

PROJECT TITLE

Mapping photosynthetic stress in a new Africa-centric worldwide panel of *Arabidopsis thaliana*

CONSORTIUM

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SUMMARY OF THE REPORT

Natural variation in photosynthetic efficiency represents a novel source of information to improve our basic understanding of the biology of photosynthesis and the ecological trade-offs to increasing yield via modifications of this pathway. In this project we will use a new collection of *A. thaliana* accessions, including populations from some of the Earth's most challenging environments in Afro-alpine East Africa, Israel and Saudi Arabia to identify novel genetic variants underlying individual differences in photosynthetic efficiency and stress response.

Natural populations of the primary molecular model plant, *Arabidopsis thaliana*, are particularly powerful for learning about local adaptation and the inter-relation of traits. Extensive research has focused on *A. thaliana* accessions collected from across Europe, including comparative assessments of physiological trait values, trait mapping, and population history reconstruction. However, recent work showed that these intensively-studied European accessions primarily represents a recently expanded lineage and only contains a limited subset of the variation in the *A. thaliana* species.

Through field collection and collaboration, we have assembled a set of *A. thaliana* accessions from South Africa, Ethiopia, Morocco, Israel and Saudi Arabia. We gathered these together with other representative worldwide samples to produce a set of 360 accessions spanning a total latitudinal range of over 100 degrees with altitudes from sea level to 4000m. Now, we are working with collaborators to phenotype these accessions for diverse traits to produce an integrated map of phenotypic variation across the *A. thaliana* species distribution.

In this project we surveyed variation in photosynthetic parameters in this new *A. thaliana* diversity panel to identify the genetic bases of variation in photosynthesis. This project is a collaboration with Prof. Mark Aarts and Tom Theeuwens at Wageningen University using the Phenovator platform, which has already been used extensively for other *A. thaliana* natural and recombinant populations.