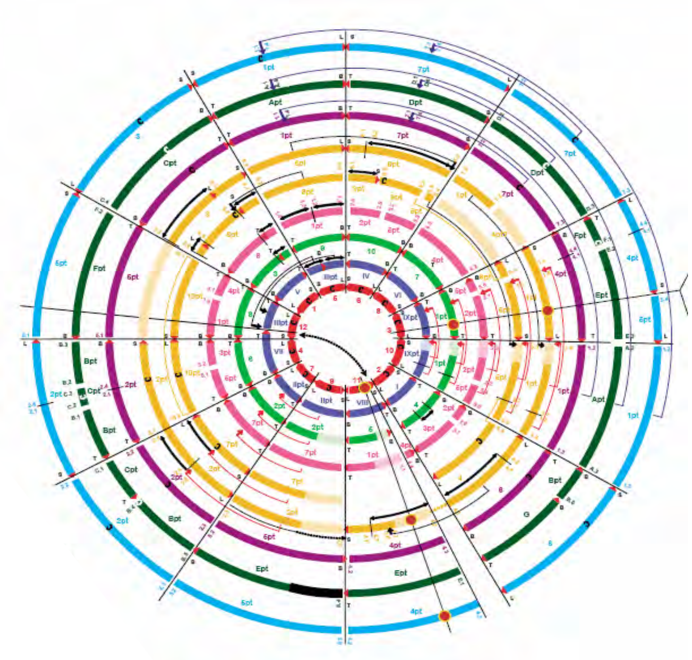
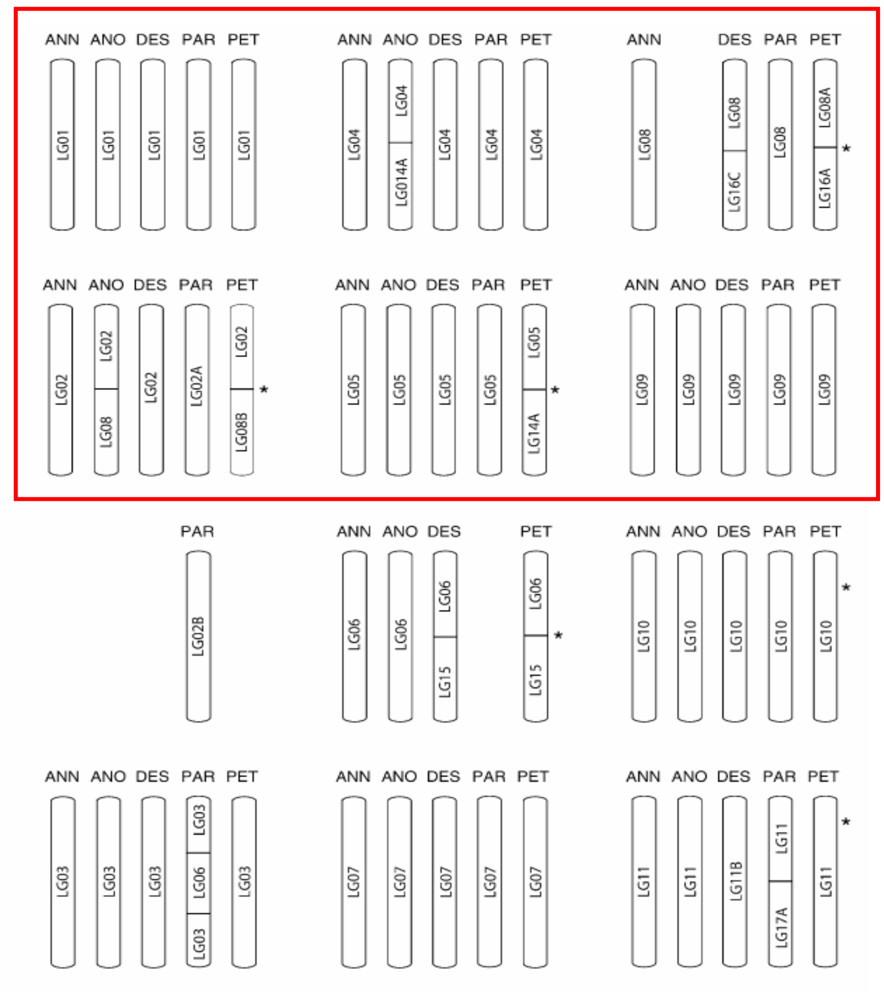
Genome and chromosome synteny and collinearity

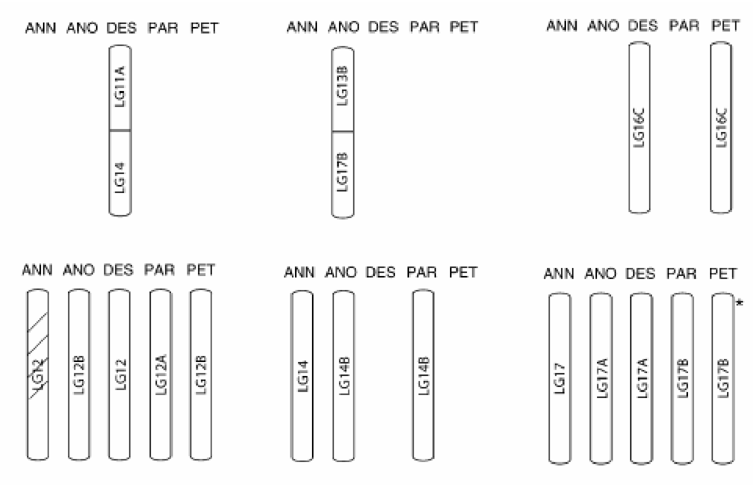


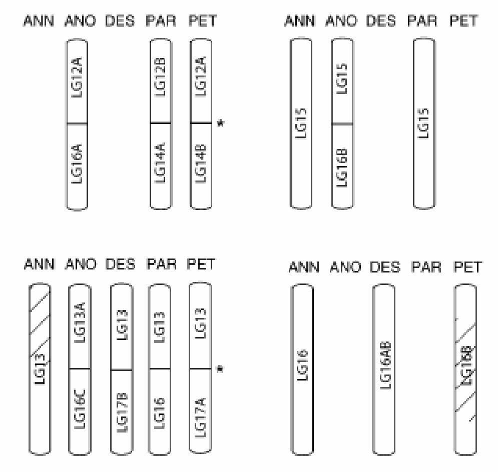
High level of genome collinearity between *Helianthus* species (*Asteraceae*)

