J.; Skarlupka, J.H.; Jewell, K.A.; Suen, G. **Correlating feed efficiency with ruminal bacterial, fungal, and archaeal community composition in dairy cows over two lactations**. *Dairy* 2025, 6, 8, doi: 10.3390/dairy6010008.

**Full text access:**

<https://www.mdpi.com/2624-862X/6/1/8>

**Abstract:** Dairy cows rely on their complex rumen microbial community to convert host-indigestible feed into nutrients usable for host growth, maintenance, and milk production. Previous work by our group found that the rumen bacterial community is dynamic over the course of two lactations and that cows with high and low milk production efficiency (MPE) have different taxa associated with either phenotype. Here, we characterized the ruminal fungal and archaeal communities to determine if these microbial populations exhibit properties similar to that of the rumen bacteria with respect to MPE over time. Our results show a decrease in fungal diversity over the course of both lactation cycles with an increase during the transition period. The fungal community had only a few taxa associated with efficiency. For the ruminal archaea, we found no change in diversity across both lactation cycles and only taxa in the genus *Methanospora* were found to be more abundant in high-MPE cows. Given that our previous study used 454 pyrosequencing, we also sought to determine if a resequencing of these communities using Illumina-based technology would alter our previous findings. We found that resequencing showed no significant deviation from our original broad conclusions, with the exception of some minor taxonomic associations.

Liang, J.; Lv, L.; Sun, L.; Chen, L.; Zhang, G.; Zhang, P. **Metagenomic analysis reveals the community composition and functional characteristics of ruminal microbes in fermenting lignocellulosic biomass in vivo and in vitro.** *Journal of Environmental Chemical Engineering* 2025, 13, 115851, doi: 10.1016/j.jece.2025.115851.

**Full text access:**

<https://www.sciencedirect.com/science/article/abs/pii/S2213343725005469>

**Abstract:** This study aims to reveal the microbial community, carbohydrate-active enzymes, and functional genes during in vivo and vitro ruminal fermentation of corn stover by metagenomic analysis. Results showed that degradation of corn stover showed high degradation efficiency in both situations. Degradation efficiencies of cellulose and hemicellulose reached 40.2 % and 50.4 %, and 54.3 % and 61.2 %, respectively, during in vitro and in vivo fermentation. *Ruminococcus*, *Prevotella*, *Butyrivibrio*, *Fibrobacter*, *Piromyces*, *Neocallimastix*, and *Orpinomyces*, etc. were the core bacterial and fungal genera. Principal co-ordinates analysis further confirmed that structure of fungal and bacterial communities dynamically changed, and the change patterns of community were different during in vivo and vitro fermentation. Co-occurrence network showed the complex competitive and synergistic relationship between fungi and bacteria. Most carbohydrate-active enzymes families of in vitro fermentation were lower than those of in vivo fermentation after 12 h fermentation, but higher in later fermentation. Expression of functional genes related to acetate production in vitro fermentation was higher than that of in vivo fermentation, and propionate production were lower than of in vivo fermentation. These findings provide insights and guidance for application of ruminal microbes in anaerobic fermentation.

**REVIEW**

Sreeremya, S. **Neocastilligmycota SP in Cowdung Helping in Biomethanation.**  
*Journal of Research in Microbiology and Immunology* 2025, 7, 7.

**Full text access:**

[https://www.researchgate.net/publication/388362839\\_Neocastilligmycota\\_SP\\_in\\_Cowdung\\_Helping\\_in\\_Biomethanation-Review?tp=eyJjb250ZXh0Ijp7ImZpcnN0UGFnZSI6ImhvbWUiLCJwYWdlIjoic2VhcmNoIiwicG9zaXRpb24iOiJwYWdlSGVhZGVyIn19](https://www.researchgate.net/publication/388362839_Neocastilligmycota_SP_in_Cowdung_Helping_in_Biomethanation-Review?tp=eyJjb250ZXh0Ijp7ImZpcnN0UGFnZSI6ImhvbWUiLCJwYWdlIjoic2VhcmNoIiwicG9zaXRpb24iOiJwYWdlSGVhZGVyIn19)

**Abstract:** Mammalian herbivores do not produce the cellulolytic or hemi-cellulolytic enzymes to degrade ingested plant material; instead they mainly rely on symbiotic associations with microorganism (i.e. anaerobic fungi, bacteria, the methanogenicarchaea and protozoa) that reside within their gut. Within this microbial consortium, the anaerobic fungi are known to be key players in the degradation of the lignocellulosic plant fibre in the rumen.