

Towards understanding the genetic mechanisms of drought response in barley using functional genomics

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Responding to water deficit plants close their stomata in order to limit the transpiration. Although that strategy evolved as the most rapid water-saving mechanism, it comes at the cost of restriction of the CO₂ assimilation ability, and it is extremely important for organic matter production in photosynthesis process. Consequently, a slower or inhibited CO₂ assimilation diminished the photosynthetic rate. One of many possible ways to increase the barley yield under climatic changes is improving its photosynthetic efficiency under climatic changes scenarios. Taking these under consideration we were more than surprised when discovered phenotype of barley TILLING mutant *hveral.b* under severe drought stress. *ERA1* (*Enhanced response to ABA 1*) encodes β -subunit of farnesyltransferase. Here, we present the potential regulatory role of ERA1 in the drought signaling network in barley. Mutation in HvERA1 confers drought tolerance manifested by faster stomatal closure and better photosynthesis than its wild type. Moreover, our transcriptomic analysis combined with physiological assays demonstrated that under prolonged drought stress the role of *HvERA1* is linked to the metabolism of galactolipids, that build the chloroplast membranes. It might result in the protection of *hveral.b* photosystem and thus, in its better photosynthesis performance under water stress. Together, these results indicate the possible mechanism of the primary cause of the observed alterations in the *hveral.b* mutant. Moreover, our recent studies also confirmed engagement in very early response to water deficit which makes *HvERA1* promising candidate to struggle with climatic changes.