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

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







Lai *et al.* 2005, *Genetics* 171

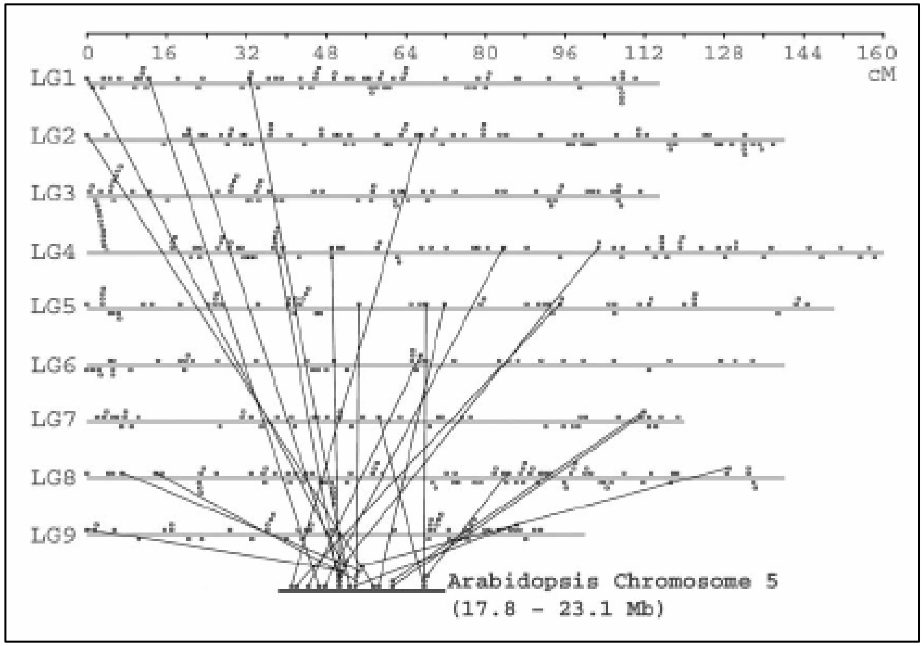
Segments containing inversions are indicated by hatched lines.

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

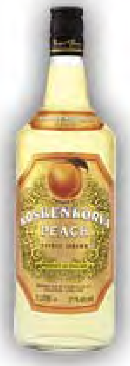


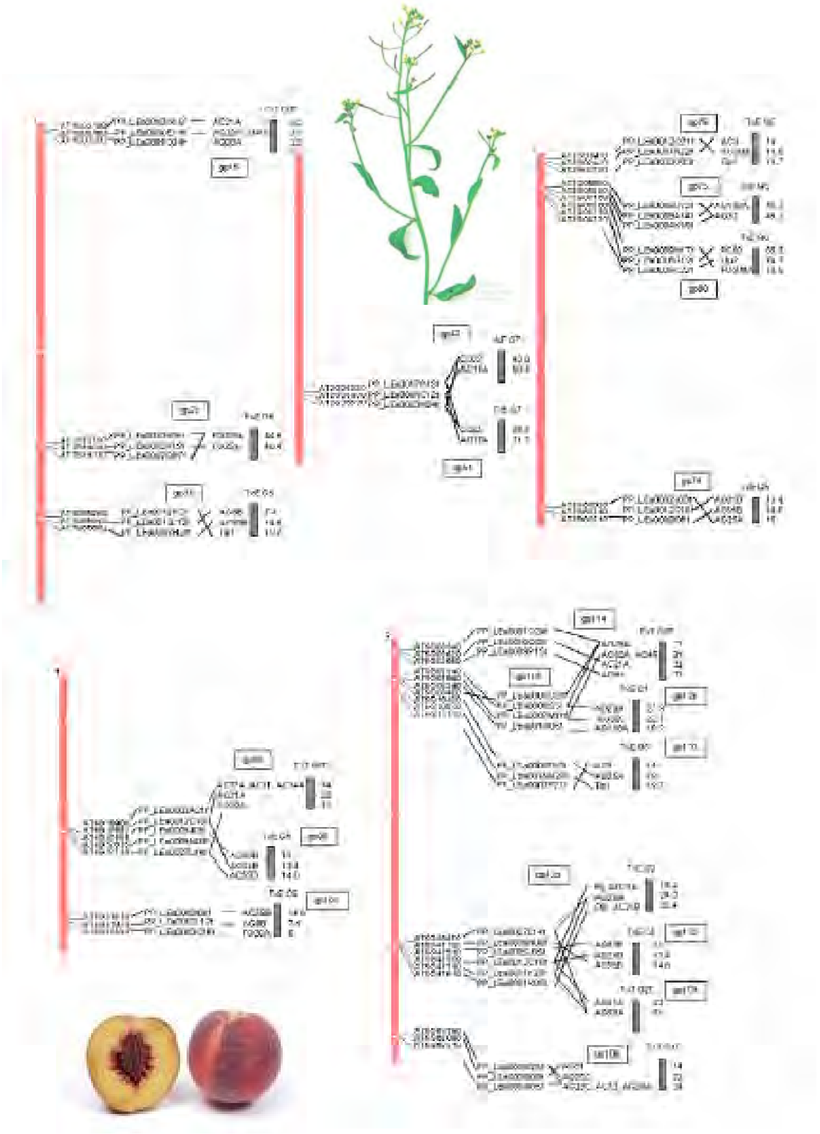
Physical positions of conserved orthologous sequences in a 5.5-Mb region of Arabidopsis chromosome 5 and their corresponding mapped positions on the nine linkage groups of *Lactuca sativa* (LG 1–9)

Timmis *et al.* 2006

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

Sook Jung*[1], Dorrie Main[2], Margaret Staton[1], Ilhyung Cho[3], Tatyana Zhebentyayeva[1], Pere Arús[4] and Albert Abbott[1]



