

Genome editing for drought in barley: a review on the topic and case-study

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Drought is the concern of a large geographical area of the world and represents probably the most serious environmental factor affecting the productivity of agronomical important crops, with devastating economical and sociological impact. Climate models indicate that drought – as well as extreme weather - episodes will become more frequent due to the long-term effects of global warming. Taking into consideration the ever growing worldwide population and the resulting ever increasing demand in food supply, it appears urgent to provide new crops which will produce more even when submitted to drought or high temperatures.

Phytohormones play pivotal role in plant growth and development and mediate a wide range of mechanisms of adaptation toward environmental pressure. They control root/shoot biomass and architecture, changes in water transport and gas exchange, and affect yield-related parameters such as alteration of grain-filling rate. Abscisic acid (ABA), ethylene and cytokinins (CKs) are the 3 most important phytohormones playing an important role during drought tolerance.

Conventional breeding relies on a pool of described genetic variation, mapped QTL (quantitative trait loci) and laborious and time-consuming back-crossing procedures, which are necessary for introgression of desired QTL alleles into elite cultivar backgrounds. Conventionally, new alleles have been introduced also by random mutagenesis, but again following screening and stabilization of advantageous traits is a long-term process. High-throughput sequencing in the last decade resulted in the availability of raw genome sequences of all important crop plants including cereals. Targeted genome editing, represented by the CRISPR Cas⁹ system, has the potential to accelerate plant breeding, providing the means to modify genomes rapidly in a precise and predictable manner.

In our laboratory, we have a long-standing history on understanding the role of CK during barley development. Recently, we turn our focus on the relation between CK and drought tolerance or yield improvement, using the CRISPR-Cas⁹. Two targets are addressed at the moment: the CK histidine kinase receptor HvHK3, and the CK-dependent glycosyltransferase.