RESEARCH

Nash, K.; Vinzelj, J.; Pratt, C.J.; Elshahed, M.S.; Youssef, N.H. ***Piromyces struthionis*, sp. nov., a new anaerobic gut fungus from the feces of ostriches.** *Mycologia* 2025, *117*, 1044-1056, doi:10.1080/00275514.2025.2549866.

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Abstract: Anaerobic gut fungi (AGF; *Neocallimastigomycota*) are a clade of basal, zoospore-producing fungi within the subkingdom Chytridiomyceta and known inhabitants of the alimentary tract of animal hosts. To date, 22 genera and 38 species have been described, most originating from herbivorous mammals. Here, we report on the isolation and characterization of a novel species of *Neocallimastigomycota* from an avian host. Multiple AGF strains were isolated from ostrich feces obtained from a local farm in Oklahoma (USA). All strains formed small, irregular-shaped white colonies with darker centers, displayed a filamentous rhizoidal structure with monocentric thallus developmental patterns, and produced mostly monoflagellated zoospores. The type strain produced terminal sporangia that were predominantly globose, often exhibiting cup-shaped and occasionally elongated sporangiophores. Sporangiophores characteristically exhibited constrictions at irregular intervals, giving them a beads-on-a-string-like appearance. Phylogenetic analysis using the partial nuc 28S rDNA D1–D2 regions (D1–D2 28S), ribosomal internal transcribed spacer 1 (ITS1), and RNA polymerase II large subunit (RPB1) grouped all isolates as a separate species within the genus *Piromyces*. Transcriptomic analysis indicated an average amino acid identity (AAI) of 80.34% (± 3.27%) between the type species and members of the genus *Piromyces* and 62.93–76.05% between the type species and all other AGF taxa outside *Piromyces*. Based on the morphology, phylogenetic analysis, and AAI values, we propose accommodating these strains as a novel species of *Piromyces*, for which the name *Piromyces struthionis* is proposed. The type strain for this species is Ost1.

Dai, H.; Gao, J.; Wei, Y.; Wang, Q.; Zhu, W.; Cheng, Y. **Mining expansin-like proteins from rumen microbiota and functional characterization of two anaerobic fungal expansin-like proteins.** *Journal of Animal Science and Biotechnology* 2025, *16*, 155, doi:10.1186/s40104-025-01287-6.

Full text access:

https://link.springer.com/article/10.1186/s40104-025-01287-6

Abstract: **Background:** Sustainable livestock production is essential for food security and environmental management. Lignocellulosic biomass can be used in animal feed, thereby reducing feed production costs and enhancing sustainability. Expansin-like proteins (ELPs) play essential roles in plant cell wall degradation, yet their functions remain largely underexplored in rumen microbes. The purpose of this study was to investigate the effects of rumen microbial ELPs on lignocellulose degradation. **Results:** This study systematically identified 396 ELPs within the rumen microbiota, uncovering remarkable diversity, particularly among anaerobic fungi. Three representative ELPs from *Pecoramyces ruminantium* F1 (*PF*Loos_1, *PF*SWO1_1, *PF*SWO2_1) were selected for biochemical characterization. While *PF*SWO2_1 could not be expressed, *PF*Loos_1 and *PF*SWO1_1 exhibited significant synergy with cellulases. The CBM10-containing *PF*SWO1_1 demonstrated superior thermal stability (up to 65 °C) and substrate affinity, increasing rice straw hydrolysis efficiency by 21.6% (reducing sugar yield) compared to cellulase alone. Structural analyses revealed that CBM10 enabled *PF*SWO1_1 to preferentially bind complex substrates, whereas the single-domain *PF*Loos_1 targeted simpler substrates. Notably, ELP pretreatment of corn stover significantly improved fermentation quality (pH and lactic acid) and nutritional value (neutral detergent fiber, acid detergent fiber, and water-soluble carbohydrates). **Conclusions:** These findings indicate that ELPs are abundant in the rumen and play a synergistic role in lignocellulosic biomass conversion.

Deshpande, P.; Dhakephalkar, P.K. **From gut to green energy: the essential role of anaerobic fungi in sustainable biofuel production.** *Sustainable Energy & Fuels* 2025, 10.1039/D5SE00240K, doi:10.1039/D5SE00240K.

Full text access:
https://pubs.rsc.org/en/content/articlelanding/2025/se/d5se00240k

Abstract: Anaerobic fungi, primarily found in the digestive tracts of herbivores, possess remarkable capabilities to degrade lignocellulosic biomass, positioning them as pivotal contributors to sustainable biofuel production. This review explores the enzymatic arsenal of these fungi, which includes cellulases, hemicellulases, and cellulosomes comprising glycoside hydrolases (GHs), carbohydrate esterases (CEs), polysaccharide lyases (PLs), and carbohydrate-binding modules (CBMs), emphasizing their superior efficiency in breaking down recalcitrant plant materials compared to other microorganisms. We highlight their potential in bioenergy applications, such as enhancing biomethane production through synergistic interactions with methanogens. Furthermore, the review underscores the unique characteristics of anaerobic fungi, including hydrogenosome-driven metabolism, their adaptation to diverse anaerobic environments, and their role in reducing the environmental impact of biofuel production. While challenges in cultivation, genetic engineering, and large-scale application persist, advancing research into these microorganisms could unlock innovative solutions for lignocellulosic biomass utilization, paving the way for a greener energy future. This review sheds light on their untapped biotechnological potential and offers a roadmap for addressing existing barriers to their application.