

PROJECT TITLE

Phenotyping early vigour in barley seedlings

CONSORTIUM

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SUMMARY OF THE REPORT

Early vigour is a trait of high relevance for plant breeders since it has been shown to influence drought tolerance, nutrient uptake, weed competitiveness and yield. Despite this, studies of seedling growth have so far been limited, which could be explained by the difficulties to screen for this trait under field conditions. However, the recent development of high-throughput image analysis now enables non-destructive time-course studies of early seedling growth under a controlled environment. Thus, platforms like APPP-B at IPK in Gatersleben, Germany, is a valuable resource that can provide breeders and researchers with a deeper understanding of the underlying genetic factors that control biomass growth and information about associated quantitative trait loci (QTL). This platform has previously demonstrated the advantage of studying seedling growth over time in a non-destructive way, when it was used for the daily assessment of biomass, from the seedling stage to flowering, in a European two-row spring barley panel. This study revealed several QTL, specific for early and late growth stages, but also showed that the best result for marker-assisted selection was when favorable alleles for high biomass at booting stage was combined with favorable alleles for seedling biomass.

In our project, a panel of 259 genotypes balanced for row-type (consisting of 247 Nordic spring barley breeding lines, cultivars, land races and 12 historic genotypes from IPK's gene bank) was evaluated in three consecutive experiments for seedling biomass development from nine days after sowing (DAS) to DAS 22 using the LemnaTec facility at IPK. In addition to seedling biomass, traits such as tiller number, plant height, fresh and dry weight of above ground biomass, plant width and compactness, chlorophyll fluorescence and relative chlorophyll content were evaluated.

High quality data were obtained for all examined traits and genome-wide association studies (GWAS) revealed several QTL, many of them within regions harboring already known phenology-related genes, but some also within regions where no obvious candidate genes were found and a couple of them that might be unique for Nordic barley material. The results obtained from this transnational project will provide the Nordic breeder's with valuable information regarding the regulation of early vigour and photosystem II efficiency but also identify genotypes promising for improvement of those traits. Furthermore, the balanced set allow for detection of both QTL shared between, but also unique for the two row types. The outcome of the association mapping will be further explored for candidate genes and favorable allele combinations.