GWAs identifies candidate polymorphisms involved in the mineral depletion of *Arabidopsis thaliana* under elevated CO_2

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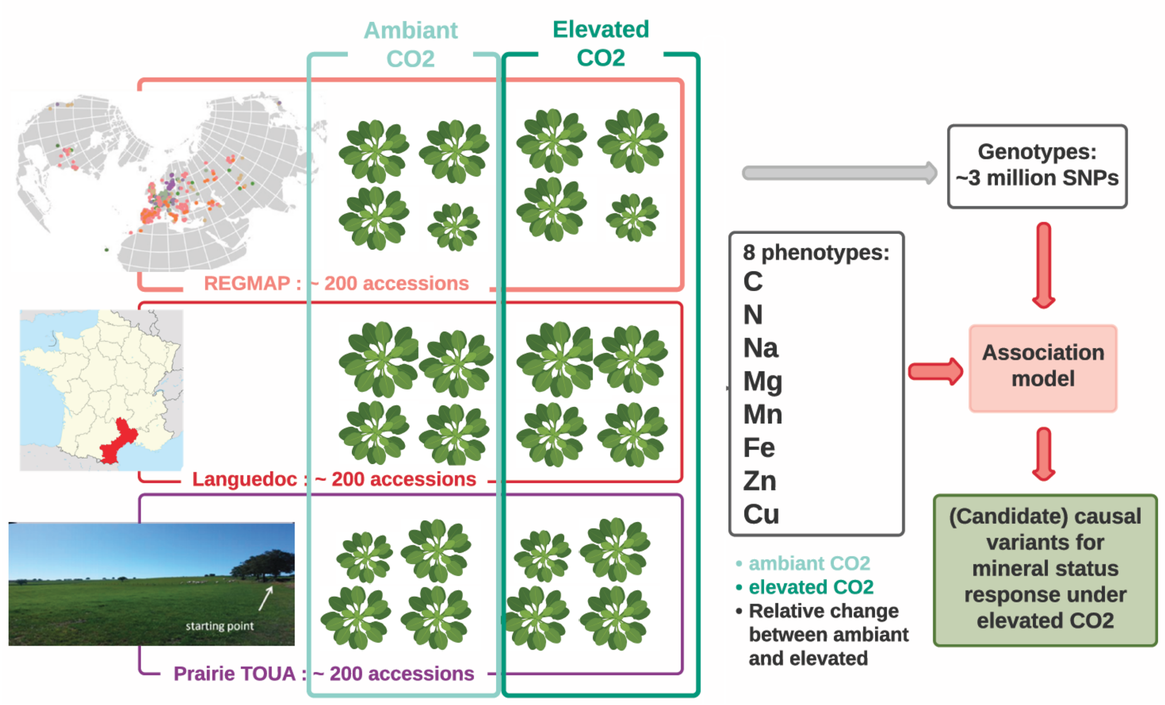
Introduction and methods

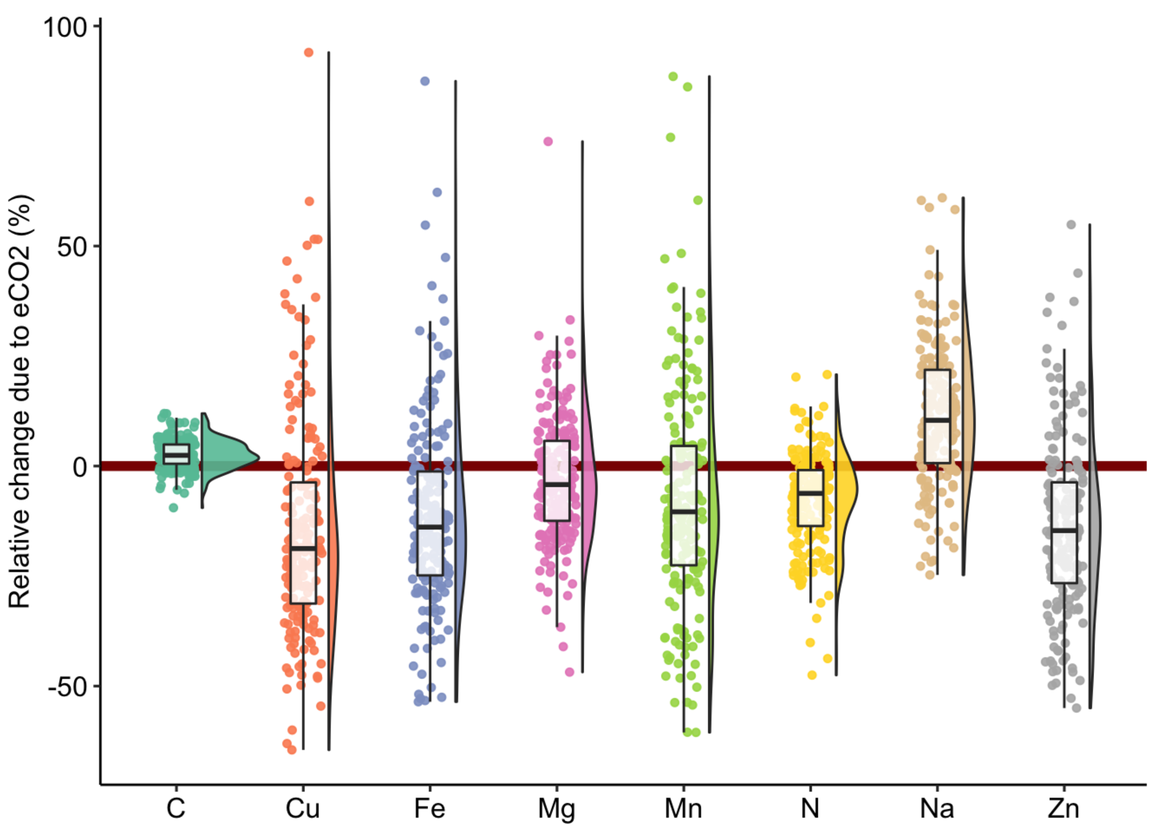
In the decades to come, atmospheric CO_2 concentration is expected to steadily increase. This comes as a serious threat to food security, as the ionome of C3 plants declines when exposed to high CO_2 conditions (Zhu and Ziska 2018). Identifying polymorphisms underlying such intra-specific diversity could not only be a way to understand this response, but also to breed more resilient crops.

