

The main goal of presented project will be the identification of components that are responsible for a cross talk between two groups of phytohormones: strigolactones (SLs) and abscisic acid (ABA). Both phytohormones are derived from carotene, and it was proposed that both of them might be involved in similar developmental processes, however interaction between SLs and ABA, at biosynthesis and signalling stage remains unclear. **Recent, unpublished results, obtained in Department of Genetics University of Silesia (DGUS) indicated that mutation in SL receptor also results in insensitivity to ABA. Based on this result we assume that that signalling pathways of both phytohormones might be interconnected.** To uncover the molecular basis of this interaction we are planning to perform detailed analysis of the gene expression, protein-protein interactions and protein phosphorylation, after ABA and SL treatment of *Arabidopsis thaliana* and *Hordeum vulgare* (barley) SL insensitive mutants. The platform for two different plant species will be used, to perform comparative analysis between mono- and dicotyledon species. This approach allows us to describe the mechanisms that are universal in plant kingdom. The reason that we are going to use *A. thaliana* is that the mutant line disturbed in SL receptor AtD14 was already identified (Waters et al., 2012) and since that time it is a model species in plant science and references for transcriptome analysis are available. On the other hand barley, a monocotyledon species, is a research object of DGUS team and mutant line disturbed in SL receptor HvD14 was recently identified in DGUS (Marzec et al., 2016). Also in that case references for transcriptomic studies are available.

For both species a parent variety and the mutant affected in SL receptor will be investigated (*atd14* and *hvd14.d*, for *A. thaliana* and barley, respectively). Our preliminary results indicated that mutation in barley SL receptor HvD14 results in insensitivity of *hvd14.d* line to ABA treatment during seed germination and stomata closure. **Thus, hypothesis that mutation in SL receptor impairs ABA signal transduction pathway, can be drawn.** To provide a comprehensive molecular analysis of proposed interaction between signalling pathways of SLs and ABA we are planning to perform an innovative research presented in this project proposal. Using mentioned plant material and various research techniques (described below) the following questions will be answered:

1. *What differences in expression level of ABA-induced and ABA-repressed genes will be observed in parent varieties and SL receptor mutants, in response to ABA treatment?*
2. *What differences in expression level of ABA-induced and ABA-repressed genes will be observed in parent varieties and SL receptor mutants, after SL treatment?*
3. *How mutation in SL receptor affects phosphorylation of proteins involved in ABA signalling?*
4. *What is an impact of ABA treatment for the interaction between SL signalling components?*
5. *Whether the proteins from SL and ABA signalling pathways are able to interact to each other?*

The obtained answers will allow us **to describe molecular basis of cross talk between SLs and ABA in mono- and dicotyledon species.** Additionally during this project the **function of previously identified barley genes encoding components from SL signalling pathway will be experimentally confirmed** . To check the interaction between analysed proteins, various constructs for bimolecular fluorescence complementation (BiFC) in *Nicotiana benthamiana* (tobacco) protoplasts will be developed, and this set of constructs will be **a valuable tool for further investigation of SL and ABA signalling pathways in plants.**