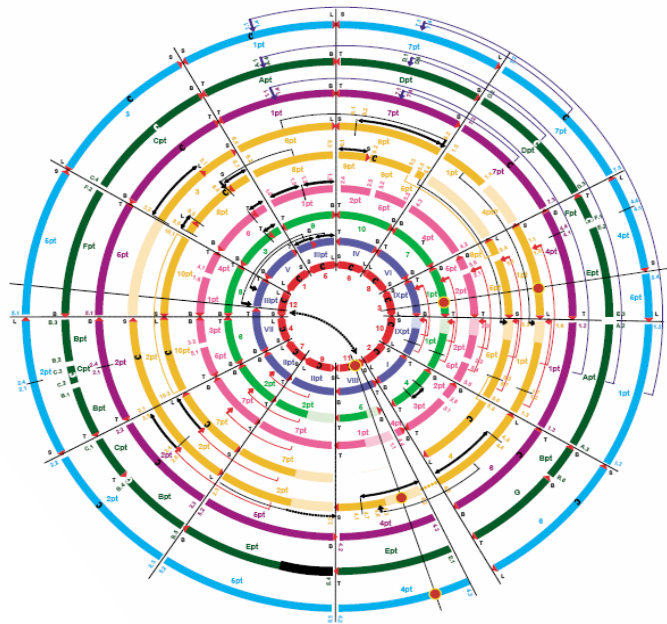


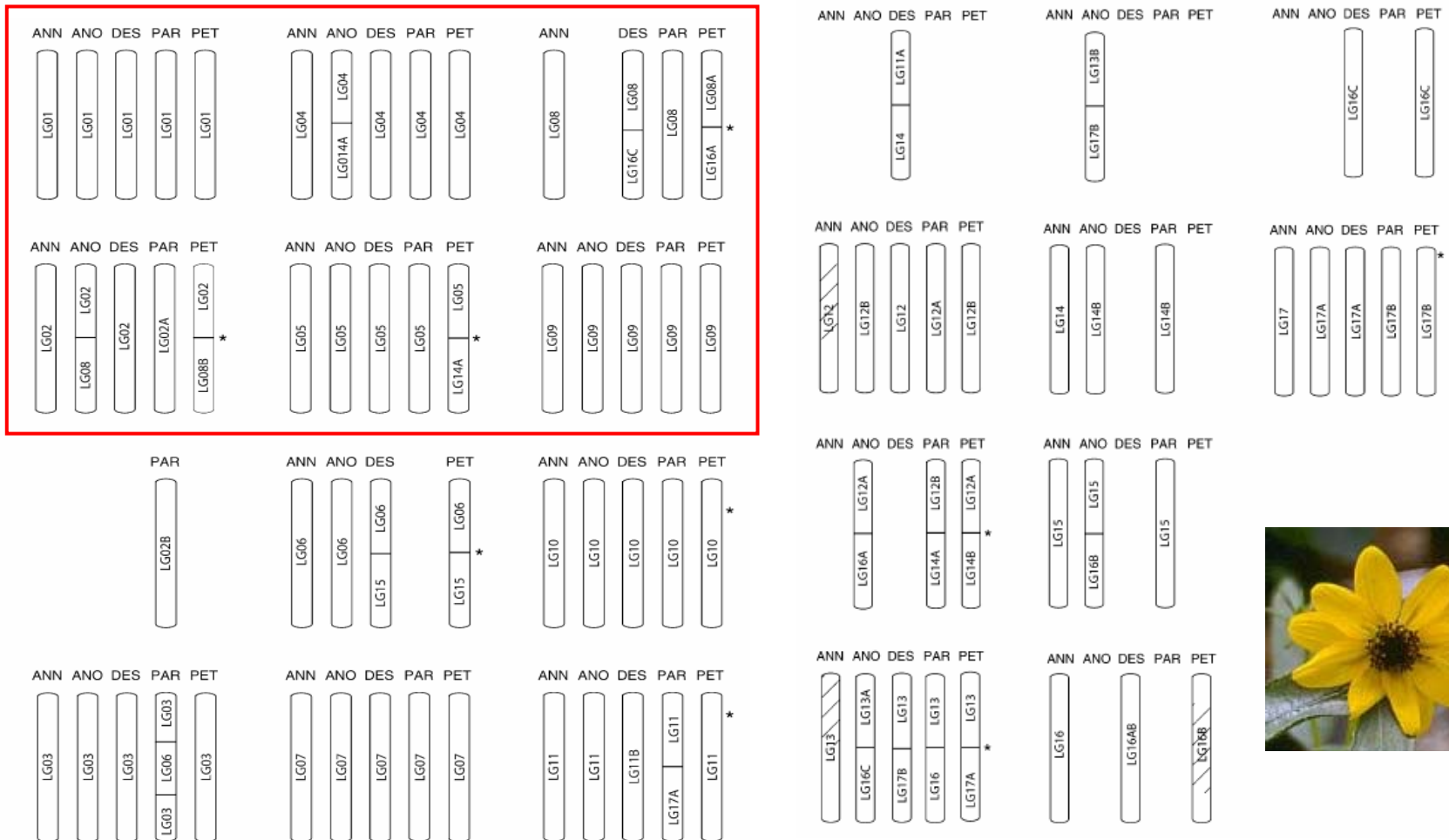
# Genome and chromosome synteny and collinearity



# High level of genome collinearity between *Helianthus* species (*Asteraceae*)

*Helianthus annuus* (ANN), *H. petiolaris* (PET): parental species

*H. anomalus* (ANO), *H. deserticola* (DES), and *H. paradoxus* (PAR): diploid hybrid derivatives

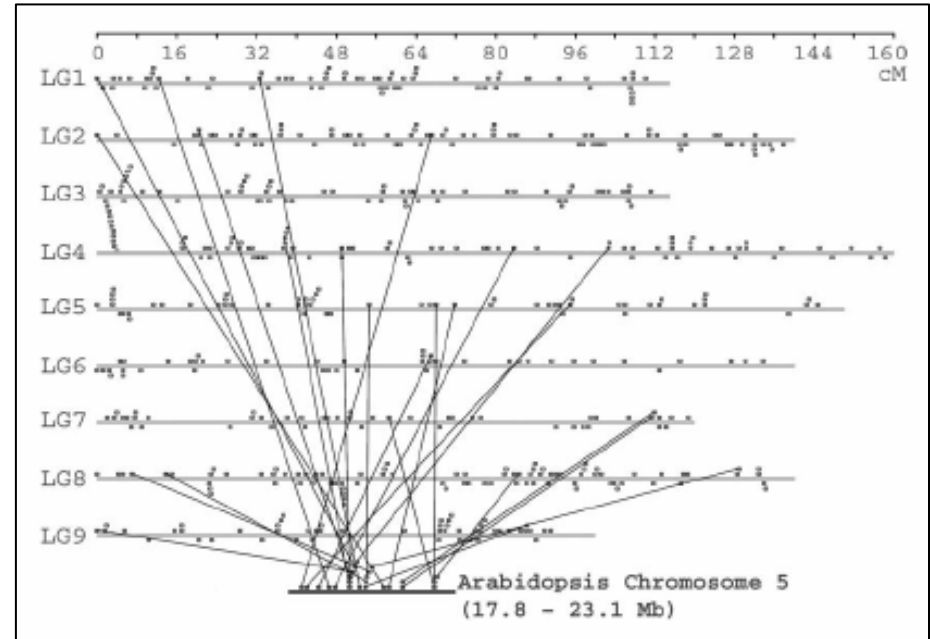


Segments containing inversions are indicated by hatched lines.

