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## Exploiting omics of *Brassica napus* core diversity populations to address trait genetics and polyploid genome evolution associated with breeding method

### Background:

Omics technologies and data resources have provided unprecedented opportunities to address issues or questions that are impossible to be addressed before. For example, high throughput mapping of genetic factors controlling important traits, not only DNA, but also RNA and epigenetic elements, and their links. More importantly, these have exposed potential of breeding technology innovation to sharply shorten breeding period as well as increase trait selection efficiency.

### Objective:

To use multi-omics technologies and resources of 2800+ *B. napus* accessions to tackle high throughput mapping of genetic elements controlling important traits and to establish relationships between causal DNA elements and gene expression regulation and trait variation.

### Methods:

A *B. napus* pan-genome was constructed from step-wise integrating de novo whole genome assemblies, de novo local assemblies and re-sequencing reads of genotypes selected from 2800+ accessions. Of the 2800+ accessions population, subpopulations were subjected to RNA-seq, Hi-C, ATAC-seq and ChIP-seq, and phenotyping of metabolites (metabolomics), disease resistance and agronomic and quality traits. The analyses of GWAS, eQTL, TWAS and colocalization analysis were respectively conducted and integrated. Genome editing, transgenics and other genetic and biochemical approaches were employed to study gene function and molecular mechanisms.

### Results:

Hundreds of loci controlling traits of disease resistance, seed quality, plant architecture, physiology and yield components were identified by GWAS, mGWAS and TWAS based on SV and SNP. More than three hundred thousand eQTLs that cis- or/and trans-regulate expression of more than seventy thousand genes. The genes in mapping regions were pinpointed by the two pipelines of candidate gene exclusion/selection developed in our lab: one is comparative genomics analyses between mapped regions of segregant population's parents, accessions and subgenomes A and C; the second is comprehensive analyses integrated with GWAS, eQTL, TWAS and colocalization analysis, which enable high-throughput identification of SV/SNP-gene expression-trait variation links. Some putative genes were validated for their functions by gene editing, Arabidopsis mutants and/or other genetic approaches. Genetic architectures of important traits were dissected, for example, those of flowering time, seed and oil quality and disease resistance.

Population genomics studies revealed that molecular mechanisms of polyploidy genome evolution, majorly subgenomic asymmetry that was observed in individual genomes (see References) and polyploid genomic plasticity, in which asymmetry in recombination and spatial interactions of the subgenomes A and C may play a crucial and central role.

### Conclusions:

The comprehensively integrated analyses of multi-omics data enable high throughput identification of genetic loci for important traits and some causal genes, and further establishment of SV/SNP-gene expression-trait variation links. The subgenomic asymmetry in recombination and plasticity provides a direction for development of new genetic improvement strategies to broaden genetic variation.

### References:

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