

## Dehydrin genes expression and transpiration intensity of drought stressed maize (*Zea mays* L.)

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### Abstract

Drought is the most significant environmental stress worldwide and improving yield under drought is a major goal of plant breeding. The significance of drought increases with the time of its effect during the vegetation period and with its occurrence in the critical phases of the plants' development. For maize (*Zea mays* L.), critical periods are flowering and early maturity. The objective of the work was to determine the intensity of stress response of maize plants using physical (sap flow) and molecular methods to quantify stress reaction with respect to the plant's growth phase and drought intensity.

The experiment was performed on plants of drought-resistant maize line 2087 (breeding material provided by CEZEA Čejč, Czech Republic). A container experiment was established in natural conditions with limited irrigation. Four variants were maintained under different soil moisture conditions from phase BBCH 40: Variant A: control (90% available water holding capacity, AWHC); variant B: mild stress (50% AWHC); variant C: moderate stress (25% AWHC); and variant D: high stress (15% AWHC). Transpiration was monitored by continuous measuring of xylem sap flow. The EMS 62 measuring system (EMS Brno, CZ) uses the 'stem heat balance' method. Plant biomass for assessing the expression of the selected genes *DHN1* and *DHN2* was sampled on four terms (BBCH 63, 67, 75, 83-85). Total RNA was isolated from 100 mg leaf discs taken from the second youngest leaf. qPCR was performed with gene-specific primers for *DHN1* and *DHN2*. Gene expression was

evaluated as normalised relative gene expression. The results were values of gene expression relative to the value of internal calibrator, i.e. value of expression in the first taking of the control variant.

Intensity of drought confirmatively influenced plant transpiration only in the two most stressed variants. A significant dependence between the average diurnal values of sap flow and volumetric soil moisture appeared only in the moderate-stressed variant C ( $r=0.528^{**}$ ,  $P\leq 0.01$ ) and in high-stressed variant D ( $r=0.395^{**}$ ,  $P\leq 0.01$ ). Significant differences were found out in transpiration ( $P\leq 0.05$ ). At the beginning of the measured period (flowering), transpiration in variants C and D was by 60% lower than transpiration of the control. At the end of the growing period, (BBCH 83-85), the transpiration flow was almost comparable in all experimental variants.

Expression of both evaluated genes *DHN1* and *DHN2* was detected from the beginning of the experiment (BBCH 63) also in plants grown under the optimum moisture conditions. The level of *DHN2* expression was 1000× higher at the beginning of the assessment than the level of *DHN1* expression. Increasing expression of both genes was observed up to the second sampling. At this time high increase in *DHN1* and *DHN2* expression was observed mainly in the high-stressed variant (*DHN1* 10<sup>5</sup>× and *DHN2* 10<sup>3</sup>×) compared to the control.

### Keywords

Drought tolerance, gene expression, qPCR, stem heat balance

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