

PROJECT TITLE

BARLEY-ROOTS 2.0: Enhancing drought resilience in barley through characterization of natural gene functions via high-throughput root phenotyping.

CONSORTIUM

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SUMMARY OF THE REPORT

One of the biggest challenges humanity faces is providing food for the constantly growing population, particularly as climate change intensifies and arable land becomes increasingly scarce. For agriculture, drought is a catastrophic climate occurrence and one of the costliest natural disasters worldwide. In comparison to all other crops, barley inherently exhibits a higher level of abiotic stress tolerance. The highly divergent wild barley nested association mapping (NAM) population, HEB-25, has revealed drought tolerance across multiple drought-related experiments. HEB-25 contains genes and alleles critical for adaptation to biotic and abiotic stress conditions, as evidenced by 35 so far published studies (<https://wcms.itz.uni-halle.de/download.php?down=59144&elem=3363880>).

To validate drought stress effects, a selection of HEB-25 lines was backcrossed by breeders in Morocco, Turkey and Germany with current elite varieties. In the proposed DPPN project, we validated the root and shoot drought resilience of 54 backcrossed HEB-25 lines, as well as six nearly isogenic heterogeneous inbred family (HIF) pairs, under both drought stress and control treatments using FZ Jülich's GrowScreen-Rhizo 3 system. The study enabled the characterization of mechanisms responsible for drought adaptation through ongoing comprehensive physiological analyses, including fully automated high throughput root and shoot image analysis under automated watering according to the implemented drought scenario.

In the aftermath of the drought experiment, transcriptome and methylome sequencing analyses are currently conducted within the frame of our BARLEY-RESILIENCE project (<https://forschung-sachsen-anhalt.de/project/barley-resilience-utilizing-wild-barley-27842>) to analyse the epigenetic imprinting and transcriptional regulation of candidate genes and QTLs responsible for drought tolerance based on Oxford Nanopore long-read transcriptomics. The transcriptome analysis of the DPPN material will enable the examination of the differential expression of candidate genes in a multitude of genotypes, allowing us to define their respective gene effects after the conduction of a GWAS. Additionally, methylome sequencing will provide insights into the epigenetic regulation of these candidate genes. Ultimately, this approach will enhance our understanding of the genetic factors driving drought resilience in barley by employing GWAS as well as comparative genome, transcriptome and methylome sequencing.