Influence of habitat type on the soil mycobiome of European white elm (*Ulmus laevis* Pall.)

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INTRODUCTION

Understanding the factors influencing the mycobiome is essential because fungi are involved in various aspects of plant health, nutrition, and productivity in various environmental contexts. Mycorrhizal fungi are a specific part of soil mycobiome, which protects plants against detrimental environmental drivers. A comprehensive understanding of mycobiome assembly associated with elm trees is crucial for their sustainable management. European white elm (*Ulmus laevis* Pall.), one of Poland's native elm species, has been chosen for research as it is widely distributed across the country. Our understanding of the mycorrhizal symbiosis of elm trees is limited and until now, the mycorrhizal status of elms remains unclear. Addressing research questions will illuminate the soil mycobiome's role in *U. laevis* development across diverse environments.

MATERIALS AND METHODS

To determine the structure of soil fungal communities of *U. laevis* eighteen locations, representing both forest (riparian and mixed forests) and non-forest (forest nurseries, urban, rural, and postindustrial areas) habitats were chosen (Fig. 1.).

At each location, the same elm trees were sampled during the two sampling periods – spring and autumn 2021. Collected soil samples were analysed using Next Generation Sequencing on the MiSeq Illumina platform with ITS2 region of fungal rDNA (gITS7/ITS4 primers). Obtained DNA sequences were identified using UNITE and INSD databases and assigned to the trophic modes using the FungalTraits.