# Limited synteny between *Arabidopsis* and *Asteraceae* species

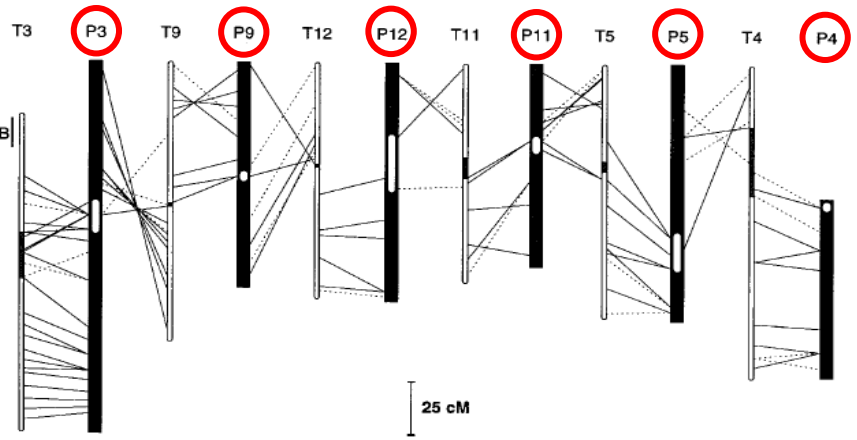
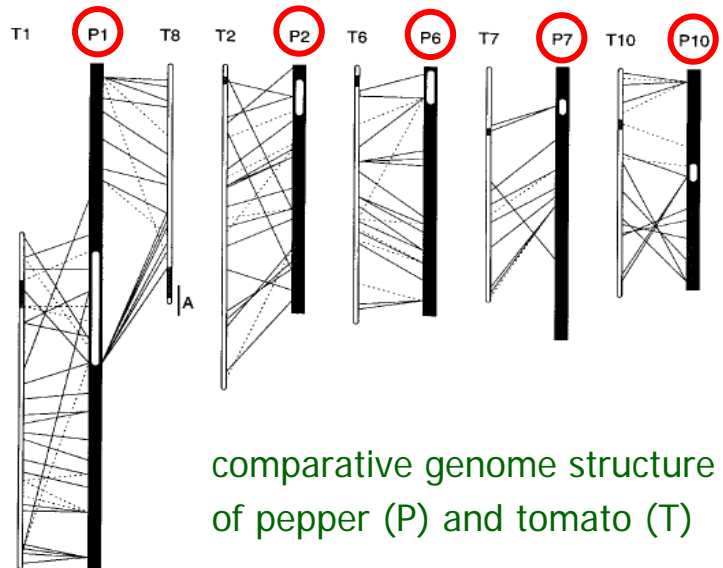


- what is the level of synteny between the model species *Arabidopsis thaliana* and *Asteraceae* species (*Compositae*)?
- macrosyntenic patterns covering large segments of the chromosomes were not evident
- significant levels of local synteny (microsynteny) were detected at a fine scale; the syntenic patches are often not colinear



Physical positions of conserved orthologous sequences in a 5.5-Mb region of Arabidopsis chromosome 5 and their corresponding mapped positions on the nine linkage groups of *Lactuca sativa* (LG 1–9)

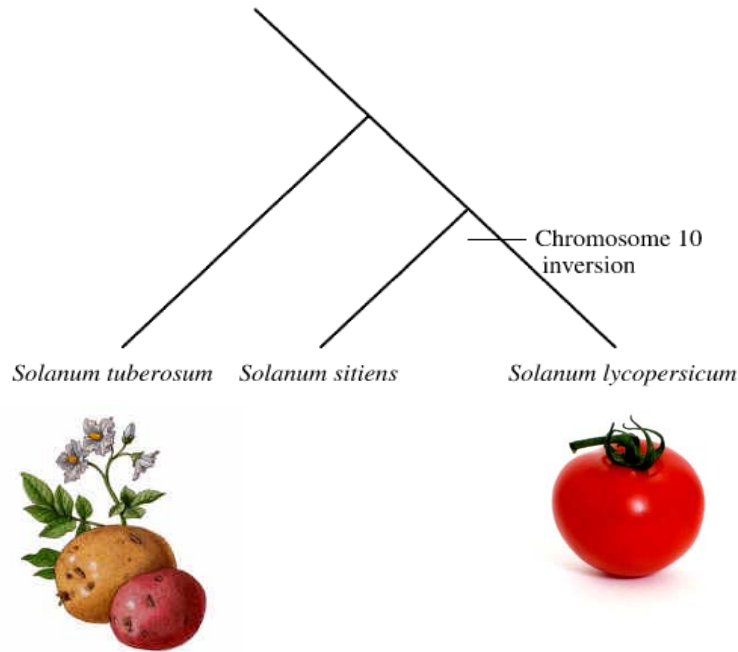
# Genome synteny between pepper ( $n=12$ ; *Capsicum*) and tomato ( $n=12$ ; *Solanum lycopersicum*)



- 18 homeologous linkage blocks cover 98.1% of the tomato genome and 95.0% of the pepper genome
- 30 breaks as part of 5 translocations, 10 paracentric inversions, 2 pericentric inversions, and 4 disassociations or associations of genomic regions that differentiate tomato, potato, and pepper



# Genome synteny between *Solanaceae* species in the molecular phylogenetic context



- comparative mapping studies showed that tomato (*Solanum lycopersicum*) and potato (*Solanum tuberosum*) are differentiated by a series of whole-arm paracentric inversions of chromosomes 5, 9, 10, 11, and 12

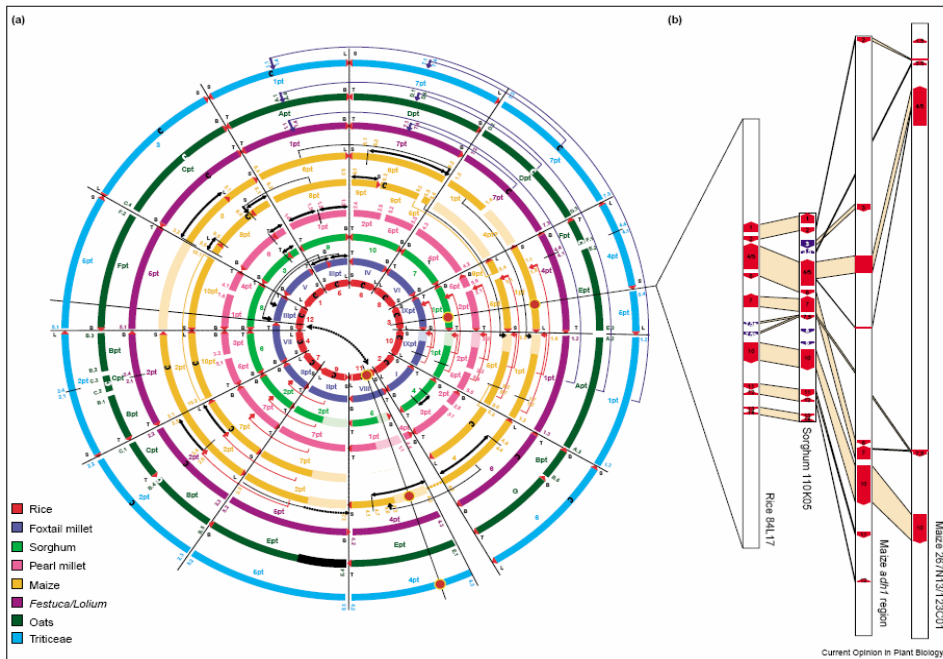
- the chromosome 10 inversion arose within the tomato lineage after the split from the common ancestor with potato

# Crop Circle: collinearity between grass genomes



Crop Circle diagram showing the currently known relationships between the genomes of eight species belonging to three different subfamilies

Right-hand side: microcolinearity of Adh-orthologous regions of rice, sorghum and the two maize homoeologs (genes are indicated by red and blue arrows).