In this work, we screened three populations of ecotypes, originating from local, regional and world-wide (Horton and Bergelson 2012), (Arouisse and Kruijer 2020) geographic scales grown in soil in contrasted CO_2 conditions (eCO_2=900ppm, aCO_2 =400ppm), and characterized the phenotypic variability observed in their ionome response to high CO_2. The **relative changes** of each element under elevated CO_2 were computed as $\frac{\text{element}_{eCO_2} - \text{element}_{aCO_2}}{\text{element}_{aCO_2}} * 100$

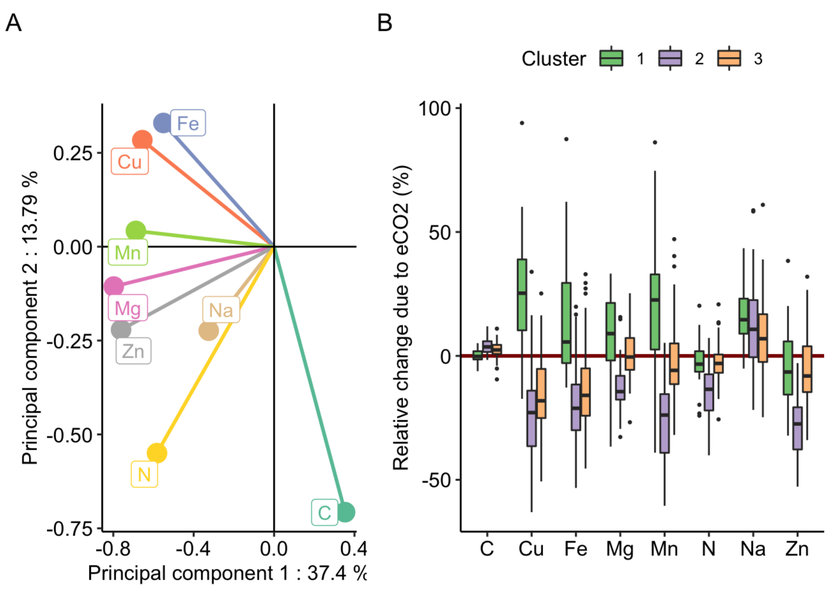


Phenotype to genotype associations were conducted by **Linear Mixed Models, accounting for population structure while testing the influence of genomic variants** in the `statgenGWAS` R package (van Rossum and Kruijer 2020).

