

Mustard



Family of Brassicaceae



<http://www.nglish.com>



www.alimentarium.org



www.natureinbottle.com



www.vietnamesische-rezepte.de



www.eurekalert.org



www.shutterstock.com

Glucosinulates

- Well-studied secondary metabolism pathway
- Stored in Vakuoles
- Hydrolysed by myrosinase
- Products (isothiocyanates, thiocyanates, and nitriles) as defence against herbivores
- Flavor compounds

vocabulary

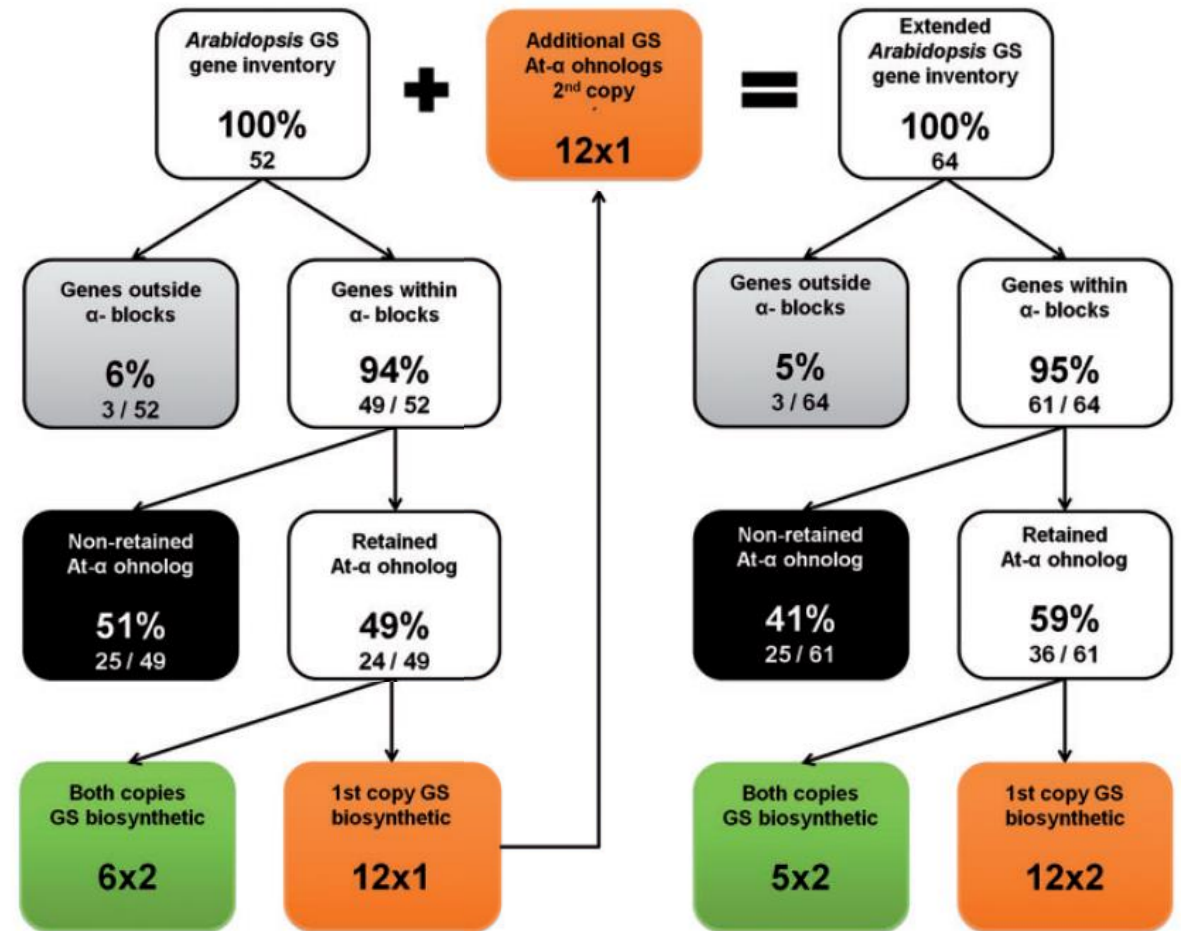
- Synteny - physical co-localization of genetic loci on different chromosomes
- Homoeologous/ohnolog genes – homologous gene pairs
- homoeologous gene expression dominance – uneven expression between homoeologous genes