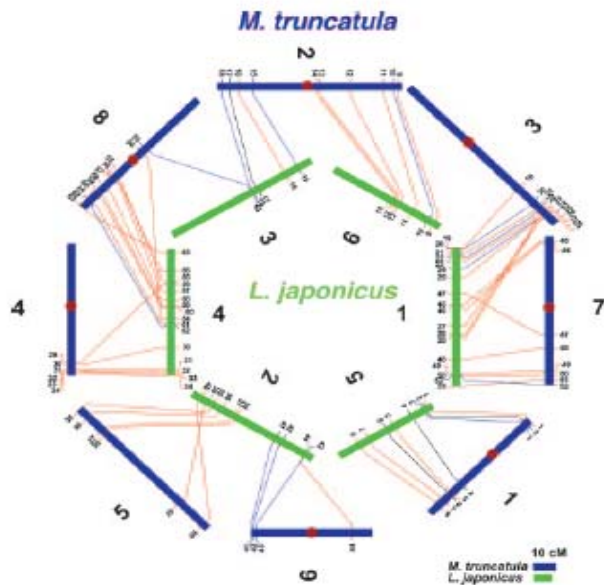


- the most comprehensive comparative dataset obtained to date
- What is the extent of collinearity at the DNA-sequence level?
  - Many small rearrangements that disturb collinearity in orthologous chromosome regions.

# Level of genome conservation between legume species (*Fabaceae*)

## Macrosyntentic relationship of *Medicago truncatula* and *Lotus japonicus*

Line color indicates the number of conserved genes between two clones: black, two; blue, three to four; red, five or more.

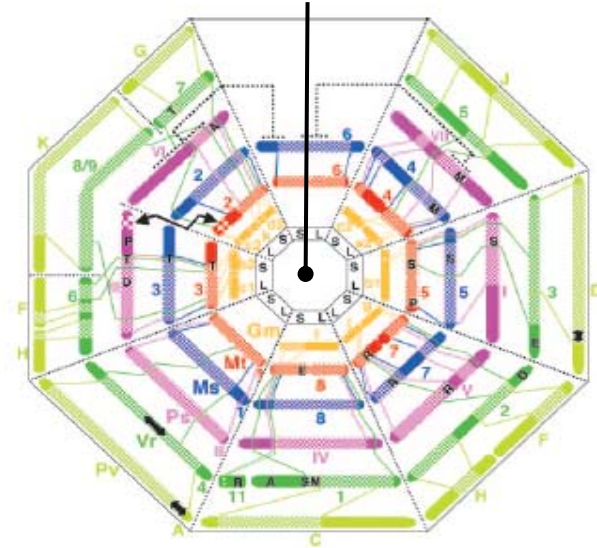


*Medicago truncatula* (n=6)  
*M. sativa* (n=16)  
*Pisum sativum* (n=7)  
*Glycine max* (n=20)  
*Vigna radiata* (n=11)  
*Phaseolus vulgaris* (n=11)  
*Lotus japonicus* (n=6)

- broad conservation of genome macrostructure
- chromosomal rearrangements that may underlie the variation in chromosome number between the species



*Lotus japonicus*

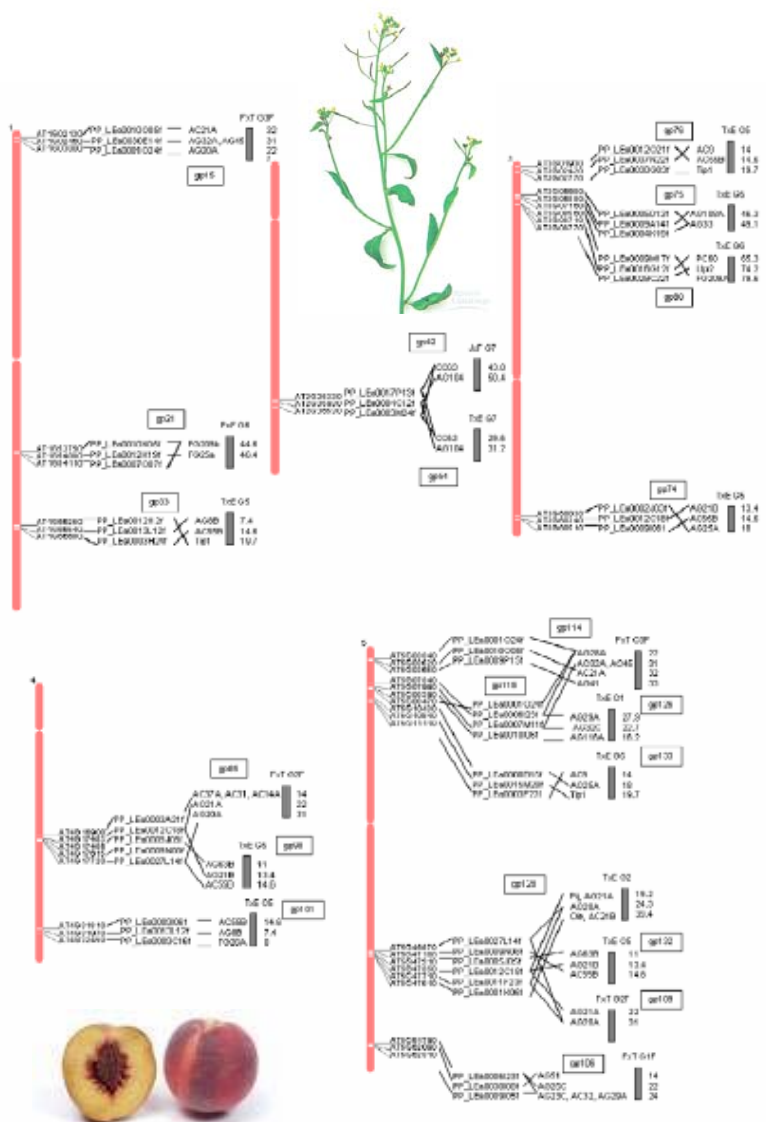


Consensus comparative map data for 6 legume species

- comparison between *M. truncatula*, *L. japonicus* and *G. max*  
 → high conservation between the genomes of *M. truncatula* and *L. japonicus*, whereas lower levels of conservation were evident between *M. truncatula* and *G. max*

# Synteny conservation between the *Prunus* genome and both the present and ancestral *Arabidopsis* genomes

Sook Jung\*<sup>1</sup>, Dorrie Main<sup>2</sup>, Margaret Staton<sup>1</sup>, Ilhyung Cho<sup>3</sup>, Tatyana Zhebentyayeva<sup>1</sup>, Pere Arús<sup>4</sup> and Albert Abbott<sup>1</sup>



- syntenic regions were short and contained only a couple of gene pairs
- all the *Prunus* linkage groups containing syntenic regions matched to more than two different *Arabidopsis* chromosomes
- conserved syntenic regions in the pseudoancestral *Arabidopsis* genome: in many cases, the gene order and content of peach regions was more conserved in the ancestral genome than in the present *Arabidopsis* region

