

REVIEW

Singh, G.; Lavika; Nandini; Abhay; Deepika; Thakur, N.; Kaura, R.; Kaur, S.; Saini, H.S.; Khulape, S.; et al. **Rumen mycobiome dynamics and dairy productivity: functional contributions of fungi to milk yield in bovine ruminants.** *Frontiers in Fungal Biology* 2026, Volume 7 - 2026, doi:10.3389/ffunb.2026.1878257.

Full text access:

<https://www.frontiersin.org/journals/fungal-biology/articles/10.3389/ffunb.2026.1878257/full>

Abstract: The rumen microbiome is a key factor influencing feed efficiency and milk production in ruminants. However, most studies have focused on the bacterial and archaeal components, with the fungal fraction of the rumen being relatively understudied. The unique ability of anaerobic rumen fungi of the phylum *Neocallimastigomycota* to colonize and degrade lignocellulosic biomass in the rumen through mechanical disruption of plant cell walls has now made them well known as important functional members of the rumen ecosystem. These fungi are armed with a plethora of carbohydrate-active enzymes degrading fiber and increase the availability of substrates for microbial fermentation. This leads to increased production of volatile fatty acids, especially acetate, which is a major precursor for milk fat production. Recent research evidence has indicated that rumen fungal communities are associated with feed efficiency, fermentation dynamics, and milk composition traits such as fat and protein content in bovine ruminants such as cattle and buffalo. However, most of the studies available are correlative, and the direct causal relationships between fungal activity and milk productivity are poorly delineated. High-throughput sequencing and multi-omics approaches have broadened our knowledge of fungal diversity and function; however, there are still limitations in reference databases and methodological biases. This review summarizes the current knowledge of the diversity, ecological roles, and functional contributions of anaerobic rumen fungi, with special reference to their association with milk production. It also highlights significant methodological and conceptual gaps and proposes future avenues for the integration of fungal ecology into microbiome-based approaches to improve dairy productivity. We need a holistic multi-kingdom view of the rumen microbiome to design efficient and sustainable dairy production systems.

RESEARCH

Morris, A.; Mills, T.; Miller, S.L.; Pratt, C.J.; Marek, S.; Wang, Y.; Elshahed, M.S.; Youssef, N.H.; Vinzelj, J. **Description of *Gopheromyces tardescens*, gen. nov., sp. nov., *Gigasporangiomyces pilosus*, gen. nov., sp. nov., *Kelyphomyces adhaerens*, gen. nov., sp. nov., and proposal of *Testudinimycetaceae*, fam. nov.** *International Journal of Systematic and Evolutionary Microbiology* 2026, 76, doi: 10.1099/ijsem.0.007196.

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Abstract: Anaerobic gut fungi (AGF, *Neocallimastigomycota*) represent a phylum of zoospore-producing fungi inhabiting the gastrointestinal tracts of herbivores. Twenty mammalian-affiliated genera (M-AGF) and two tortoise-affiliated genera (T-AGF) have been described so far. Here, we report on three additional novel T-AGF isolates obtained from Texas tortoises (*Gopherus berlandieri*; GX isolates) and African spurred or sulcata tortoises (*Centrochelys sulcata*; SR and TM isolates). Phylogenetic analysis using the D1-D2 regions of the large ribosomal RNA subunit (D1-D2 LSU), RNA polymerase II large subunit, internal transcribed spacer-1 (ITS-1) region and transcriptomics-enabled phylogenomic analysis clustered these strains into three distinct, deep-branching clades, closely related to previously described T-AGF genus *Testudinimycetes*. All isolates displayed filamentous rhizoidal growth patterns and produced monoflagellated zoospores. Unique morphological characteristics included the production of elongated, thick, nucleated structures in GX isolates, the formation of thin hair-like projections on sporangial walls in SR isolates and irregularly shaped sporangia in TM isolates. All strains grew optimally at 32–35 °C and showed distinct substrate utilization capacity (e.g. growth on pectin, chitin, galactose). LSU analyses revealed GX isolates as the first cultured representatives of tortoise-affiliated but previously uncultured lineage NY56, while SR and TM strains have not been encountered in prior culture-independent AGF surveys. We propose to accommodate these isolates in three new genera and species – *Gopheromyces tardescens* (GXA2), *Gigasporangiomyces pilosus* (SR0.6) and *Kelyphomyces adhaerens* (TM0.3). Furthermore, based on the ecological, physiological and phylogenetic distinctions between T-AGF and M-AGF, we propose to establish a new family (*Testudinimycetaceae*) to accommodate the genera *Testudinimycetes*, *Gopheromyces*, *Gigasporangiomyces* and *Kelyphomyces*.

RESEARCH

Vinzelj, J.; Morris, A.; England, E.E.; Elshahed, M.S.; Youssef, N.H. *Joblinomyces undulatus*, sp. nov., a novel anaerobic fungus from the feces of a Boer goat. *Mycologia* 2026, 1-10, doi:10.1080/00275514.2026.2687342.

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Abstract: Members of the phylum Neocallimastigomycota, often referred to as anaerobic gut fungi (AGF), primarily inhabit the gut of herbivorous animals. To date, 25 AGF genera have been described, but only five harbor more than one species. Here, we report on the isolation and characterization of novel AGF isolates from the feces of a Boer goat. The isolates formed small, mostly round, dense colonies on agar roll tubes and produced flaky, loosely clumped white biomass in liquid medium. Microscopic features included monoflagellated spherical zoospores and monocentric filamentous thallus. Sporangia were spherical or ovoid, although elongated and oddly shaped sporangia were also observed. Zoospore release was observed through ruptures in the sporangial wall. Phylogenetic analysis using the ribosomal internal transcribed spacer 1 (ITS1) and the 28S nuc rDNA D1–D2 region (28S) showed the isolates to be most closely related to *Joblinomyces apicalis*, the only described species in the genus *Joblinomyces* (0.00–1.30% divergence in ITS1, 2.50–3.82% in 28S). Transcriptomic sequencing and subsequent analysis of the *RPB1* (largest subunit of RNA polymerase II) region and average amino acid identity (AAI) value comparison clearly showed a high level of AAI sequence divergence (70.11–75.40%, average $72.53 \pm 1.43\%$) when compared with all other genera within the order Neocallimastigales. Based on morphological and phylogenetic analyses, we propose to accommodate these isolates as a novel species within the genus *Joblinomyces* and propose the name of *Joblinomyces undulatus*. The type strain for this species is JC3.3.