

SIGNALOAS -Dissection of the signaling function of O-acetylserine in plants

DESCRIPTION FOR THE GENERAL PUBLIC

Objectives: Primary metabolites, such as amino acids, often function as signals to trigger transcriptional responses in plants. However, the molecular mechanisms of the signal transduction are not known in detail. One of such signal molecules is the precursor of cysteine, O-acetylserine (OAS), which links the three assimilatory pathways of carbon, nitrogen, and sulfur. The level of OAS regulates expression of a group of genes, so called “OAS cluster”. The aim of this project is dissecting the physiological role of the proteins encoded by the OAS cluster genes and characterization of the molecular mechanisms of the signaling and regulatory role of OAS in plants.

Research to be carried out: The project has been divided into three main work packages. Each of them consists of several separate experimental tasks. We will (1) use available Arabidopsis genetic resources to test how each mutation affects OAS level in plants and identify the mechanisms causing OAS increase at the beginning of the night. We will (2) identify the transcription factors responsible for altered gene expression upon OAS trigger and find the mechanism of their activation/repression by OAS. We will then (3) address in detail the function of the OAS cluster genes, particularly *SDI1* and *LSU1*, which act as multipliers of OAS signal. These proteins interact with a number of other proteins and modulate their function. We will dissect their protein interaction networks and test how changes in OAS level affects the expression of downstream genes controlled by each “multiplier” of OAS signal.

Reasons for choosing this research topic: OAS is a metabolite synthesized from serine and acetyl-CoA by serine acetyltransferase, a component of cysteine synthase enzymatic complex. OAS serves as a substrate for cysteine biosynthesis catalyzed by a second component of the complex, O-acetylserine (thiol) lyase. In addition to the metabolic role of OAS in sulfur assimilation (the only known metabolic function), the signaling and regulatory function of OAS in plants has been suggested by numerous published and unpublished data. Our preliminary work identified the OAS cluster genes with expression positively correlated with OAS level. Dissection of the molecular mechanisms responsible for the observed effect would revolutionize our understanding of control of sulfur metabolism and its links to carbon and nitrogen metabolism. SIGNALOAS provides a unique opportunity of collaboration between the German and Polish partners, each of them focusing on one of concurrent topics related to the signaling function of OAS in plants. The combined effect of collaboration and joint results of different experimental approaches will exceed the results which would be obtained by single partners working separately. Due to this synergistic approach, we expect a substantial advancement of knowledge.