

RESEARCH

Ullah, A.; Khalil, A.A.K.; Ali, S. **Anaerobic gut fungi as biocatalytic platforms for circular lignocellulosic biorefineries: Enzymes, consortia, process integration and biosafety.** *Biomass and Bioenergy* 2027, 217, 110047, doi: 10.1016/j.biombioe.2026.110047.

Full text access:

<https://doi.org/10.1016/j.biombioe.2026.110047>

Abstract: Lignocellulosic residues are abundant renewable carbon sources, but their microbial conversion remains constrained by plant-cell-wall recalcitrance, enzyme cost, pretreatment severity and incomplete carbon recovery. Anaerobic gut fungi of the Neocallimastigomycota provide a distinctive biological solution because they combine invasive rhizoidal growth, extensive carbohydrate-active enzyme repertoires, fungal cellulosomes and hydrogenosome-linked fermentative metabolism. These traits allow direct colonization and deconstruction of untreated or mildly pretreated plant biomass under oxygen-free conditions. This review integrates taxonomy, enzyme architecture, syntrophic metabolism, process engineering and biosafety considerations to evaluate anaerobic gut fungi as practical biocatalysts for circular biorefineries. Particular attention is given to the transition from discovery-oriented enzyme studies toward programmable fungal-bacterial and fungal-archaeal consortia, consolidated hydrolysis, feedstock-specific pretreatment, product steering and reactor-scale control. The evidence indicates that anaerobic gut fungi are most promising where mechanical penetration, low-enzyme operation and compatibility with wet agricultural residues are required. However, industrial translation requires faster cultivation, stable inoculum systems, improved genetic and omics tools, rigorous containment, and quantitative techno-economic and life-cycle assessment. A development roadmap is proposed for converting these organisms from biological curiosities into safe, standardized and regionally adaptable platforms for biomass valorization. The revised synthesis emphasizes strain- and enzyme-tool development aimed at higher-yield cellulase-complex secretion and an integrated full-chain biorefinery concept linking low-severity pretreatment, fungal hydrolysis, partner metabolism, product recovery and residue

valorization. It further separates experimentally demonstrated anaerobic fungal functions from proposed programmable configurations and introduces quantitative benchmarks for conversion, residence time, carbon recovery, process stability and biosafety-governed scale-up.



RESEARCH

Wang, W.; Tian, Y.; Guo, W.; Dong, Y.; Mi, J.; Ahmad, A.A.; Jing, X.; Long, R.; Sun, X.; Deng, Q., et al. **Age-related shifts of dissolved hydrogen and its impact on rumen fermentation dynamics and microbial communities in goats (*Capra hircus*)**. *BMC Microbiology* 2026, 26, 778, doi:10.1186/s12866-026-05563-x.

Full text access:

<https://doi.org/10.1186/s12866-026-05563-x>

Abstract: The rumen is a complex anaerobic fermentation ecosystem in which microbial communities undergo dynamic changes during host development, influencing fermentation efficiency, hydrogen utilization, and methane (CH₄) production. However, how rumen maturation reshapes hydrogen redistribution and the associated microbial interactions remains poorly understood. This study compared rumen fermentation characteristics, microbial communities (bacteria, archaea, fungi, and protozoa), and Gibbs free energy profiles between 0.5-year-old and 2-year-old goats to elucidate age-related changes in hydrogen metabolism. Adult goats exhibited significantly higher concentrations of dissolved methane (dCH₄), dissolved hydrogen (dH₂), and total short-chain fatty acids (SCFAs), including acetate, propionate, and butyrate, than young goats ($P < 0.05$). Thermodynamic analyses indicated that glucose fermentation and methanogenesis were energetically feasible under rumen conditions ($\Delta G < 0$), while age-related differences in Gibbs free energy (ΔG) suggested altered hydrogen partitioning during rumen maturation. The mature rumen was characterized by enrichment of carbohydrate-fermenting microorganisms, particularly *Segatella*, *Anaeroplasma*, and the anaerobic fungus *Cyllamyces*, which were positively associated with glucose conversion pathways, metabolic hydrogen, and SCFA production. In contrast, younger goats showed enrichment of amino acid metabolism pathways together with microbial taxa associated with early rumen development, including *Christensenellaceae_R-7_group* and *Caecomyces*. The archaeal community also shifted with age, with significantly higher abundances of *Methanosphaera* and *Methanosarcina* in adult goats, consistent with enhanced hydrogen utilization through methanogenic pathways. Functional predictions further revealed enrichment of

carbohydrate and energy metabolism in adult goats, whereas amino acid metabolism predominated in young goats. These findings demonstrate that rumen maturation is accompanied by coordinated changes in microbial community structure, metabolic hydrogen redistribution, and thermodynamic characteristics, resulting in a transition from amino acid-oriented metabolism in young goats to a more specialized carbohydrate-fermenting ecosystem in adults. This integrated analysis identifies key microbial groups involved in hydrogen turnover and may provide new insights into the microbial mechanisms underlying rumen maturation, offering potential targets for improving feed efficiency and mitigating methane emissions in ruminants.



