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# BRASSICA ALLOTRIPLOIDS, A SOLUTION TO DEAL WITH HAMPERED MEIOTIC RECOMBINATION

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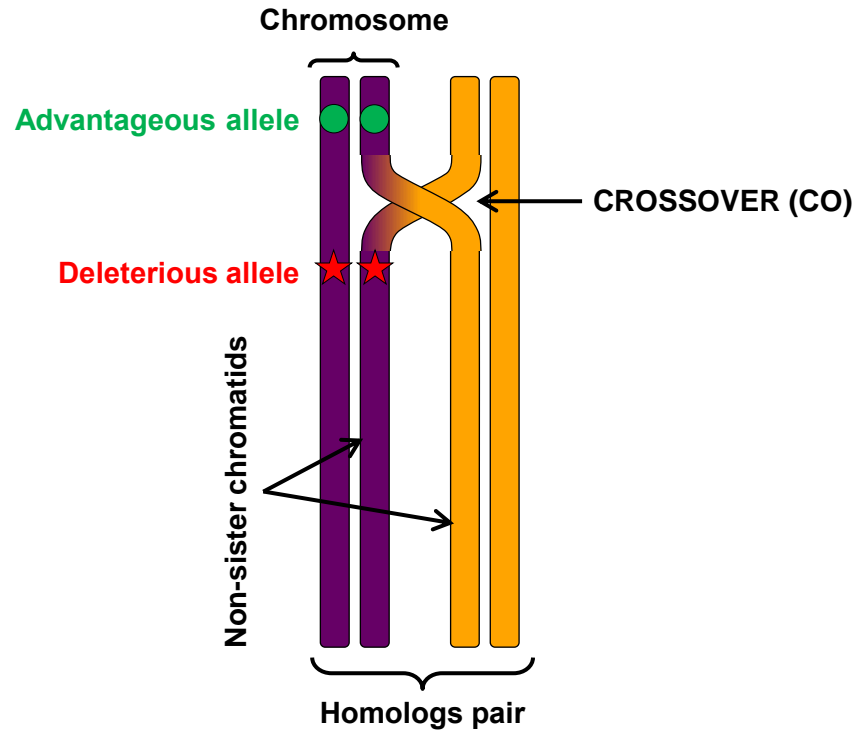
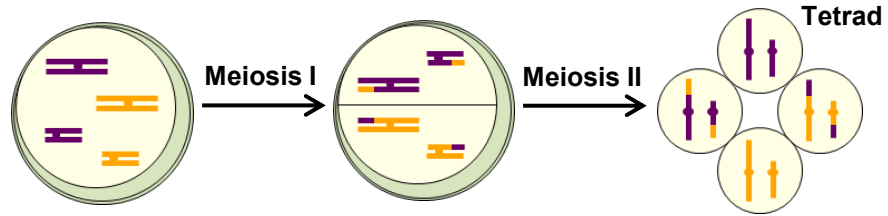
21<sup>st</sup> Crucifer Genetics Conference  
Saint-Malo, 01<sup>st</sup> July 2018



# SCIENTIFIC CONTEXT

## Meiotic recombination process in brief, from its roles to its limits

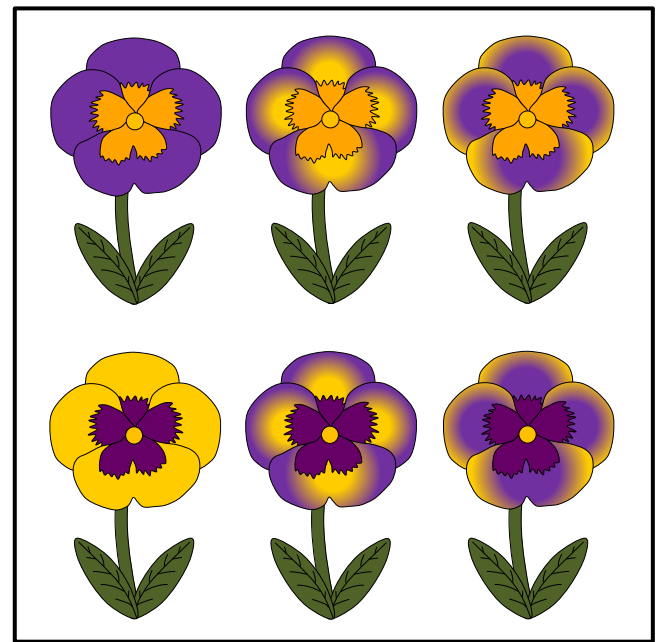
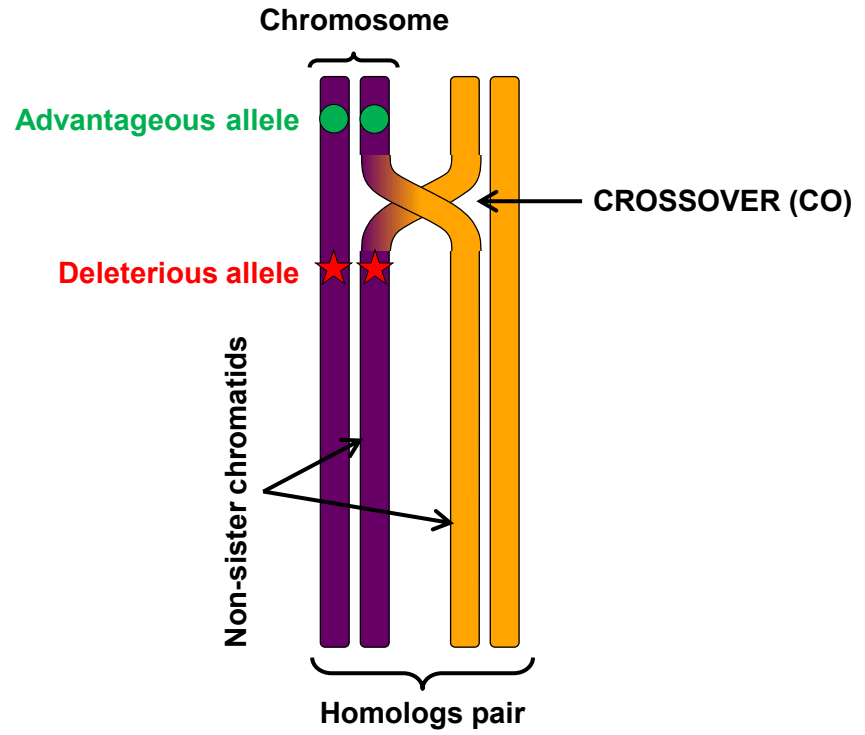
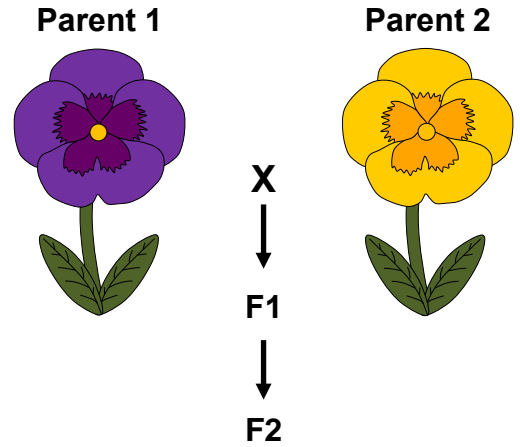
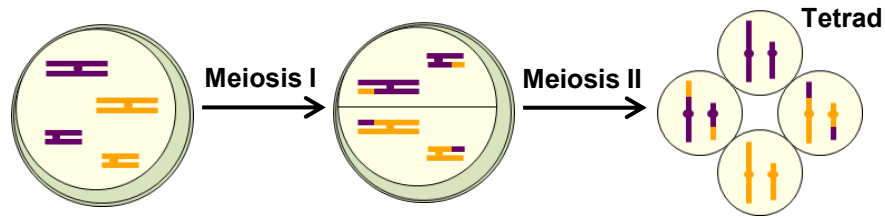
- ❖ Ensures the formation of well-balanced gametes



