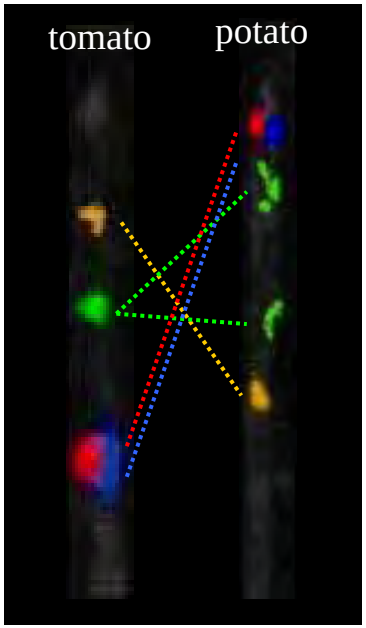


Contemporary plant cytogenetics

- chromosome number changes ($\rightarrow$ karyotypic variation)

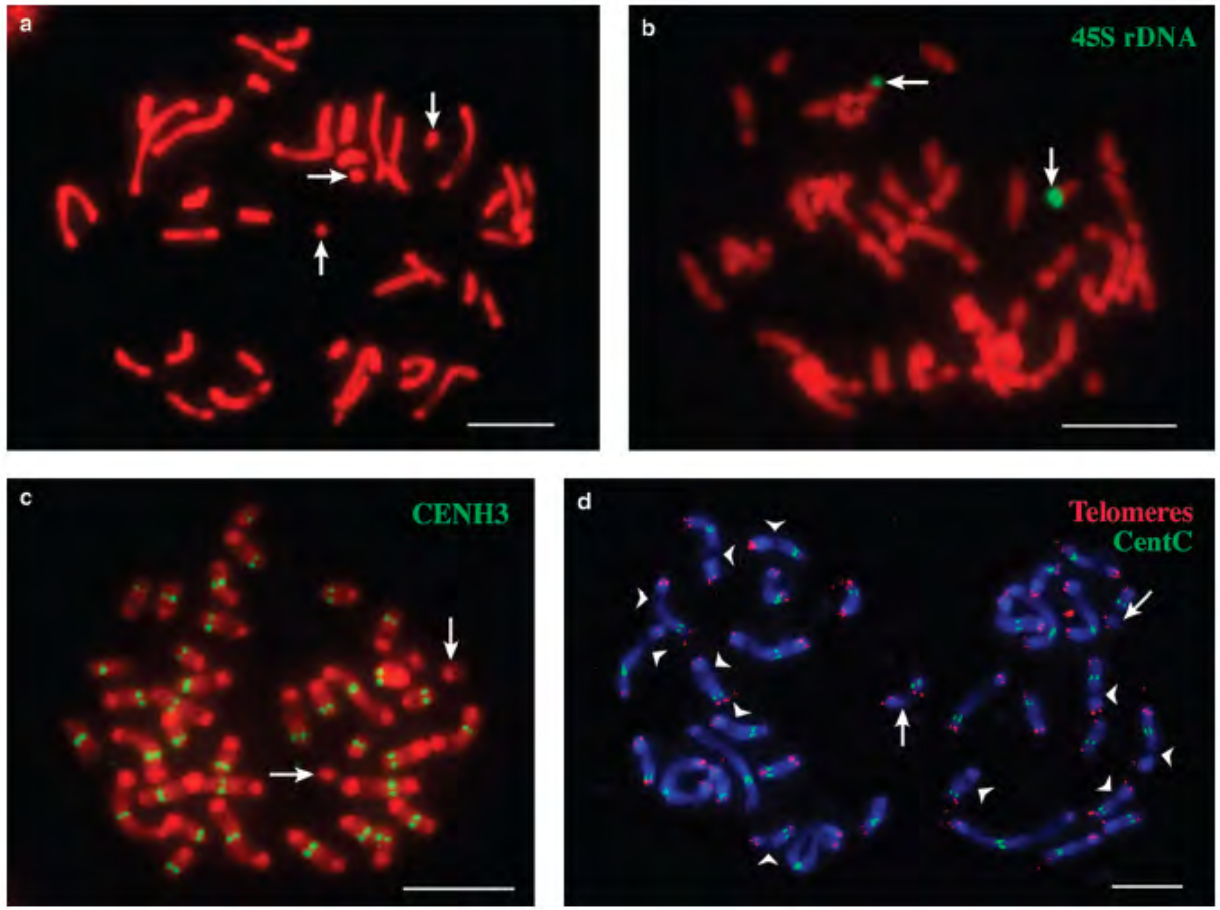
- structural chromosome changes (e.g. centromere repositioning)

- collinearity and karyotype evolution (cross-species FISH and chromosome painting)

Extraordinary Tertiary Constrictions of *Tripsacum dactyloides* Chromosomes: Implications for Karyotype Evolution of Polyploids Driven by Segmental Chromosome Losses

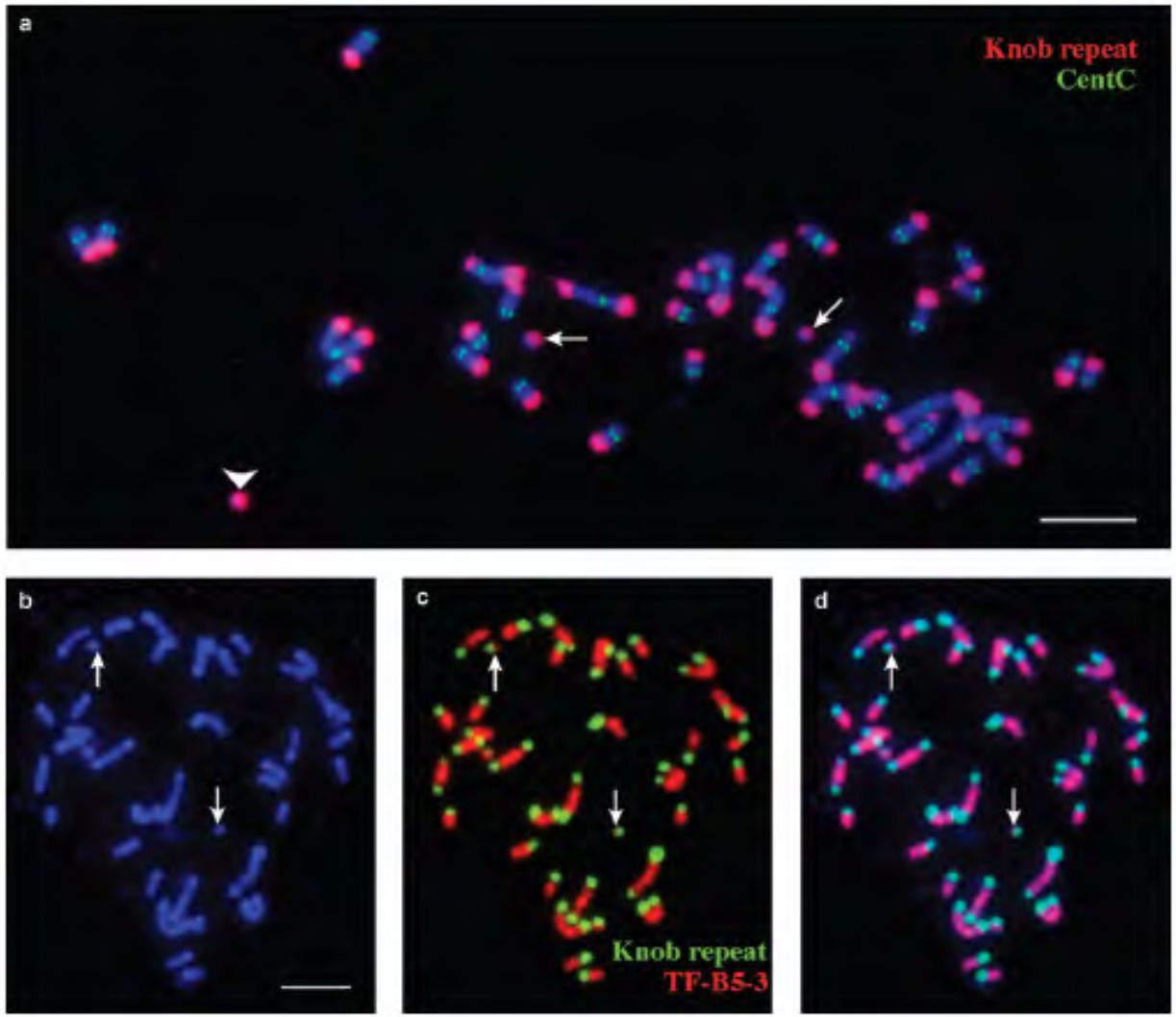
Dal-Hoe Koo and Jiming Jiang[1]

Department of Horticulture, University of Wisconsin, Madison, Wisconsin 53706



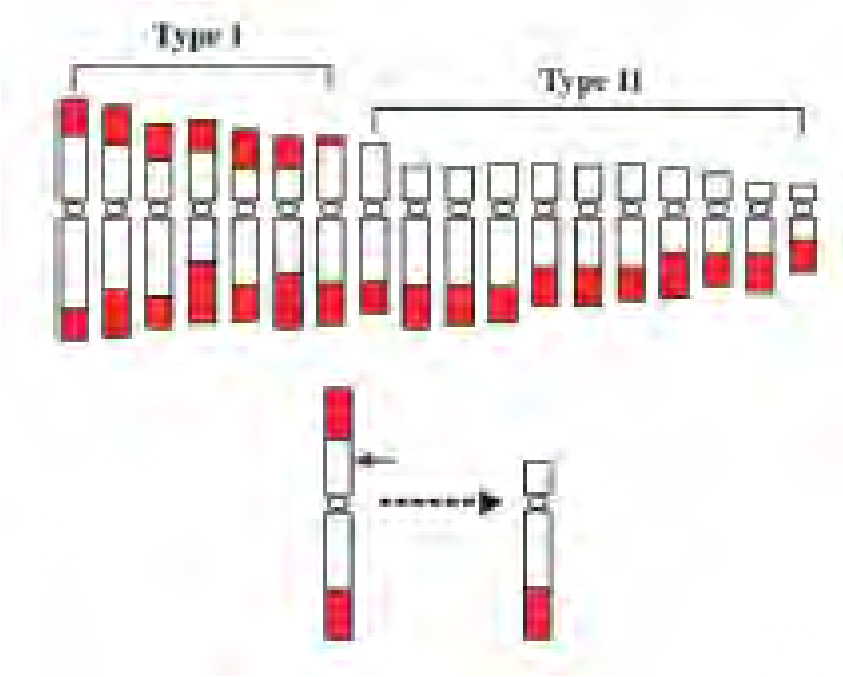
Genetics 179 (2008)

