



Book of Abstracts

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Microbial characterization of Tangel Humus and the influence of bioinformatic pipeline selection on metabarcoding results

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Tangel humus is characterized by strongly reduced carbon turnover and the accumulation of organic matter, resulting in the formation of thick organic layers. However, the underlying causes of this organic matter accumulation remain poorly understood, and insights into the microbial community within Tangel humus are still lacking. Thus, we conducted a detailed investigation of microbial diversity, activity and abundance across different layers of a Tangel humus profile in the Wetterstein mountains (Tirol, Austria), together with analysis of chemical properties.

Our results showed nutrient-poor conditions, especially in deeper humus depths, and a clear microbial zonation along the depth profile of 50 cm. Specifically, microbial diversity declined with depth, accompanied by pronounced shifts in microbial community composition. The observed decrease in microbial abundance and diversity, together with the established nutrient deficiencies in deeper depths, likely contributes to the reduced C-turnover and Tangel humus formation.

Because metabarcoding results depend on bioinformatic processing, we further evaluated how pipeline selection influences diversity outcomes. Since no universally standardized bioinformatic pipeline for metabarcoding analysis exists, results may vary depending on the chosen pipeline and parameter settings. Thus, we compared the processing of fungal ITS2 sequences derived from environmental samples using an ASV-inferring pipeline and an OTU-based pipeline with different similarity thresholds. This comparison revealed inconsistent diversity estimates and taxonomic composition when processing settings were not harmonized between pipelines. Across all approaches, differences in taxon abundance heterogeneity and detection capacity were evident. Based on these findings, we provide practical recommendations for improving reproducibility and comparability in future metabarcoding studies.