Hofberger et. Al (2013)

- *Arabidopsis thaliana* compared to *Aethionema arabicum*
- *A. arabicum* similar GS chemotype as Brassicaceae crown group
- Earliest diverged clade („ancient“)
- Last WGD shared (At-alpha)
- Synteny conserved in At-alpha blocks

Distribution of GS pathway genes

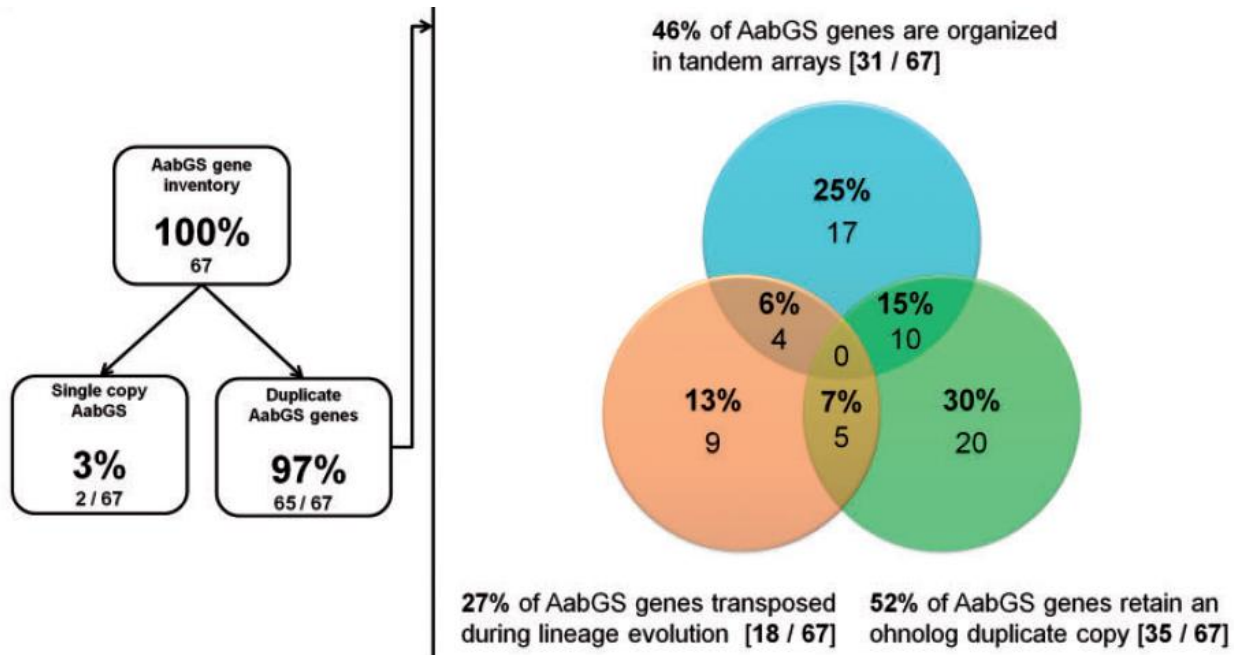
- 59% of GS genes with retained ohnolog copy
- Average: 22%



Canonical set of *Arabidopsis* glucosinolate (AtGS) genes (Sønderby et al. 2010)