# SCIENTIFIC CONTEXT

## Meiotic recombination process in brief, from its roles to its limits

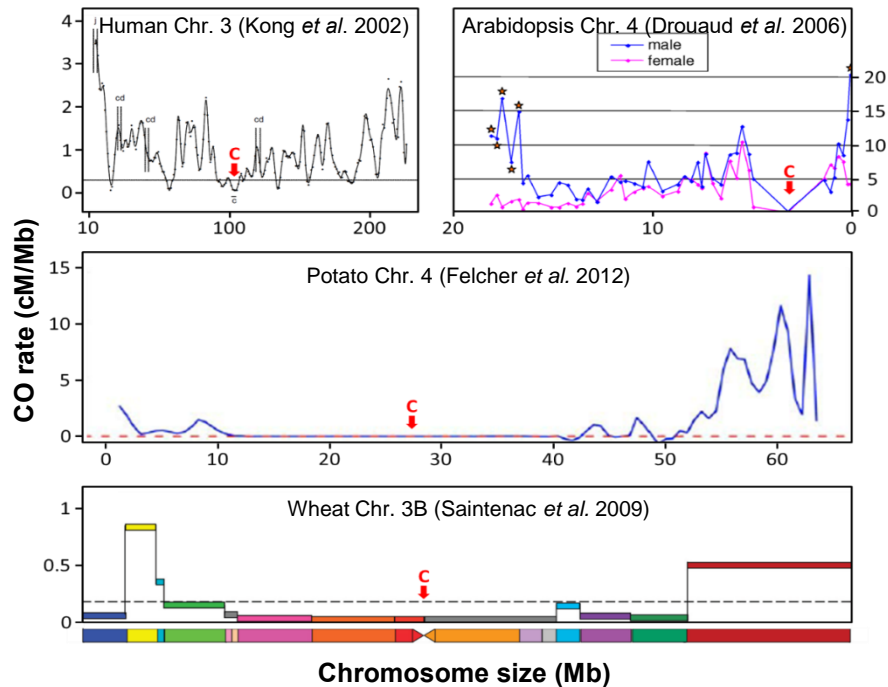
- ❖ Ensures the formation of well-balanced gametes & the generation of diversity



## Meiotic recombination process in brief, from its roles to its limits

❖ But number and distribution of crossovers are tightly controlled

- ✓ Per pair of homologs, rarely more than 3 COs occur
- ✓ COs distribution is NOT homogenous along the chromosomes

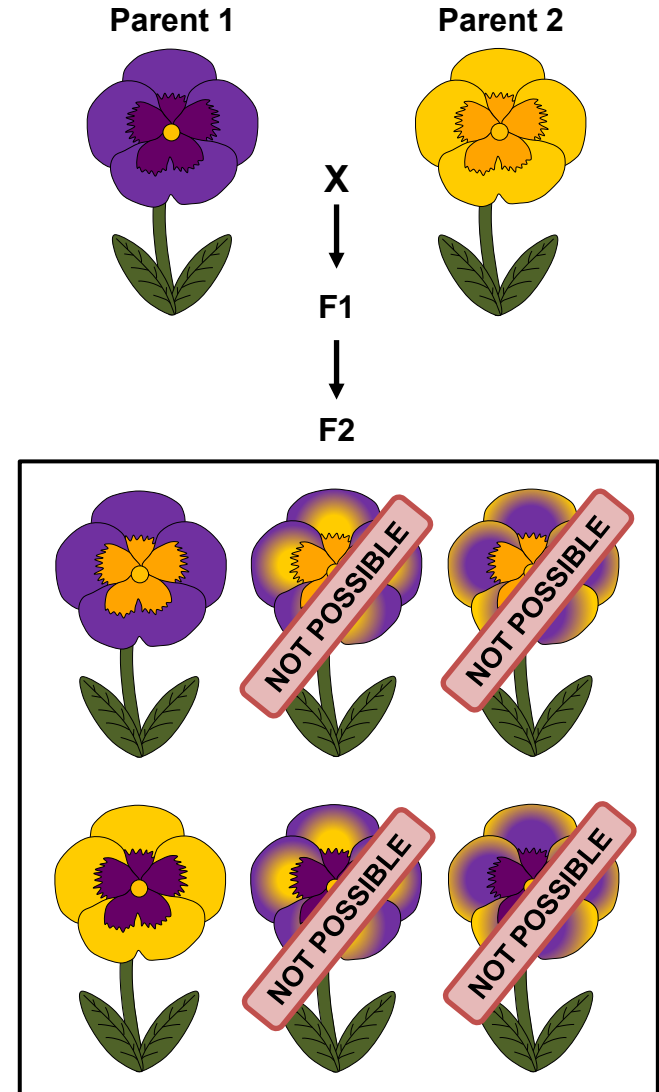
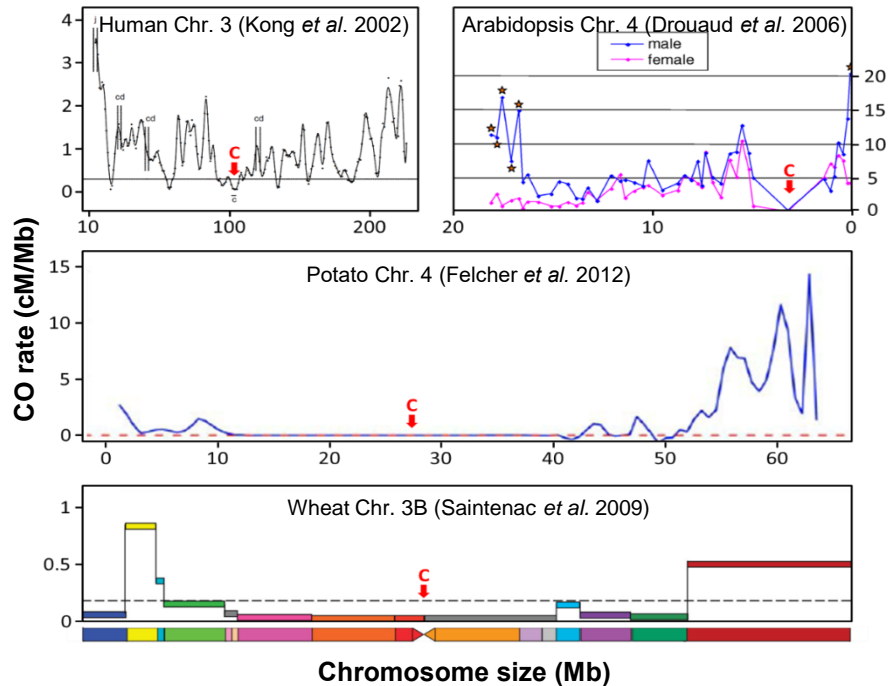


# SCIENTIFIC CONTEXT

## Meiotic recombination process in brief, from its roles to its limits

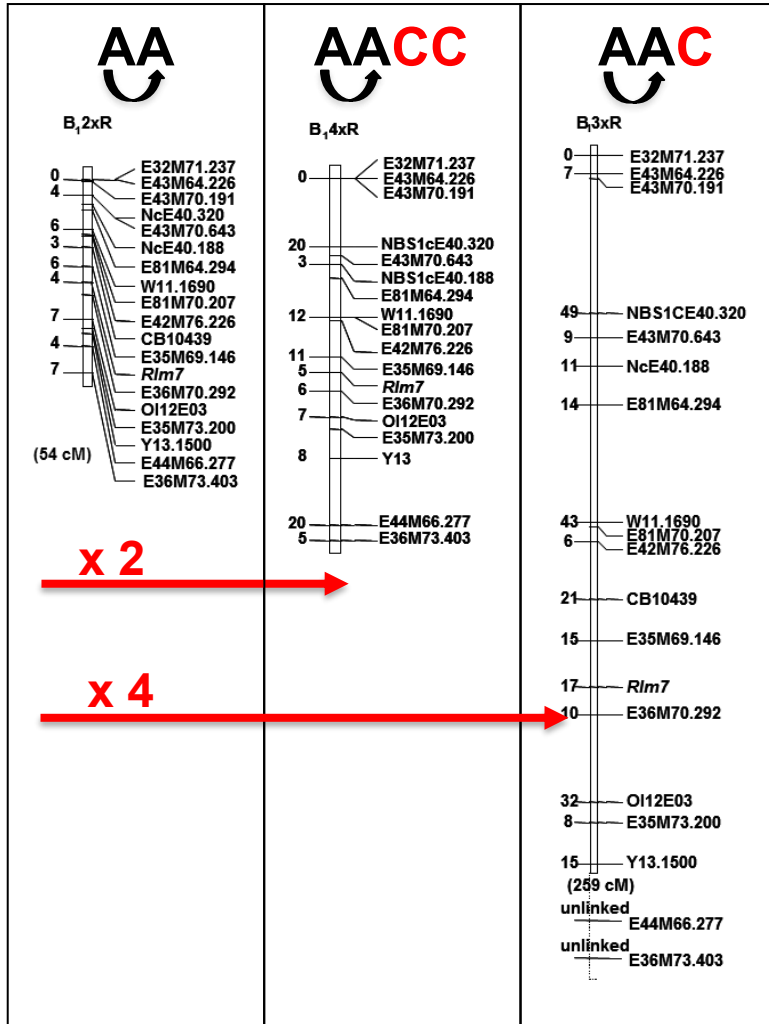
❖ But number and distribution of crossovers are tightly controlled

