

**PROJECT TITLE**

Mapping elemental composition in a new Africa-centric worldwide panel of *Arabidopsis thaliana*

**CONSORTIUM**

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# SUMMARY OF THE REPORT

Soil composition and climatic factors can influence availability of nutrients and exposure of a plant to trace elements. In response, plants may evolve to differ in nutrient processing and trace element homeostasis. Understanding the factors that contribute to these differences is useful to improve our understanding of basic biological and ecological mechanisms and can be applied to improve crop varieties for challenging environments.

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 have gathered these together with other representative worldwide samples to produce a set of 400 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.

Here, surveyed and mapped the genetic bases of variation in elemental processing in collaboration with David Salt and Paulina Flis at the University of Nottingham. The project uses our new diversity panel of *A. thaliana* samples from Africa and other worldwide locations. The work will benefit from complementary phenomics for life history, drought stress and photosynthesis parameters as well as population genetics analyses to identify the loci underlying adaptation in these samples.