Throughout modern history, some tree species experienced an unforeseen decline due to the expansion of specialized pests, leaving a path of dead and damaged trees in their wake. The first such incident that comes to mind is the Dutch Elm Disease (DED) epidemic that struck elm trees in Europe and North America in the mid-20th. Soon, many elms were gone and these environmentally tolerant, beautiful and valuable timber trees became truly forgotten for a long time. Before, elms had been widely used as ornamental trees to embellish avenues and gardens across Europe due to its aesthetically pleasing shape and tolerance of pollution, compacted soil, and drought. Compared with the data from the 1970s, research indicates a significant increase in the population of one of the three elm trees native to Poland - European white elm (*Ulmus laevis)* in Poland, which may be related to the fact that it is the most resistant to DED compared to the other two native elm species (*Ulmus glabra* and *Ulmus minor*).

Ulmus laevis is a hardwood deciduous tree which grows in river margins and damp bottom land forests, tolerating flooding for some periods of the year. In Poland European with elm is mostly an admixture species in the natural riparian communities and especially in oak-hornbeam forests. The dying out of other "riparian" trees (pedunculate oak, especially ash) caused elm to appear again in the interest of foresters. However, the loss of suitable habitats due to human-induced changes in riparian forests, combined with the effect of Dutch elm disease (DED), has compromised the survival of many *U. laevis* populations.

The fungal microbiome (i.e., the mycobiome) has a central function in soil ecological processes because it is composed of functionally distinct groups that are required for organic matter decomposition and nutrient fluxes among different kingdoms. The special part of mycobiome constitutes mycorrhizal fungi. Mycorrhizal fungi, in concert with soil fungi of other trophic groups, colonize plant roots, forming the root-associated mycobiome (RAM). RAM provide benefits to the host by improving plant nutrition and health, but they can also inflict diseases or parasitize host resources. Because of the multifaceted involvement of fungi for the health, nutrition and productivity of different ecosystems, it is important to understand the factors that influence root associated fungal microbiomes (RAMs). Therefore root-associated mycobiomes of elm grown in highly diverse environmental conditions has been selected as the main subject of this project. Understanding the forces that govern the assembly of RAFMs accompanying elms is key to the sustainable management of European white elm.

The main objectives of this project are to reveal mycobiome community structure accompanying roots of *U. laevis* and correlate the composition and abundance of fungi from different trophic groups with a variety of white elm life-history characteristics. Depending on the purpose (field samples or samples from a pot experiment), an amplicon-based (nrITS) metagenomics approach (NGS) or Sanger sequencing will be applied for the molecular analysis of environmental samples. Special emphasis will be placed on the mycorrhizal symbiosis of European white elm, an exceptionally unexplored and often misinterpreted phenomenon regarding elm trees. However there has been little progress so far in understanding the mycorrhizal relationships of elm trees, even though this is an important and interesting tree species from the perspectives of future forestry and urban environments. Therefore great part of the project will be dedicated to **“mycorrhizal switching”** in studied elm species, with respect to different environmental variables (tree age, season, health status, habitat, edaphic parameters). To reach this goal, the work will be centred and organised on answering the four research questions listed below. Answering these questions will shed light on the role of the mycobiome in development of European white elm in very different environmental conditions.

The proposed approach will be a **pioneering** effort in analyzing of root mycobiome of elm trees with *U. laevis* as an object of research. This sort of ambitious, original, and innovative research, conducted in very diverse environmental settings (nurseries, natural forests, rural and urban habitats) has not been conducted yet in Europe concerning elm trees. These settings enable to study correlations between major environmental variables and the diversity patterns of root mycobiome in tested elm species. I hypothesize that the patterns of different land-use influence the establishment of RAMs communities, resulting in different community composition and diversity among landscapes. Due to the finance and time limitation ***U. laevis*** **has been selected as an object of research**.

I ask four interlinked research questions:

Q1. How do different types of environments (natural alluvial forest and oak-hornbeam forest, forest nursery, urban areas, roadside avenues, and disturbed sites) shape mycobiome communities accompanying roots of *U. laevis* and which environmental factors (e.g., soil chemistry, tree species composition) are the main drivers of the mycobiome community?

Q2. How does the mycobiome community accompanying roots of *U. laevis* respond to tree age and season?

Q3. How the mycobiome community is influenced by tree decline caused by DED?

Q4. How do neighborhoods of trees with arbuscular or ectomycorrhizal symbiosis influence type of mycorrhizal colonization of elm seedlings in a pot experiment?