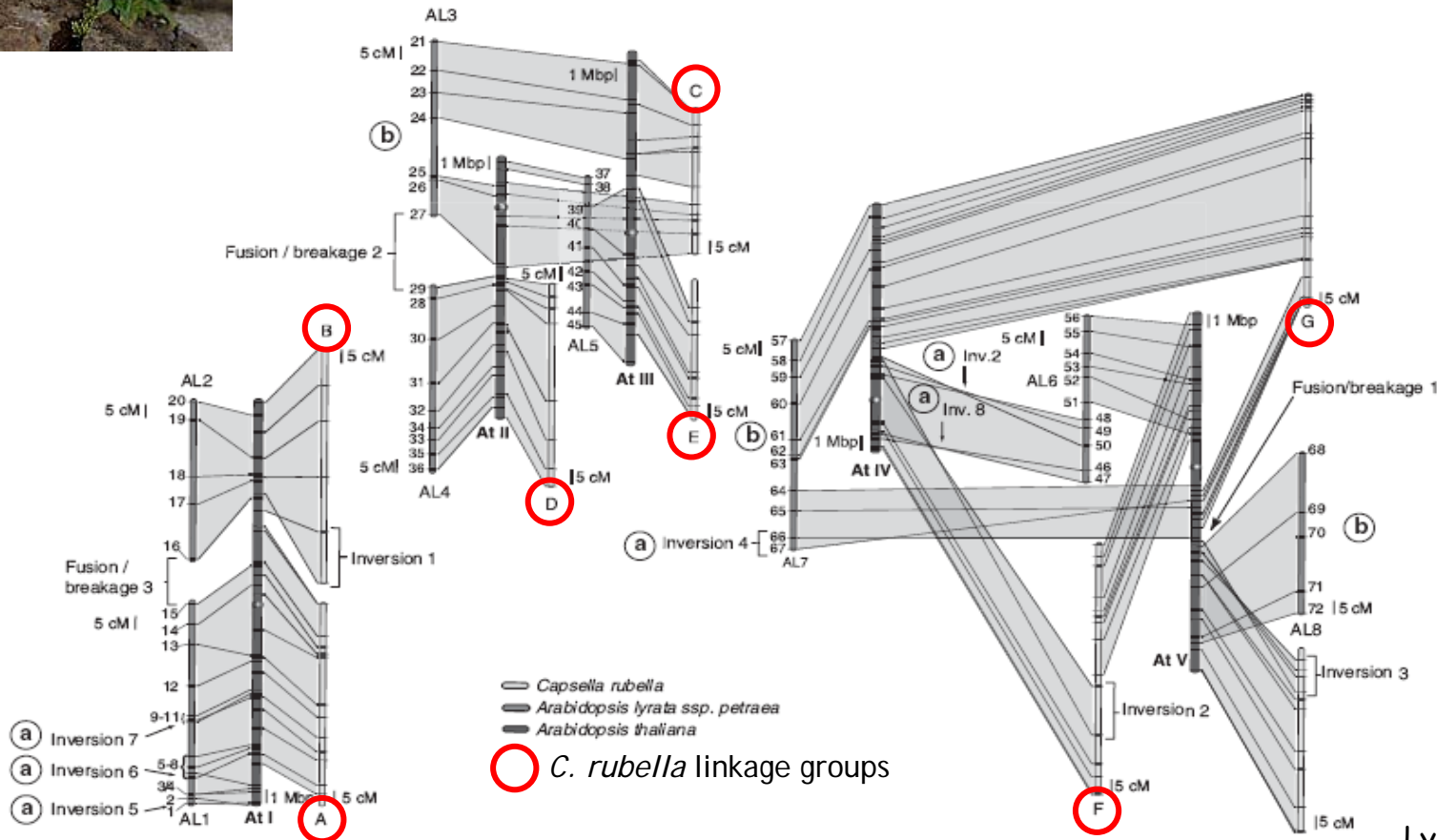




# Genome collinearity in crucifers (*Brassicaceae*)

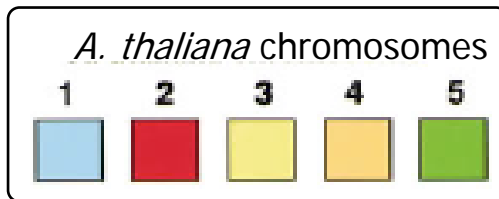
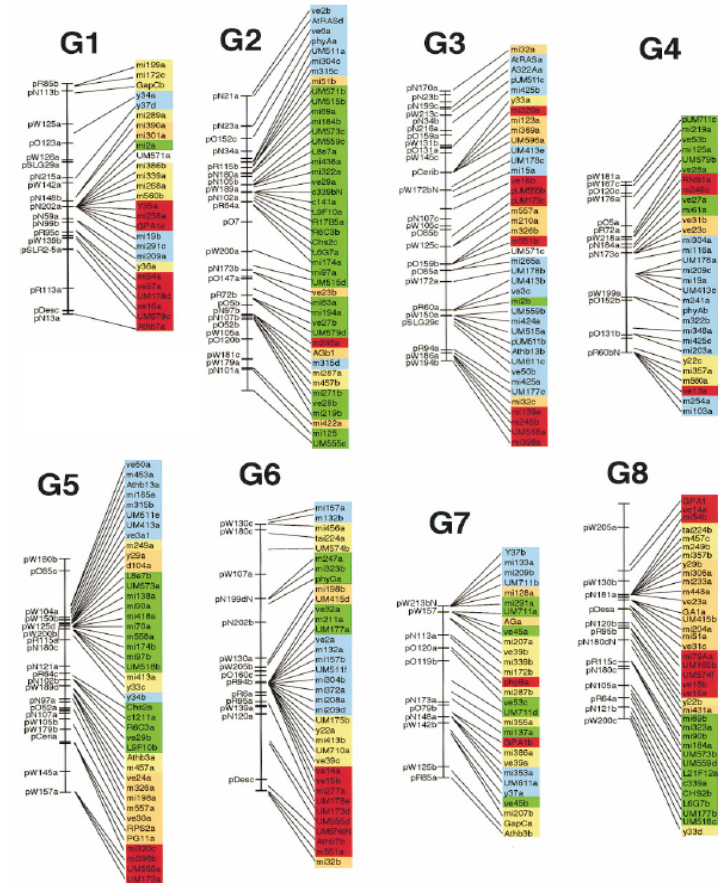


- eight linkage groups of *Arabidopsis lyrata* and *Capsella rubella* (n=8) show a high level of collinearity to the five chromosomes of *A. thaliana* (n=5)
- *A. lyrata* and *C. rubella* genomes exhibit almost identical structure



# Genome collinearity in crucifers: *Arabidopsis* - *Brassica*

Eight linkage groups (G1-8) of *B. rapa* compared to five *A. thaliana* chromosomes



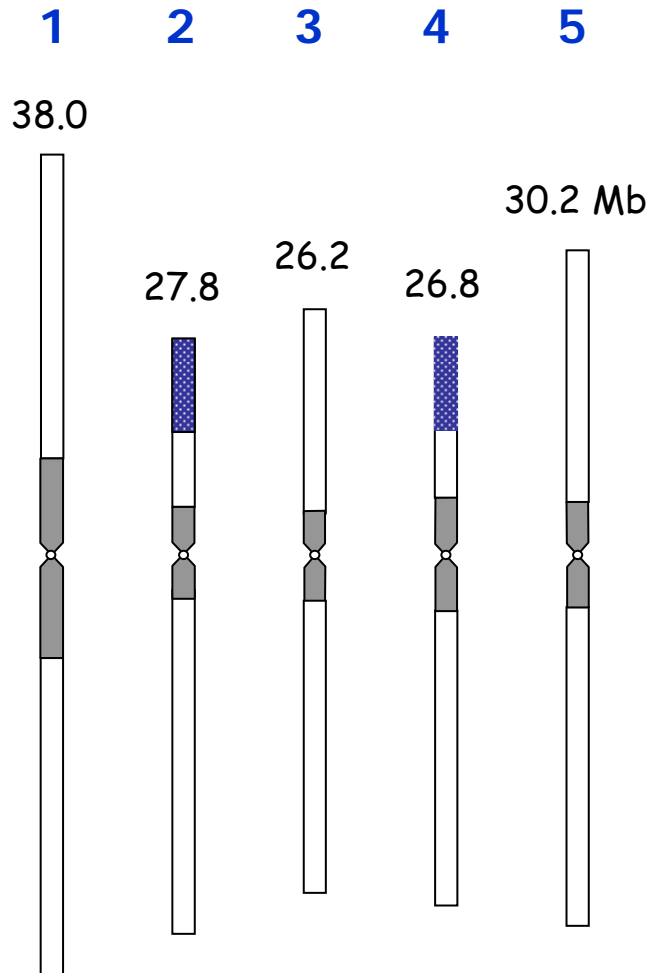
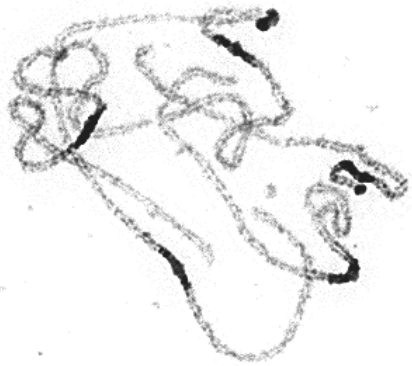
- B. rapa* and all modern diploid *Brassica* species have triplicated genomes and probably descended from a hexaploid ancestor

