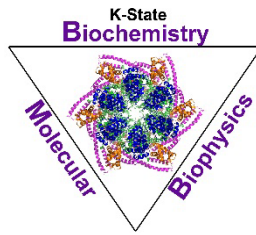


Ackert Hall, Room 120
Wednesday, February 19, 2025
4:00 P.M.



Coffee and Cookies
Chalmers Hall, Room 168
3:45 P.M.

Biochemistry
&
Molecular
Biophysics

Seminar

**ECOLOGICAL, SELECTIVE AND GENOMIC FORCES SHAPING ENZYME
AND DEFENSE METABOLITE EVOLUTION ACROSS THE BRASSICALES**

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Plant Specialized metabolism is key to how plants adapt to abiotic and biotic interactions. This creates highly lineage specific chemical compositions that are often associated with co-evolutionary theory. We are using the glucosinolates within the Brassicales to test how chemical diversity is shaped across genomic, geographic and phylogenetic scales.

Geography and Fluctuating Selection: To understand the interplay between glucosinolates and selection, we studied the 1001 Arabidopsis accession collection. Measuring the glucosinolate chemotyped showed that local adaptation differs with fluctuating selection in central Europe and directional selection in Iberia. This mapped to two major known loci containing extensive genetic heterogeneity including convergent evolution caused by structural variation. Recreating the phenotypic consequence of this structural variation in single gene variants showed that these loci are under fluctuating selection such that the optimal chemotype is highly specific to the year and location. This shows that there are different selective forces across the geographic range of the species and that local adaptation is not a linear process.

Genomic and Phylogenetic Evolution: Studying these loci across the Brassicaceae, shows that simple presence absence variation hides a complicated genomic process involving segmental and distal duplications. This enabled a high rate of independent gene loss across the lineages. Extending this to species with novel glucosinolates showed that the creation of novel patterns relied equally on distal gene duplication and gene loss but not whole genome duplications. Extending this across the Order showed that distal duplication and neofunctionalization is the key process to creating metabolic diversity and not whole genome duplications.