Extraordinary Tertiary Constrictions of *Tripsacum dactyloides* Chromosomes: Implications for Karyotype Evolution of Polyploids Driven by Segmental Chromosome Losses



Extraordinary Tertiary Constrictions of *Tripsacum dactyloides* Chromosomes: Implications for Karyotype Evolution of Polyploids Driven by Segmental Chromosome Losses

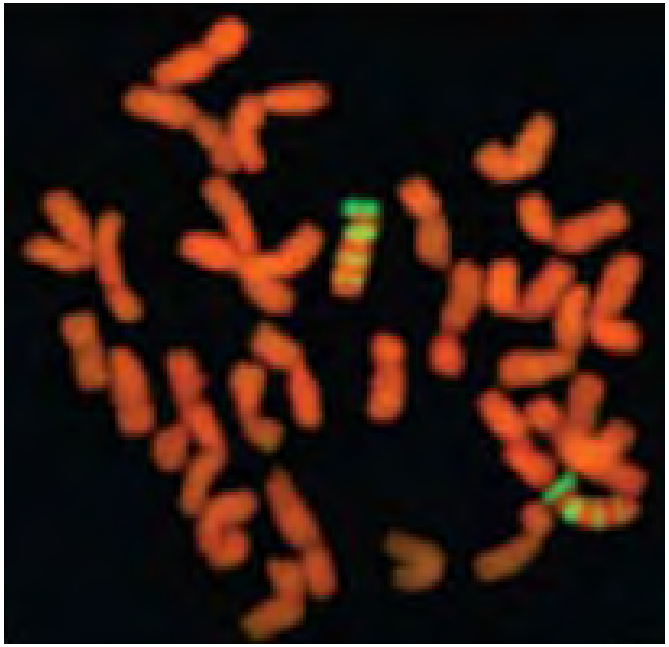
n=18



An ideogram of the karyotype and a model of segmental chromosome loss in *T. dactyloides*.

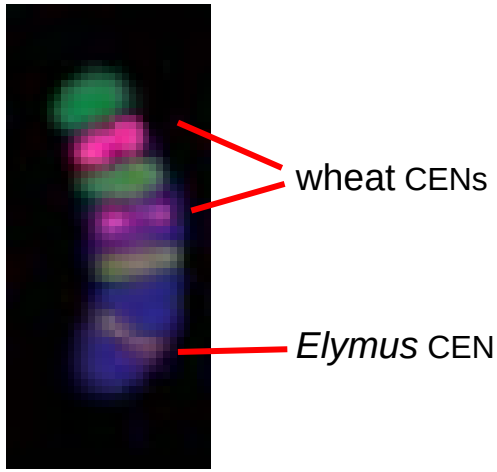
Type II chromosome is the product of a terminal deletion of a type I chromosome. The small arrow points to the deletion breakpoint that is possibly linked to a tertiary constriction.

The origin of a "Zebra" chromosome in wheat



2 zebra z5A

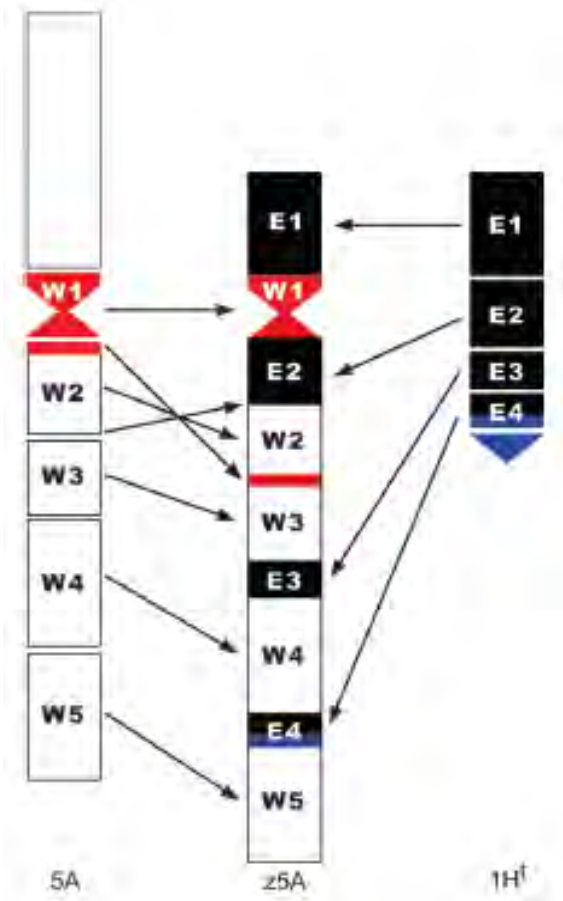
+ 40 wheat chromosomes



z5A

Zhang et al. 2008, *Genetics* 179

The origin of a "Zebra" chromosome in wheat via nonhomologous recombination



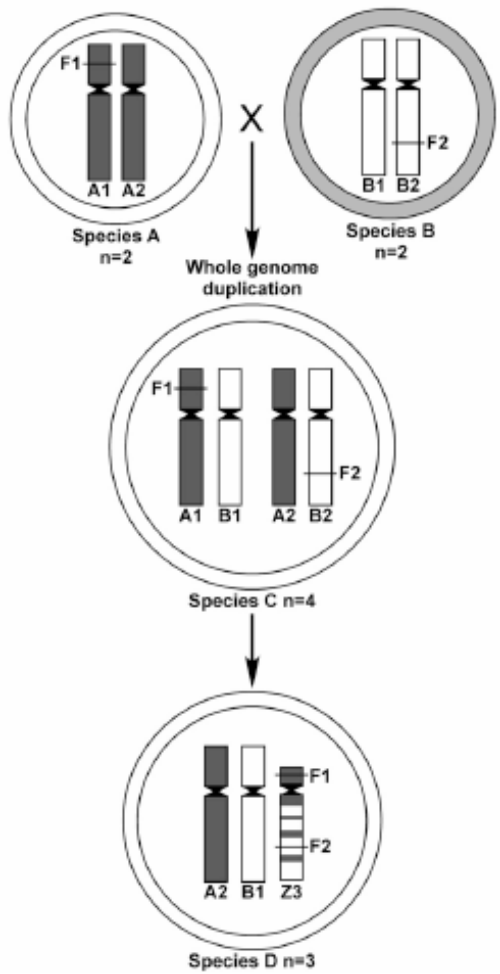
Chromosome z5A might have originated from nonhomologous recombination between 5A and 1HtS chromosomes.

1) Initially, at least five breaks occurred in chromosome 5A, resulting in six chromatin blocks.

2) Four breaks in the 1HtS telosome split it into five chromatin blocks.

3) Rejoining of the prealigned 5AL and 1HtS blocks resulted in the formation of chromosome z5A.

It was accompanied by the complete loss of 5AS, including the telomere and the loss of a very small distal centromeric end of 1HtS.

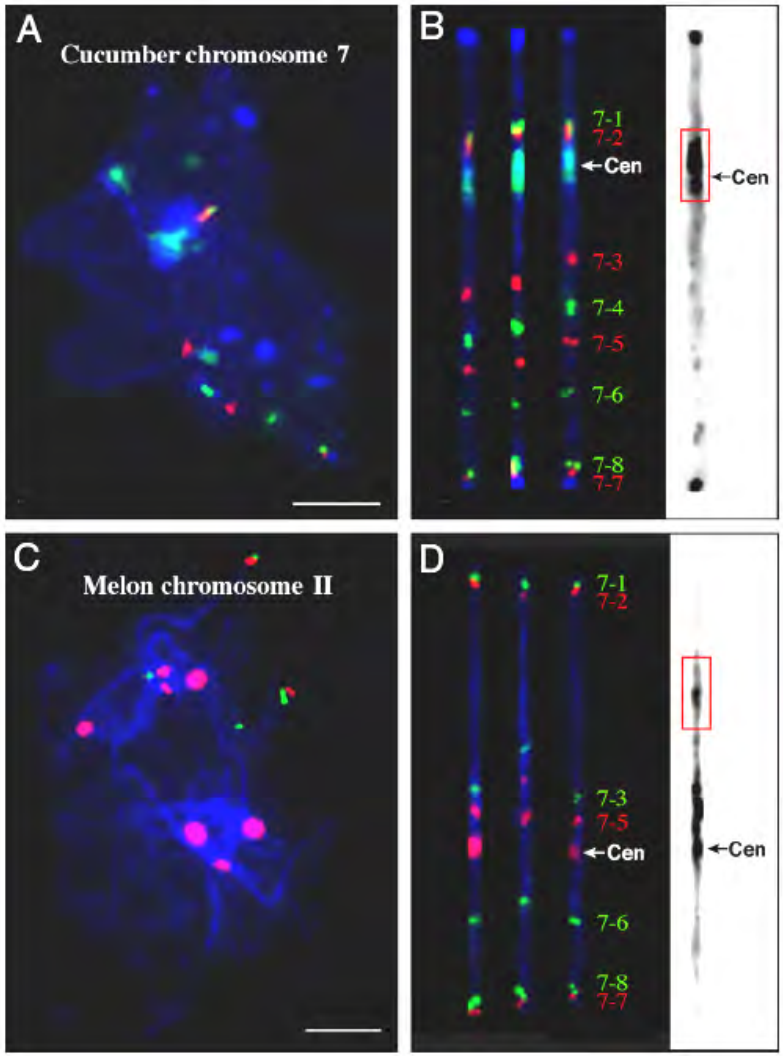


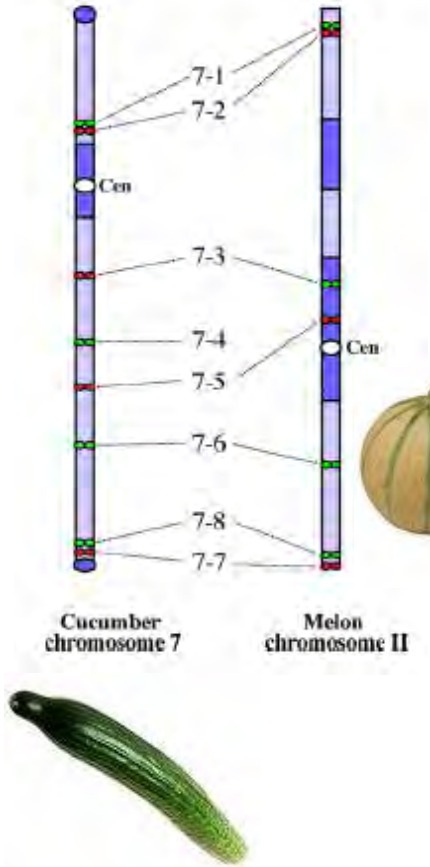
Novel mechanism of step changes in chromosome number (chromosome number reduction)