- the duplications were accompanied by an exceptionally high rate of chromosomal rearrangements

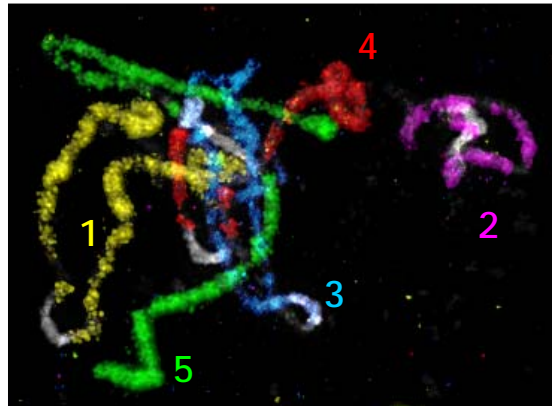
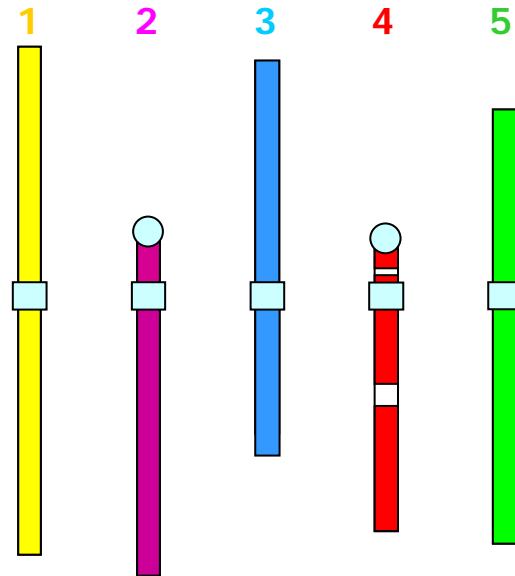
- the *B. nigra* linkage groups show a typical pattern of relatively large blocks of markers from particular *A. thaliana* chromosomes interrupted by a few markers from one or more other from *A. thaliana* chromosomes



# Painting the *A. thaliana* genome

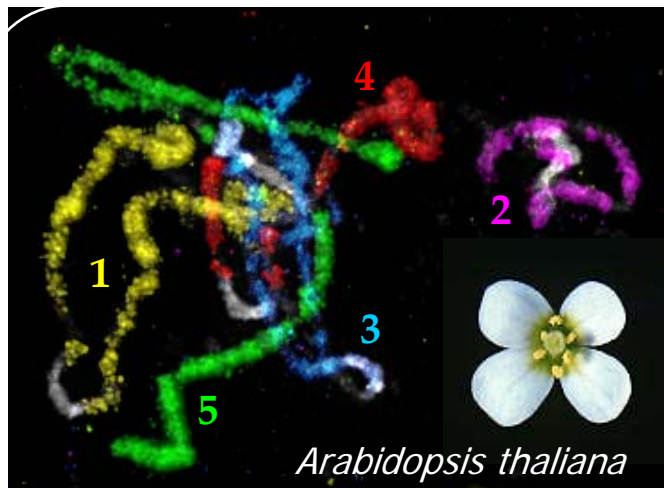


## Chromosome painting in Arabidopsis

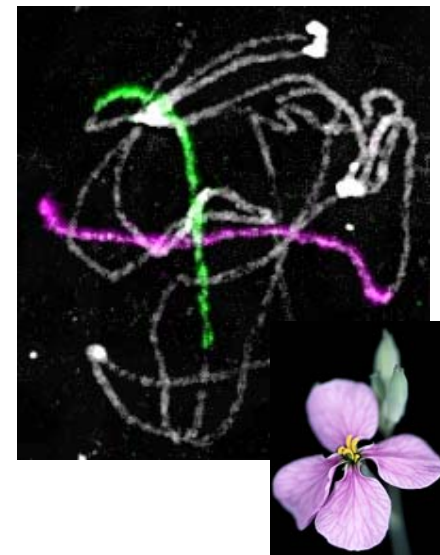


# Studying genome and chromosome collinearity across the *Brassicaceae* by comparative chromosome painting (CCP)

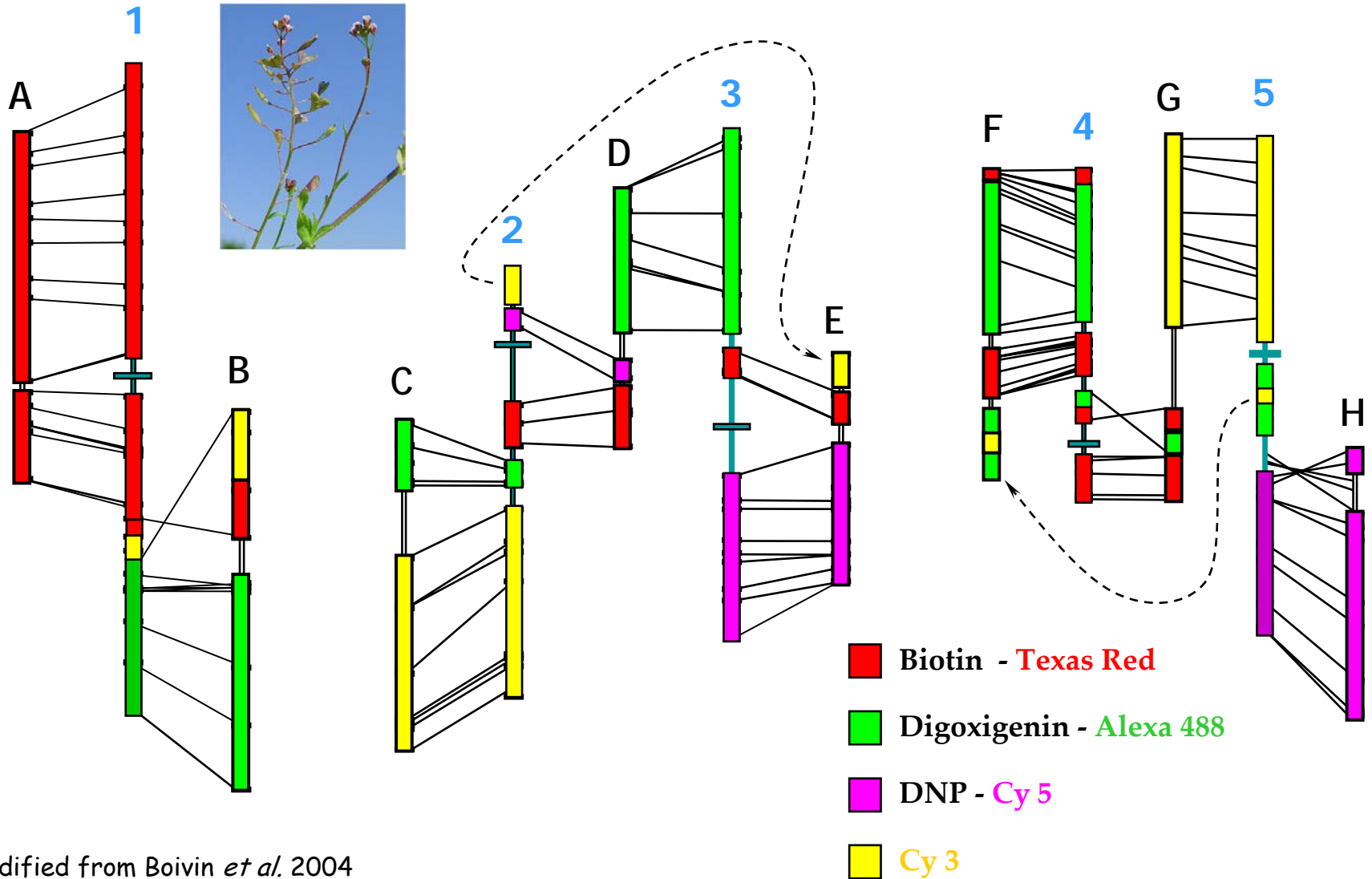
Fluorescently labelled Arabidopsis BAC contigs are hybridized *in situ* to pachytene chromosomes of other cruciferous species



