Fungi play a crucial role in the functioning of soil ecosystems, and in the case of initial soils are pioneer organisms colonizing the mineral substrate with mosses and lichens. Studies by Tedersoo et al. (2014) have shown that fungi from subtype Mortierellomycotina are common in temperate climate forests zone and relatively frequent in tundra, but their contribution in the soils of equatorial zone relative to the other groups of fungi is negligible. The frequency of Mortierella in Antarctic and Arctic soil is confirmed by many authors. Kochkina et al. (2012) show its presence in sediments of Antarctic permafrost. It is worth noting that the contribution of Mortierellomycotina fungi in samples of arctic tundra soil far excess the lichen-forming fungi from Lecanoromycetes (Tedersoo et al. 2014). Fungi from this group are characterized by low nutrient requirements as expressed in the Polish family name - which could be translated as 'starvation fungi'. Representatives of Mortierellomycotina are usually not recognized to the species level and functioning in databases as OUT's - Operational Taxonomical Unites (eg. Nishizawa and wp. 2010 Moll et al., 2016 et al.), Their distribution and habitat preferences are not known, though often they are isolated from poor, polluted, strongly acidified environments (Wagner and wsp.2013). There is a high probability that there are still undescribed species of Mortierella, because their morphology is simple and they are very tiny. It is known that certain Mortierella fungi carry symbiotic bacteria (Sato et al., 2010). At the same time the body plan of vegetative mycelium of many species, with numerous hyphal extensions called gemmae suggests that these structures represent the adaptation to symbiosis with bacteria, and that this phenomenon is represented more widely than previously thought. Conducting research on the interaction of fungi with bacteria requires initial recognition of the diversity of the fungi and checking the presence of bacteria in their hyphae. The aim of the research is to investigate a pattern of distribution of fungi Mortierellomycotina in successive zones of the mountain vegetation which should correspond to the distribution of these fungi in different biomes studied in the meridional transects by Tedersoo and al. (2014). Another research goal is to determine how many species of Mortierellomycotina are hosts for symbiotic bacteria. By obtaining axenic cultures and their barcode sequences we can identify many strains of Mortierella unrecognized and present in literature as OTUs. The subsequent analysis of large database of species-specific OTUs will provide to determine the species ranges.

We will test the following hypotheses: a) fungi from subtype Mortierellomycotina are the most varied and numerous in subalpine forests (coniferous forests) zone, which corresponds to their increased distribution in boreal forests as indicated by Tedersoo et al. (2014); b) Their diversity in soil in relation to other fungi will decrease with the transition to the deciduous forests zone and snow zone; c) In the alpine zone they will be found a few species from the group, but will dominate taxa associated with bacteria; d) All Mortierellomycotina representatives living under extremely unfavorable climatic conditions in initial soils are hosting endosymbiotic bacteria inside hyphae. Research methods will include new generation sequencing for 36 soil samples from the three mountain ranges (the Tatras, the Alps, the Rocky Mountains) from six zones of vegetation. The 180 soil probes will serve as a source of Mortierellomycotina strains. Fungi will isolated using a moist chamber method and selective media method. Pure cultures will be characterized by analysis of the sequence of the ITS rDNA region, described morphologically and documented. The presence of bacteria inside the hyphae will be performed by PCR from DNA obtained from surface sterilized mycelium using specific bacterial primers. The presence of a band of the expected length will confirm the presence of bacteria in the hyphae. Representatives of Mortierellomycotina belong to the one of the oldest terrestrial fungal taxa - demonstration of the widespread participation of endosymbiotic bacteria inside their hyphae may shed a new light on the process of early lands colonization - not by plants living in mycorrhiza with fungi, but even earlier by microbial consortia and symbiotic associations of fungi and bacteria.