

Natural Variation and Comparative Genomics

J. Chris Pires (Chair)
piresjc@missouri.edu
 University of Missouri



Ya-Long Guo (Co-Chair)
yalong.guo@ibcas.ac.cn
 Institute of Botany, Chinese Academy of Sciences



Recently developed Open Tools and Resources for Arabidopsis Researchers

AraShare (www.arashare.cn), a stock center to share Arabidopsis seeds among colleagues, was established in China to facilitate research in Arabidopsis.

Recent or Future activities of Subcommittee members

Beside the model species *Arabidopsis thaliana*, there have been many species in the family Brassicaceae and order Brassicales that have been sequenced to facilitate comparative genomics. With respect to natural variation within species, numerous populations have been sequenced or have had pan-genomes made to facilitate population genomics and association studies. With the divide shrinking between “model species” studied by a large consortium and creating genomic resources for any species of interest to a single investigator, the subcommittee is overwhelmed with reporting on all the resources and studies within genera like Arabidopsis and Brassica, let alone all the other related species. Our basic understanding of natural variation and genome evolution is exploding along with this research area’s ability to support applied efforts ranging from crop improvement to the conservation of biodiversity.

Selected Publications

- Hepworth J, Antoniou-Kourounioli RL, Berggren K, Selga C, Tudor EH, Yates B, Cox D, Collier Harris BR, Irwin JA, Howard M, Säll T, Holm S, Dean C.. 2020. Natural variation in autumn expression is the major adaptive determinant distinguishing Arabidopsis FLC haplotypes. *Elife* 9: e57671.

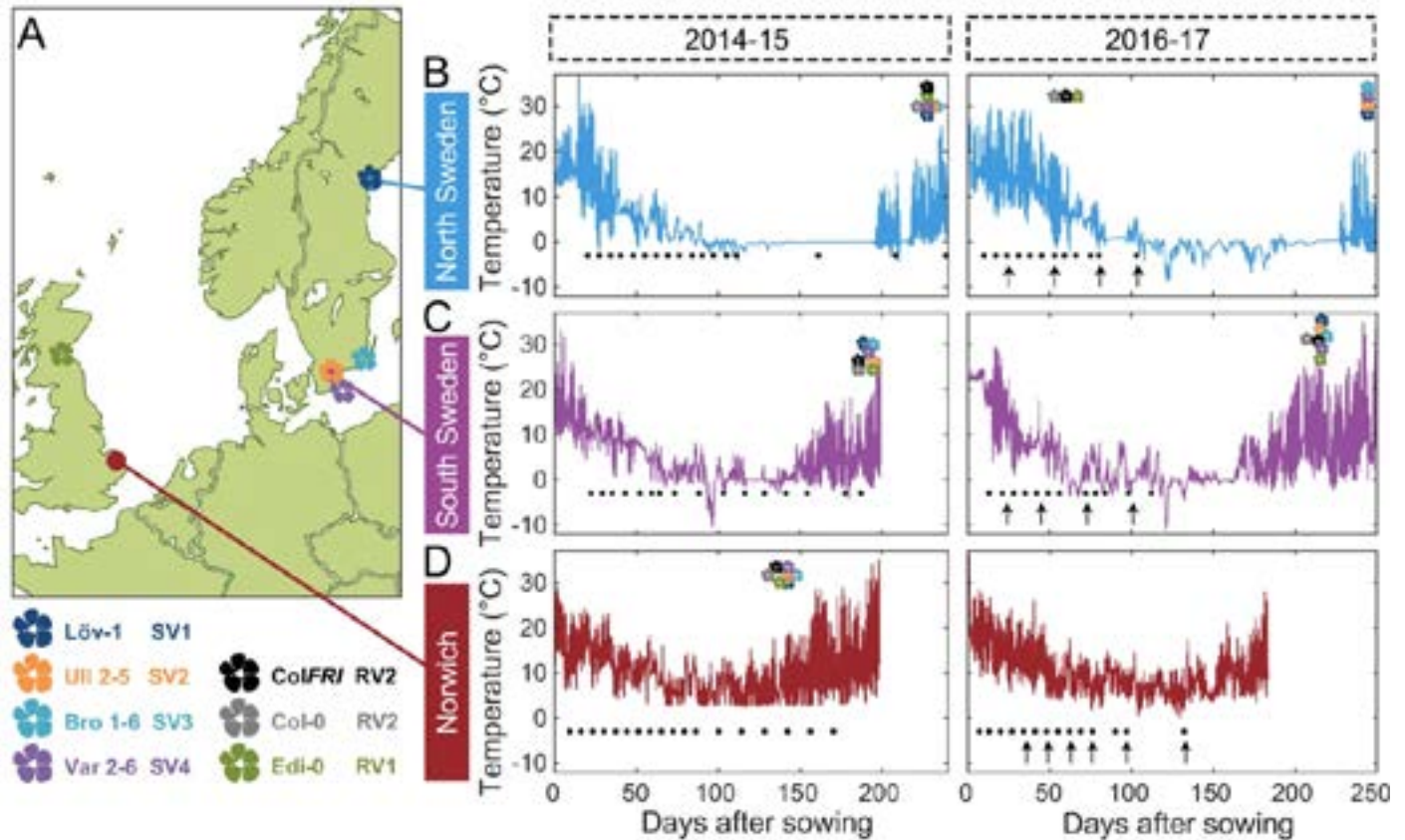
This study reveals how expression variation through non-coding *cis* variation at FLC has enabled Arabidopsis accessions to adapt to different climatic conditions and annual fluctuations