Ionome response to eCO_2 is highly variable among Arabidopsis ecotypes

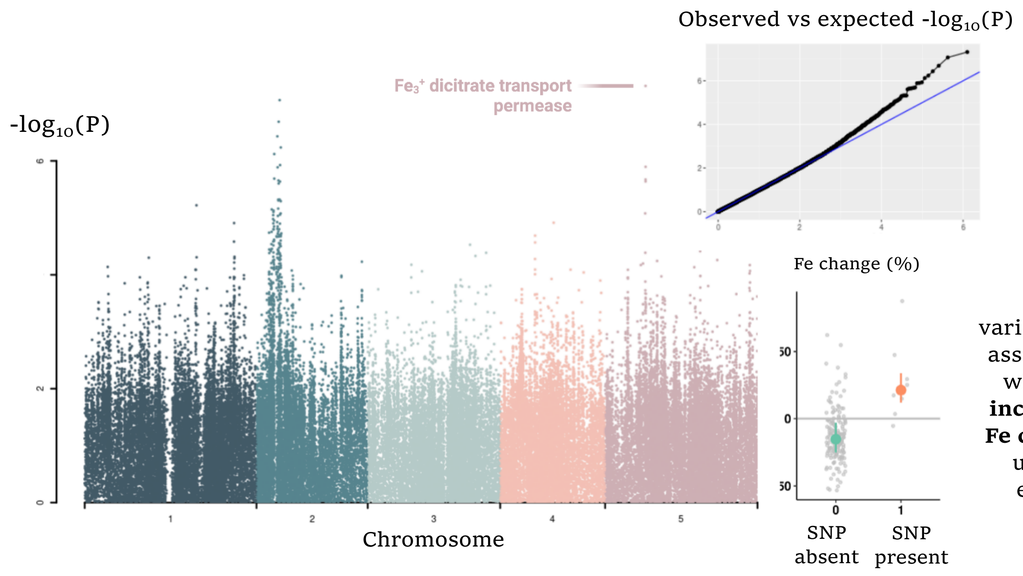


Relative changes in 8 elements were measured in the shoots of REGMAP acessions. It shows that mineral content declines globally under eCO_2, and there is an **antogonistic response of mineral elements versus carbon content**.



Ionomic changes contributions to PCA components under eCO_2 for the three populations are shown. K-means multivariate clustering of the REGMAP accessions depending on their mineral content variation highlights a group of **26 tolerant ecotypes** with a preserved ionome under eCO_2.

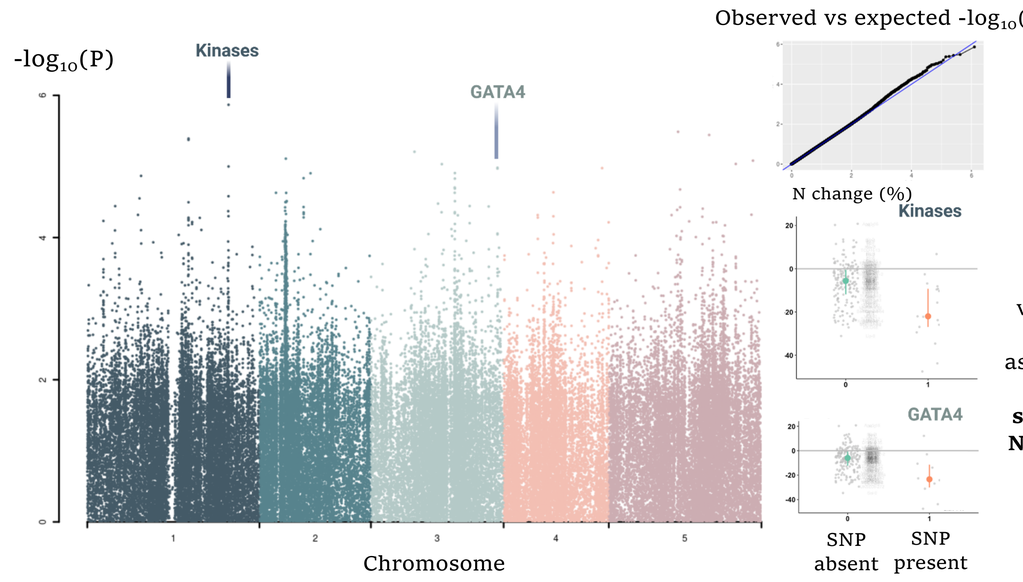
GWAs on Fe change under eCO_2



Top variants are associated with an **increased Fe content** under eCO_2

4 strong signal SNPs near AT5G21070, a Fe_3^+ dicitrate transport system permease, form a haplotype of interest.

GWAs on N change under eCO_2



Top variants are associated with a **stronger N decline** under eCO_2

5 strong signal SNPs near GATA4, a putative actor in N pathways, and 4 strong signal SNPs near kinases form haplotypes of interest.

Perspectives

Functional study of candidate genes for the control of Fe and N accumulation in shoots will be carried out by examining mutant lines, and measuring the expression of genes close to top variants in promising haplotaypes. New candidates can also be identified by exploring other mineral elements, the local and regional populations, and exploiting local score metrics in Manhattan plots.

References

Arouisse, Bader, and Willem Kruijer. 2020. "Imputation of 3 Million SNPs in the Arabidopsis Regional Mapping Population." *The Plant Journal* 102 (4): 872–82. https://doi.org/10.1111/tpj.14659.

Horton, Matthew W, and Joy Bergelson. 2012. "Genome-Wide Patterns of Genetic Variation in Worldwide Arabidopsis Thaliana Accessions from the RegMap Panel." *Nature Genetics* 44 (2): 212–16. https://doi.org/10.1038/ng.1042.

van Rossum, Bart-Jan, and Willem Kruijer. 2020. *statgenGWAS: Genome Wide Association Studies*. https://CRAN.R-project.org/package=statgenGWAS.

Zhu, Chunwu, and Lewis H. Ziska. 2018. "Carbon Dioxide (CO 2) Levels This Century Will Alter the Protein, Micronutrients, and Vitamin Content of Rice Grains with Potential Health Consequences for the Poorest Rice-Dependent Countries." *Science Advances* 4 (5). https://doi.org/10.1126/sciadv.aaq1012.

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