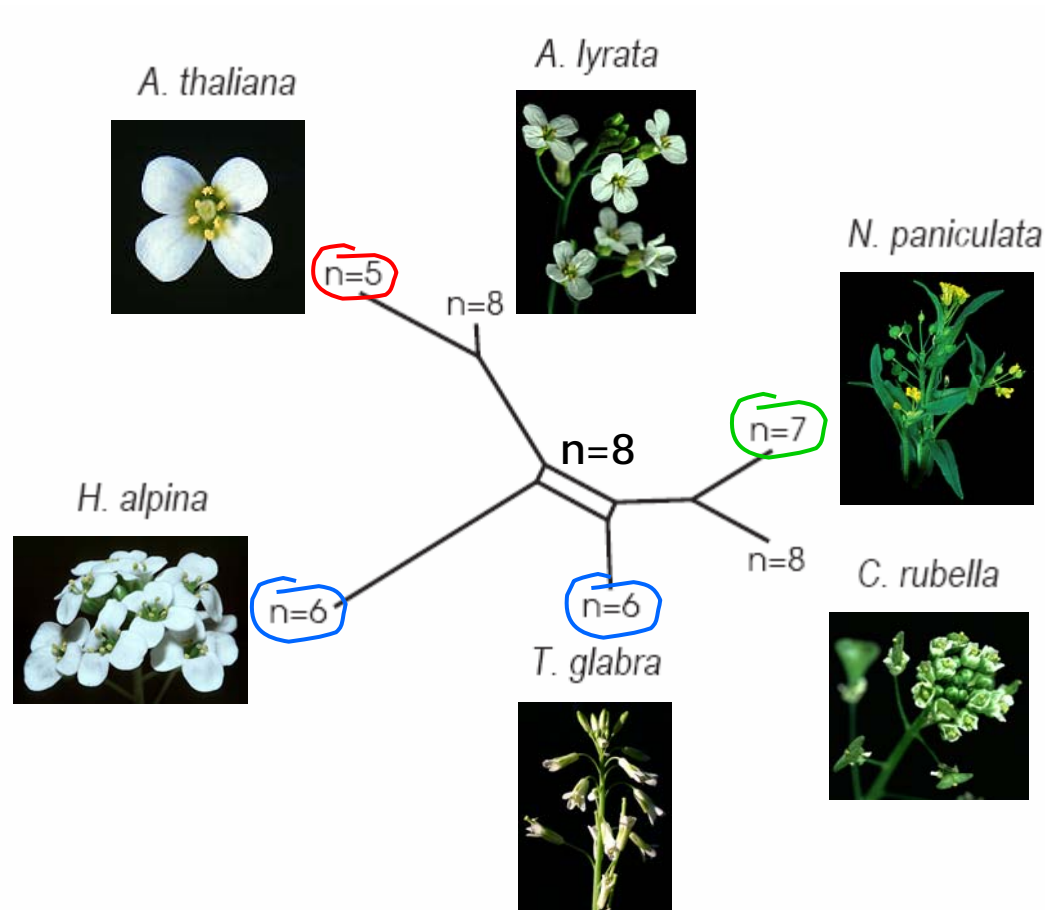
CCP  
→



# CCP in *Brassicaceae*: Arabidopsis BAC contigs designed according to the Arabidopsis-*C. rubella* comparative map



# Chromosome collinearity between *A. thaliana* and closely related *Brassicaceae* species



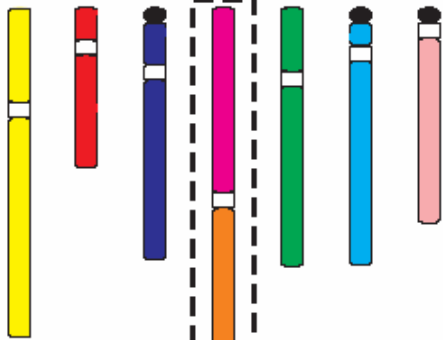
# Chromosome homeology and chromosome number reduction in *Neslia paniculata* ( $n=7$ )



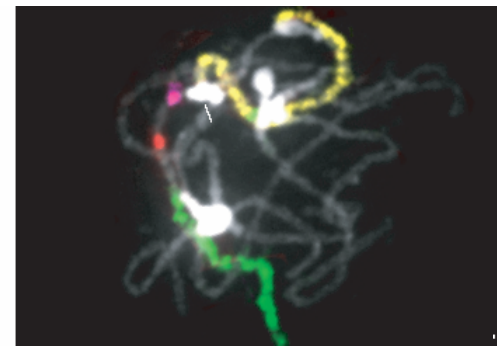
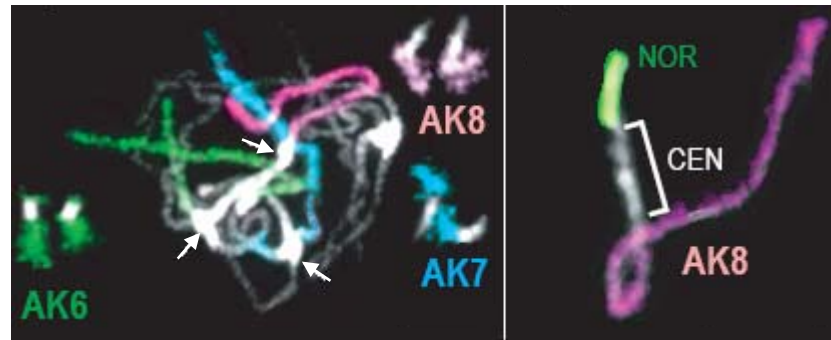
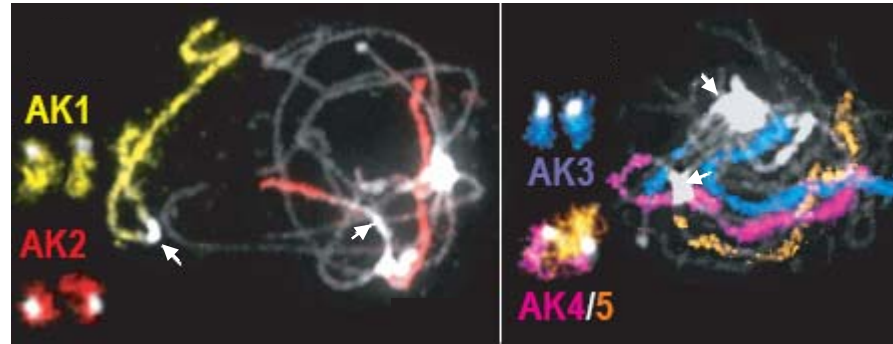
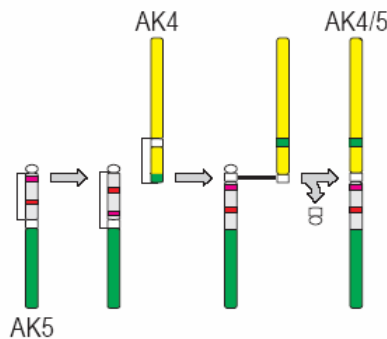
Ancestral Karyotype