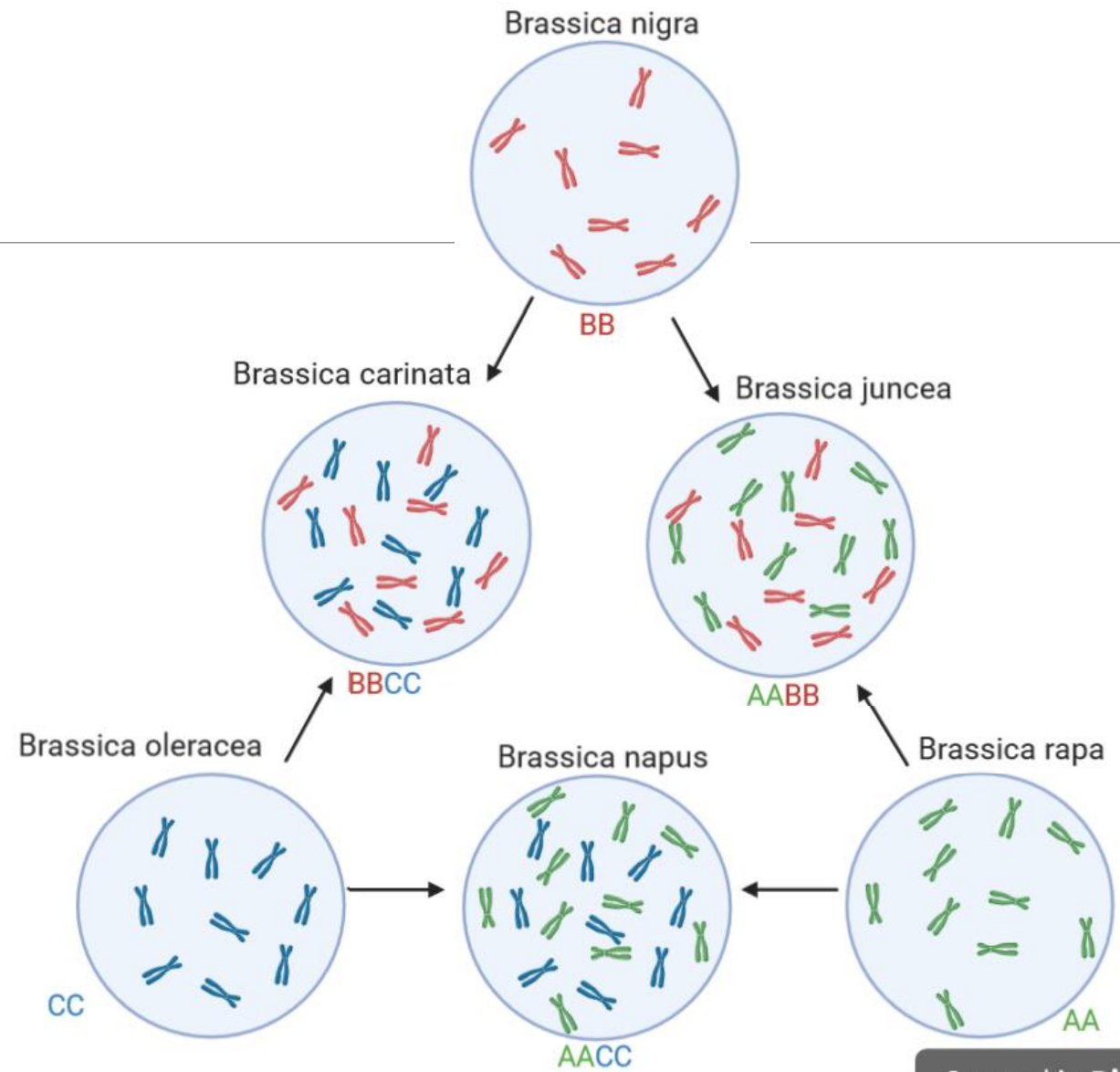
Extended set of *Arabidopsis* glucosinolate (AtGS) genes (this study)

