

PROJECT TITLE

Fine-mapping a QTL for photosynthetic efficiency in *Cardamine hirsuta*

CONSORTIUM

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SUMMARY OF THE REPORT

Crop yield is determined by the available solar irradiation energy, the radiation interception efficiency, the light conversion efficiency and the harvest index. From this factorial analysis, photosynthetic efficiency emerges as the most potent factor for yield improvement. Enhancement of crop photosynthesis would be an important step in improving yield, contributing to sustainable development without sacrificing more arable land for use in agriculture. We aimed to contribute to this effort by identifying and characterizing the precise DNA polymorphism(s) that influence photosynthetic efficiency in natural populations of *Cadamine hirsuta* in the context of the broader aim to discover and characterize natural genetic variation affecting photosynthetic efficiency, leaf development, and seed yield.

We previously detected a QTL for photosynthetic efficiency (θ_{PSII}) in a recombinant inbred line (RIL) population using the Phenovator platform. We have now attempted to both validate and fine-map this QTL in a single experiment, which was feasible due to the high throughput and high reproducibility of the platform. Before the experiment we selected a heterogeneous inbred family (HIF) that segregated in a region broadly covering the QTL for validation of its effects. But rather than performing QTL validation immediately we also selected a set of 22 segregating recombinant HIFs, chosen such that if the QTL could be validated and its position was accurately estimated, it would be fine-mapped sufficiently to start considering candidate genes. As it stands we have been able to validate the presence of a QTL affecting θ_{PSII} in the original QTL interval, and the fine-mapping, which requires genotyping, is ongoing.

The founder strains of the RIL population in which the QTL for θ_{PSII} was detected were collected from environments contrasting in seasonal and diurnal changes in temperature (extremes). We therefore hypothesized that the QTL reflected differentiation driven by these environmental differences. We tested this hypothesis by evaluating the change of the allelic effects of the QTL on θ_{PSII} in response to transient changes in temperature. We found that a rapid decrease in air temperature leads to a corresponding change in θ_{PSII} independent of allele at the QTL. But θ_{PSII} in plants with the allele from the strain collected in an environment where such temperature changes are more likely to occur recovered faster than in those with the alternative allele.

To summarize, we have validated a QTL affecting θ_{PSII} in *Cardamine hirsuta* and obtained evidence supporting the hypothesis that the differentiation at the QTL is driven by local adaptation. We also collected data that may allow fine-mapping the QTL towards identifying the causal gene and the specific polymorphisms underlying the QTL effects, which would allow gaining a deeper understanding of photosynthetic adaptation to temperature and offer the opportunity to apply this knowledge in crop improvement.