DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

Root nodules are characteristic structures for plant symbiosis with nitrogen-fixing bacteria. This specific organ develops on the roots of plants derived from Fabaceae family, as in model species *Medicago truncatula* and *Lotus japonicus*. There are two types of root nodules: determinate-type, which exhibits temporary meristematic activity and indeterminate-type root nodules with persistent meristematic zone, which allows constant nodule growth. *Lotus japonicus* forms determinate nodules, while *Medicago truncatula* – indeterminate type. Both types of root nodules have one main goal – to create low-oxygen concentration environment which allows living in them bacteria to fix atmospheric nitrogen. Plants cannot directly assimilate atmospheric nitrogen and its accessibility in soil is limited. However, species from Fabaceae family evolved the ability to establish symbiosis with nitrogen fixing bacteria, called rhizobia. As a result of symbiosis, plants receive nitrogen from bacteria, whereas bacteria obtain products of photosynthesis. Knowledge concerning root nodule development is still limited. It is assumed that auxin, along with its transporters, play an important role in the process of symbiosis. Auxin is a plant hormone, which is essential in many morphogenetic processes and its polar transport is dependent on the asymmetric localization of family of PIN proteins in plasma membrane. However, still little is known about which specific PIN proteins are crucial for nodulation and whether it is associated with the type of the nodule. Therefore, the aim of this project is to investigate the role of PINs in nodulation in both model plants – *Medicago truncatula* and *Lotus japonicus*. Although majority of PIN proteins are plasma membrane located, there is a group which localizes specifically in the endoplasmic reticulum, which was found for *Arabidopsis thaliana*. Those PIN proteins mediate auxin flux from cytosol to the ERs' lumen.

This project concerns basic studies on model plants, however, many of the species belonging to Fabaceae family are crops, which are important for agriculture. Because of symbiosis with rhizobia, they exhibit a high protein content and are its important source in human and livestock nutrition. Results obtained within this project can result in developing new technics in nodulation intensification and generation of highly efficient crops.