Abiotic and biotic stresses consist serious problems for agriculture. Global climate changes resulting in salinization and desertification make the situation even more difficult, not only for the future of agriculture but also for our environment. Therefore, an understanding of the signaling pathways that control the stress tolerance of plants is extremely important these days. This knowledge is necessary to build strategies to cope with the negative effects of harsh environmental conditions on plant development and growth.

The project is focused on SNF1-related kinases 2 (SnRK2s), plant specific kinases which are involved in the regulation of plant tolerance to water deficit and salinity. Based on phylogenetic analysis the SnRK2 family members have been divided into three groups. The classification correlates with their response to a plant hormone, abscisic acid (ABA). Group 1 consists of kinases not activated by ABA, group 2 – not activated by ABA or activated very weakly, and group 3 - strongly activated by ABA. The most extensively studied are ABA-activated kinases, which play a key role in ABA signal transduction. Several cellular substrates of these kinases have been identified (e. g., ions channels involved in stomatal closing, aquaporins, ABA-dependent transcription factors). Much less is known on the SnRK2s, which belong to group 1 of the SnRK2 family - kinases not dependent on ABA. They are activated extremely rapidly (within seconds to minutes) in response to osmotic stress and regulate root growth and architecture in salt stress conditions.

Our recent phosphoproteomics data indicate that certain of RNA binding proteins, which are involved in pre-mRNA alterative splicing and/or miRNA biogenesis, are potential substrates of ABA-non-activated SnRK2s. We were able to confirm that some of them are indeed phosphorylated by the kinases studied. These results indicate that SnRK2s might regulate gene expression not only at the level of transcription but also post transcriptionally in response to salinity. During realization of the project we plan to confirm phosphorylation *in vitro* and *in vivo* of all RNA-binding proteins selected, identify phosphorylated residues, and to establish the role of these phosphorylations in respect to miRNA biogenesis and pre-mRNA alternative splicing. We will analyze the effect of phosphorylation of RNA-binding proteins on their subcellular localization, RNA binding, and protein-protein interactions.

I our research we plan to apply multidisciplinary approach: plant physiology, molecular biology, biochemistry, biophysics, and bioinformatics using both classical methodology, as well very modern scientific techniques, such as new generation RNA sequencing and proteomics.

The results obtained during realization of the project should provide new data on the role SnRK2s and important insights into the mechanisms regulating miRNA biogenesis and pre-mRNA alternative splicing in plants. They will broaden the knowledge on signaling pathways that control plant defenses in stressful environments.

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