

PROJECT TITLE

Transferability of genomic regions associated to drought stress tolerance from early to late developmental stages of barley

CONSORTIUM

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SUMMARY OF THE REPORT

Previously, a diverse set of 156 winter barley genotypes has been characterized in greenhouse pot experiments for drought stress tolerance in early developmental stages and genomic regions associated with drought stress tolerance were identified (Wehner et al. 2015; Wehner et al. 2016a; Wehner et al. 2016b; Wehner et al. 2016c). In the EPPN Project “BarleyTransDrought” (ID 220) we aimed to investigate the same set of genotypes in field experiments (Phéno3C facility, Clermont-Ferrand, France) for the response to drought stress in late developmental stages. Main objectives of the study were to get detailed information on:

- (i) physiological changes in generative stages of barley genotypes differing in drought stress tolerance,
- (ii) correlation between drought stress tolerance in the juvenile and the generative stage,
- (iii) comparison of manually determined drought stress response with results obtained automatically,
- (iv) reaction of the same set of genotypes in both systems, and
- (v) QTL for drought stress tolerance detected in both environments as well as to develop molecular markers based on association genetics studies.

The experiment with the 156 genotypes was conducted in a block design in the Pheno3C rain-out shelter facility from September 2019 on. Due to the pandemic situation, all automated measurements and destructive samplings during the generative phase of plant development were stopped and visits were cancelled. The rain-out shelters were still used as originally planned and post-harvest measurements were conducted in 2020 as scheduled. In addition, the harvested material was transferred to the project partner for further investigations.

Due to the missing physiological data during the generative developmental stages, comparison with the drought stress response of the winter barley genotypes in the juvenile stages is not possible (i). Also, comparing the manually with the automatically derived drought stress responses is out of reach (iii). However, the comprehensive data set from the post-harvest measurements are of high value to characterize the drought tolerance of the diverse genotypes. Based on the obtained yield-related data we will correlate the level of drought stress tolerance in the juvenile and the generative stage (ii). In addition, a comparison of both growth systems regarding the plant performance during drought stress is still feasible (iv), and detection of QTL for drought stress tolerance detected in both environments can be performed as intended (v), although relying on yield-related parameters solely for the field experiments. The quantitative assessments are still in progress. We expect the results to contribute to a better understanding of drought stress tolerance in barley and to facilitate a marker-based improvement of barley breeding for drought stress tolerance.