

Coselected genes determine adaptive variation in herbivore resistance throughout the native range of *A. thaliana*

The “mustard oil bomb” is a major defense mechanism in the Brassicaceae, which includes crops such as canola and the model plant *Arabidopsis thaliana*. These plants produce and store blends of amino acid-derived secondary metabolites called glucosinolates. Upon tissue rupture by natural enemies, the myrosinase enzyme hydrolyses glucosinolates, releasing defense molecules. Brassicaceae display extensive variation in the mixture of glucosinolates that they produce. To investigate the genetics underlying natural variation in glucosinolate profiles, we conducted a large genome-wide association study of 22 methionine-derived glucosinolates using *A. thaliana* accessions from across Europe. We found

that 36% of among accession variation in overall glucosinolate profile was explained by genetic differentiation at only three known loci from the glucosinolate pathway. Glucosinolate-related SNPs were up to 490-fold enriched in the extreme tail of the genome-wide F_{ST} scan, indicating strong selection on loci controlling this pathway. Glucosinolate profiles displayed a striking longitudinal gradient with alkenyl and hydroxyalkenyl glucosinolates enriched in the West.

We detected a significant contribution of glucosinolate loci toward general herbivore resistance and lifetime fitness in common garden experiments conducted in France, where accessions are enriched in hydroxyalkenyls. In addition to demonstrating the adaptive value of glucosinolate profile variation, we also detected

long-distance linkage disequilibrium at two underlying loci, GS-OH and GS-ELONG. Locally cooccurring alleles at these loci display epistatic effects on herbivore resistance and fitness in ecologically realistic conditions. Together, our results suggest that natural selection has favored a locally adaptive configuration of physically unlinked loci in Western Europe.

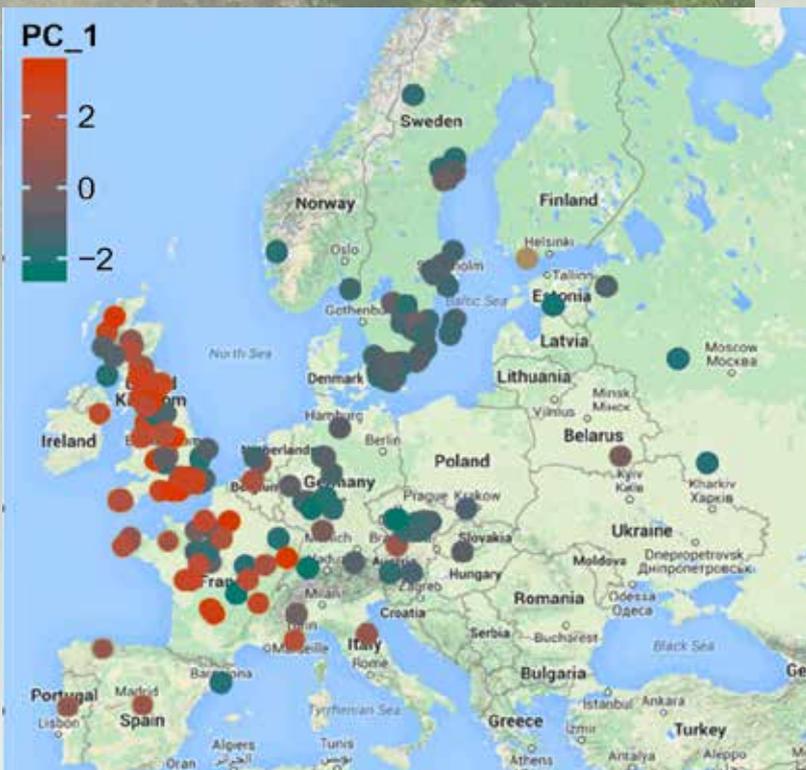


Fig.: Dots indicate collection sites, and the color reflects the score of each accession along the principal component describing GSL profile variation. The gradient from dark grey to red represents an increase in alkenyl and hydroxyalkenyl GSLs.