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Pratt, C.J.; England, E.E.; Vinzelj, J.M.; Youssef, N.H.; Elshahed, M.S. ***Anaeromyces corallioides*, sp. nov., a new anaerobic gut fungus from the faeces of cattle.** *International Journal of Systematic and Evolutionary Microbiology* 2025, *75*, doi:10.1099/ijsem.0.006719.

Full text access:

https://www.microbiologyresearch.org/content/journal/ijsem/10.1099/ijsem.0.006719

Abstract: We report on the isolation and characterization of three isolates of anaerobic gut fungi from a cattle faecal sample obtained in Stillwater, OK, USA. The isolates produced polycentric thalli with nucleated rhizomycelia, lobed appressorium-like structures, intercalary sporangia and constricted sausage-like hyphae. These morphological features are characteristic of members of the genus Anaeromyces. No zoospore production was observed during the isolation process or thereafter. The strains seemed to have propagated solely through their nucleated hyphae post initial enrichment. Phylogenetic analysis of the D1/D2 region of the large ribosomal subunit (D1/D2 LSU) rRNA, the ribosomal intergenic spacer region 1 (ITS1), RNA polymerase II large subunit (RPB1) and comparative average amino acid identity using transcriptomic datasets further confirmed the position of the type strain as a distinct member of the genus *Anaeromyces*, family *Anaeromycetaceae* and phylum *Neocallimastigomycota*. We propose to accommodate these isolates into a new species (*Anaeromyces corallioides*) within the genus *Anaeromyces*. The type strain is EE.1.

Neurauter, M.; Vinzelj, J.M.; Strobl, S.F.A.; Kappacher, C.; Schlappack, T.; Badzoka, J.; Podmirseg, S.M.; Huck, C.W.; Rainer, M. **Application of MALDI TOF and DART mass spectrometry as novel tools for classification of anaerobic gut fungi strains.** *Analytical and Bioanalytical Chemistry* 2025, 10.1007/s00216-025-05846-8, doi:10.1007/s00216-025-05846-8.

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Abstract: Anaerobic gut fungi (AGF) have emerged as promising candidates for optimized biogas and biofuel production due to their unique repertoire of potent lignocellulose-degrading enzymes. However, identifying AGF strains through standard fungal DNA barcodes still poses challenges due to their distinct genomic features. This study explored the applicability of matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI) and direct analysis in real-time (DART) mass spectrometry (MS) as alternative methods for AGF identification. Further, the capability of the methods to differentiate strains from different growth phases was investigated. The study found that both MALDI and DART were viable methods for AGF strain identification. MALDI proved to be a precise and robust technique for strain discrimination with prediction accuracies of 94% for unknown standard samples. Even at longer growth times (>3 weeks) MALDI achieved good prediction accuracies with 84%; however, younger cultures (72 h) were only predicted with 63% accuracy. The fast on-target lysis with minimal chemical demand yielded suitable spectra for strain differentiation. DART MS, while effective with prediction accuracies of samples with the same age of up to 93%, exhibited lower prediction accuracies for cultures of different ages, with 14% for young (72 h) and 71% for old (>3 weeks) samples. Further research could enhance the capabilities of these mass spectrometry methods for AGF identification and broaden their application to species-level discrimination and a wider range of AGF genera.

Cidan, Y.; Jia, W.; Hongzhuang, W.; Chang, X.; Yanbin, Z.; Kasib, K.M.; Wangdui, B.; and Li, K. **Composition and diversity of rumen mycobiota in Jiani yaks (*Bos grunniens* jiani): insights into microbial ecology and functions.** *Animal Biotechnology* 2025, *36*, 2476539, doi:10.1080/10495398.2025.2476539.

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https://www.tandfonline.com/doi/full/10.1080/10495398.2025.2476539#abstract

Abstract: This study aimed to explore the diversity and functions of rumen mycobiota in 14- (PLf) and 15-rib (DLf) Jiani yaks using ITS sequencing. A total of 1,079,105 and 1,086,799 filtered sequences were obtained for the PLf and DLf groups, respectively, with 491 ASVs common to both. No significant difference regarding the α-diversity of mycobiota within the two groups was observed. While β-diversity analysis indicated that the abundance of fifteen (15) genera in the PLf group and two (2) genera in the DLf group was found to be significantly different (p < 0.05). 16S rRNA sequencing results indicated that at the phylum level, in 14 ribs yaks Ascomycota, Basidiomycota, and Olpidiomycota, while in 15 rib yaks, Neocallimastigomycota, Mortierellomycota, and Rozellomycota were found to be significantly different ($p < 0.05$). At the genus level, *Rhodotorula*, *Kluyveromyces*, *Comoclathris*, *Arthrinium*, *Cladophialophora*, *Seimatosporium*, *Lambertella*, and *Sphacelotheca* in 14 rib yaks, and *Orpinomyces*, *Ustilago*, *Fusarium*, *Aspergillus*, *Caecomyces*, *Alternaria*, *Trichoderma* and *Acremonium* in 15 rib yaks were found to be significantly ($p < 0.05$) different. Predictive functional analysis based on ruminal fungal DNA sequences from 15-rib yaks (DLf) demonstrated that genes involved in energy metabolism were upregulated. This study sheds novel insights into how genetic variations influence gut mycobiota in Jiani yak.