- ✓ Per pair of homologs, rarely more than 3 COs occur
- ✓ COs distribution is NOT homogenous along the chromosomes



## How can we enhance meiotic recombination in *Brassica*?

❖ By exploiting *Brassica* allotriploids



(Leflon *et al.*, 2010)



*B. napus* AACCC,  
 $2n=4x=38$   
(Chalhoub *et al.*, 2014)

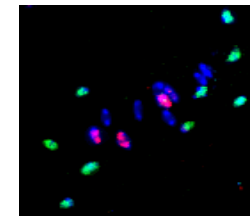


*B. rapa* AA,  
 $2n=2x=20$   
(Wang *et al.*, 2011)

X



AAC  
 $2n=3x=29$

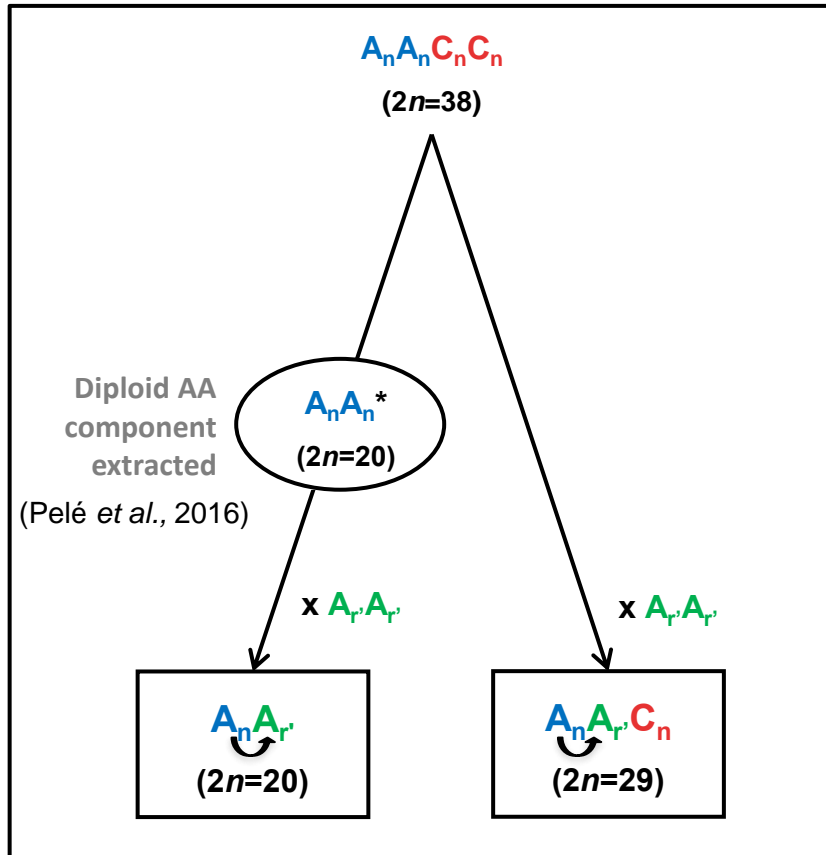


### QUESTIONS

- ✓ What about COs rate and distribution between the 10 A homologs in AACCC allotriploids?
- ✓ What about CCA allotriploids?

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

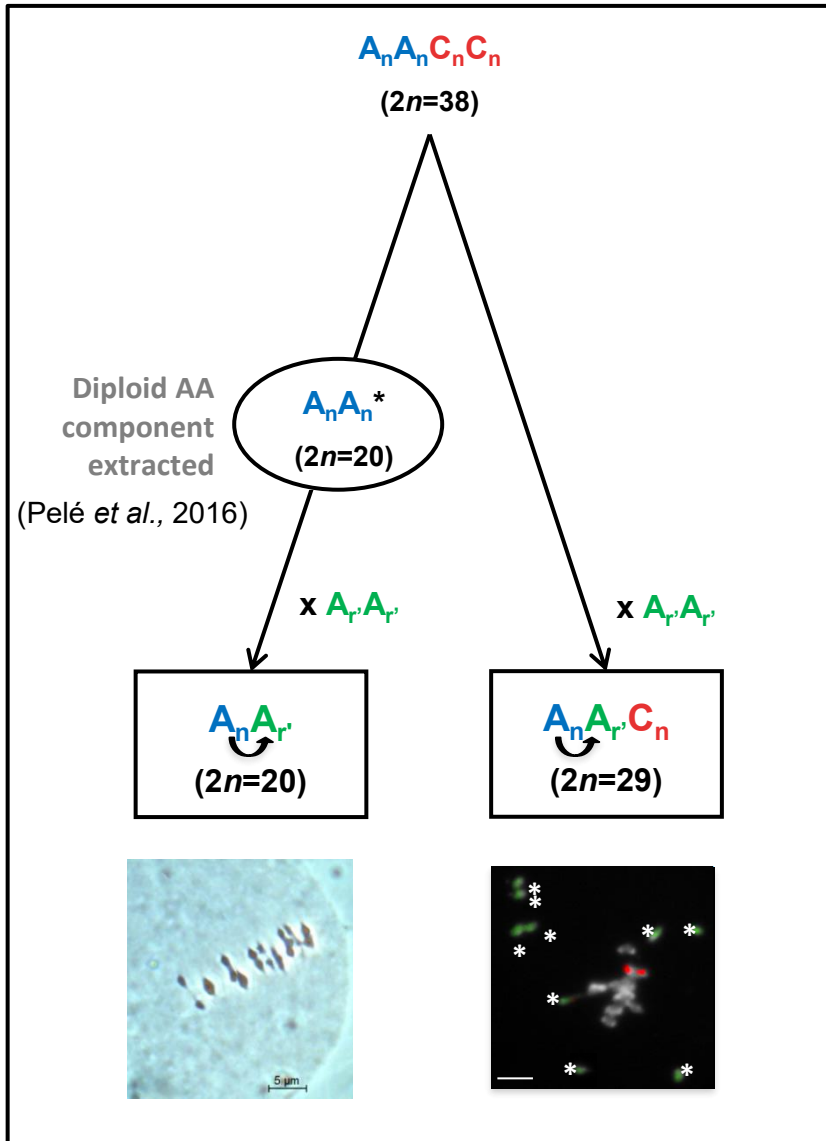
## Material & Methods



- $A_n A_n$  = A genome of *B. napus* cv. Darmor extracted
- $A_r' A_r'$  = *B. rapa* cv. Chiifu (Sequenced)
- $A_n A_n C_n C_n$  = *B. napus* cv. Darmor (Sequenced).