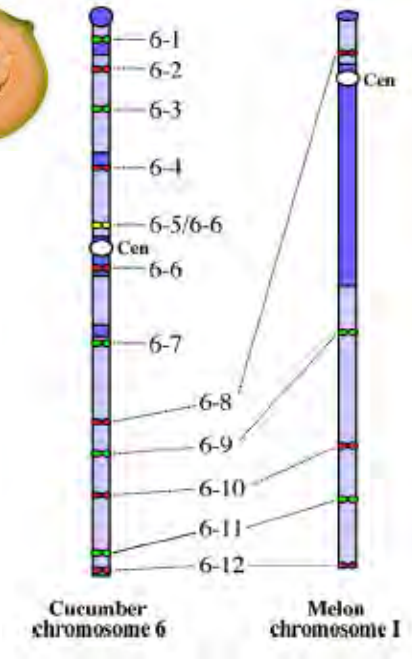
Centromere repositioning in curbit species

Cross-species fosmid FISH in cucumber and melon (*Cucurbitaceae*)

Fosmids (40 kb) are based on the bacterial F-plasmid. The cloning vector is limited, as a host (usually *E. coli*) can only contain one fosmid molecule. Low copy number offers higher stability than comparable high copy number cosmids.







Han et al. 2009, *PNAS* 106

Centromere repositioning in curbit species

- centromere repositioning (CR) extensively documented in mammalian species (e.g. 5 CRs in the donkey after its divergence from zebra)

- scarce reports on CR in other eukaryots including plants

- centromeres of cucumber and melon chromosomes are associated with distinct pericentromeric heterochromatin

Cucumis melo
2n = 24

- centromere activation or inactivation were associated with a gain or loss of a large amount of pericentromeric heterochromatin

Cucumis sativus
2n = 14

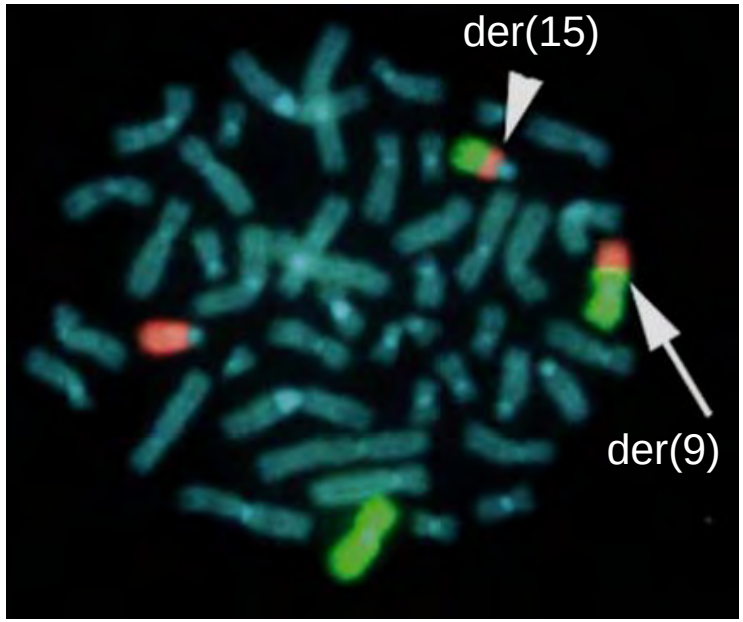
Karyotype evolution in *Brassicaceae*

Chromosome painting (CISS)

Chromosome painting generally refers to *in situ* identification of large-scale chromosome regions or whole chromosomes using chromosome-specific DNA probes (Pinkel et al. 1988, *PNAS* 85)

Chromosomal *In Situ* Suppression (CISS)

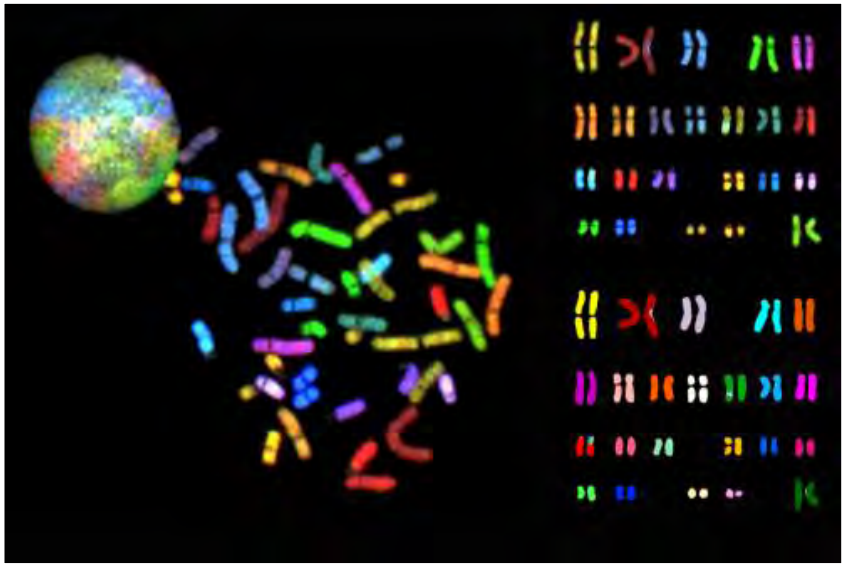
- unlabelled total genomic DNA or C_0t-1 DNA (DNA fraction enriched for repetitive sequences) are used to suppress unspecific repetitive sequences from hybridization (Lichter et al. 1988, *Hum Genet* 80)



Langer et al. (2004)

Chromosome painting in human and animal cytogenetics

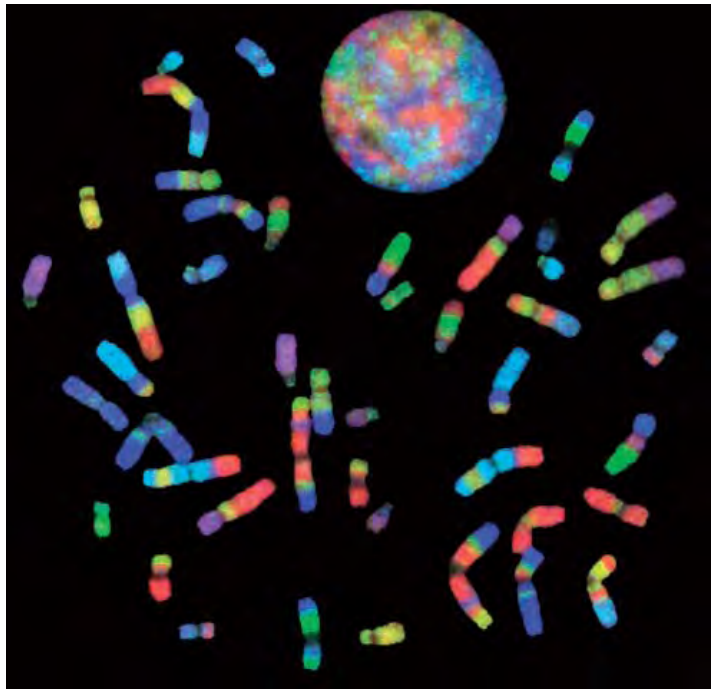
Human metaphase chromosomes after the simultaneous hybridization of 24 differentially labelled chromosome painting probes



E. Schröck, S. du Manoir, and T. Ried

Comparative chromosome painting

Human metaphase and interphase after hybridization with a chromosome-specific paint probe set derived from gibbon chromosomes



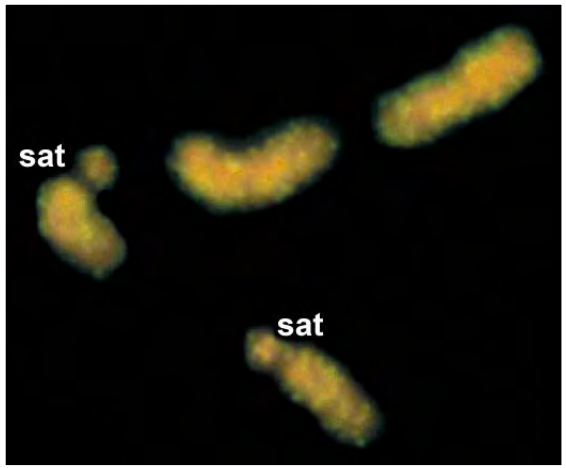
Ferguson-Smith & Trifonov (2007)

Chromosome painting in plants

All attempts at chromosome painting in euploid plants failed or yielded doubtful results (cross-hybridization to non-target chromosomes).

Reasons are the great diversity of dispersed repetitive sequences in plant genomes and their even distribution over chromosome complements.