RESEARCH

Lawson, C.E.; Howard, J.P.; Lankiewicz, T.S.; Brown, J.B.; Singer, S.W.; Martín, H.G.; O'Malley, M.A. **Carbohydrate-active enzyme architectures reflect distinct fungal and bacterial strategies for lignocellulose conversion to volatile fatty acids.** *ISME Communications* 2026, 10.1093/ismeco/ycag262, doi:10.1093/ismeco/ycag262.

Full text access:

<https://doi.org/10.1093/ismeco/ycag262>

Abstract: Anaerobic fermentation with microbial communities is an emerging platform for converting lignocellulosic biomass to biofuels and bioproducts. The process relies on diverse anaerobic microbes that interact to deconstruct and convert lignocellulosic biomass into a range of products, such as volatile fatty acids (VFAs), through arresting methanogenesis during fermentation. However, defining the distinct functional roles played by various fungi and bacteria during anaerobic biodegradation remains poorly understood. Here, we performed parallel enrichment experiments from cow faeces, goat faeces, and anaerobic digester sludge, selecting for fungal or bacterial dominated communities that convert sorghum biomass into VFAs. Subsequently, we reconstructed metabolic networks across these enrichments using recovered bacterial metagenome-assembled genomes (MAGs), fungal isolate genomes, and genome-centric metatranscriptomics. This enabled direct comparison of the carbohydrate-active enzymes and fermentation pathways expressed by bacterial and fungal communities during lignocellulose conversion to VFAs. Our findings implicate diverse bacteria affiliated with the Bacteroidales and Lachnospiraceae in the direct conversion of lignocellulosic biomass to propionate and butyrate, respectively, whereas *Neocallimastix*-dominated fungal enrichments converted lignocellulose to lactate, acetate and formate. Analysis of carbohydrate-active enzymes revealed that bacterial and fungal communities primarily targeted the same dominant lignocellulosic substrates while employing distinct enzyme repertoires and multidomain carbohydrate-active enzyme architectures, highlighting complementary enzymatic strategies for accessing and deconstructing lignocellulosic biomass. We anticipate that these findings will help inform efforts to develop synthetic consortia with tailored functionality for low-cost conversion of lignocellulosic biomass to fuels and bio-based chemicals.

RESEARCH

Nehra, C.; Bhure, M.; Shah, T.; Pandit, R.; Patil, N.V.; Patel, A.K.; Kachhawaha, S.; Kumawat, R.N.; Joshi, M.; Joshi, C.G. **A diet containing *Moringa oleifera* alters the goat rumen microbiome and improves animal performance: an insight into bacteria, ciliates and rumen anaerobic fungi.** *Scientific Reports* 2026, 10.1038/s41598-026-68655-8, doi:10.1038/s41598-026-68655-8.

Full text access:

<https://doi.org/10.1038/s41598-026-68655-8>

Abstract: In the present study, we investigated the impact of *Moringa oleifera* feed on rumen and fecal microbial communities, including bacteria, ciliates, and anaerobic fungi in lactating goats (*Capra hircus*). The goats were divided into three groups based on dietary regimes: masoor straw (MS, $n = 10$), 20% moringa leaf meal (20% MLM, $n = 10$), and 30% moringa leaf meal (30% MLM, $n = 10$), and were maintained on this diet for 180 days. Animal performance parameters, daily feed and nutrients intake, fortnightly milk yield and body weight changes, and feed digestibility were measured. Rumen digesta and fecal samples were collected at the end of the experiment, and amplicon sequencing targeting the 16 S rRNA, ciliates-specific 18 S rRNA, and rumen anaerobic fungi-specific *ITS1* genes were carried out. Moringa-fed goats showed improved nutrient utilization efficiency, body weight gain (BWG), and milk production. Linear mixed-effect model analysis demonstrated that milk yield increased significantly from third fortnight onwards in both moringa -supplemented groups. In the rumen solid and liquid fractions, a moringa diet increased the *Bacillota*:*Bacteroidota* ratio, which could be associated with lower residual feed intake, improved metabolism, and thus better body weight gain and milk yield. An increase in the proteolytic bacterial phylum *Pseudomonadota* was observed with the moringa diet, which could be linked with high protein content in the moringa and the diet containing it. In the rumen solid fraction, several plant carbohydrate degraders and fermenters such as *Coprococcus*, *Ruminococcus*, *Succinimonas*, *Mediterraneibacter*, *Cellulosilyticum*, *Butyricicoccus*, *Cellulosibacter*, *Ruminobacter*, *Saccharofermentans*, *Agathobacter* were significantly abundant in the moringa-fed group (Kruskal-Wallis, Dunn's post hoc

test, adjusted $p \leq 0.05$). Ciliates like *Enoploplastron*, *Metadinium* and *Diploplastron* significantly increased (Kruskal-Wallis, Dunn's post hoc test, adjusted $p \leq 0.05$), while *Entodinium* was reduced in the rumen digesta samples of moringa feed groups. The fibre-degrading fungal genus *Neocallimastix* was less abundant in the rumen of the goats fed with moringa. Overall, these findings suggest that moringa supplementation positively influences feed digestion, nutrient intake, body weight gain, and milk yield, possibly through modulating rumen microbial communities in the lactating goats. These findings also highlight the complex interactions between moringa-based diet and rumen microbes, which may further improve goat health and milk production. However, future experiments focusing on the analysis of phytochemical composition of moringa leaves and rumen fermentation parameters would further strengthen these findings.

