DPPN

Deutsches
Pflanzen
Phänotypisierungs-
Netzwerk e.V.

PROJECT: HEB-ROOT

Date: **05.07.2023**   **REPORTING**

ID: 11

PROJECT TITLE

Mining promising alleles of genes controlling root traits in the wild barley nested association mapping population HEB-25

CONSORTIUM

P 1	Andreas Maurer		

SUMMARY OF THE REPORT

The wild barley nested association mapping (NAM) population HEB-25 has been established as a toolbox to mine naturally occurring alleles with respect to replenishing the barley breeding pool with valuable resources. This is of particular importance in times of climate change and the increasing size of the human population. So far, more than 30 studies have been published for HEB-25, highlighting the natural diversity present in this population. However, root phenotypes had not been investigated, so far.

We used the GrowScreen-Rhizo 3 system for non-invasive phenotyping of several root characteristics in a representative subset (N=400) of the HEB-25 population to complement the above-ground phenotype data already available for HEB-25. The experiments were conducted from January 2023 - April 2023 in an augmented design in three different batches of 168 rhizotrons each. The plants were pre-germinated, transferred and finally grown in the rhizotrons for 3 weeks. Above-ground biomass was determined and root traits are currently extracted.

We aim to discover different root phenotypes that can support the breeding of stress-adapted barley through better water and nutrient accessibility. We want to explore the genetic factors explaining the different rooting behaviour by means of genome-wide association studies (GWAS) and recommend specific alleles that could be introgressed in future breeding programs.