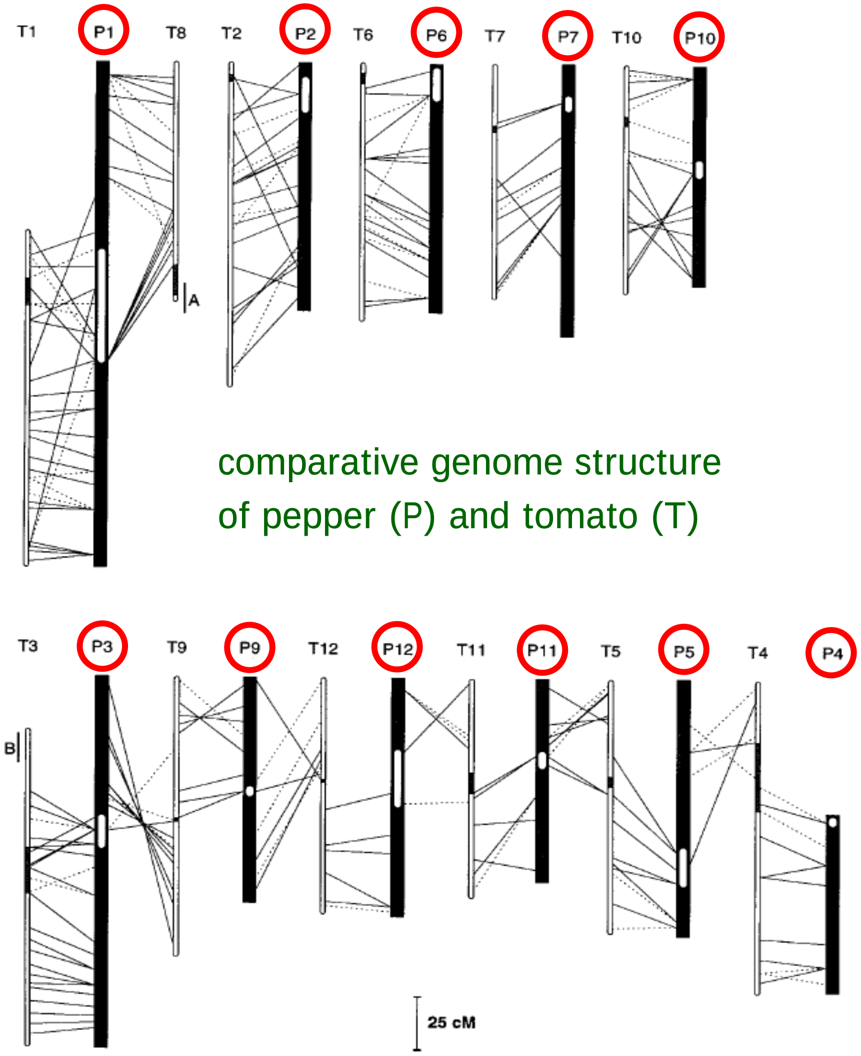


- syntenic regions were short and contained only a couple of conserved gene pairs

- 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 synteny between pepper (n=12; *Capsicum*) and tomato (n=12; *Solanum lycopersicum*)



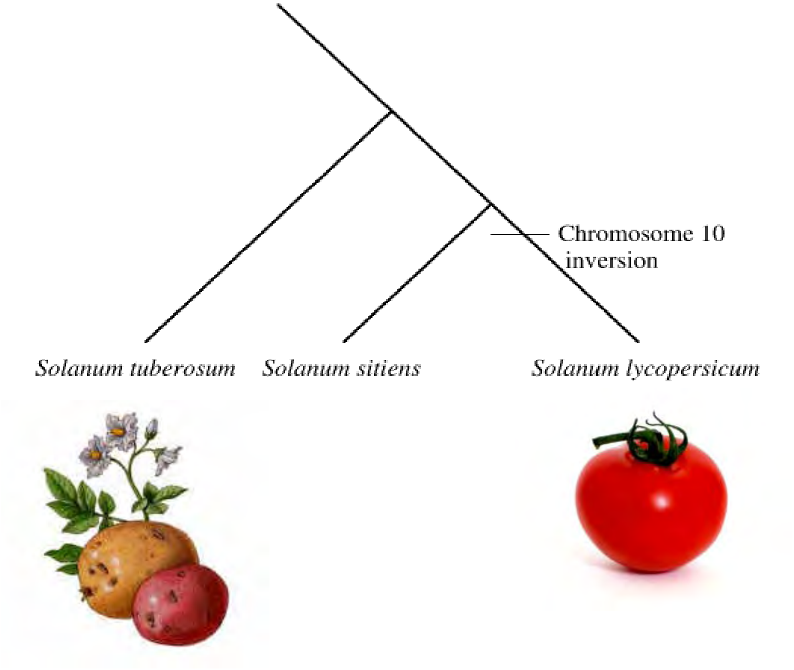
comparative genome structure of pepper (P) and tomato (T)

- 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

Livingstone *et al.* 1999

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

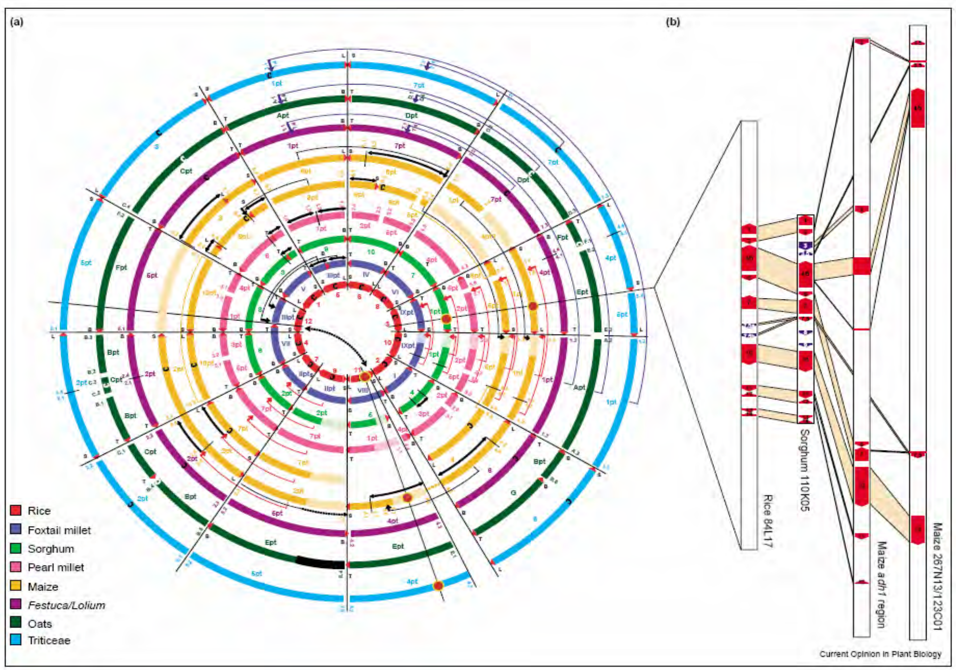
- the chromosome 10 inversion arose within the tomato lineage after the split from the common ancestor with potato

Rieseberg & Livingstone 2003

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 colinearity at the DNA-sequence level?