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

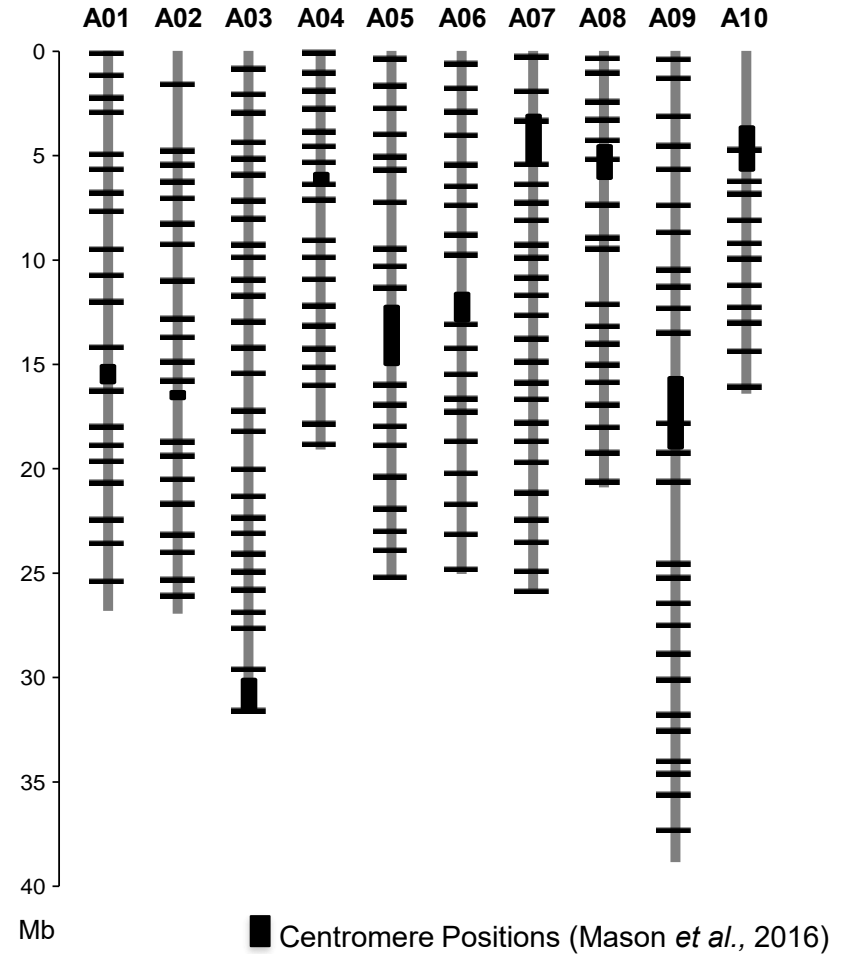
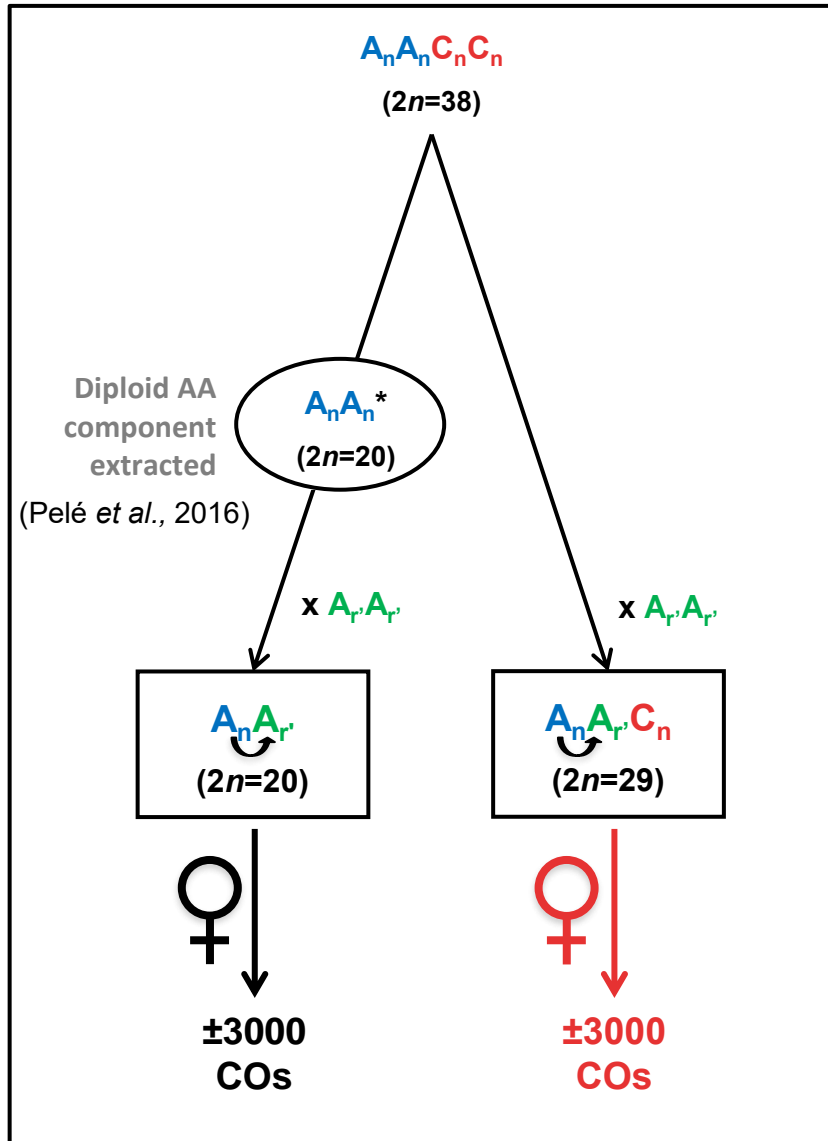
## Material & Methods





# RATE AND DISTRIBUTION OF COs IN AA VS AAC HYBRIDS

## Material & Methods

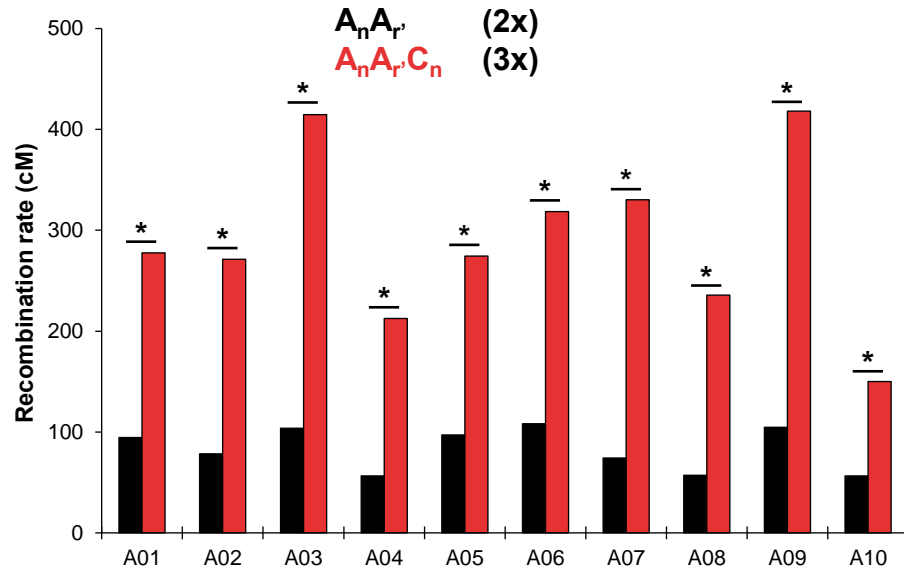


1 SNP / 1.25 Mb (SE = 0.04, n = 194)

Covering 94% of the A genome

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## CO rates between the homologous A chromosomes in AA and AAC hybrids

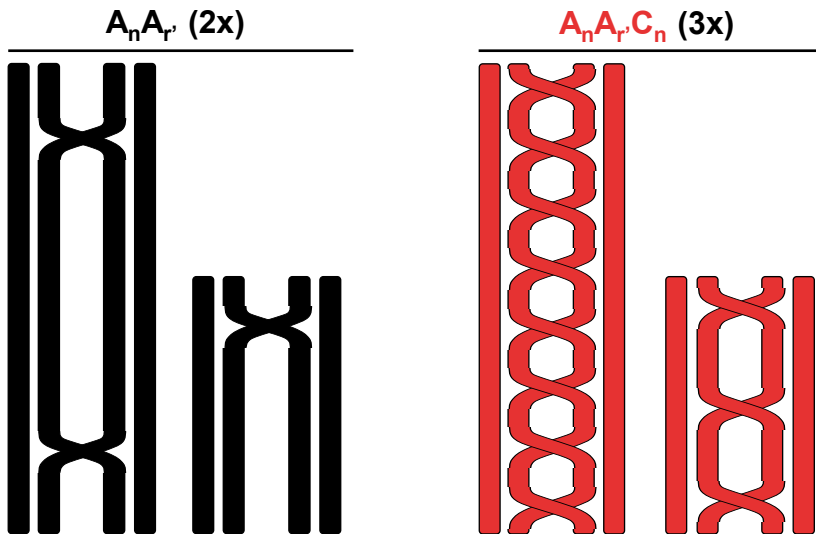
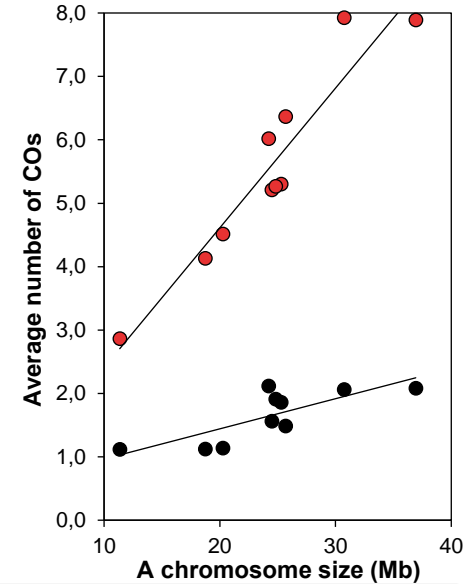
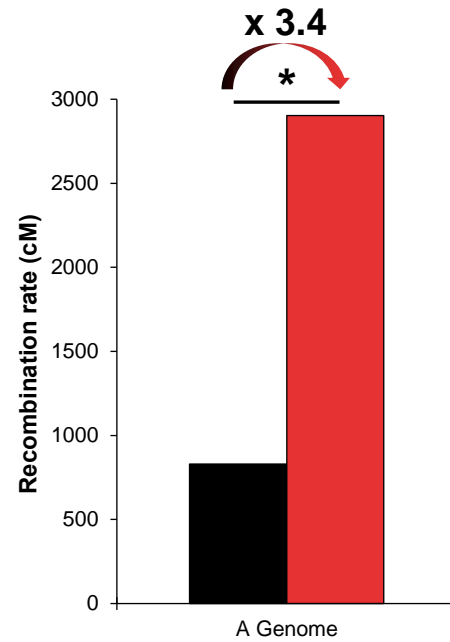
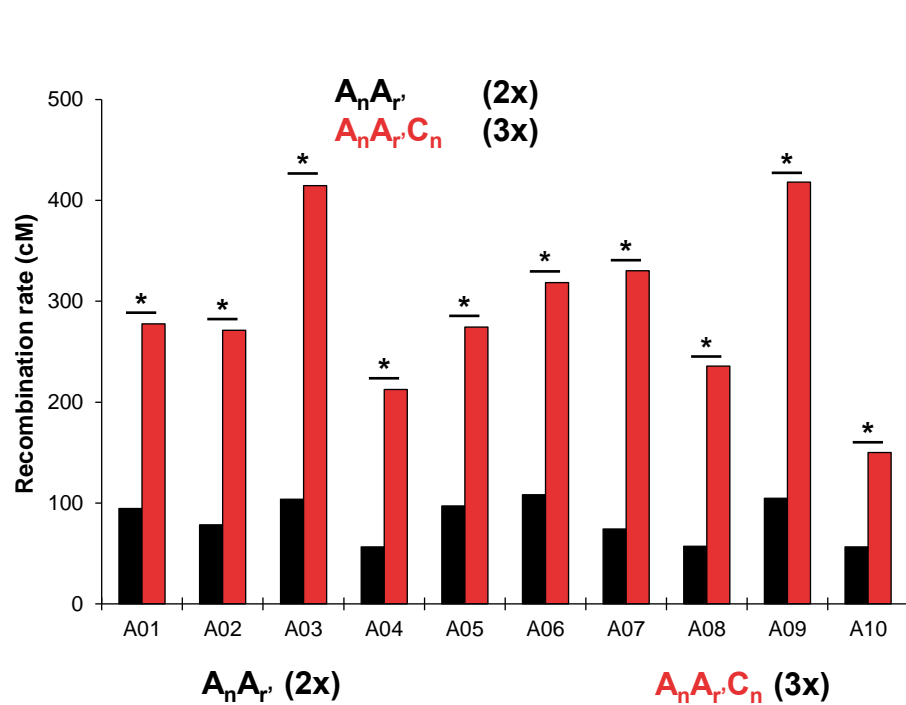


