



CONCERT-Japan 3rd call Food Crops and Biomass Production Technologies

**"Improving crop yield by enhanced plant performance
under stress conditions"
IPSC**

INTERIM REPORT

Project coordinator : Prof. Stephan Pollmann, Centro de Biotecnología y Genómica de Plantas,
Spain

Over the course of millions of years, plants have evolved in close vicinity with other organisms. Particularly in the rhizosphere, plant development and contemporary ecology has been shaped by their constant interaction with a plethora of soil microbes. Reportedly, these interactions can have direct impact on plant fitness, including stimulated plant productivity and induced resistance to pathogens. In the IPSC project we apply a holistic scientific approach to address the question of how plants benefit from the symbiosis with the root-colonizing endophytic fungus *Piriformospora indica*. The goal of the project is to disclose the molecular mechanism(s) triggered by the symbiosis with the fungus that render(s) host plants more productive in terms of biomass production and yield, and more resistant to prevailing abiotic stresses.

Given the fact that *P. indica* shows an enormously broad host spectrum, the key hypothesis of the project is that the beneficial effects of the symbiosis are based on conserved recognition and signaling processes, rather than specific host-symbiont interactions. This assumption makes it tempting to speculate that obtained data can directly be harnessed to improve the productivity and yield of agriculturally relevant crops, particularly under environmental stress condition, such as drought, salinity, and nutrient limitation, by employing a biotechnological approach. Facing the prevailing global climate change as a consequence of anthropogenic greenhouse gas emission, including current climatic models predicting temperature increases of 2-5°C, reduced annual rainfalls, and increased vapor pressure deficit and evaporation even for large parts of moderate climate regions, global food production is in jeopardy. The results of the IPSC project are expected to mitigate the risk of reduced agricultural productivity, as they will offer the possibility and accelerate the production of new high-performance crop lines through the identification of novel molecular targets and mechanisms.

In the first phase of the project, comprehensive transcriptomics and metabolomics studies have been performed. The purpose of these experiments and the subsequent detailed comparative analysis was to collect data at a depth that is sufficient to reveal differences on the molecular level, explaining the growth promotion and increased stress resistance of *Arabidopsis thaliana* plants co-cultivated with *P. indica*. The analysis has been divided into two blocks. On the one hand, the plant-microbe interaction has been studied under control conditions, i.e. without the application of any kind of extra abiotic stress. On the other hand, a number of different representative abiotic stress conditions have been studied, i.e. osmotic stress, salinity, phosphate limitation, nitrate limitation, as well as phosphate and nitrate limitation.

The preliminary analysis of the data revealed that the investigated symbiosis between *A. thaliana* and *P. indica* and the therewith associated growth promotion does not rely on a simple induction of plant hormone biosynthesis. The multiplex analysis of phytohormones and related compounds showed no significant changes in the levels of the major active plant hormones. However, based on the obtained results, it seems as if the metabolic flux into auxin conjugates (inactive storage and degradation forms, respectively, of auxin) and auxin derivatives (glucosinolates) is increased. This notion is further confirmed by the RNA-Seq data, providing evidence for the induction of genes encoding for enzymes acting in L-tryptophan (Trp) biosynthesis, indole-3-acetic acid (IAA) amino acid synthetases (GH3), and enzymes acting in the indole-3-aldoxime (IAOx) and glucosinolate pathway.

Intriguingly, a number of auxin transporter genes appear to be differentially expressed, too. More importantly, however, is the observation that alterations in calcium signaling are likely to contribute to the observed phenotypic differences. Currently, we are pursuing the hypothesis that changes in Ca^{2+} signaling translate both into the differential activity of a small number of potassium transporters/channels and the activation of a number of transcription factors. Combined with the observed improved assimilation of macronutrients and the formation of local auxin maxima driven by induced IAA transport, those molecular mechanisms could explain the increased growth of the root system of *Arabidopsis* plants that grow in symbiosis with *P. indica*.