  \- Many small rearrangements that disturb collinearity in orthologous chromosome regions.

Devos 2005

Maize-rice colinearity

Wei et al. 2007, PloS Genet 3

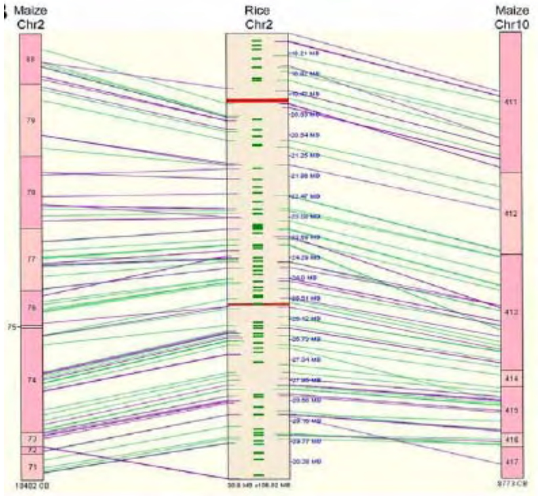
2n=20

2n=24

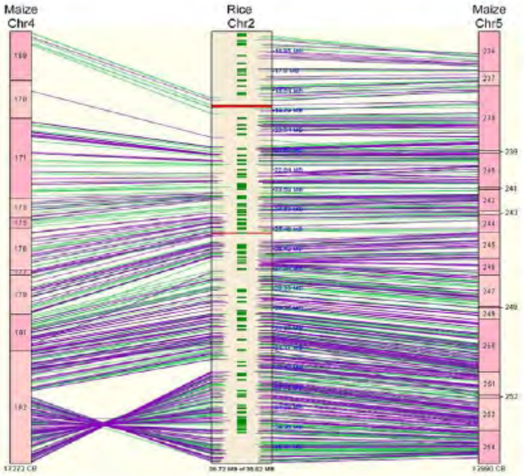
in collinear regions, 1 kb in rice corresponds to an average of 3.2 kb in maize, yet maize has a 6-fold genome size expansion. This can be explained by the fact that most rice regions correspond to 2 regions in maize as a result of its recent polyploid origin.

inversions account for the majority of chromosome structural variations during subsequent maize diploidization. There was also clear evidence of ancient genome duplication predating the divergence of the progenitors of maize and rice.

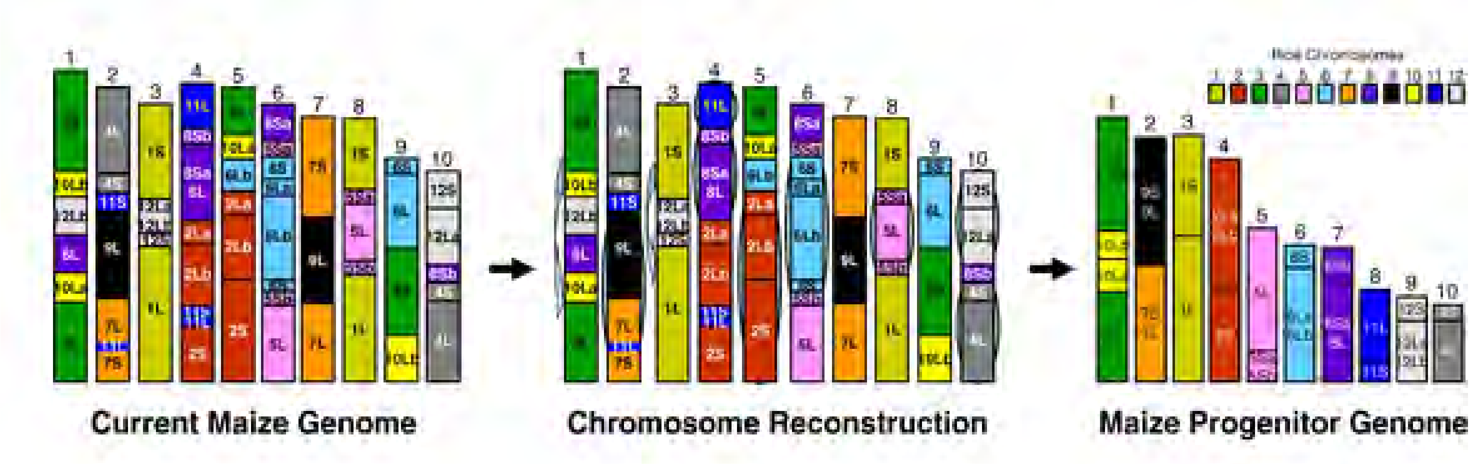
ancient whole-genome duplication in the maize/rice progenitor

