

Phenotypic and genetic diversity of root traits in DRR population of barley for selection in breeding

Shiyan Jia¹, Shree Pariyar², Henning Lenz¹, Kerstin Nagel^{1*}, Fabio Fiorani^{1*} | JPPC Group, IBG-2

In our research, the RILs and the parental lines of double round robin population of barley (Casale et al., 2022) will be used. And GrowScreen RhizoIII, which is an automated non-invasive high-throughput phenotyping system, will perform the root phenotyping in the control environment (based on Nagel et al., 2012). The phenotypic data will subsequently be correlated to genotypic data, and QTLs linked to the traits of shoot and root are identified by Genome Wide Association Study (GWAS).