Chromosome painting in *Haplopappus gracilis* (2n=4)

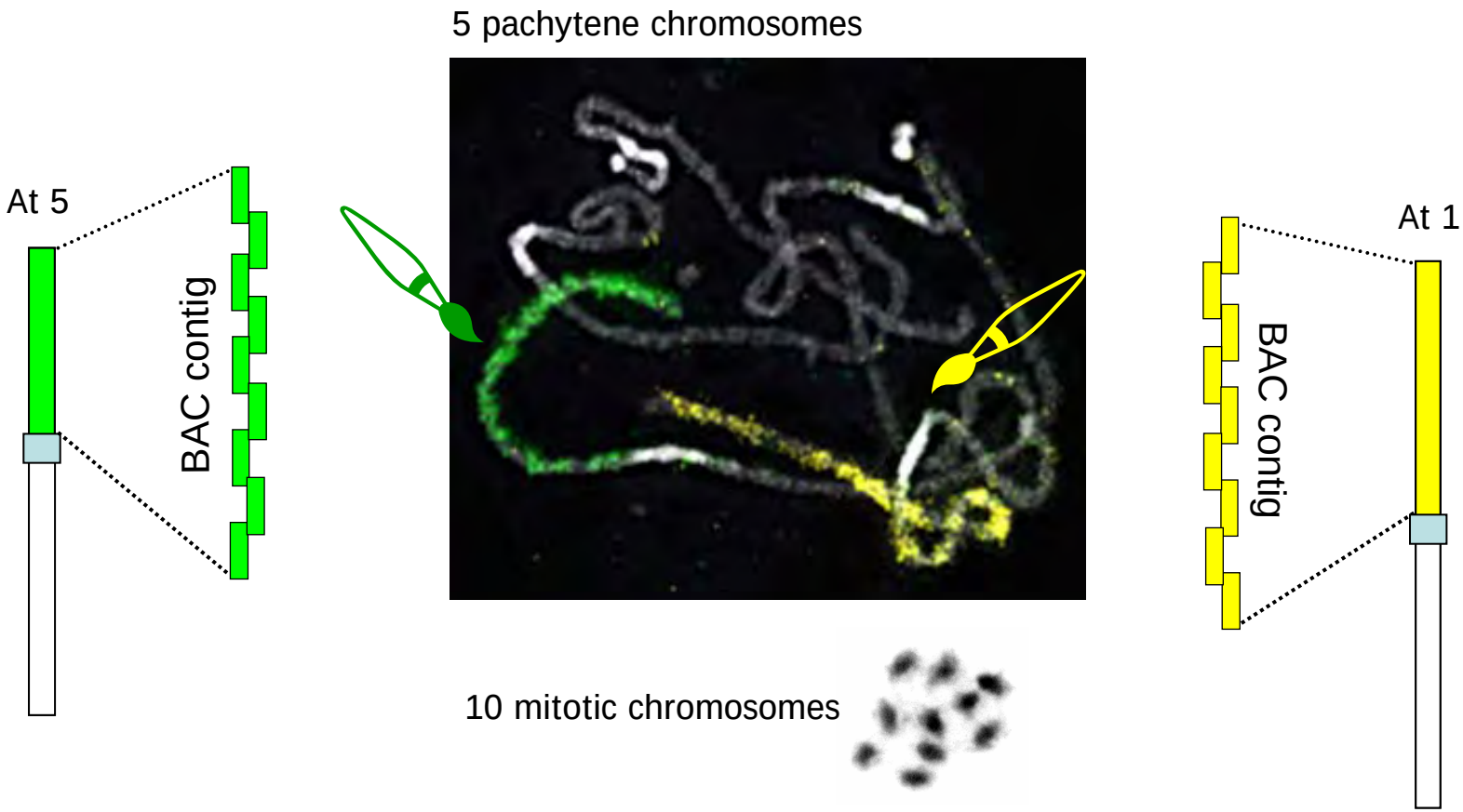


DOP-PCR amplified DNA of the non-satellite chromosome was used as a painting probe (Schubert et al. 2001)

Arabidopsis thaliana

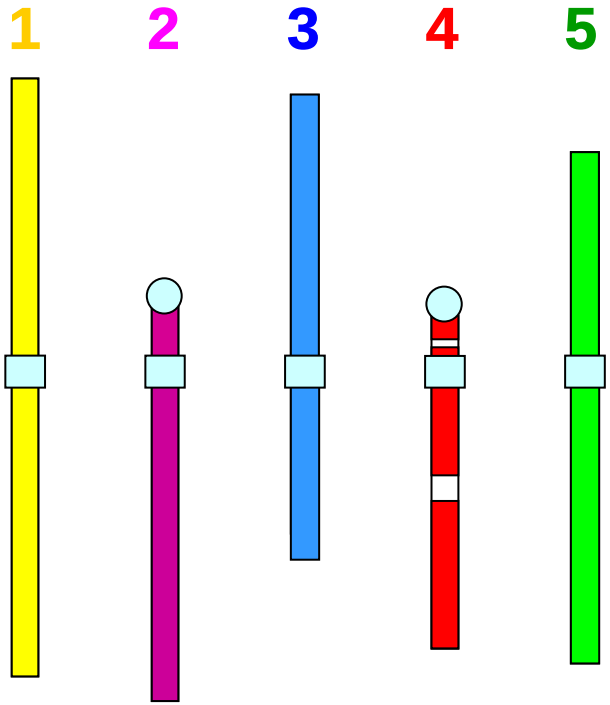
- ✓ small nuclear genome (~157 Mb/C)
- ✓ low proportion of repetitive DNA sequences (~15%)
- ✓ only five chromosome pairs (n=5)
- ✓ chromosome-specific BAC clones available

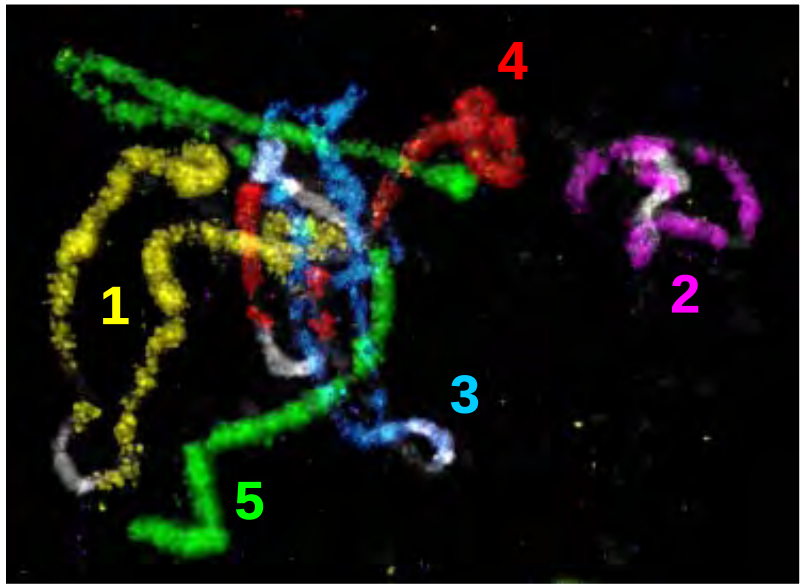
Chromosome painting in Arabidopsis using chromosome-specific BAC contigs and pachytene chromosomes

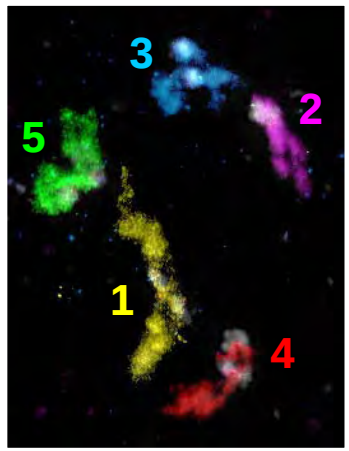


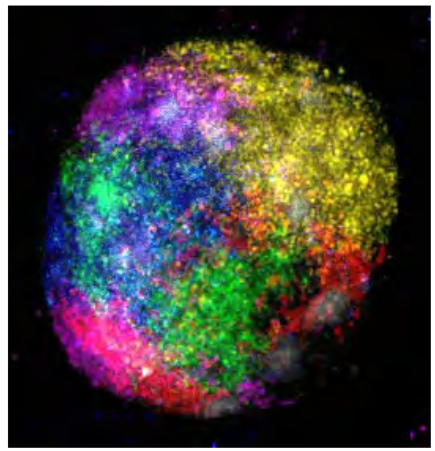
Lysak et al. 2001, 2003; Fransz et al. 2002; Pecinka et al. 2004

Multicolour chromosome painting in Arabidopsis



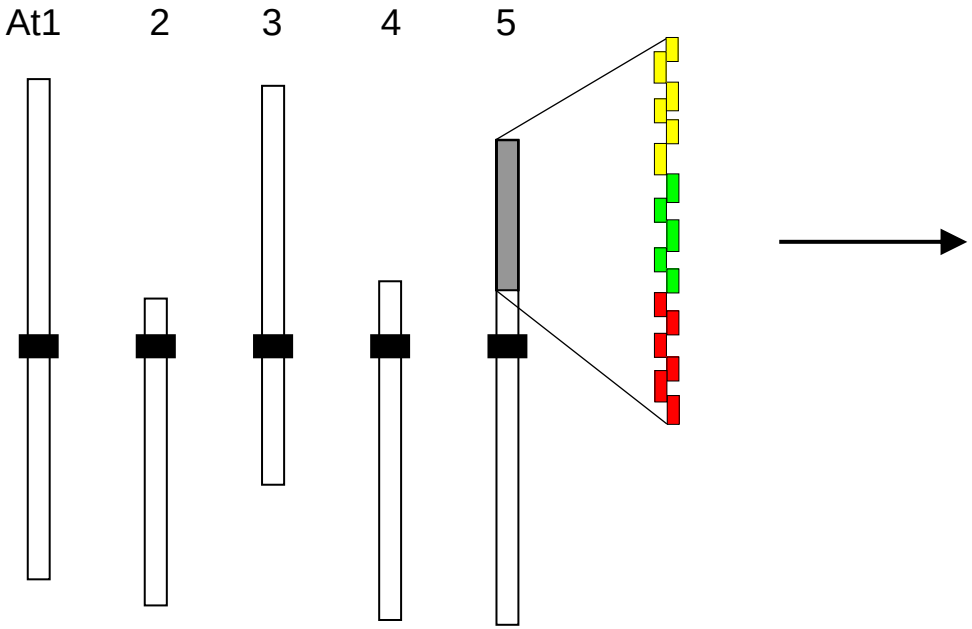






Lysak et al. 2001, 2003; Pecinka et al. 2004

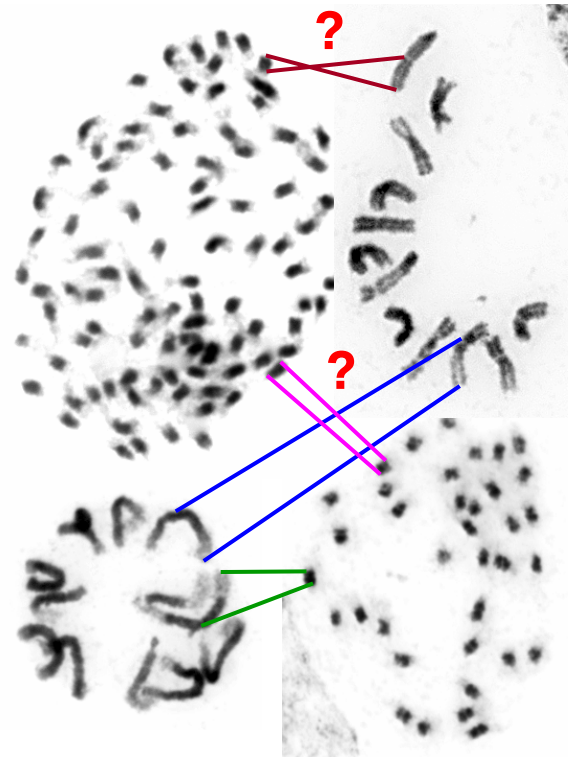
Comparative chromosome painting in *Brassicaceae*



