

There is very little risk in assuming that all eukaryotic organisms associate in multilevel, complex symbiosis with microorganisms that play diverse, often fundamental roles in host physiology. It has been proven without a doubt that this microbiota played an important role in evolution (Lynn Margulis's endosymbiotic theory, terrestrialization of plants) and has profound effects on the ecology of ecosystems and fitness of its inhabitants. Symbiotic microorganisms manifest strong effects on the community structure and the diversity of associated organisms. One of the most representative and best studied example of the importance and complexity of inherent microbiota is the human digestive tract. It is estimated that metagenome of the intestine microbiota is 100-fold larger than the human genome. The gut inhabitants play diverse, beneficial roles. Microbiome deprivation has often severe effects on human health.

The composition and role of plant microbiota is far less known, however significant progress in this field of research has been made recently. Symbiotic microorganisms, mainly bacteria and fungi were shown to play beneficial roles in plant adaptation to the environment, however environmental pollution and intensive farming has severely limited the richness and biodiversity of symbiotic microorganisms in many habitats, negatively affecting plant and ecosystem homeostasis. The positive impact of plant microbiota on host water and nutrient uptake and its pest control capabilities has been the subject of intensive research, due to possible application in agriculture and phytoremediation as an alternative to traditional farming techniques.

Among the best-described groups of plant symbiotic microorganisms are mycorrhizal fungi. However, in recent years another important group - endophytes, has emerged. Endophytes (fungi and bacteria) are ubiquitous, taxonomically diverse microorganisms that inhabit plant tissues without causing any visible symptoms of infections for at least a part of their life cycles and can increase plant biomass and can protect plants against unfavourable environmental conditions. Symbiosis with endophytes is especially important for non-mycorrhizal plants (approximately 29% of all vascular plant species), including members of the families *Chenopodiaceae*, *Caryophyllaceae*, and *Brassicaceae*.

According to our preliminary studies, seedlings of *Arabidopsis arenosa* from a population not adapted to toxic metals (reference population from a non-polluted environment) showed better adaptation to metal toxicity than seedlings from a population inhabiting a post mining waste dump. Additionally, application of seed-borne endophytes from the reference population had a positive effect on seedling (from mine dump) growth. This allowed us to hypothesize that vegetation under high metal toxicity may have limited the biodiversity of beneficial symbiotic microorganisms of *A. arenosa* seeds, what in turn had a negative effect on the plants growth and fitness. This implies that the seed microbiome can be responsible for the adaptation of the plant to the environment. It is commonly known, that seed-borne endophytes play beneficial roles in the seedling survival, defence against biotic and abiotic stresses and nutrient acquisition. The knowledge, whether toxic metals present in the soil can lead to seed endophytes deprivation in TM-adapted plant population, is not known.

In the first step of the project, the identification of fungal and bacterial seed microbiota of *A. arenosa* grown in different habitats is planned. This will give a better understanding of the biology of symbiosis and allow us to explore the relationship between abiotic environmental factors, diversity of microorganisms present in the environment and plant adaptation potential. Classical culture based technics and next generation sequencing (NGS) approaches will be used. Microorganism pure cultures will be catalogued in pure cultures bank at MCB JU. Vertical transmission seed-borne endophytes will be studied in the consecutive plant generation in TM-enriched environment and the seeds of each generation will be provided for endophyte isolation and identification. By doing so, we will answer the question, when and if TM inhibits vertical transmission of endophytes. In the next steps, screening for microorganisms with the highest potential to improve plant growth under TM in the substrate will be performed. Growth response analysis, transcriptomics and ionomics will be applied for the evaluation of the effect of the seed microbiome on plant adaptation to TM. For verification of transcriptomics data quantitative *q*PCR and HPLC will be used.

The planned study is of basic research nature, however, obtained results can be starting point a future applied project.