- Tsuchimatsu T, Kakui H, Yamazaki M, Marona C, Tsutsui H, Hedhly A, Meng D, Sato Y, Stadler T, Grossniklaus U, Kanaoka MM, Lenhard M, Nordborg M, Shimizu KK. 2020. Adaptive reduction of male gamete number in the selfing plant *Arabidopsis thaliana*. *Nat Commun* 11: 2885

This study identified the causal gene of the variation of male gamete number, and support theoretical predictions that reduced investment in male gametes is advantageous in predominantly selfing species

- Voichek Y, Weigel D. 2020. Identifying genetic variants underlying phenotypic variation in plants without complete genomes. *Nat Genet* 52: 534-540.

This study demonstrates the power of performing GWAS before linking sequence reads to specific genomic regions, which allows the detection of a wider range of genetic variants responsible for phenotypic variation



Field experimental setup.

(A) Map showing locations of field sites (dots) and the origins of five of the accessions (flowers) used in this study. These accessions, with the addition of Col-0, represent the five major and one intermediate (Löy-1) FLC haplotypes identified by Li *et al.*, 2014. The lab genotype Col FRI was also used in this study as a vernalization-requiring reference.

(B–D) Temperature profiles experienced by plants at the three field sites, North Sweden – Ramsta (B), South Sweden – Ullstorp (C) and Norwich, UK (D) (Source data 1, as from Hepworth *et al.*, 2018 and Antoniou-Kourouniotti *et al.*, 2018). Flowers above temperature profile indicate the median time of bolting of each of the natural accessions and of Col FRI (legend at bottom left corner).

Black dots below temperature profile indicate the timepoints when plant material was collected for expression analysis. Black arrows below temperature profiles indicate time of transfer to greenhouse with long-day, warm conditions to assess degree of vernalization based on bolting time.

- Wieters B, Steige KA, He F, Koch EM, Ramos-Onsins SE, Gu H, Guo YL, Sunyaev S, de Meaux J. 2021. Polygenic adaptation of rosette growth in *Arabidopsis thaliana*. PLoS Genet 17: e1008748.

This study shows that the growth rate variation is caused by multiple loci of small effect, and tests of adaptive divergence indicate that these differences may reflect adaptation to local environmental conditions

- Zust T, Strickler SR, Powell AF, Mabry ME, An H, Mirzaei M, York T, Holland CK, Kumar P, Erb M, Petschenka G, Gomez JM, Perfectti F, Muller C, Pires JC, Mueller LA, Jander G. 2020

Rapid and independent evolution of ancestral and novel defenses in a genus of toxic plants (*Erysimum*, Brassicaceae). eLife 9: e51712. The findings describe a system in which plants have naturally evolved an equivalent strategy to escape their main herbivores, and ancestral and novel chemical defenses in *Erysimum* thus appear to provide complementary rather than redundant functions.

Planning for Fourth Decadal Roadmap

- How can plants and people adapt to the changing climate in a sustainable manner?
- How do we integrate studies across disciplines, evolutionary depth (population biology to cross-clade comparisons), and various ecological challenges to answer these fundamental questions?
- As one initial step, can we better understand evolution in the context of pleiotropy (one gene affecting multiple traits) and polygenic variation (one trait is regulated by multiple genes)?