**CO rates: AA <<< AAC**

Between all homologous A chromosomes,  
extending at the whole A genome the  
results of Leflon *et al.* (2010)

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## CO rates between the homologous A chromosomes in AA and AAC hybrids



**CO rates: AA <<< AAC**

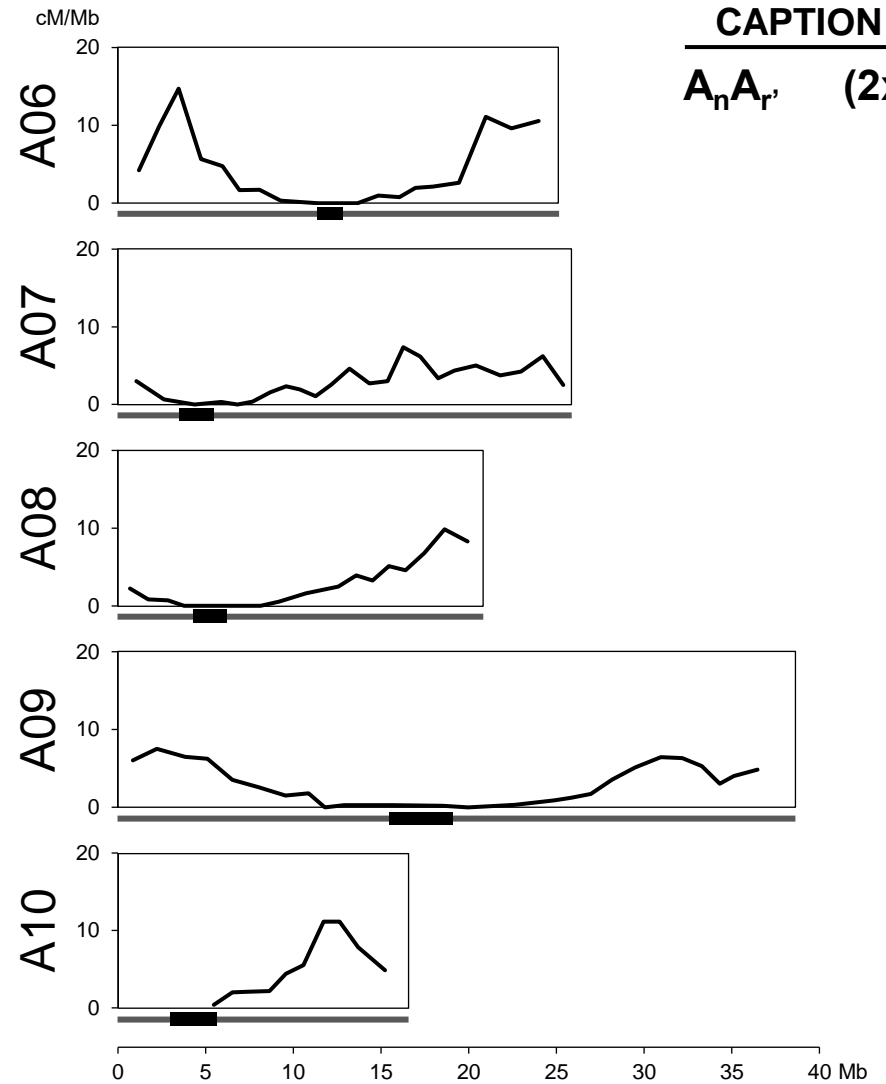
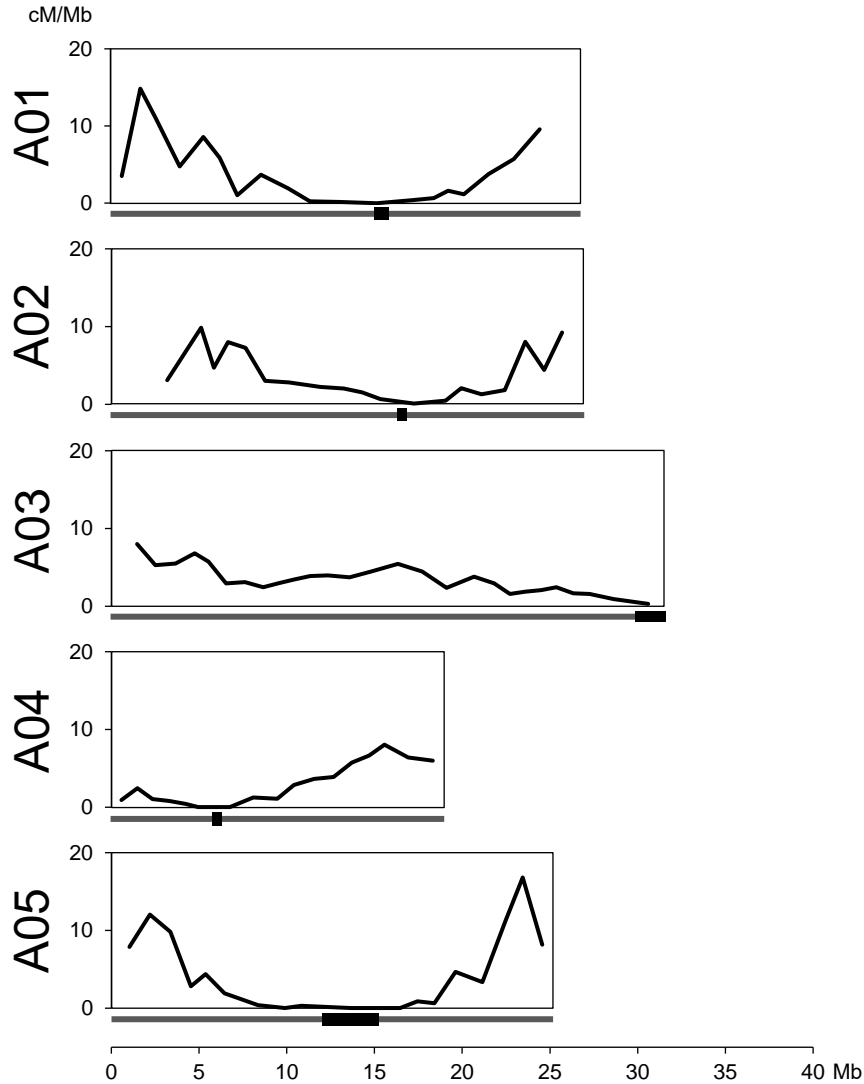
At the whole A genome the number of COs is 3.4-fold higher in AAC hybrid

The number of COs is positively correlated with the A chromosome size

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## COs distribution along the A chromosomes in the AA hybrid