Arabidopsis BAC contigs

Brassicaceae is the only plant family in which large-scale comparative chromosome painting (CCP) is feasible

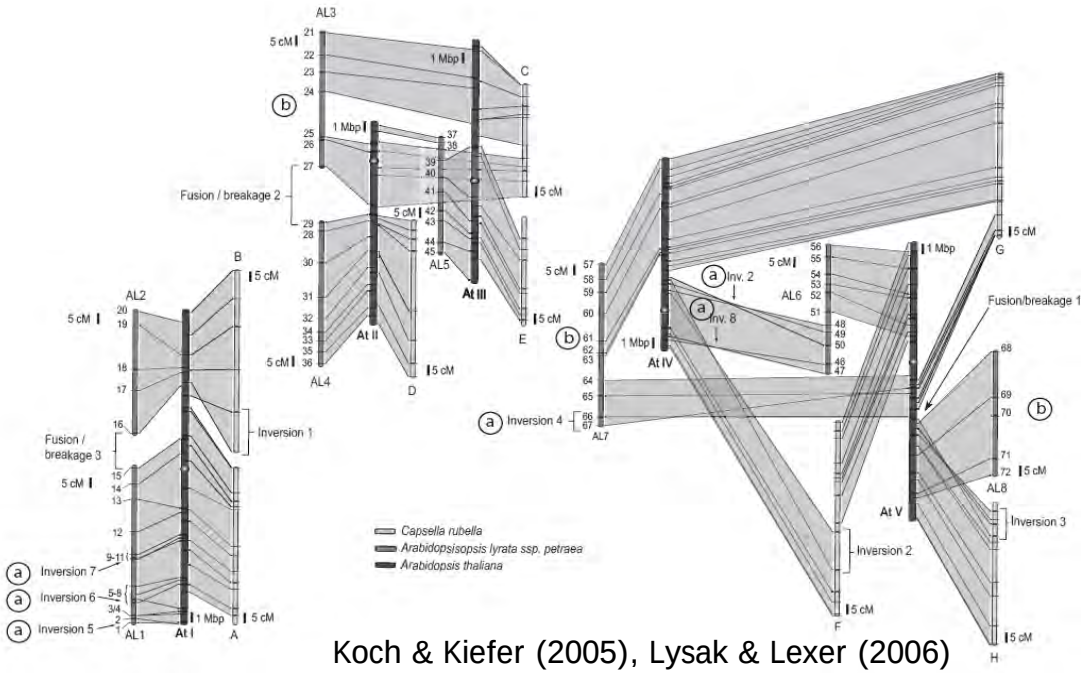
Evolutionary and comparative cytogenetics in *Brassicaceae*



- extent of chromosome homeology across the family
- chromosome number variation and karyotype evolution
- paleo- and mesopolyploid evolution
- evolutionary significance of karyotypic variation

The way to an ancestral crucifer karyotype

- ✓ comparative genetic mapping showed that karyotypes of *A. lyrata* (n=8) and *Capsella rubella* (n=8) are almost identical



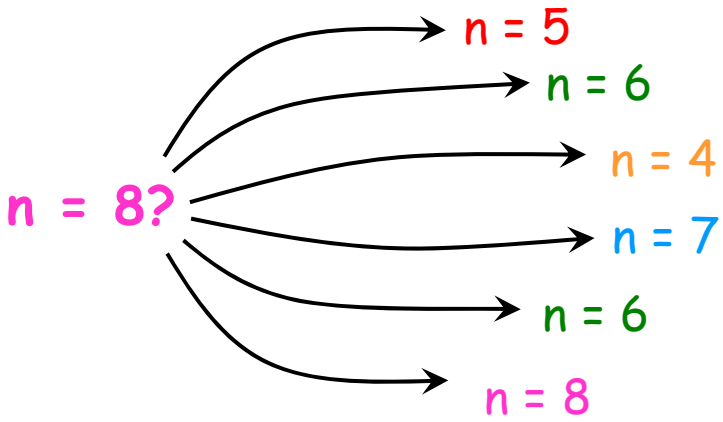
Koch & Kiefer (2005), Lysak & Lexer (2006)

- ✓ x=8 is the most frequent base number found in all *Brassicaceae* lineages, in consequence, x=8 is regarded as an ancestral chromosome number of the family

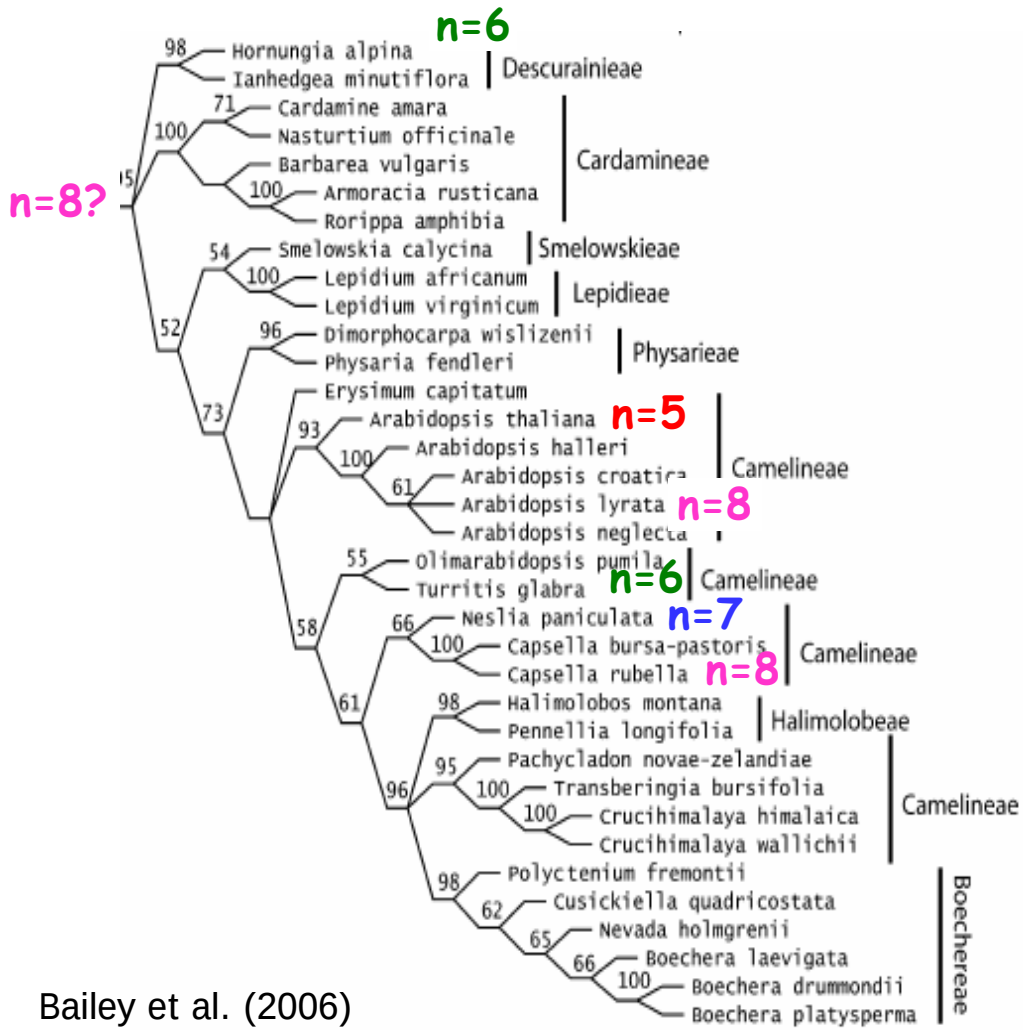
Mechanisms of chromosome number reduction in *Arabidopsis thaliana* and related Brassicaceae species

Martin A. Lysak*†, Alexandre Berr‡, Ales Pecinka‡, Renate Schmidt§, Kim McBreen¶, and Ingo Schubert‡

Proc. Natl. Acad. Sci. USA 103: 5224-5229 (2006)



revealing the extent of chromosome homeology and reconstructing evolutionary scenarios of chromosome number reduction...

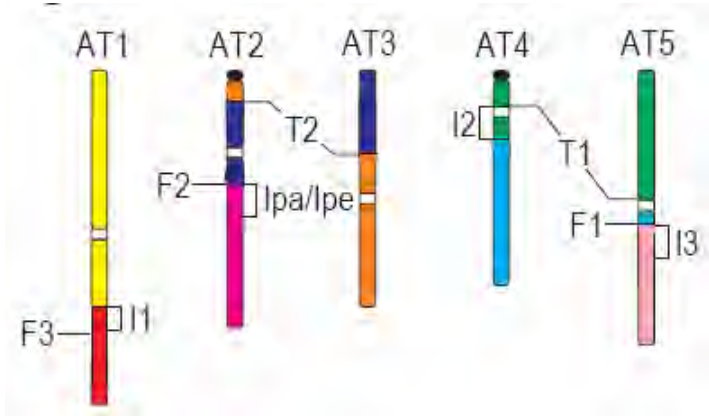


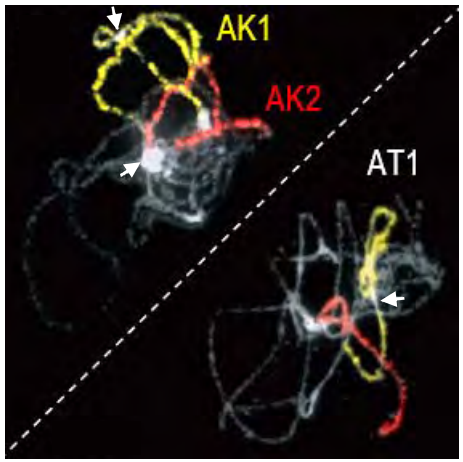
Bailey et al. (2006)