*Neslia*

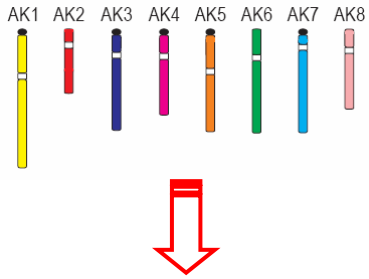


AK4/5

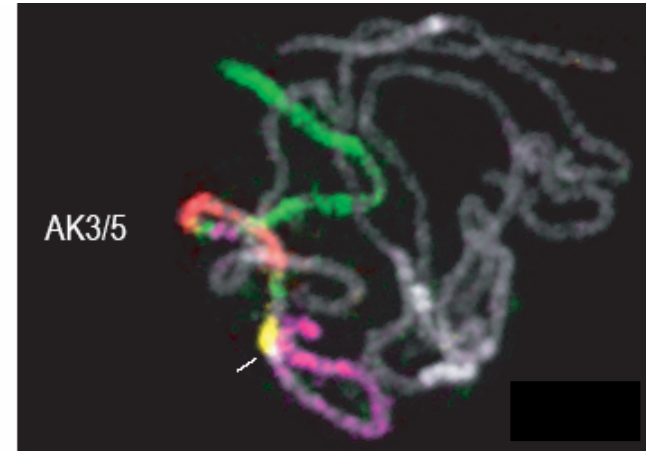
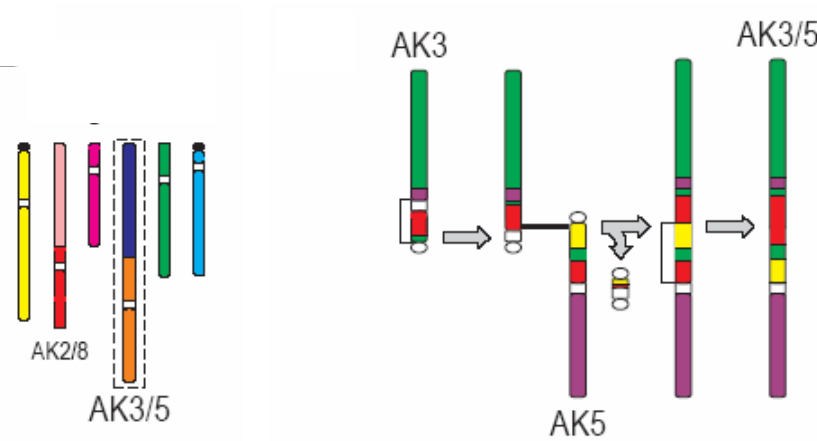


# Chromosome homeology between the Ancestral Karyotype and two n=6 species

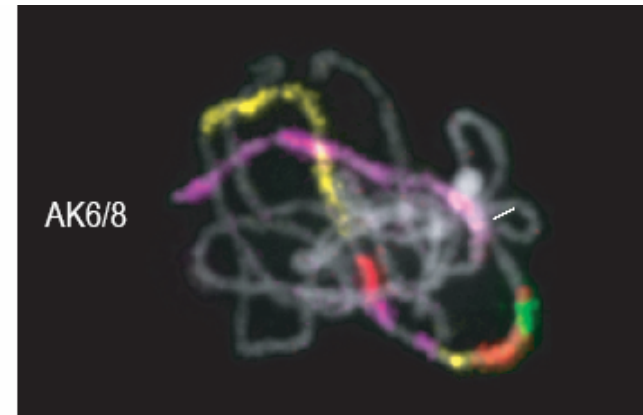
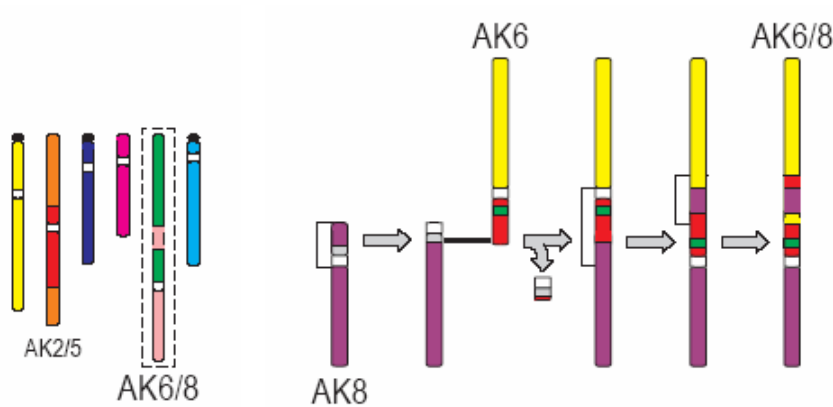
Ancestral Karyotype



*Turritis glabra* (n=6)

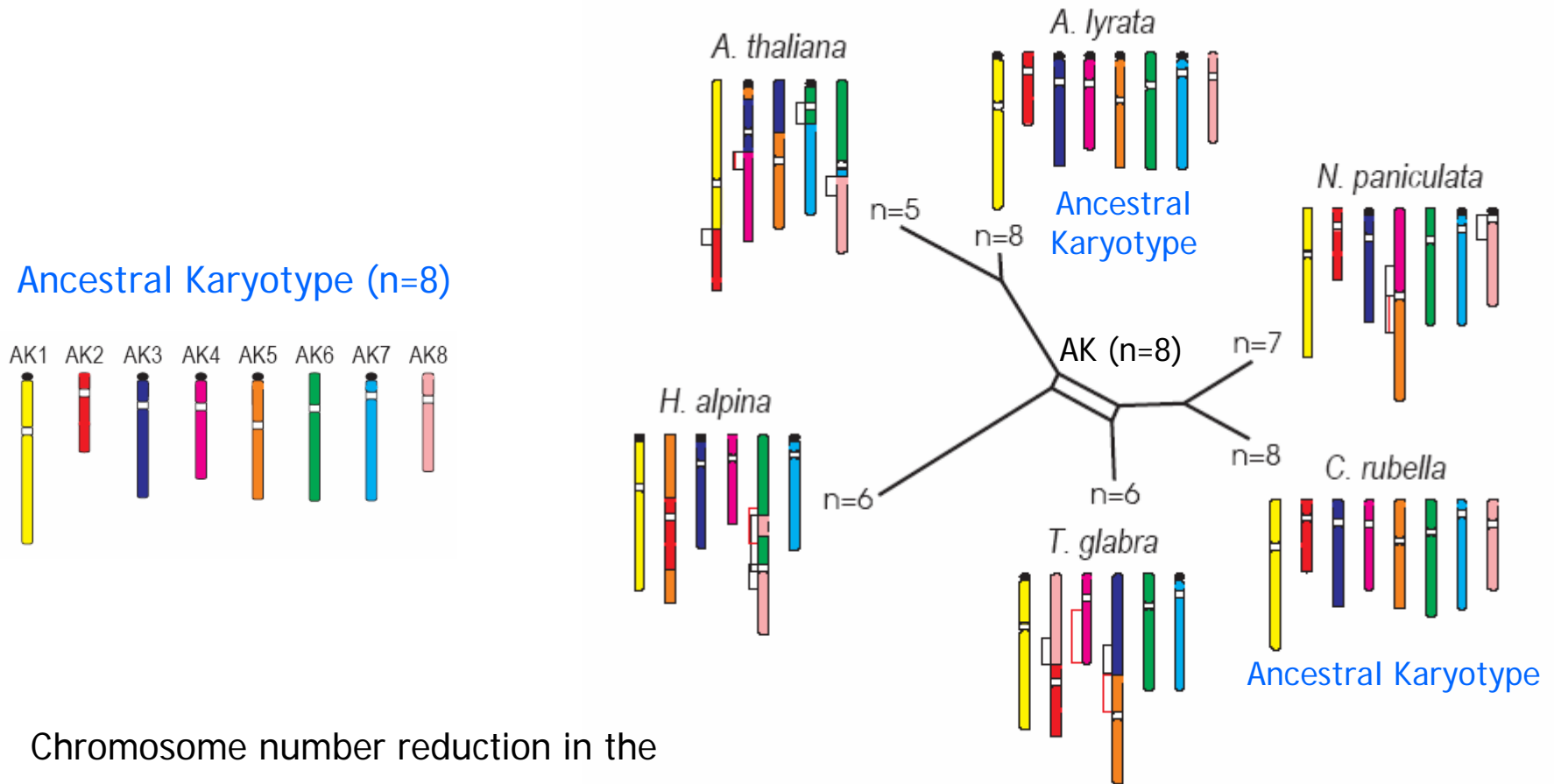


*Hornungia alpina* (n=6)



