

Plants and related microorganisms are an effective tool for cleaning contaminated environments. Phytoremediation is an environmentally friendly method widely used to clean soils contaminated with petroleum hydrocarbons (PH) and/or heavy metals (HM). Recent evidence has indicated that the phytoremediation of contaminated soils can greatly benefit from plant-bacterial associations. The most important role in this process is played by plant growth-promoting bacteria (PGPB) that inhabit the rhizosphere zone, as well as the interior of plant tissues. These bacteria can stimulate the degradation of pollutants, contribute to the mobilisation and uptake of heavy metals by plants and improve plant growth under PH and HM exposure. In general, plant-associated bacteria play a key role in the adaptation of a host plant to a polluted environment. PGPB use a variety of bacterial mechanisms that are responsible for an increase in the plant biomass and/or metal bioavailability, thereby resulting in an increase in metal uptake. The bacterial mechanisms of plant growth-promotion involve phosphate solubilisation of minerals such as phosphorus, the production of phytohormones (e.g., auxins), siderophores, HCN, ammonia, nitrogen fixation and the synthesis of 1-amino-cyclopropane-1-carboxylic acid deaminase (ACCD). It has been suggested that cooperation between plant growth-promoting bacteria and hydrocarbon and heavy metal-tolerant plants may result in a more effective phytoremediation of soil that has been contaminated with these compounds. In this process PGPB would be applied in order to accelerate the degradation and accumulation of toxic compounds. nevertheless, a detailed description of the above mentioned cooperation is still not entirely understood. As was shown above, although there are many potential mechanisms that can be activated during the bacterial-assisted phytoremediation of heavy metals and petroleum co-contaminated soils, the real process of their interactions in the contaminant-plant-bacteria system is still unknown.

Thus, the aim of the proposed project is a comprehensive analysis of cooperation between plants and bacteria during the bacterial assisted-phytoremediation of soil co-contaminated with petroleum hydrocarbons and heavy metals using *Zea mays*. On the one hand a global analysis of the gene expression (RNA-Seq) of *Z. mays* exposed to PH and HM stress in both soil systems - bioaugmented with live and dead PGPB, as well as in control plants treated with water, will be studied. Furthermore, the activity of the plant stress defence mechanisms and stress symptoms in plants will be investigated. These analyses will provide information about the molecular and physiological response of plants to the introduction of PGPB in the tested conditions. On the other hand, a study concerning bacterial activity during ongoing processes is also planned. It will be performed by studying the transcription level of the microbial genes encoding the proteins involved in the degradation of hydrocarbons and plant growth promotion in soil and tissues of *Z. mays*. Quantifying the expression of the bacterial functional genes in soil subjected to bacterial-assisted phytoremediation is a key step in monitoring bacterial activity during the ongoing processes. Such analyses will enable the bacterial mechanisms of the plant growth promotion that occur in the soil and interior of tissues of *Z. mays* during bioremediation study to be determined. In addition to testing the bacterial activity during phytoremediation, it is also necessary to analyse the composition of the bacterial communities inhabiting rhizosphere and tissues of *Z. mays* using high-throughput sequencing analysis of 16S rRNA gene. Only such a comprehensive analysis will enrich our understanding about the plant-bacteria interactions during bacterial-assisted phytoremediation. There is a lack of reports in the literature that integrate all of these types of analyses in regards to plants exposed to contaminants, especially those exposed to a combination of organic and inorganic compounds.