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Shi, Q.; Wang, D.; Duan, C.; Li, Y.; Tu, T.; Zhu, W.; Cann, I.; Cheng, Y. **Anaerobic fungal carbohydrate-binding modules exhibit preference for fusion to hemicellulases and enhance their enzymatic hydrolysis.** *Journal of Agricultural and Food Chemistry* 2026, doi:10.1021/acs.jafc.5c11503.

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Abstract: As auxiliary components of the carbohydrate active enzymes (CAZymes), carbohydrate-binding modules (CBMs) influence the enzymatic hydrolysis of substrates. To investigate the role of anaerobic fungal CBMs in lignocellulose degradation, an architectural analysis of bacterial and fungal CBM-containing protein sequences was completed. Results indicated that 67.9% of the fungal CBMs were incorporated into the plant-biomass-degrading enzymes and 51.1% of the anaerobic fungal CBMs were biased to be fused with the hemicellulose-degrading enzymes. Based on the transcriptomic data of anaerobic fungus *Pecoramyces ruminantium* F1, three upregulated CBM-fused hemicellulose-degrading enzyme gene clusters were identified. Results suggested that the fused CBMs retained the enzymatic function of the associated CAZymes. Importantly, the CBM1 domains of acetyl xylan esterase (AxeA16138) and α-L-arabinofuranosidase (AraA02173) possessed a crucial role to promote the xylanase-mediated hydrolysis of hemicellulose. These results demonstrated that anaerobic fungal CBMs harbor substantial potential to enhance hemicellulose degradation.

Xu, J.; Ma, J.; Lin, H.; Yan, S.; Niu, H. **Metagenomic and metabolomic analyses of rumen fiber digestion in Mongolian cattle fed fresh grass versus hay.** *Microbiology Spectrum* 2026, *0*, e03051-03025, doi:10.1128/spectrum.03051-25.

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Abstract: Mongolian cattle exhibit exceptional roughage tolerance due to their rumen microbiome's robust fiber-degrading capacity, enabling efficient utilization of low-quality forage under the Mongolian Plateau's seasonal fluctuations. This study compared rumen microbial composition, CAZyme profiles, fermentation parameters, and metabolic pathways in cattle fed fresh grass (FG) versus hay to elucidate microbe-metabolite interactions underlying fiber digestion. Thirty non-pregnant female Mongolian cattle (460 ± 35 kg, 3–4 years old) were randomly divided into two groups (n = 15/group): one grazed on FG, the other housed and fed autumn-harvested hay (HG). Six animals per group were subsampled for rumen fluid collection and multi-omics analyses (n = 6/group, total n = 12). Compared with the FG group, the HG group showed an increased molar proportion of acetate and a higher acetate-to-propionate ratio, along with reduced molar proportions of propionate and butyrate in rumen fermentation parameters. Metagenomic analysis revealed a higher abundance of Bacteroidales bacteria and anaerobic fungi (including *Neocallimastix* sp. JGI-2020a and *Piromyces* sp. E2) in the HG group. Functional annotation further indicated enriched carbohydrate metabolism pathways in the HG group, along with a greater diversity of CAZymes, particularly those involved in hemicellulose and pectin degradation. Metabolomics identified 13 differentially abundant carbohydrate metabolites, with gluconolactone upregulated in the HG group. Additionally, carbohydrate metabolism pathways identified in the metabolome corroborated the reliability of the metagenomic functional annotations. Correlation network analysis revealed positive associations of Bacteroidaceae bacteria, *Neocallimastix* sp. JGI-2020a, and *Piromyces* sp. E2 with acetate, hemicellulose-degrading GHs, and carbohydrate metabolic pathways. In conclusion, hay feeding enhanced ruminal fiber degradation in Mongolian cattle through increased Bacteroidales and anaerobic fungi, diversified CAZymes (especially hemicellulases/pectinases), and upregulated carbohydrate metabolism, reflecting microbial adaptation to low-quality forage.