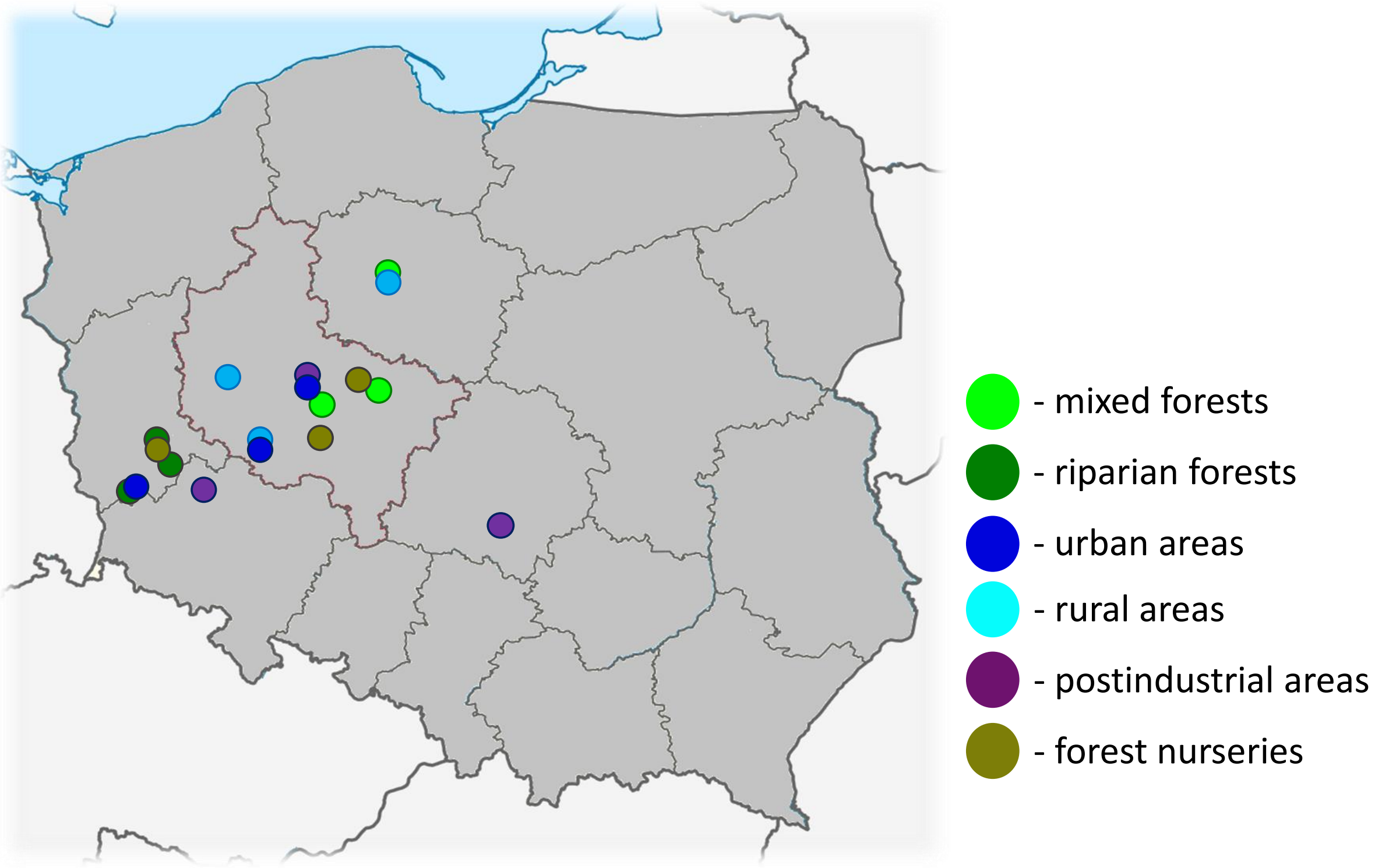

Fig. 1. Studied plots representing six different habitat types.

RESEARCH QUESTIONS

- **Q1.** How do different types of habitats (riparian forest and mixed forest, forest nursery, urban, rural, and postindustrial areas) shape soil mycobiome communities of *U. laevis*?
- **Q2.** How does the soil mycobiome community accompanying the roots of *U. laevis* respond to the season (spring, autumn 2021)?

RESULTS

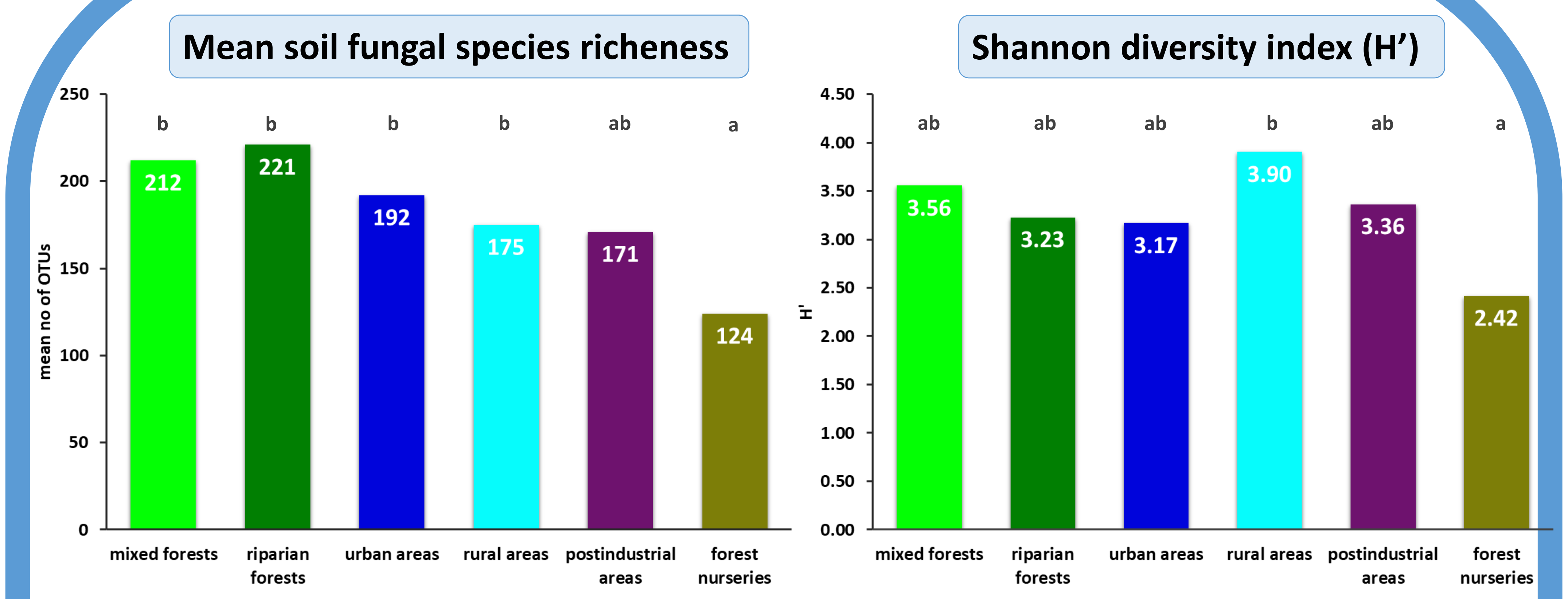

Fig. 2. Mean species richness and Shannon diversity indices of soil fungi from all trophic groups in different habitat types. Different letters indicate significant differences (Tukey's tests, $p < 0.05$).