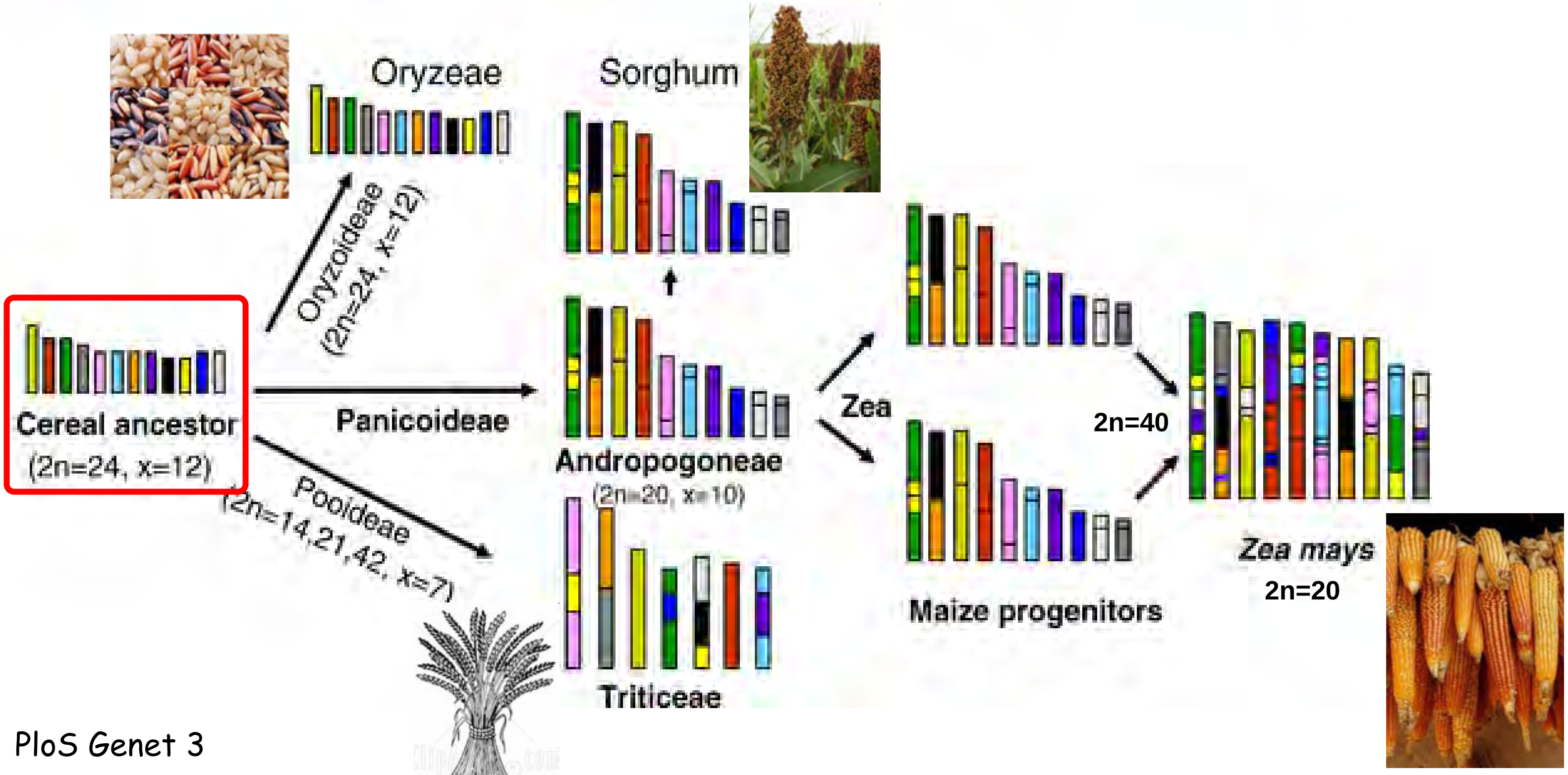


recent allotetraploidy in maize



Change of chromosome numbers during speciation of cereals





Wei et al. 2007, PloS Genet 3

Shared duplications between rice (2n=24) and wheat (2n=42) and evolution of grass genomes

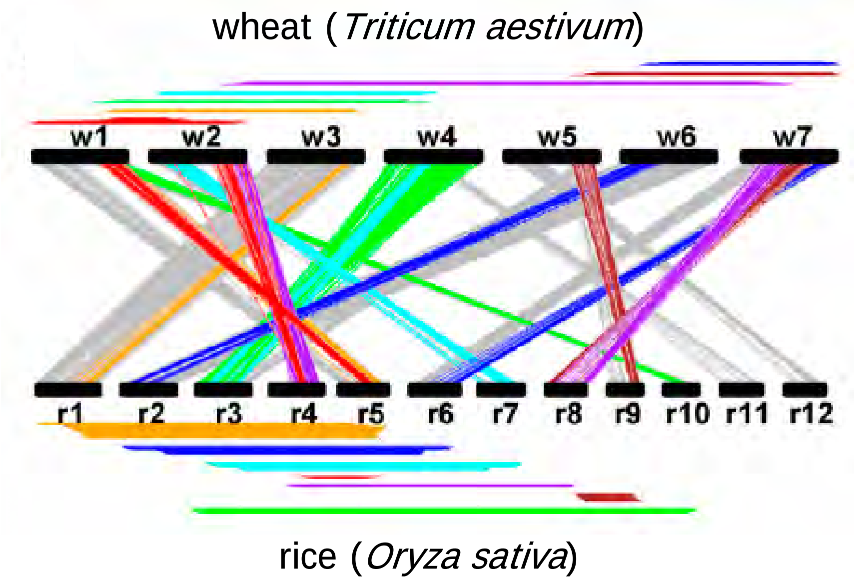
- comparing 42,654 rice gene sequences with 6,426 mapped wheat ESTs (sequence alignment and statistical analysis)

- identified 29 inter-chromosomal duplications covering 72 % of the rice genome and 10 duplication blocks covering 67.5 % of the wheat genome

- orthologous relationships between the two genomes assessed: 13 blocks of colinearity representing 83.1 and 90.4% of the rice and wheat genomes, respectively

- integration of the intraspecific duplications data with colinearity relationships revealed seven duplicated segments conserved at orthologous positions → common orgin (also maize and sorghum)