- ❖ CO rates increase gradually from centromeres toward chromosome extremities

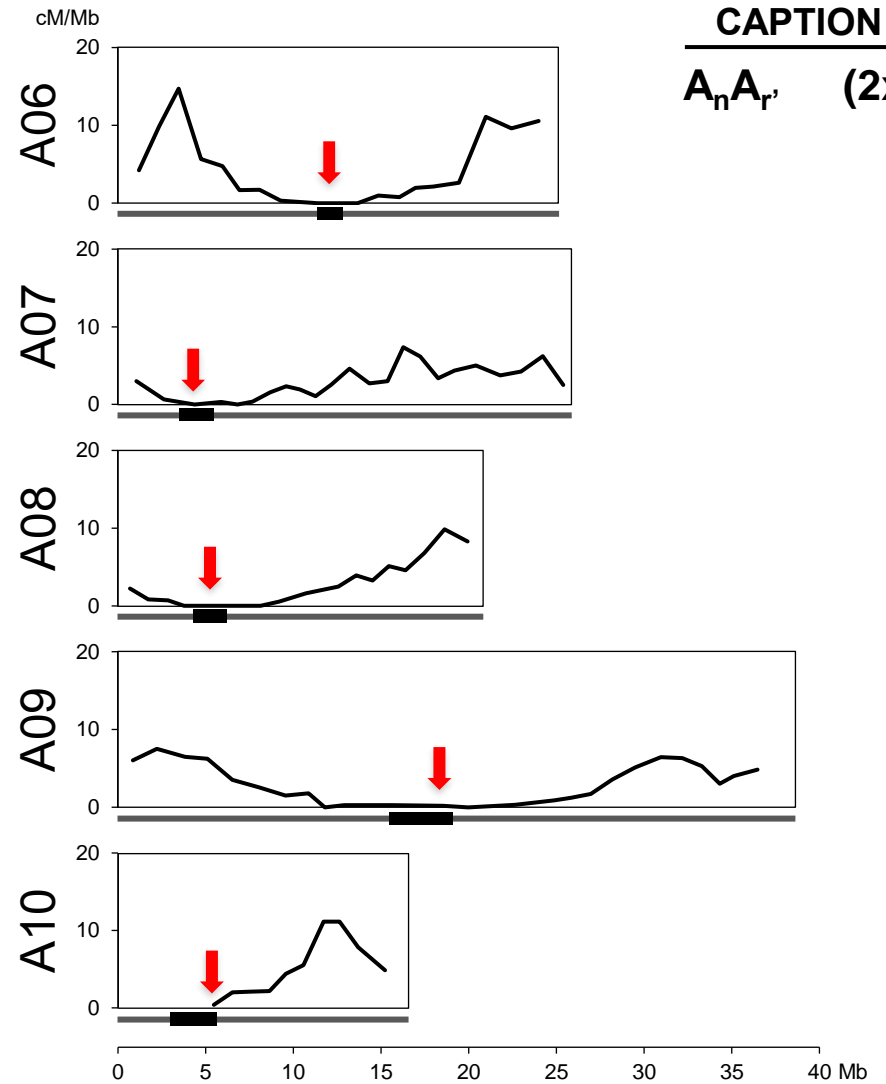
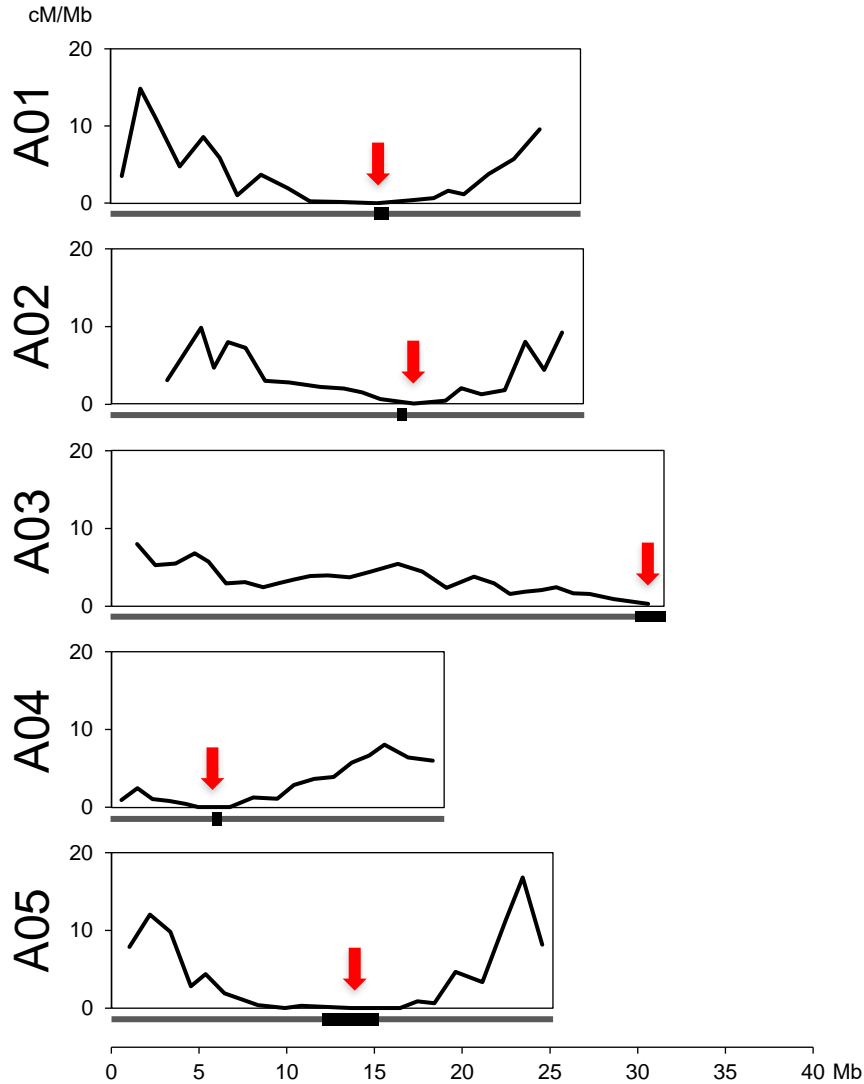


**CAPTION**  
**A<sub>n</sub>A<sub>r</sub>' (2x)**

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## COs distribution along the A chromosomes in the AA hybrid

- ❖ ~10% of the A genome is totally deprived of COs, especially close to the centromeres

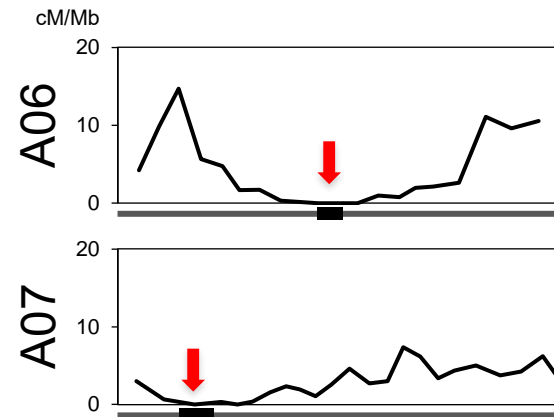
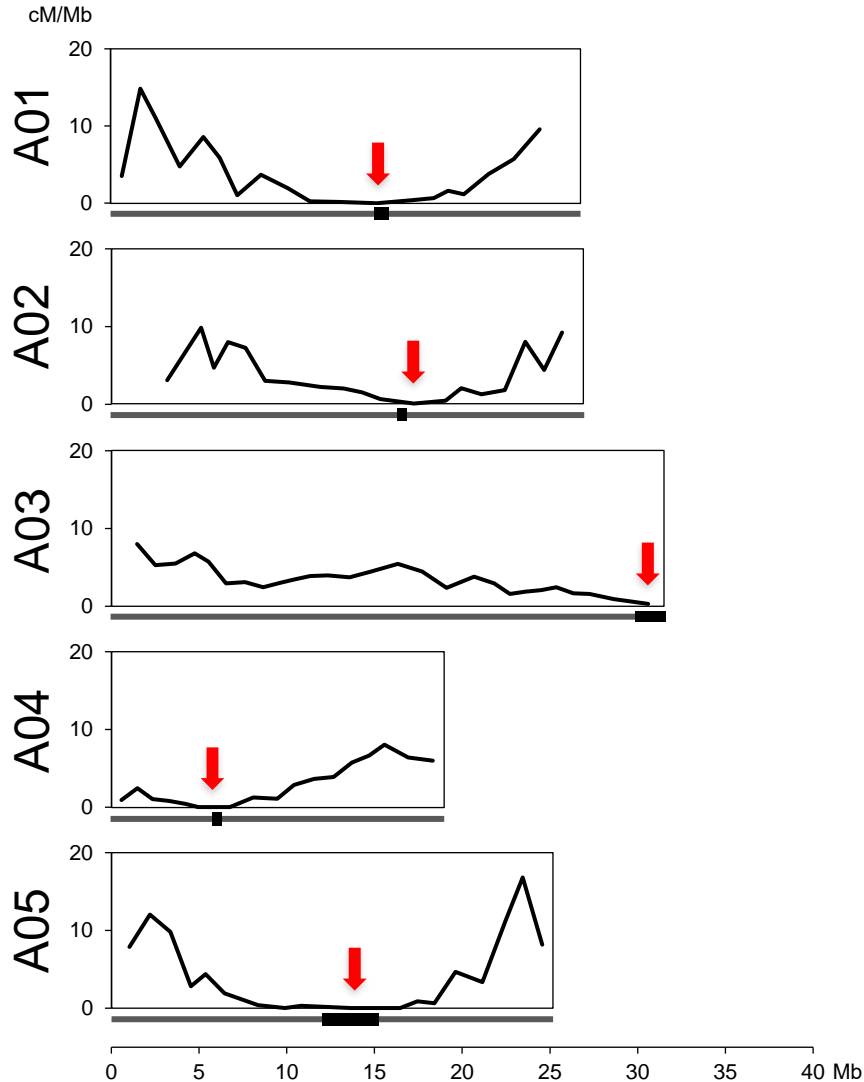


