

IDENTIFICATION OF NEW TARGETS FOR IMPROVING ABIOTIC STRESS TOLERANCE IN PLANTS

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Water availability is one of the main limitations for crop productivity. As droughts get more frequent and severe, it is important to improve plant's drought tolerance. One strategy to reach this goal is the development of chemical compounds that are able to manipulate ABA signaling, thus promoting stomata closure and reducing water consumption^[1]. The main goal of this project is to search for new targets other than ABA receptors that contribute to plant stress tolerance, and which can be regulated by small molecules in order to activate drought resistance in crops. First, we conducted a chemical screening testing more than 1200 natural-like compounds on the stress-inducible *pMAPKKK18-LUC*⁺ reporter line^[2], in order to identify small molecules with the ability to activate stress response. Several molecules have been selected as potential hits, including indole-3-acetonitrile, which caused the greatest activation of the reporter; moreover, we identified a novel compound that strongly activated the reporter line and was chosen for further characterization. Differential expression of *MAPKKK18* in response to the hits was verified by qPCR. Physiological assays, including germination, root growth, and stomatal closure, are currently being conducted in both WT and mutant plants affected in different elements of ABA and drought stress signaling pathways to evaluate the biological activity of this compound. In addition, RNA-Seq analysis has been performed with the novel compound to gain insights into the molecular pathways triggered by this molecule and its potential role in plant stress responses. A forward chemical genetic screening is now ongoing to identify the molecular targets of the most promising compound by mapping-by-sequencing. Lastly, the best targets will be characterized, thus enabling their development to improve plant stress tolerance. This last objective involves the generation of tools such as overexpression lines and loss-of-function mutant alleles through CRISPR/Cas9, as well as their characterization at the physiological and molecular levels. Overall, in this project we will contribute to the discovery of new natural compounds, as well as their targets, that can be used to enhance stress responses of plants and allow us to cope with the droughts to come.

References

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