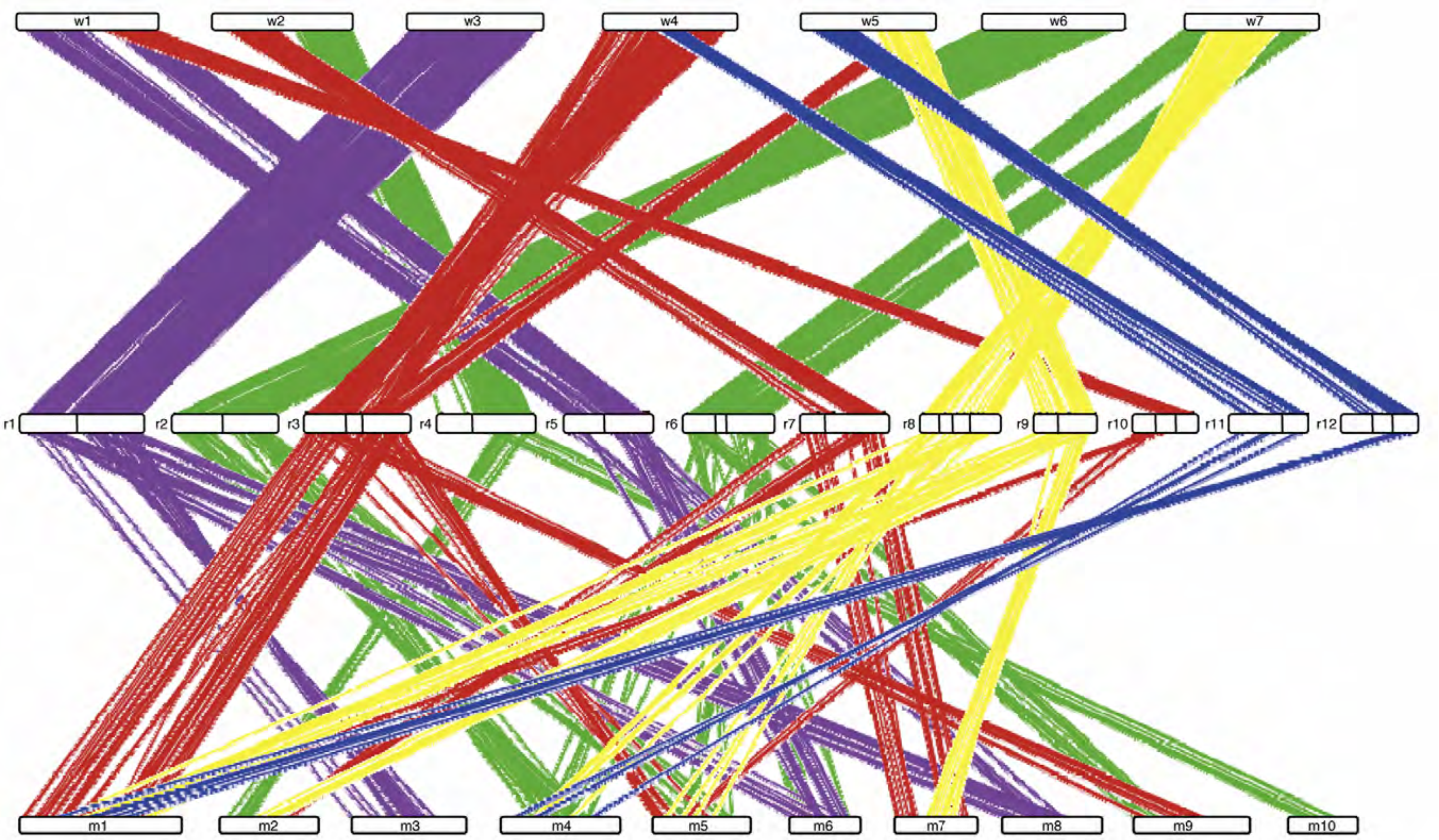
Seven duplicated regions shared between wheat and rice



- → a model of grass genome evolution from a common ancestor with n=5 through a series of whole genome and segmental duplications, chromosome fusions, and translocations

Salse et al. 2008, Plant Cell

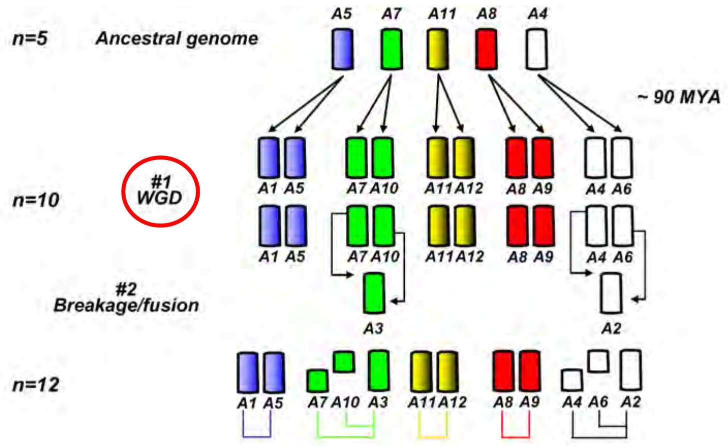
Synteny between cereal genomes (wheat, rice, and maize)

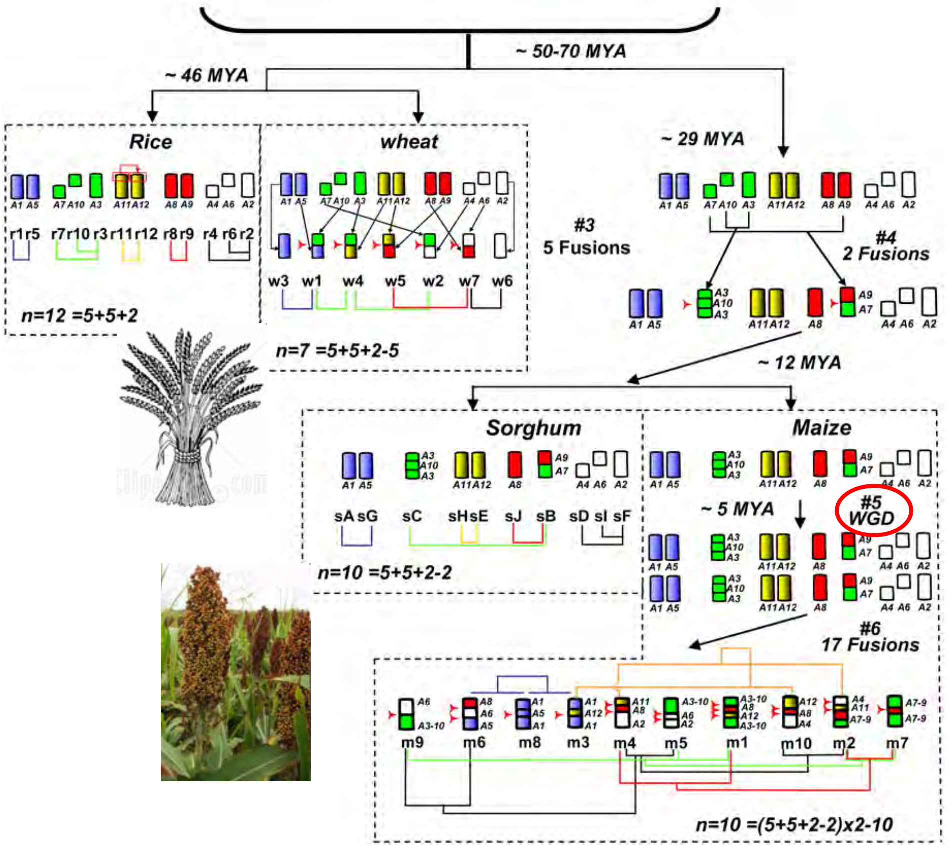


five colours represent the orthologous relationships referring to the five ancestral chromosomes