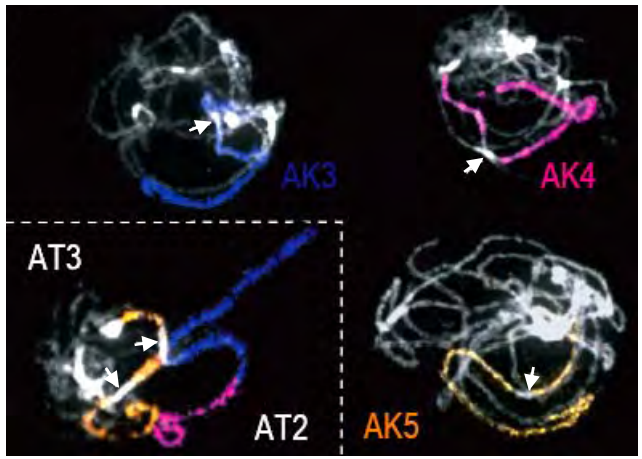
The origin of the *A. thaliana* karyotype from a tentative Ancestral Karyotype (n=8)

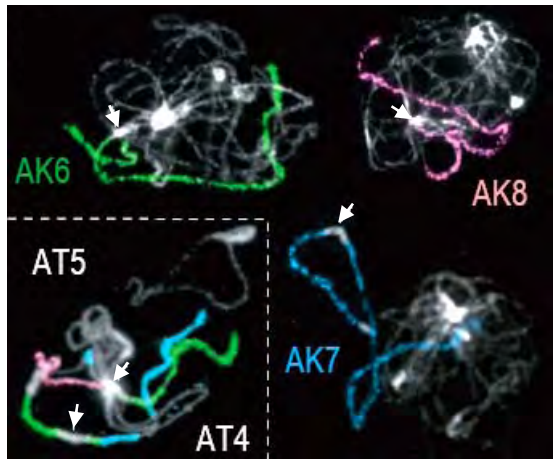
Ancestral Karyotype (n=8)

A. thaliana (n=5)



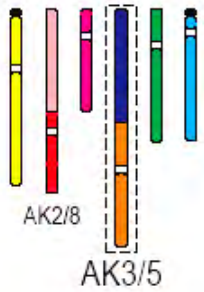


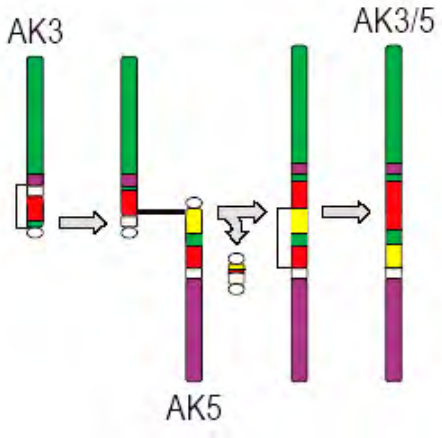


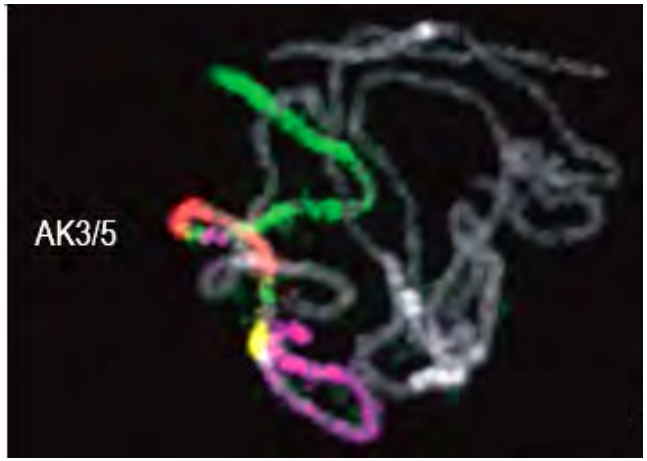


Chromosome number reduction in *Turritis glabra* (n=6) and *Hornungia alpina* (n=6)

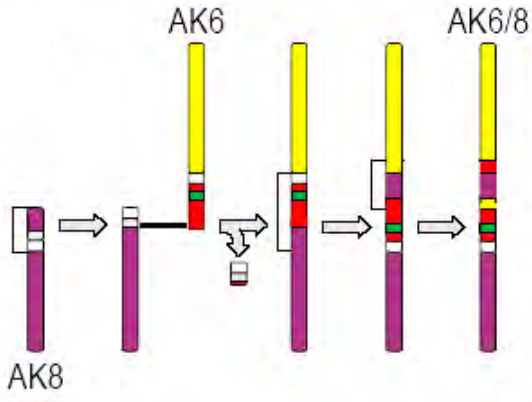
Turritis glabra (n=6)

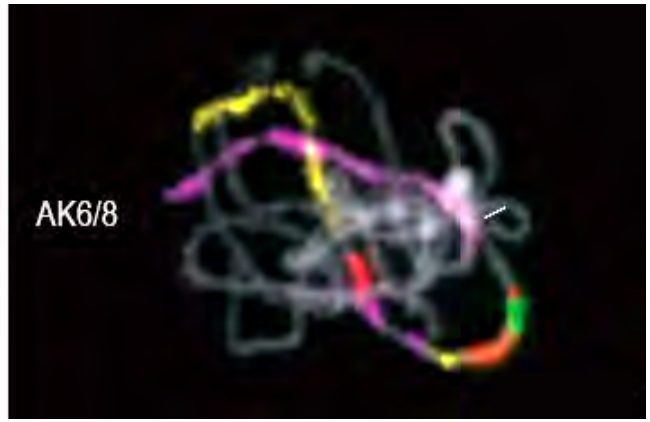




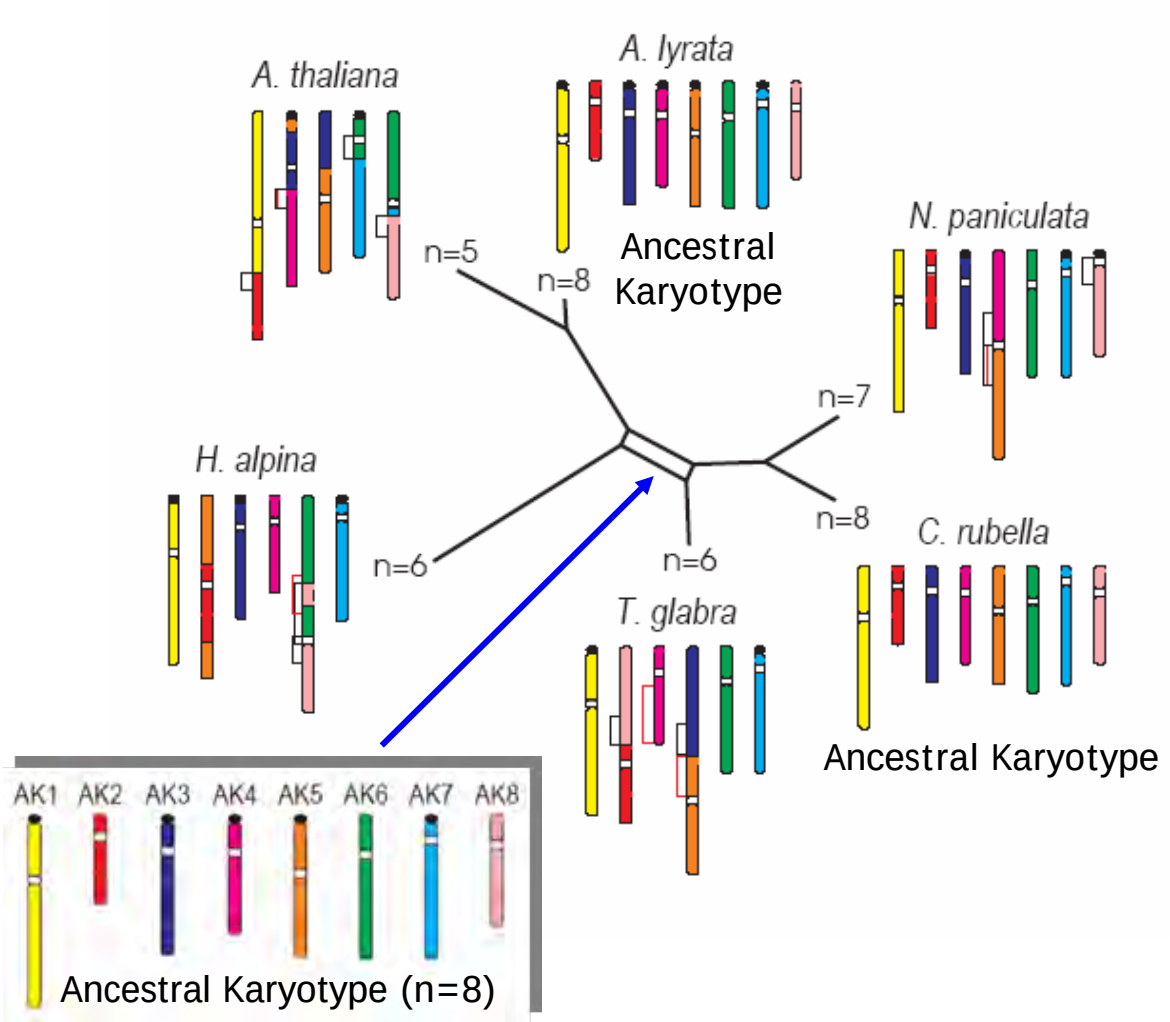


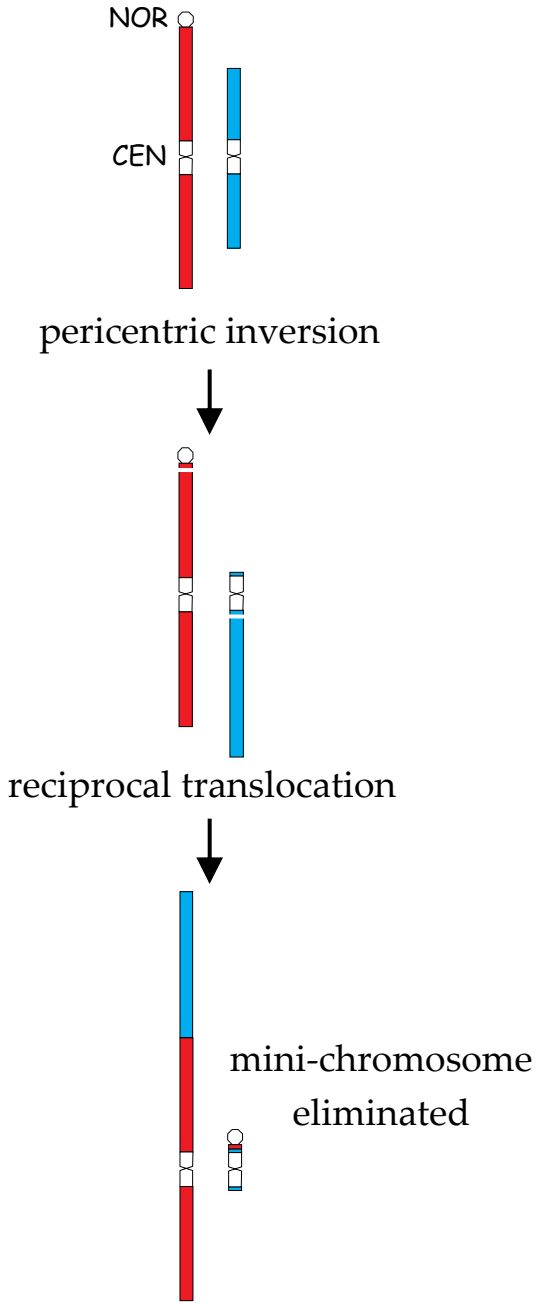
Hornungia alpina (n=6)



