

The bulk soil is considered as a nutrient-poor environment; therefore, microorganisms developed mechanisms allowing them to successfully colonize niches with better nutrient supply, such as plant rhizosphere. In opposition to the bulk soil, the rhizosphere is a 'hot spot' of microbial activity assuring rich nutrient environment for the growth of microorganisms. Rhizosphere is also characterized by strong intra- and interspecies interactions, where the microorganisms compete for nutrients and ecological niche. This environment creates a kind of a microbial market, the place of an active exchange between 'sellers' and 'buyers', which are: the microbes (plant beneficial or pathogenic bacteria, fungi, viruses or protozoa) and their hosts (plants) or vice versa. This microbiological 'stock exchange' is subjected to 'rises' and 'falls' depending on both: the composition and availability of nutrients, secondary metabolites, and signal molecules penetrating the environment. These interactions result in the composition of microorganisms colonizing the particular environment and significant modification of the host's resistance. An important strategy of rhizosphere bacteria to compete with other microbes is production of growth-suppressing secondary metabolites such as e.g. antibiotics, toxins and biosurfactants. Also, the addition of beneficial microorganisms to the natural environment of plants can improve plant's health and fitness by better uptake of nutrients, increasing plant's growth, protection of the plant against pathogens or improvement of stress tolerance. Among the beneficial microorganisms, especially the rhizosphere-associated bacteria play an important role for plant development. The plant growth-promoting rhizobacteria (PGPR) enhance plant growth but also inhibit the growth and development of fungal and bacterial plant pathogens on the plant root system.

A strain P482 is the second representative of the little known and newly established species of *Pseudomonas donghuensis*, described in 2014. This strain seems to be very interesting due to the production of antimicrobials, which have not been described so far for the *Pseudomonas* genus. It also possesses the features of the strain capable of promoting plant growth and protecting plant tissue against bacterial and fungal pathogens, as it is able to protect plant tissue against plant pathogenic bacteria and to colonize the roots of maize, potato and tomato plants. Our recent research allowed us to determine the genetic background of P482, important for synthesis of the antimicrobials produced by this strain. Those genes are localized among 800, which are unique for this strain in comparison to the closely related species. The more, we have found that the production of those antimicrobials depends on the availability of specific nutrients and iron ions. Hence, one may assume that in the rhizosphere environment the specific genes responsible for the production of the metabolites with antimicrobial properties are switched on. Similarly, the genes important for the survival, and adaptation of these bacteria to the rhizosphere environment are activated. The activation of those genes depends on the root exudates, plant and microbial signal molecules and microbial metabolites of microorganisms inhabiting the rhizosphere. Therefore, the aim of the proposed study is the identification and analysis of the molecular mechanisms important for P482 strain interaction with roots of maize and tomato.

In the proposed study we will apply the combination of innovative molecular strategies: i) sequencing of RNA (RNA-seq) which is based on sequencing of the globally and specifically activated genes in the given environment; here it will be used to analyze the response of P482 to the maize and tomato root exudates or root colonization; ii) the *in vivo* expression technology - IVET, which is a molecular 'promoters trap' of the genes specifically activated in the given environment; here it will be used to identify genes of P482 activated in the rhizosphere of maize and tomato; iii) microarray technology, which allows studying the genes of maize and tomato plants which are switched on in response to the presence of P482 in the root environment of these plants. The project will also use ecological analyzes to: a) determine the population dynamics of P482 and its negative mutant in the *gacA* gene (*gacA* gene encodes the regulatory protein relevant for secondary metabolite synthesis) in the rhizosphere of the tested plants; b) determine the ability of P482 to promote the plant growth and fitness. Survival studies of strain P482 and its *gacA* mutant in rhizosphere and plant colonization ability of those strains will be carried out using the green fluorescent protein (GFP) variant of P482. This will allow for microscopic observations of the effectiveness of the colonization. The ability of P482 and its *gacA* mutant to promote maize and tomato growth will be reflected by the increase in the root mass and length, the number of branches and the increase in stem length

The proposed project aims to gain fundamental knowledge concerning the plant-bacterium interaction and does not assume gaining economic profits, however, the result obtained in the course of the project may have an impact on the future more applicable research proposals. Broadening the knowledge concerning the antimicrobial activity of P482 strain in the rhizosphere environment of different plant species would make possible undertaking further studies on elaboration of novel strategies of combating plant pathogenic bacteria and fungi. Facing the need of search of novel, environmentally friendly strategies of combating plant pathogens, this research project fits the European Commission regulations, concerning the limited usage of chemicals for plant protection.