



Abstract

# Fungal Communities in Pine Deadwood <sup>†</sup>

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Forest management strategies aim to keep forests in the best possible condition. They may allow for adaptation to new conditions or promote proactive measures. As a result of ongoing climate change, the amount of dead wood in forests is increasing. Dead wood can provide food and habitat for many micro and macro-organisms such as fungi, bacteria, plants, insects, and small rodents. It, therefore, has a beneficial effect on increasing biodiversity. Fungi can decompose dead organic matter into simple compounds easily assimilated by plants. In this way, they influence the circulation of elements in nature. The decomposition of wood is widely observed, yet it still holds many secrets. Observing natural processes in nature and studying them in detail can contribute to a better understanding the biodiversity of organisms invisible to the naked eye.

The study aimed to analyse the species biodiversity of fungal communities inhabiting dead pine wood during the first stages of the decomposition process.

The study area was a stand of trees damaged as a result of the hurricane that occurred in Poland in August 2017. The Faculty of Forestry and Wood Technology of the Poznań University of Life Sciences and the Gniezno Forest District signed an agreement. As a result, a reference area in a damaged pine stand in the Gniezno Forest District was set apart. There are no plans for forest management in the area. In the establishment reference area, it is possible to study one of the most common processes in nature (wood decomposition) from its first stages.

Ten locations were designated in the study area, each of which contained three types of trees: windrows (trees lying with their root system on the ground), windbreaks (trees without a crown, with their root system underground), and standing trees (live, control).

Samples were taken in November 2018. The test material consisted of pieces of wood taken with a sterile Pressler auger, which were then ground in a cryogenic mill. DNA was extracted using the Bead-Beat purification Kit, and amplification of the ITS1 rDNA region was performed using specific primers. The PCR product was then sequenced using Illumina SBS technology (Genomed S.A.). The results were subjected to bioinformatics and statistical analysis, while the obtained sequences were compared with reference sequences deposited in the NCBI database and UNITE using the BLAST algorithm. Based on the available literature, the trophic functions performed by the identified taxa were determined.

NGS Illumina sequencing of pine wood samples yielded an average of 8150 OTUs per tree type. Of these, 69.23% were sequences of culturable fungi, 15.08% of non-culturable fungi, 9.30% were sequences of organisms belonging to other Kingdoms, and 5.79% of sequences not deposited in the database. The clusters whose species occurred most abundantly were Ascomycota, Basidiomycota, and a negligible number of Mucoromycota. A number of species common to each tree type were shown. With regard to trophic functions, the following were identified: saprotrophs, pathogens, lichenising fungi, and endotrophic.



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The results indicate a high taxonomic richness of the fungal communities in the first stages of the decomposition process. The greatest biodiversity is characterised by windrows. The proportion of species from the Ascomycota cluster dominates. Threatening root system pathogens such as *Armillaria* spp. and *Heterobasidion* spp. for young stands were identified. The conducted studies are a prelude to long-term observations on changes occurring in fungal communities during decomposition processes of dead pine wood.

**Supplementary Materials:** The following are available online at <https://www.mdpi.com/article/10.3390/IECF2022-13112/s1>.

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