Duplicate distribution

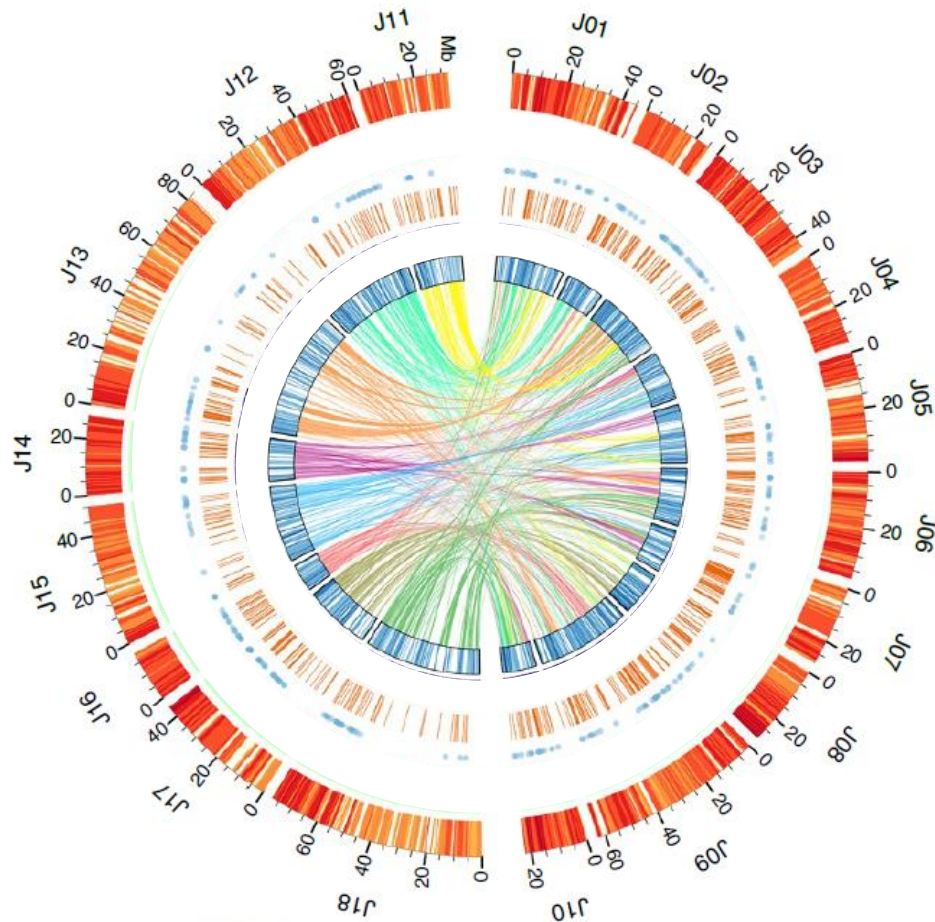


- tandem duplicates (blue)
- retained ohnologs (green)
- gene transposition duplicates (orange)
- GS genes more often as duplicates than other genes
- WGD and TD accelerated genetic versatility of GS
- Possibly hold true for other secondary metabolites and for other plants

Triangle of U

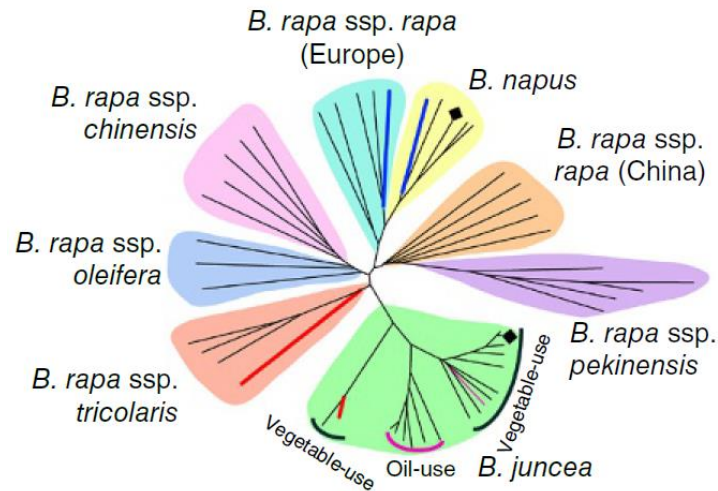
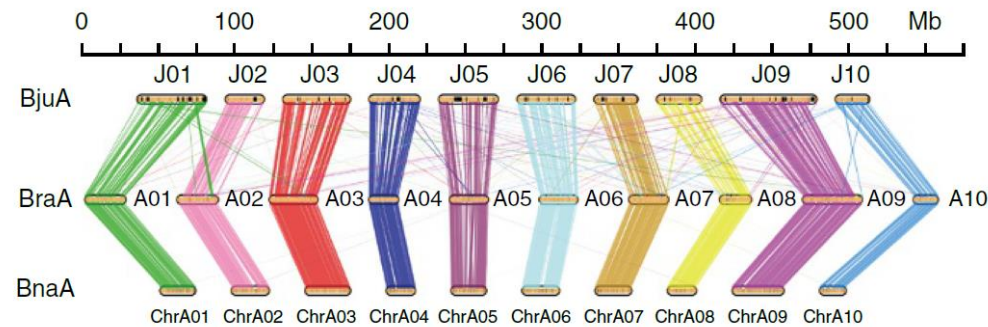