**CAPTION**  
**A<sub>n</sub>A<sub>r</sub>' (2x)**

# RATE AND DISTRIBUTION OF COs IN AA VS AAC HYBRIDS

## COs distribution along the A chromosomes in the AA hybrid

❖ ~10% of the A genome is totally deprived of COs, especially close to the centromeres



**CAPTION**  
**A<sub>n</sub>A<sub>r</sub>' (2x)**

### In AA hybrid

Expected Recombination landscapes are  
observed along each A chromosome

With:

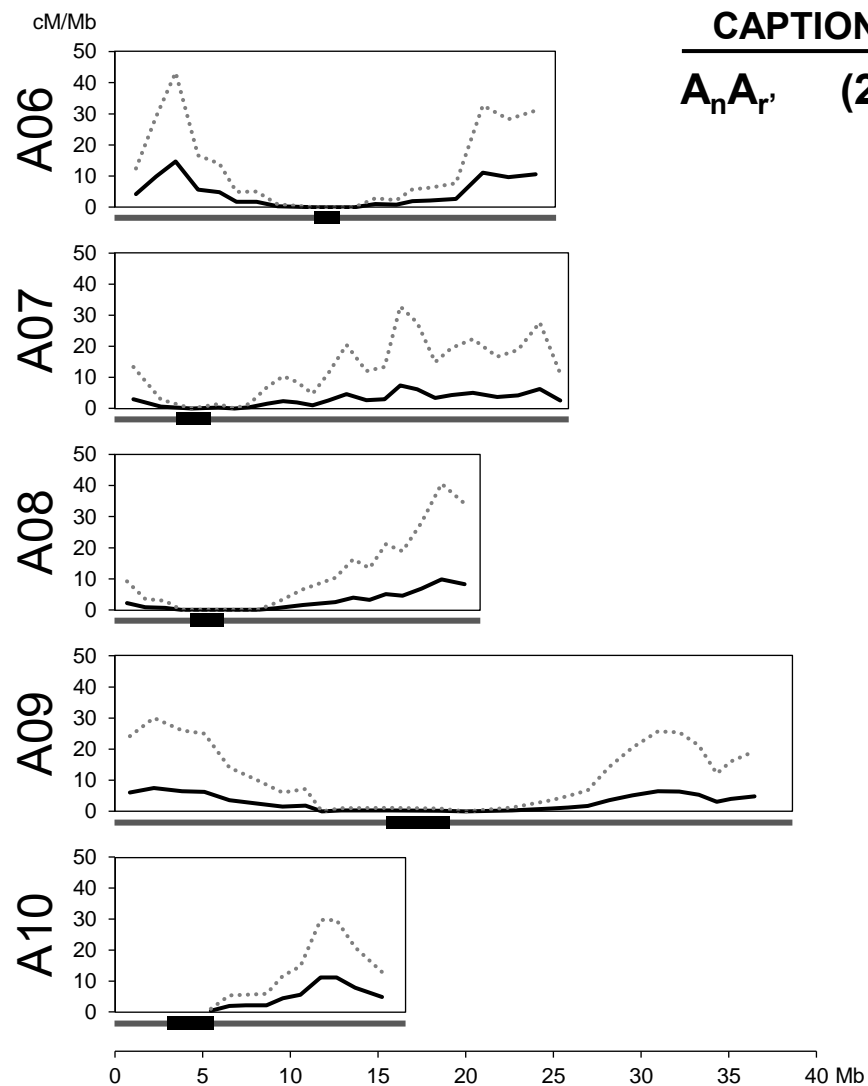
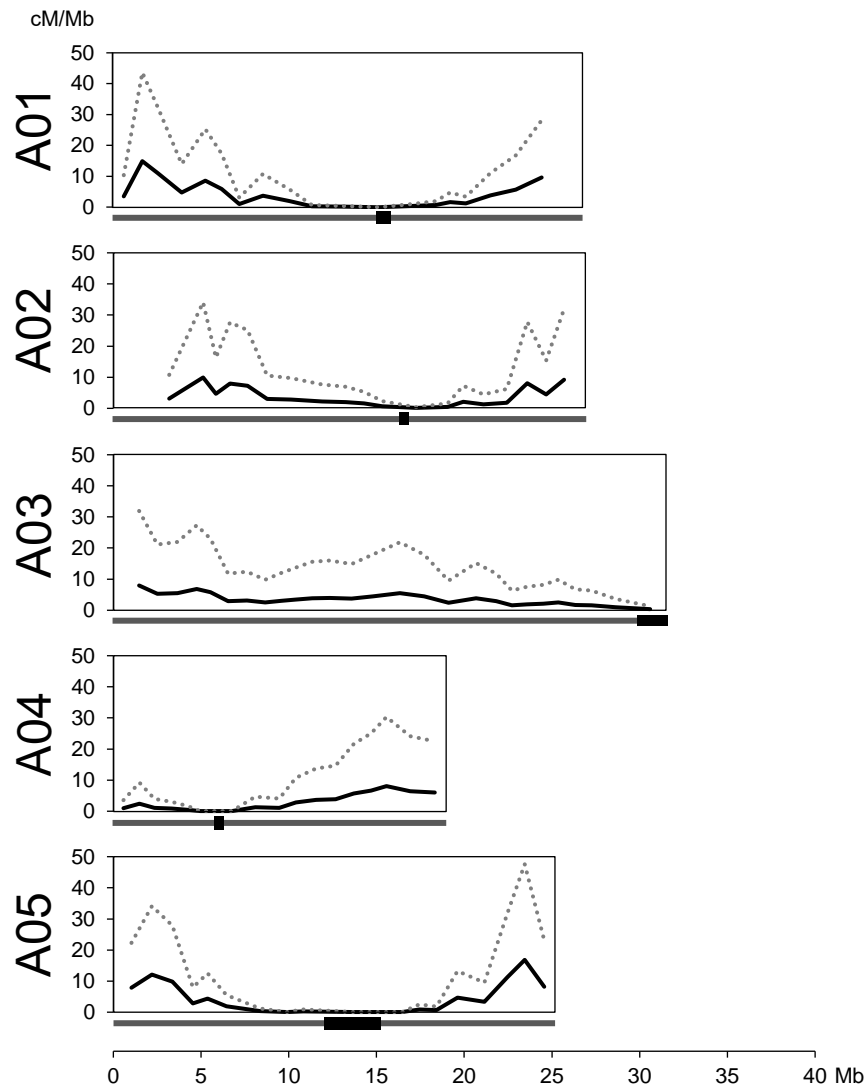
- ✓ No CO in the vicinity of centromeres
- ✓ Gradient for CO rates along chromosome arms

**What is going on in AAC hybrid?**

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## COs distribution along the A chromosomes in the AAC hybrid

❖ Does CO rates increase proportionally along the A chromosomes compared to the AA hybrid?