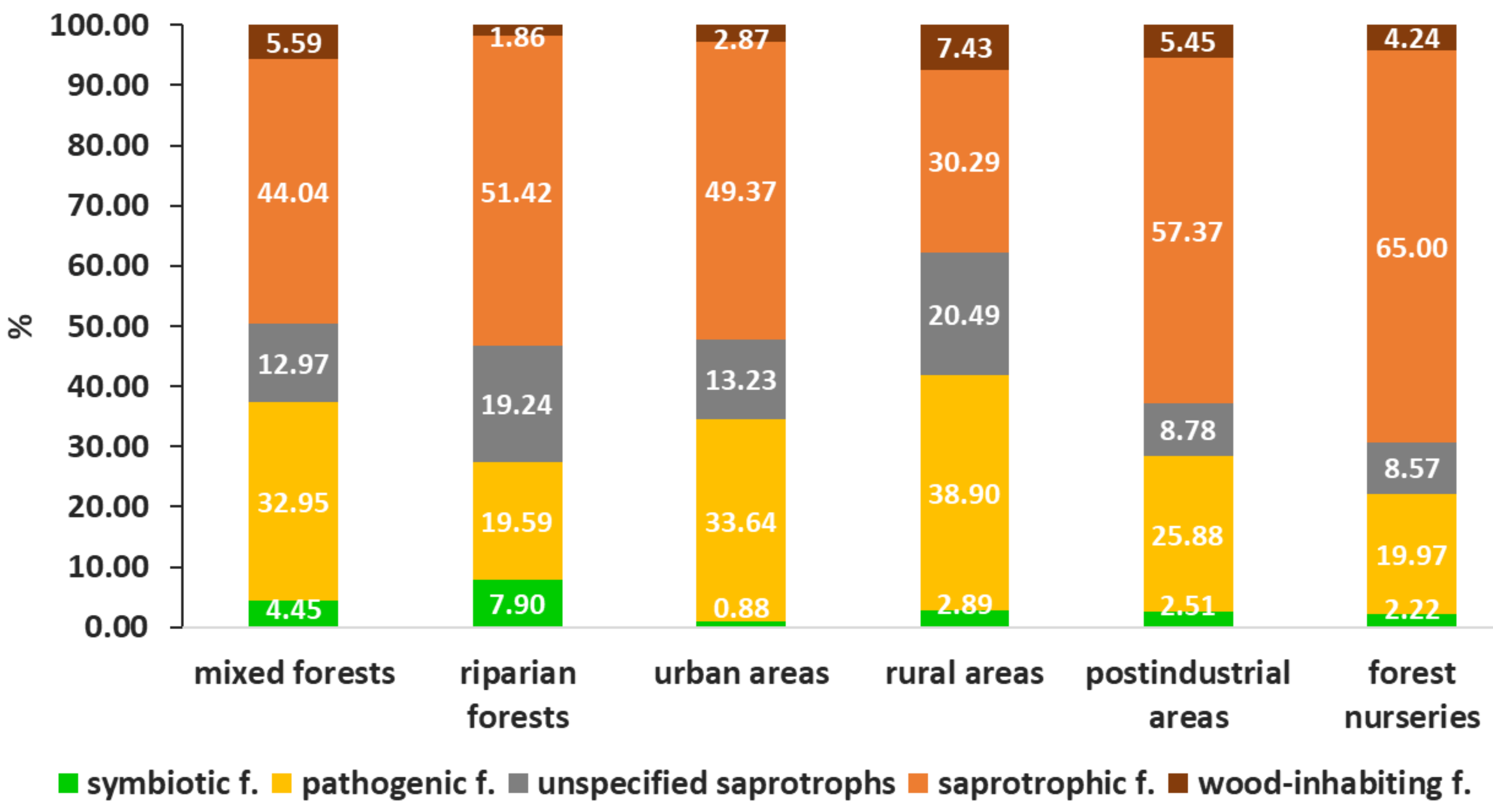

Fig. 3. Relative abundance (%) of soil fungi from different trophic groups in different habitat types.