B. Juncea genome comparison



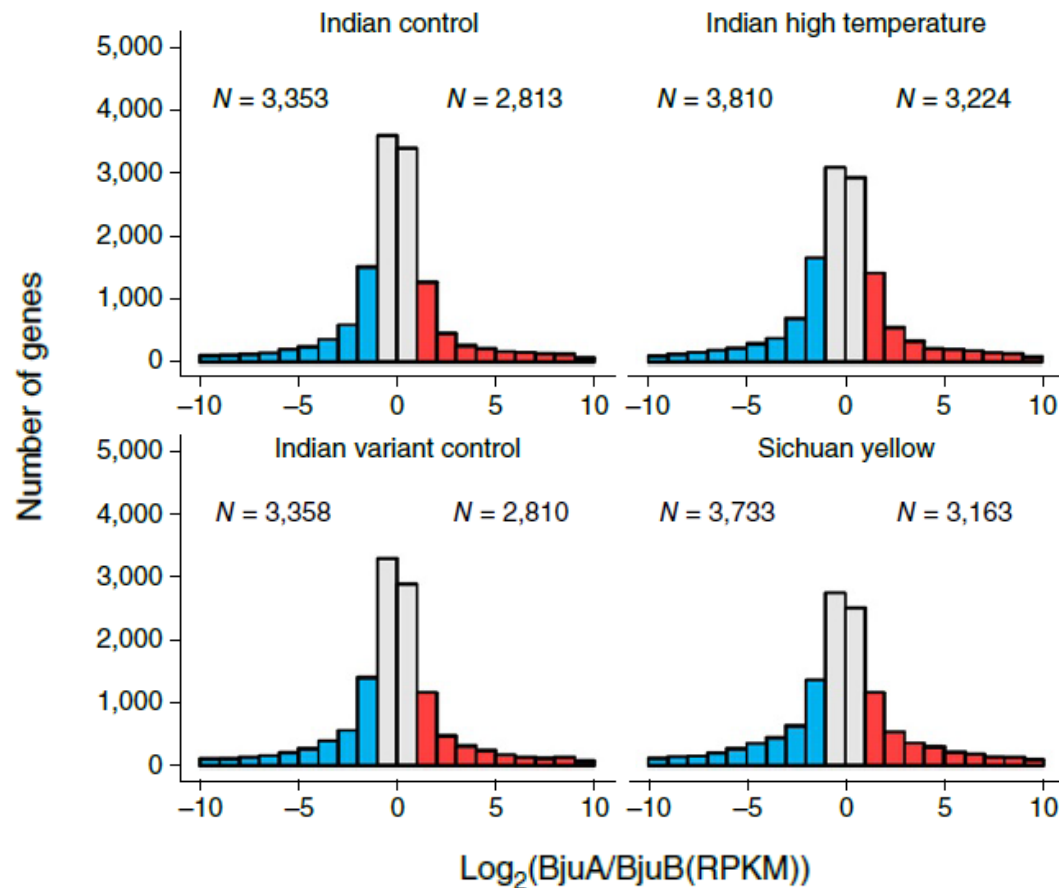
- Left: *B. Juncea* B
- Right: *B. Juncea* A
- Many homologous genes
- → lost genes/pseudogenes

Synteny of the A genome across species



- Chromosomal rearrangements between juncea and rapa
- Not expected, if A genome obtained from same species
- Analysis of SNPs → neighbor-joining tree
- different origins
- *B. Juncea* A from *B. rapa* ssp. *Tricoloris* (Asia)
- *B. napus* A from *B. rapa* ssp. *Rapa* (EU)
- *B. Juncea* with monophyletic hybridisation event