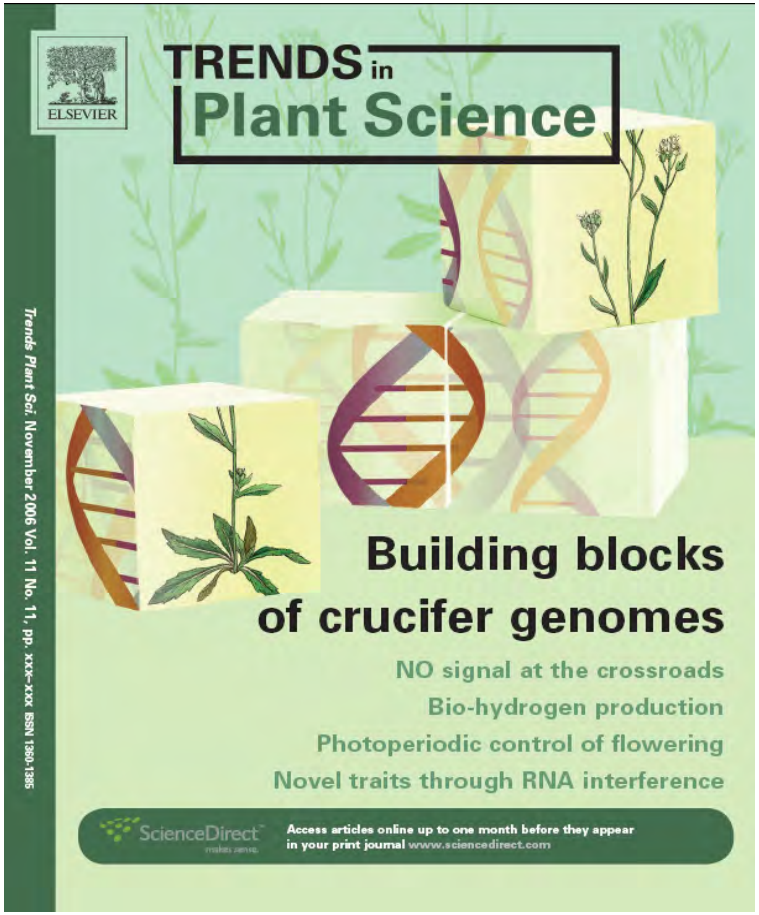


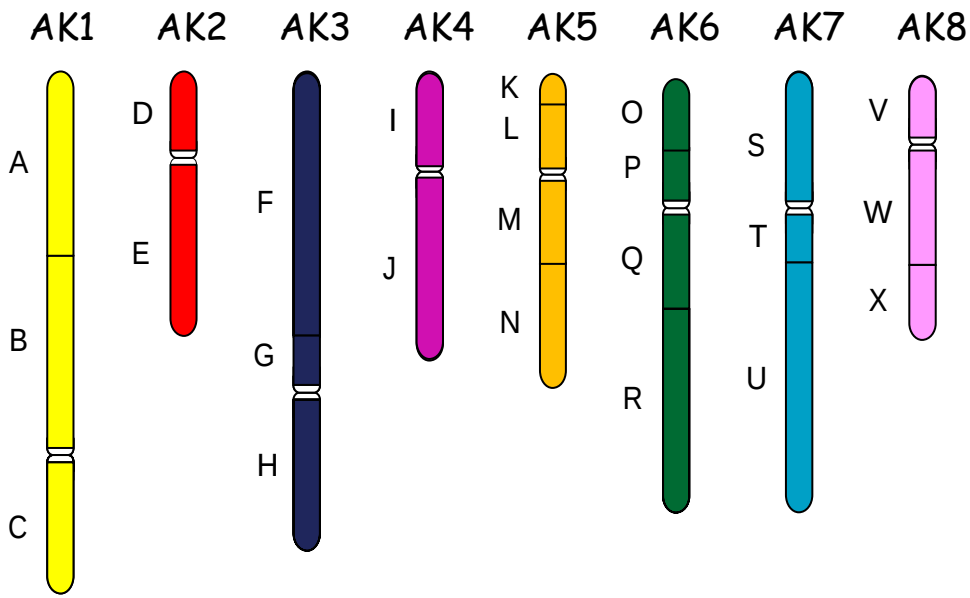
Chromosome number reduction followed different scenarios and involved different ancestral chromosomes





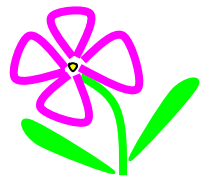
Ancestral Crucifer Karyotype (ACK): 8 ancestral chromosomes and 24 conserved genomic blocks





Crucifera ancestralis

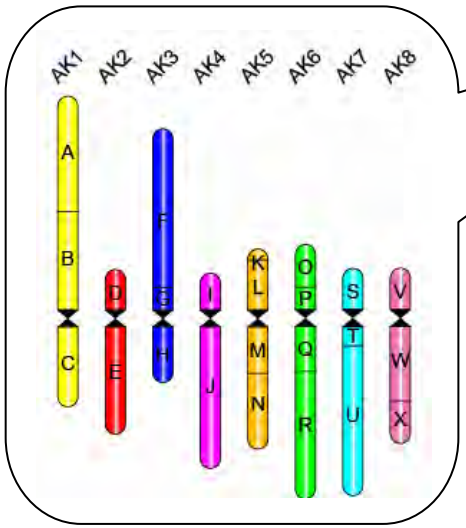
(n=8)



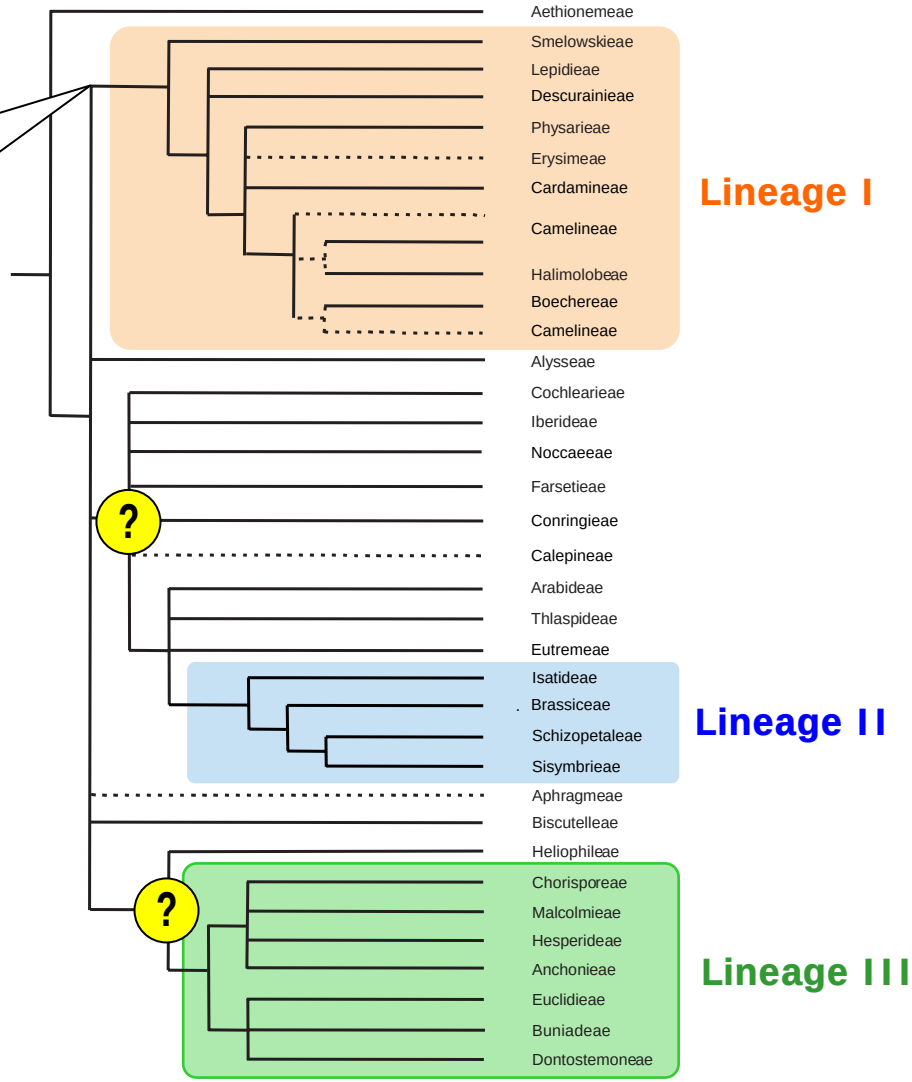
Schranz, Lysak & Mitchell-Olds (2006)

