

RESEARCH

Deng, M.; Sun, L.; Yu, C.; Li, C.; Zhang, Q.; Yang, S.; Yang, S.; Yu, C. **Altitude drives the divergence of rumen fungal communities between cattle and yak in Yunnan plateau.** *Microbial Pathogenesis* 2026, 213, 108358, doi: 10.1016/j.micpath.2026.108358.

Full text access:

<https://www.sciencedirect.com/science/article/pii/S0882401026000847>

Abstract: To investigate the effects of host species and altitude differences on the rumen fungal community (RFC), this study selected Zhongdian yellow cattle and Zhongdian yaks from high-altitude regions (Shangri-La, 3600 m) and Jiangcheng yellow cattle and Jiangcheng water buffalo from low-altitude regions (Jiangcheng, 1100 m) in Yunnan Province as research subjects. The ITS2 high-throughput sequencing (HTS) technology was applied to analyze the composition and diversity of their rumen fungi. The results showed no significant differences in the RFC between different host species within the same altitude environment ($P > 0.05$), whereas significant differences were observed in the fungal community structure between different altitude groups ($P < 0.01$). This indicates that under consistent dietary conditions, altitude is the primary factor driving differences in the RFC, while the influence of host species is relatively limited. Our study provides a theoretical basis at the fungal level for understanding the mechanisms of interaction between plateau ruminants and microorganisms.

Koitto, T.; Pohto, A.; Sidorova, E.; Vuong, T.V.; Penttilä, M.; Master, E.R. **Functional characterization of a dockerin-containing expansin-like protein from the anaerobic fungus *Neocallimastix californiae***. *Biotechnology for Biofuels and Bioproducts* 2026, doi:10.1186/s13068-026-02744-8.

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<https://link.springer.com/article/10.1186/s13068-026-02744-8>

Abstract: (Background) Anaerobic microbes produce multienzyme complexes known as cellulosomes to enhance the degradation of cellulosic substrates. These complexes localize diverse enzymes onto a protein scaffold, where proteins are anchored by dockerin domains. Although the cellulosomes of anaerobic fungi incorporate a broad array of cellulolytic enzymes, they remain largely unexplored. Notably, some fungal cellulosomes reportedly comprise expansin-like proteins with potential to disrupt cellulose networks. While two bacterial cellulosomal expansin-like proteins have been characterized, no fungal cellulosomal expansin-like proteins have been functionally characterized to date. (Results) Sequence analyses of expansin-like proteins from the anaerobic fungus *Neocallimastix californiae* revealed similar N-terminal domains among proteins with or without appended dockerins. Those without dockerins, however, consistently lacked the first conserved aromatic residue that forms the substrate binding surface of the C-terminal family 63 carbohydrate binding module. One cellulosomal expansin-like protein from *N. californiae* (*NcaEXLX1*) was recombinantly expressed with and without (*NcaEXLX1tr*) the dockerin domains. The adsorption characteristics of *NcaEXLX1* and *NcaEXLX1tr*, and impact on cellulase (*Cel7B*) activity, were then investigated using quartz crystal microbalance with dissipation (QCM-D). *NcaEXLX1* exhibited higher binding to cellulose nanofibrils (CNF) compared to *NcaEXLX1tr*. Despite the lower binding of *NcaEXLX1tr* to CNF, both *NcaEXLX1* and *NcaEXLX1tr* enhanced the action of *Cel7B* to similar extents. (Conclusions) This study reports the production and characterization of a fungal cellulosomal expansin-like protein. The corresponding *NcaEXLX1* protein and truncated variant were shown to enhance the activity of an endoglucanase, similar to observations made with non-cellulosomal expansin-like proteins. Notably, the improvement in cellulase activity upon the addition of *NcaEXLX1* or *NcaEXLX1tr* was not correlated to extent of substrate binding.