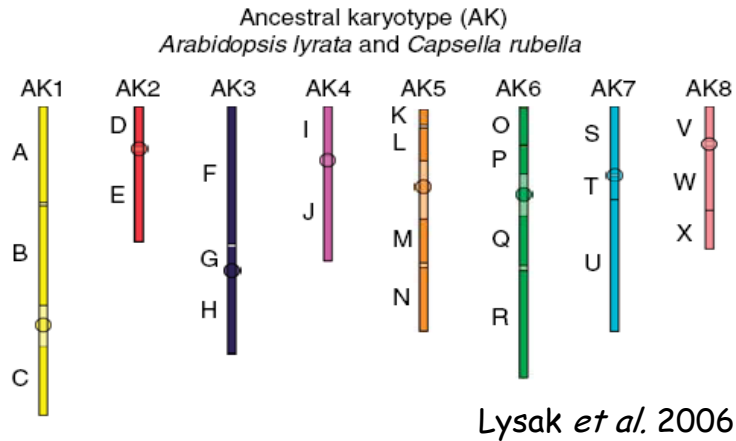


# There is high level of chromosome homeology and collinearity shared by *A. thaliana* and its close relatives

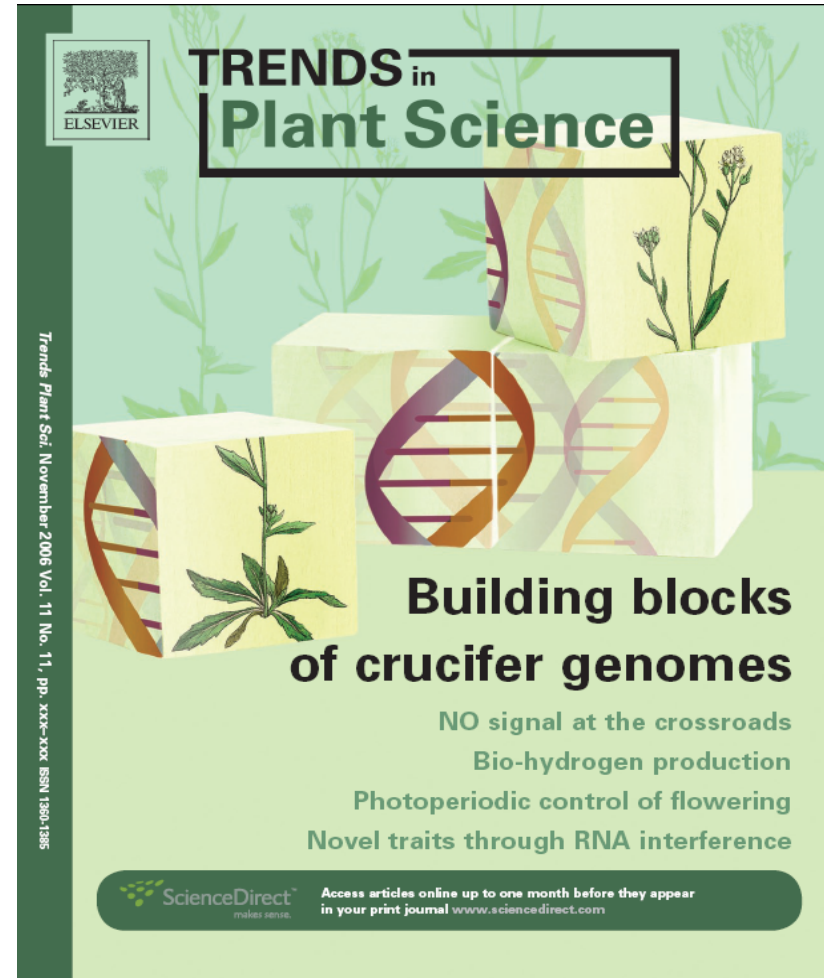


Chromosome number reduction in the Arabidopsoid clade followed different scenarios and involved different ancestral chromosomes

# The ABC's of comparative genomics in the *Brassicaceae*: Ancestral Karyotype



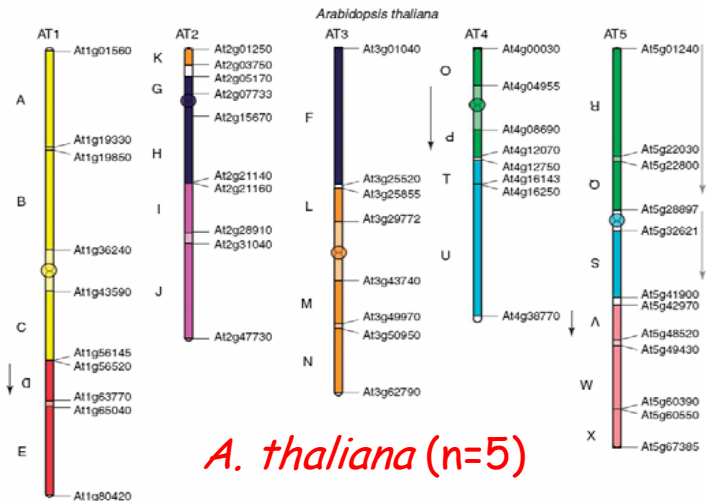
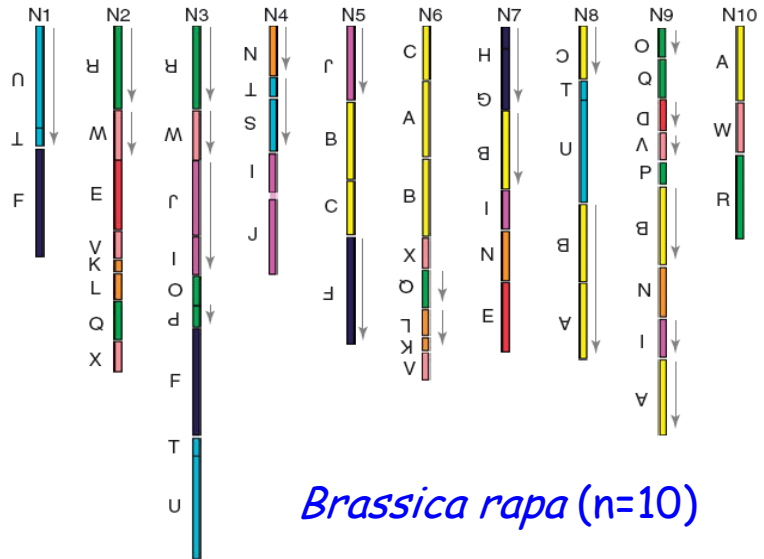
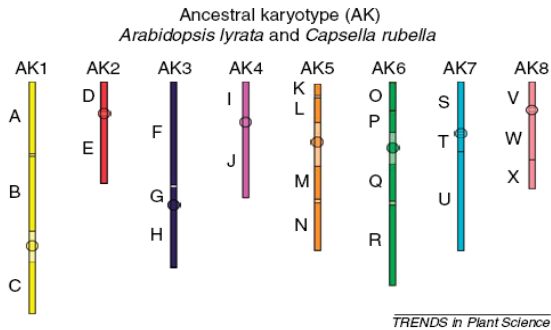
- unified comparative genomic framework across *Brassicaceae*
- system of 24 conserved chromosomal blocks (A-X)
- order, orientation and color-coding of the blocks are based on their positions in the Ancestral Karyotype ( $n = 8$ )
- the building blocks can be rearranged to model the genome structures of *A. thaliana*, *A. lyrata*, *Capsella rubella*, *Brassica rapa* and other crucifers



Schranz, Lysak & Mitchell-Olds 2006

# 24 ancestral building blocks were identified to model karyotypes of *A. thaliana*, *B. rapa* and other crucifer species

## Ancestral Karyotype (n=8)



Genomic building blocks based on the ancestral karyotype will facilitate genome comparisons across *Brassicaceae*