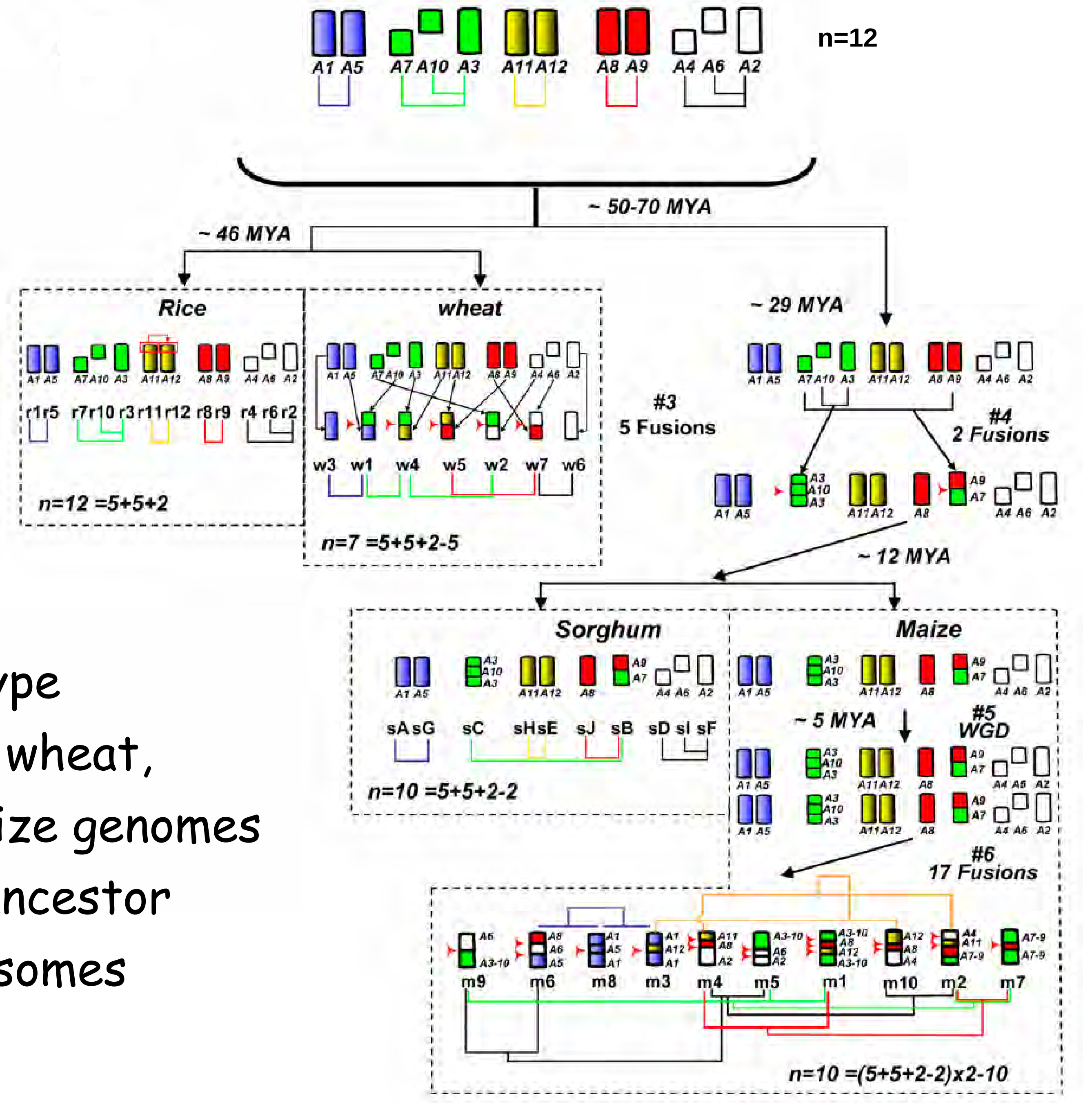
Bolot et al. 2009, *Curr. Opin. Pl. Biol.*

Model of karyotype evolution in rice, wheat, sorghum, and maize genomes from a common ancestor with n=5 chromosomes





Salse et al. 2008, Plant Cell



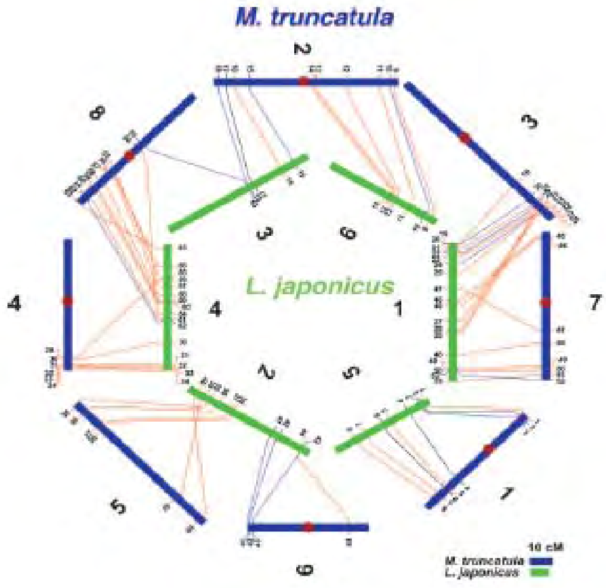
Model of karyotype evolution in rice, wheat, sorghum, and maize genomes from a common ancestor with n=5 chromosomes

Salse et al. 2008, Plant Cell

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

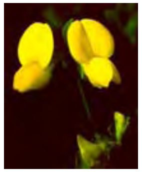
Macrosyntenic relationship of *Medicago truncatula* and *Lotus japonicus*

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

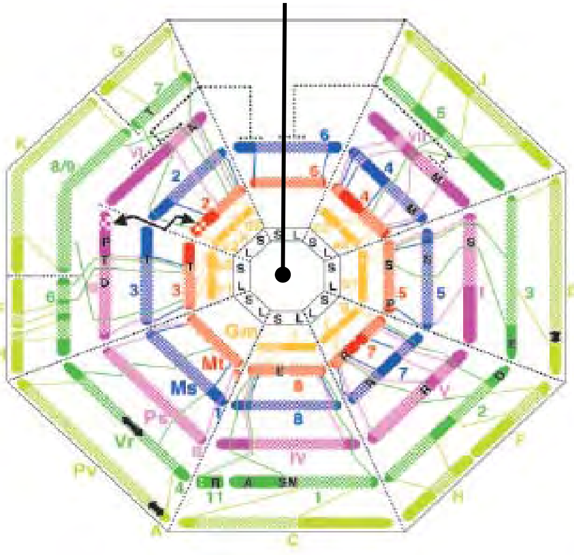


Medicago truncatula (n=6)
M. sativa (n=16)
Pisum sativum (n=7)
Glycine max (n=20)
Vigna radiata (n=11)
Phaseolus vulgaris (n=11)
Lotus japonicus (n=6)