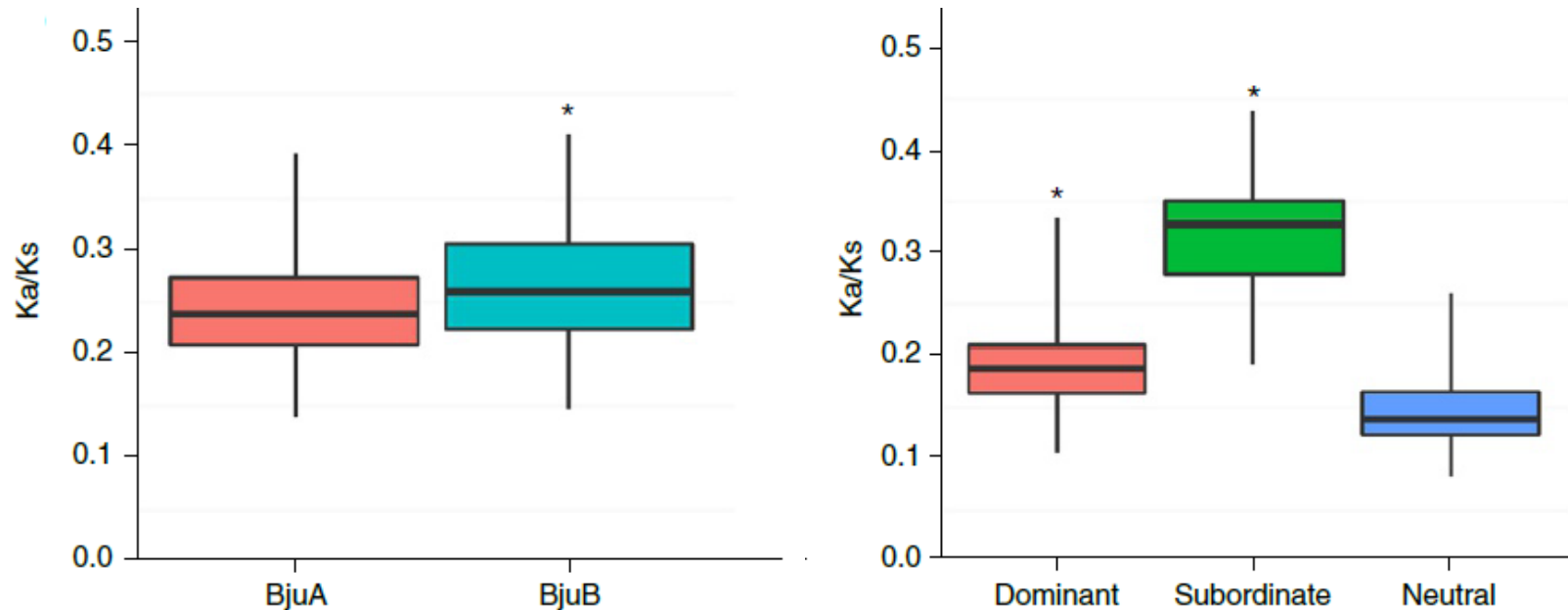
Genome-wide transcriptional levels



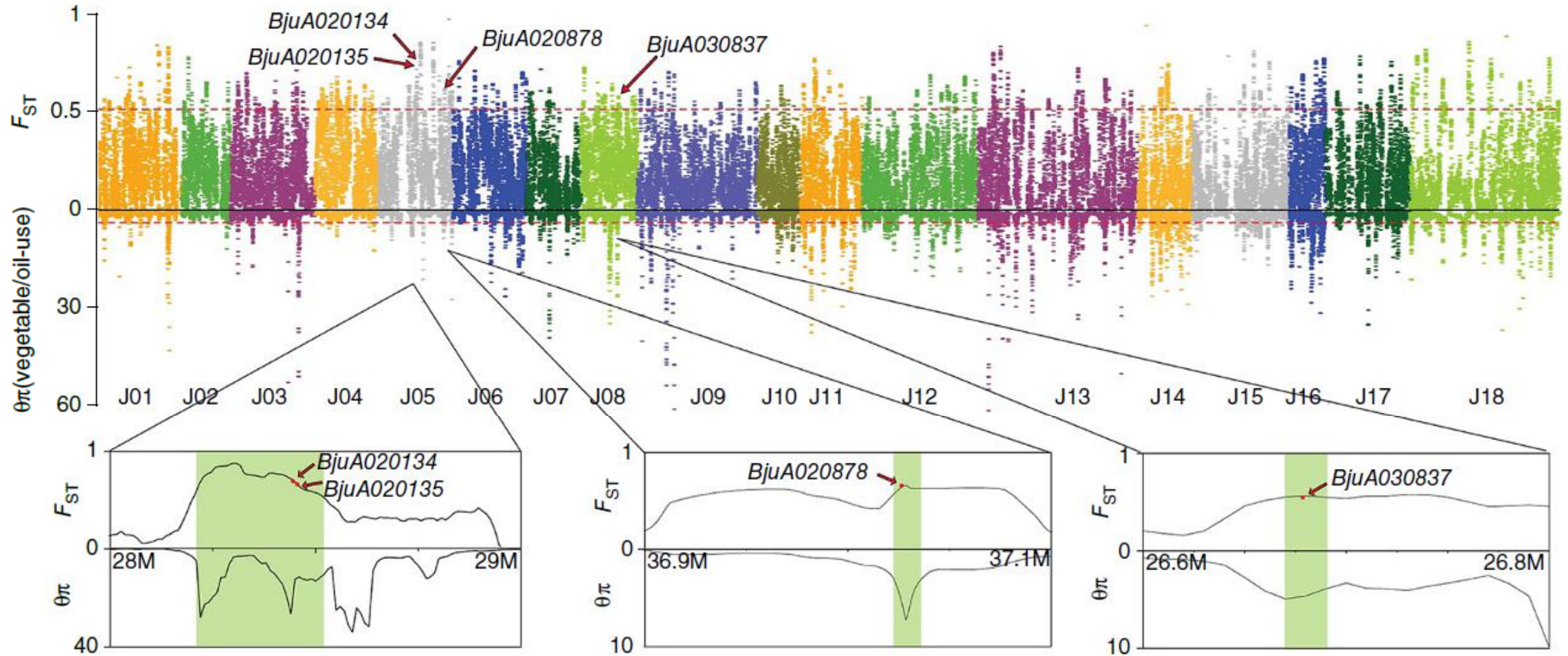
- 16.2% of genes homoeologous expression dominance
- BjuB slightly more dominant in most cases
- primarily in secondary metabolism

Genomic selective pressure

- non-synonymous/synonymous substitution
- asymmetric evolution of the subgenomes
- Dominant and subordinate genes evolved more quickly



Selective sweep regions



Conclusion

Acceleration of genetic versatility of plant secondary metabolism by WGD and TD

Evolutionary stability of this versatility

Increased selection potential of genes with homoeolog expression dominance

Sources

- Halkier, B.A., and Gershenzon, J. (2006). BIOLOGY AND BIOCHEMISTRY OF GLUCOSINOLATES. *Annual Review of Plant Biology* 57, 303-333.
- Hofberger, J.A., Lyons, E., Edger, P.P., Chris Pires, J., and Eric Schranz, M. (2013). Whole Genome and Tandem Duplicate Retention Facilitated Glucosinolate Pathway Diversification in the Mustard Family. *Genome Biology and Evolution* 5, 2155-2173.
- Yang, J., Liu, D., Wang, X., Ji, C., Cheng, F., Liu, B., Hu, Z., Chen, S., Pental, D., Ju, Y., *et al.* (2016). The genome sequence of allopolyploid *Brassica juncea* and analysis of differential homoeolog gene expression influencing selection. *Nature Genetics* 48, 1225-1232.
- Yoo, M.J., Szadkowski, E., and Wendel, J.F. (2013). Homoeolog expression bias and expression level dominance in allopolyploid cotton. *Heredity* 110, 171-180.