Phenoxy herbicide MCPA (2-chloro-4-methylphenoxyacetic acid) is widely used in agriculture to control broadleaf weeds. Although its application has helped to increase crop yields and its value, MCPA is also recognized as a source of potential adverse environmental contamination. Its extensive use and wrong storage practices may promote contamination of soil matrices, surface- and groundwaters and in consequence increased inhibition of plant development and soil toxicity. Hence, there is an urgent need to search for nature-based solutions (NBS) and understand the synergy between soil microorganisms and plant secondary metabolites (PSMs) in term of effective elimination of MCPA from the environment. This can be obtained by developing bioremediation methods.

Bioremediation typically involves the ability of microorganisms (i.a. bacteria) to utilize contaminants to less toxic or non-toxic compounds. Soil bacteria inhabiting the root zone of plants (rhizosphere) also show biodegradation activity (i.e. rhizodegradation). The activity of rhizosperic bacteria can be enhanced by plant exudates released into the root zone. This exudatch, which are rich in special chemical compounds (including PSMs), can stimulate and accelerate the degradation of pollutants by rhizospheric bacteria. Therefore, the subject of our research is to assess the impact of PSMs on the activity of bacteria inhabiting agricultural soil in order to stimulate the process of MCPA biodegradation.

Our previous study showed that plant secondary metabolite: syringic acid can mitigate the toxic effect of MCPA, enhance the occurrence of MCPA-degradative genes (on DNA level) and improve the removal of MCPA. To complete the established goals, it is essential to continue experiments for the evaluation of the influence of selected PSMs on soil bacteria activity and biodegradation of MCPA. **Hence, we selected structurally related PSMs such as: syringic acid, caffeic acid, vanillic acid, rosmarinic acid and salicylic acid in order to examine their effect on: 1) functional genes expression which are responsible for the first steps of MCPA biodegradation, and 2) removal of MCPA from studied matrices.**

Through employment of RNA-based molecular and chemical approach our present study can: fulfill our previous results; assess and quantify the activity of bacterial strains stimulated with selected PSMs under stress conditions and hence give better understanding of what is actually happening in the environment. In conclusion, this scientific project will create an extensive database in scope of biological sciences, which can be used for solving already existing and future problems in term of organic pollutants removal from natural ecosystems.