Trends Plant Sci. 11

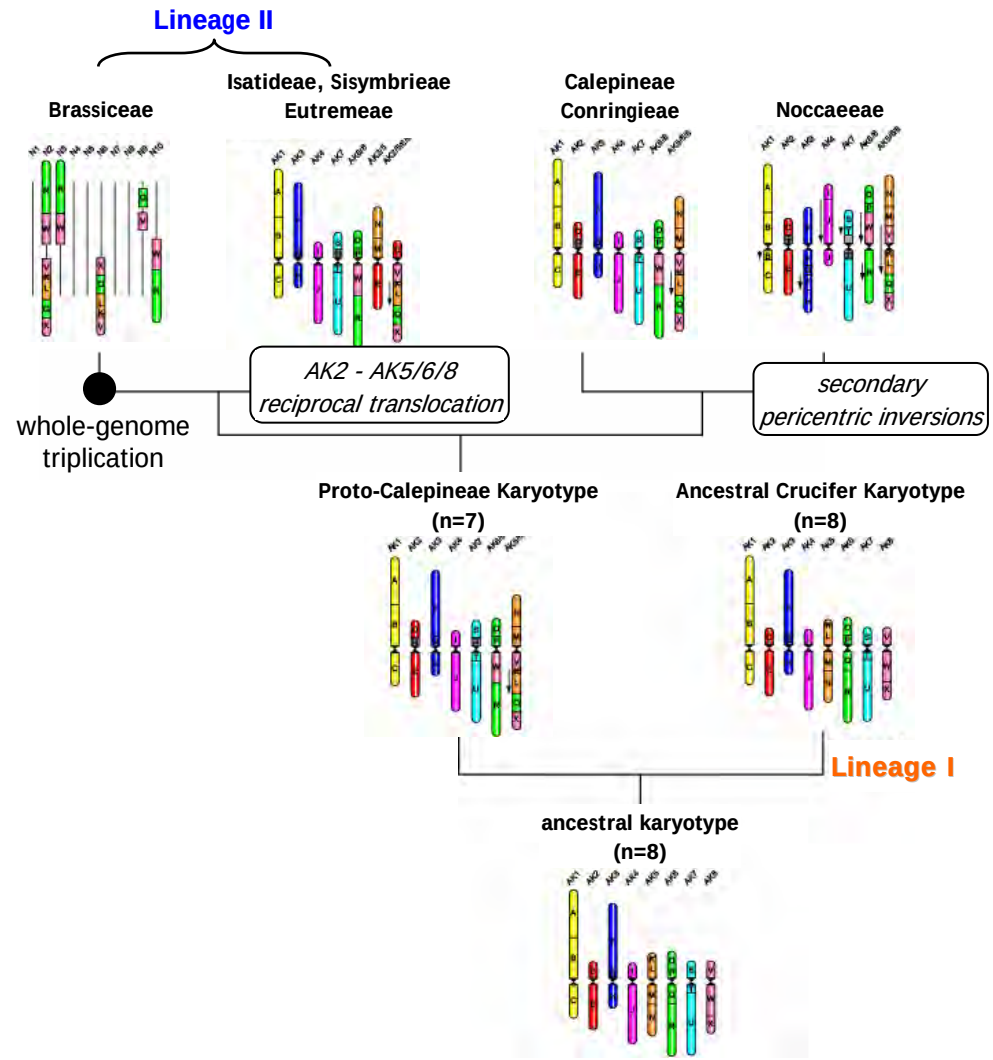
Karyotype evolution in *Brassicaceae*



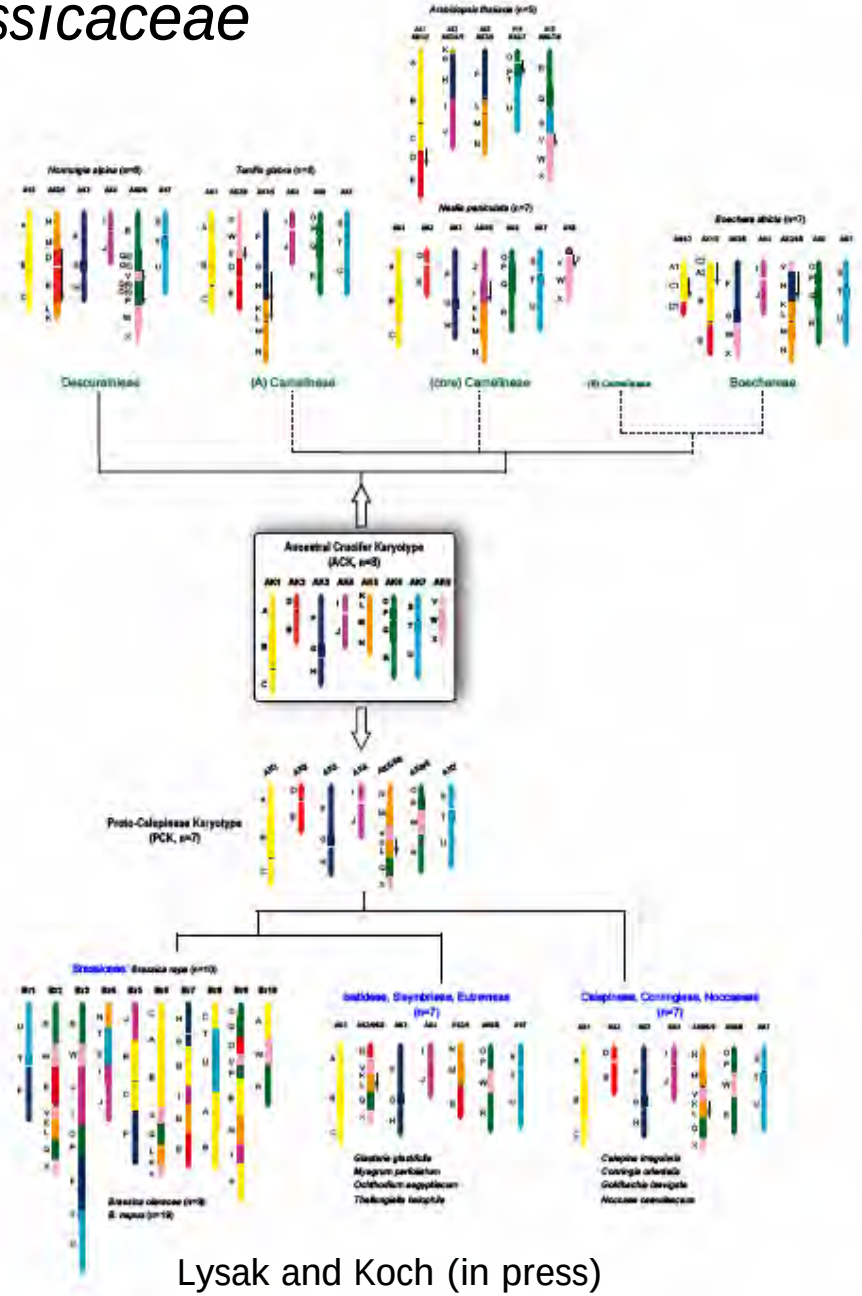
Ancestral Crucifer Karyotype
(n=8)



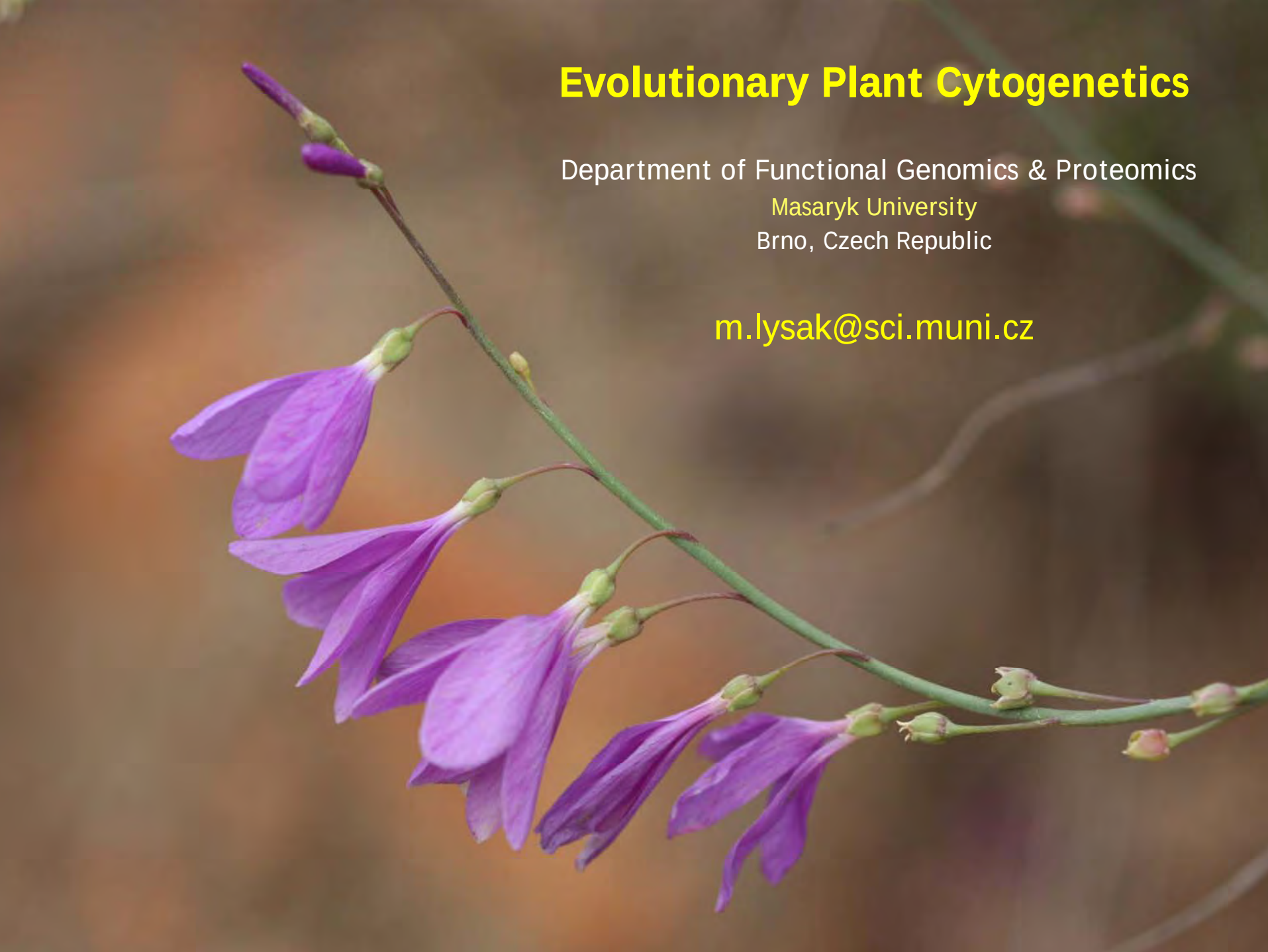
ACK: reconstructing karyotype and genome evolution across *Brassicaceae*



Mandakova and Lysak (2008) Plant Cell 20



Lysak and Koch (in press)



Evolutionary Plant Cytogenetics

Department of Functional Genomics & Proteomics
Masaryk University
Brno, Czech Republic

m.lysak@sci.muni.cz