- 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

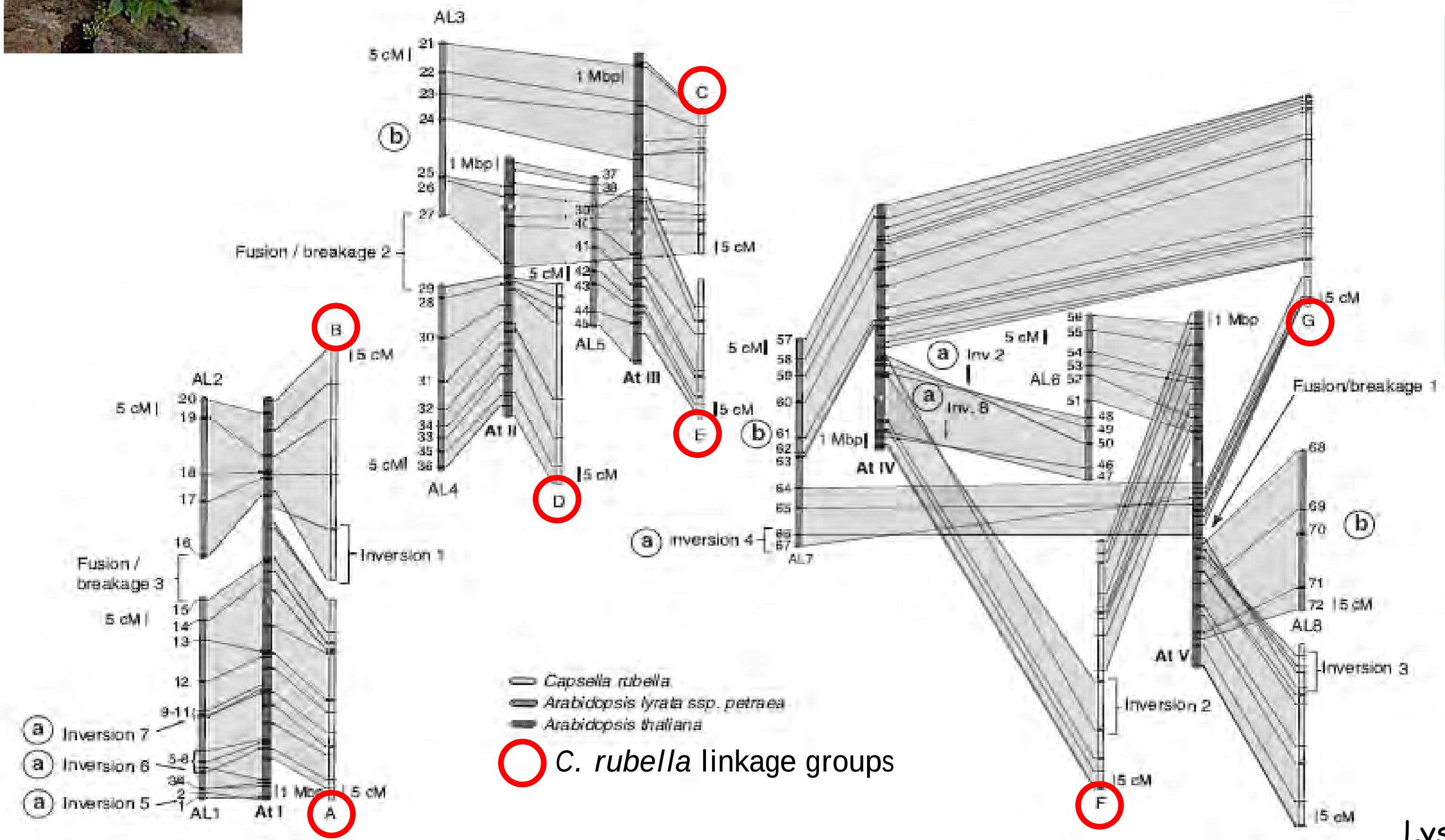
- comparison between *M. truncatula, L. japonicus* and *G. max*

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

Choi *et al.* 2004

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

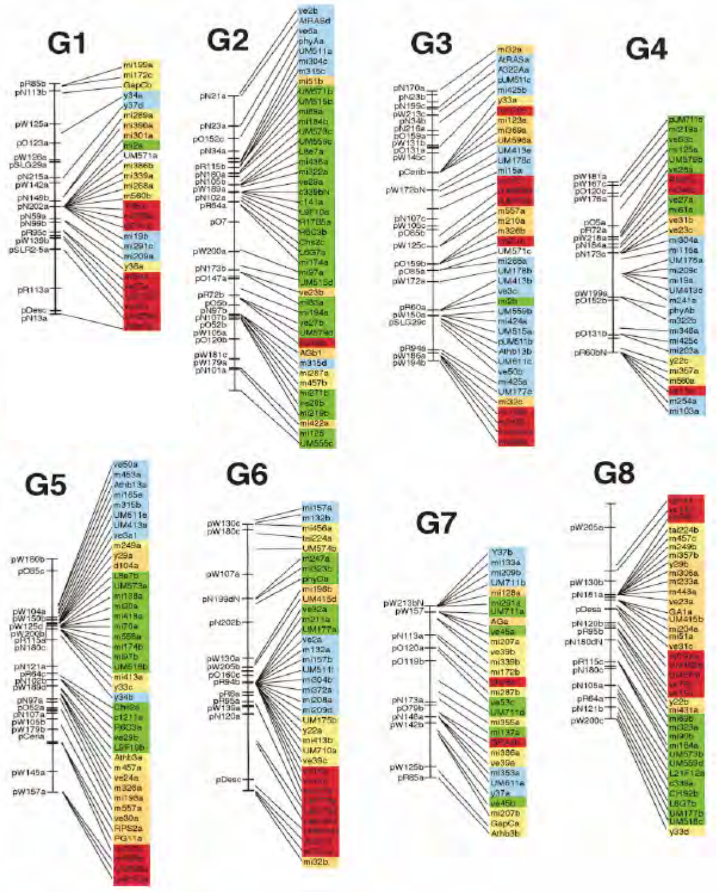


C. rubella linkage groups

Lysak & Lexer 2006

Genome collinearity in crucifers: Arabidopsis - *Brassica*

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



A. thaliana chromosomes

1	2	3	4	5
🟦	🟥	🟨	🟧	🟩

- *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

Lagercrantz 1998