PROJECT TITLE

Characterising autotoxicity tolerance in crops releasing natural herbicides.

CONSORTIUM

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SUMMARY OF THE REPORT

To suppress competitors, some plant species have evolved a biochemical strategy called allelopathy: these 'donors' secrete herbicidal chemicals ('allelochemicals') to inhibit neighbours. Allelopathy can be exploited in agriculture to combat weeds because many crops have the capacity to synthesize such allelochemicals. However, a major caveat of allelopathic crops is that allelochemicals can also inhibit the growth of the donor, a phenomenon known as 'autotoxicity', with consequences for crop growth and yield. While little is known about the mechanisms by which donors counteract autotoxicity, understanding these processes is crucial to efficiently use these endogenous weed suppression strategies in sustainable agricultural practices.

The overall aim of our project has been to identify the genetic factors that confer tolerance to autotoxicity in barley (*Hordeum vulgare*). Barley is an ideal model to screen for allelochemical autotoxicity tolerance: it produces many effective allelochemicals and is tractable to quantitative trait loci (QTL) mapping. The proposed research uses the recombinant inbred barley composite cross II (CCII) panel, which was generated by inter-crossing 28 diverse landraces and early cultivars, and selfing the progeny for 58 generations.

In the pilot experiment at FZJ, we noticed that DMSO, the solvent that we use for resuspending the allelochemicals, had detrimental effects on barley growth when applied in a soil environment. This was unexpected, as in our preliminary experiments using hydroponic culture, we had never noticed such an effect. As a result, we had to exclude allelochemicals from the EPPN study. Instead, we decided to phenotype the root architecture of the barley lines in order to identify the genetic basis of root growth and root architecture. We detected substantial variation in root growth and biomass among the CCII parental landraces; these data are currently explored for genetic associations, using genome-by-sequencing data generated by our collaborators.