varied with sampling location and period, with the highest values recorded in the microbial mats of the lake on Irizar Island. Differences in growth on various culture media, together with molecular and quantitative analyses, indicate taxonomic, quantitative, physiological and biochemical heterogeneity of bacterial communities in freshwater microbial mats of the Maritime Antarctic.

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https://doi.org/10.30970/apmicro.2026.61

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REPRESENTATIVES OF THE GENUS *TRICHODERMA* COLONIZING ROTTING WOOD IN FOREST-PARK ZONES OF THE WESTERN FOREST-STEP OF UKRAINE

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Abstract. In this work we aimed to study mycobiome composition of species inhabiting decomposing wood of forest steppe area. Material was collected in several parts of deciduous forest. We obtained 115 Trichoderma strains by isolating fungi on PDA medium from decaying trees. Next Sanger sequencing of ITS region as well as TEF1 gene was performed for each strain in order to identify their species belonging.
Keywords: *Trichoderma*, Western Forest-Step of Ukraine.

Members of the genus *Trichoderma* are dominant xylotrophic and soil ascomycetes that play a key role in the degradation of lignocellulosic substrates and the maintenance of microbiological balance in forest ecosystems. In the mosaic ecosystems of the Western Forest-Steppe of Ukraine (particularly the Podillia and Opillia regions), the colonization of decaying wood by this group of microorganisms is determined by biotopic factors and the specifics of the mycocenosis.

In the decaying wood of deciduous (*Quercus robur*, *Fagus sylvatica*, *Carpinus betulus*) and mixed stands of the Western Forest-Steppe, species such as *Trichoderma harzianum*, *Trichoderma viride*, *Trichoderma koningii*, *Trichoderma atroviride*, and *Trichoderma citrinum* (teleomorph *Hypocrea citrina*) are most frequently identified. They act as secondary colonizers and saprotrophs, displacing primary wood-decaying basidiomycetes (Błaszczyk et al., 2015).

Colonization of dead wood is carried out through a powerful cellulolytic and hemicellulolytic enzymatic complex (endoglucanases, cellobiohydrolases, β-glucosidases). This enables *Trichoderma* to break down complex biopolymers of plant cell walls into simple sugars, accelerating humification and the carbon cycle in parkland and natural forest stands (Druzhinina et al., 2011).

In degraded wood, *Trichoderma* strains actively suppress the development of phytopathogenic and wood-decaying fungi through a threefold action: mycoparasitism: direct coiling around pathogen hyphae and secretion of lytic enzymes (chitinases, β-1,3-glucanases); antibiosis: secretion of volatile and non-volatile metabolites (leptomycins, trichocin-like compounds); competition: rapid substrate acquisition and nutrient uptake (Chan et al., 2023).

Preserving fallen logs and dead wood in the forest parks of the Western Forest-Steppe is a critical factor in supporting the species diversity of *Trichoderma*. These microorganisms not only accelerate the utilization of woody debris but also serve as a natural reservoir of antagonists against pathogens causing root and stem rots (*Armillaria* spp., *Heterobasidion* spp.).

The forest-park territory of the Western Forest-Steppe zone of Ukraine has previously attracted the attention of Ukrainian mycologists (Heluta et al., 2014), but its mycobiota has not been investigated using molecular methods. Therefore, the goal of this study is the identification and collection of species inhabiting decaying wood.

The research material – specifically fallen dead wood – was collected in forest-park zones belonging to the Western Forest-Steppe region of Ukraine.

Samples were placed on Petri dishes with PDA medium for fungal isolation. The germinating mycelium was subsequently subcultured onto fresh dishes until pure cultures were obtained. DNA extraction was performed on mycelium harvested from agar plates. PCR was carried out using two primer pairs (ITS1 and ITS4, ef1 and ef2) targeting the ITS region and the *TEF1-α* gene. Strain identification to the species level was conducted by comparing sequences with those available in the BLASTn database. Phylogenetic analysis was performed in MEGA11.

A total of 115 strains of the genus *Trichoderma* were isolated from the wood. Molecular analysis identified 9 species: *T. atrobrunneum*, *T. atroviride*, *T. citrinoviride*, *T. hamatum*, *T. harzianum*, *T. longipile*, *T. pararogersonii*, *T. pleuroticola*, and *T. simmonsii*. Out of the 115 strains, only 58 were identified to the species level. Based on *TEF* sequences, a Neighbor-Joining tree was constructed, with the majority of strains belonging to the Harzianum clade/group.

It is known that *Trichoderma* species are difficult to identify via molecular analysis (Jaklitsch & Voglmayr, 2015). Analyzing strains at the species level usually requires the amplification of a larger number of genomic fragments. In our study, the ITS region demonstrated poor utility as a species-level marker for *Trichoderma* strains from the studied area, whereas *TEF* exhibited higher specificity in identification.

Within the Hamatum species complex, ITS is not a sufficiently informative marker, whereas phylogenetic analyses based on the *TEF* gene fragment allow assigning *T. atrobrunneum* to the *T. pleuroticola* group in a sister clade to the Hamatum species group. All strains identified to the species level according to Cai and Druzhinina (2021) are amenable to molecular identification, which adds significance to our results.

Overall, nine species were identified, with *T. atroviride* being dominant. All strains not assigned to a specific species belong to the polyphyletic *T. hamatum* species complex, the identification of which requires further molecular and ecological analysis. *T. pararogersonii* is reported for the first time in Ukraine. The strains obtained in this study will be used for subsequent ecological analysis.

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https://doi.org/10.30970/apmicro.2026.62

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COMPARATIVE CHARACTERISTICS OF SOME THERMAL WATER MICROBIOTA SAMPLES OF WESTERN UKRAINE

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Abstract. The physicochemical characteristics of thermal waters, particularly temperature, mineralization, and concentrations of major ions and dissolved gases, represent major environmental