Two-way ANOSIM/ Bray-Curtis measure	
Habitat type	
R	0,35
p	**0,0001**
Season	
R	0,03
p	0,3357

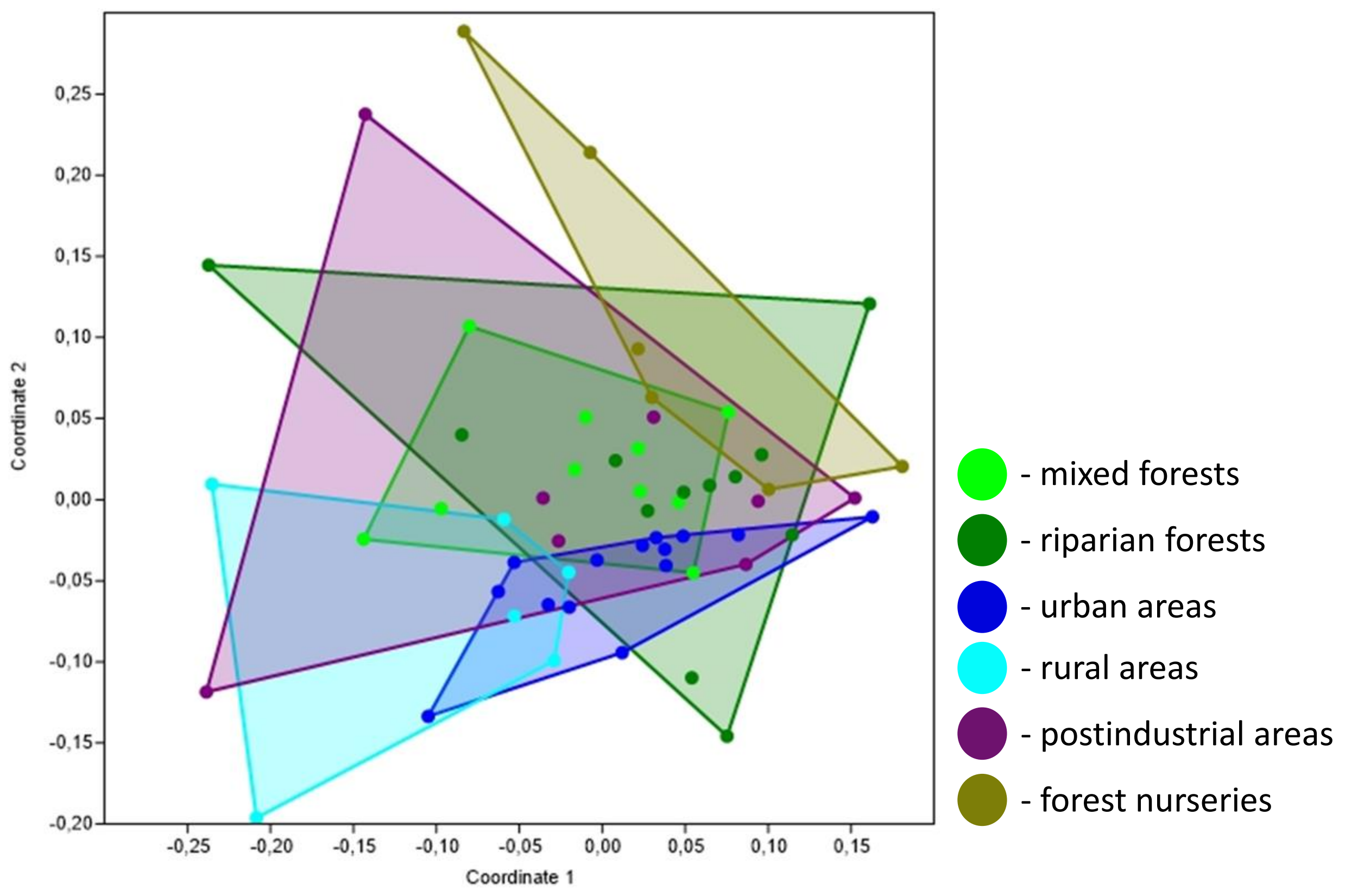

Fig. 4. The NMDS plot of Bray-Curtis dissimilarity measure visualizing the differences between the habitat types.

CONCLUSIONS

- The mean species richness (OTUs) and the Shannon index values (H') exhibit significant differences among the studied habitat types (Fig. 2).
- The highest share of symbiotic fungi was found in forest habitats (Fig. 3).
- The type of habitat significantly affects the structure of soil fungal communities ($p < 0.05$) (Fig. 4).
- The season does not significantly affect the structure of soil fungal communities ($p > 0.05$) (Fig. 4).

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