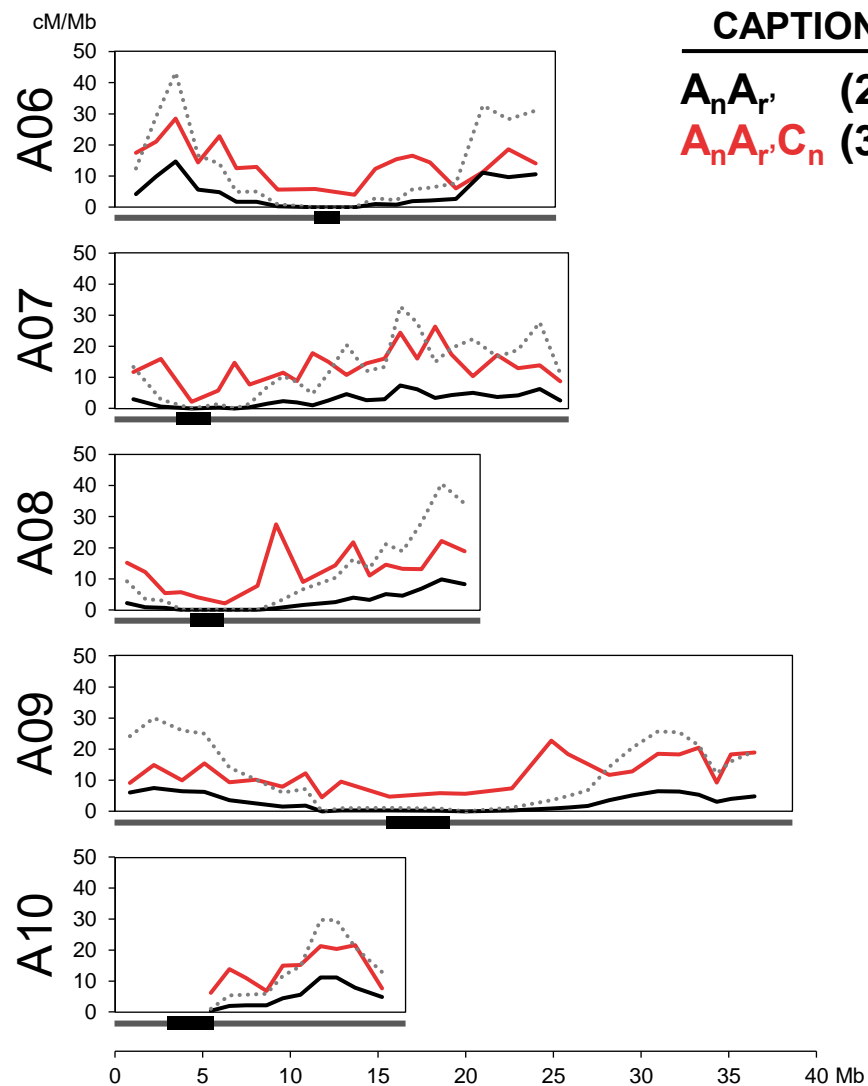
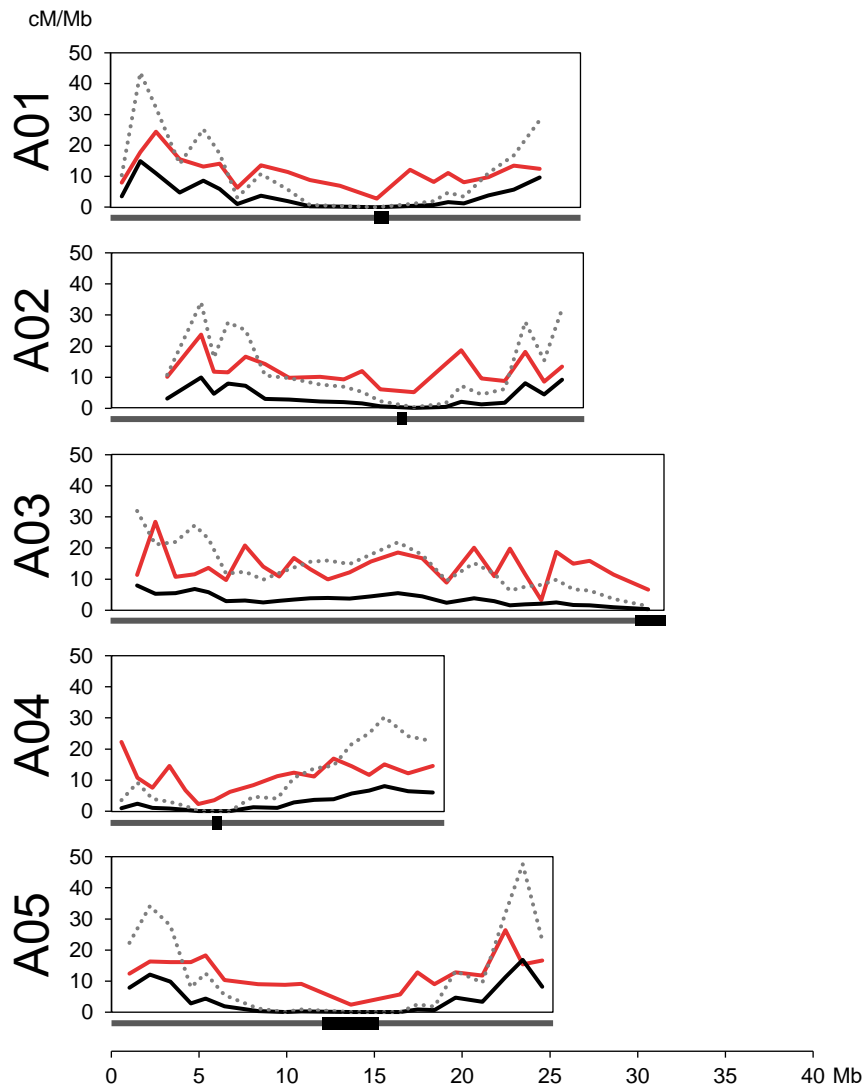


**CAPTION**  
 **$A_n A_r$  (2x)**

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## COs distribution along the A chromosomes in the AAC hybrid

❖ Does CO rates increase proportionally along the A chromosomes compared to the AA hybrid? **NO**



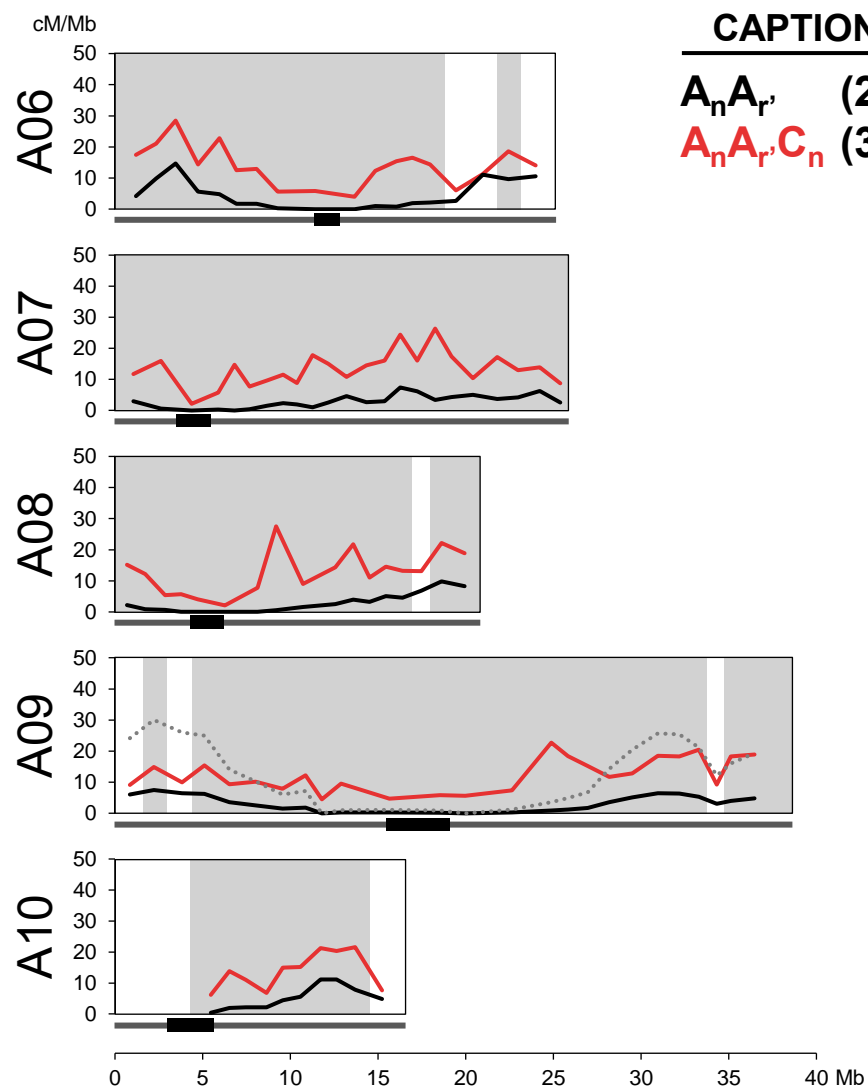
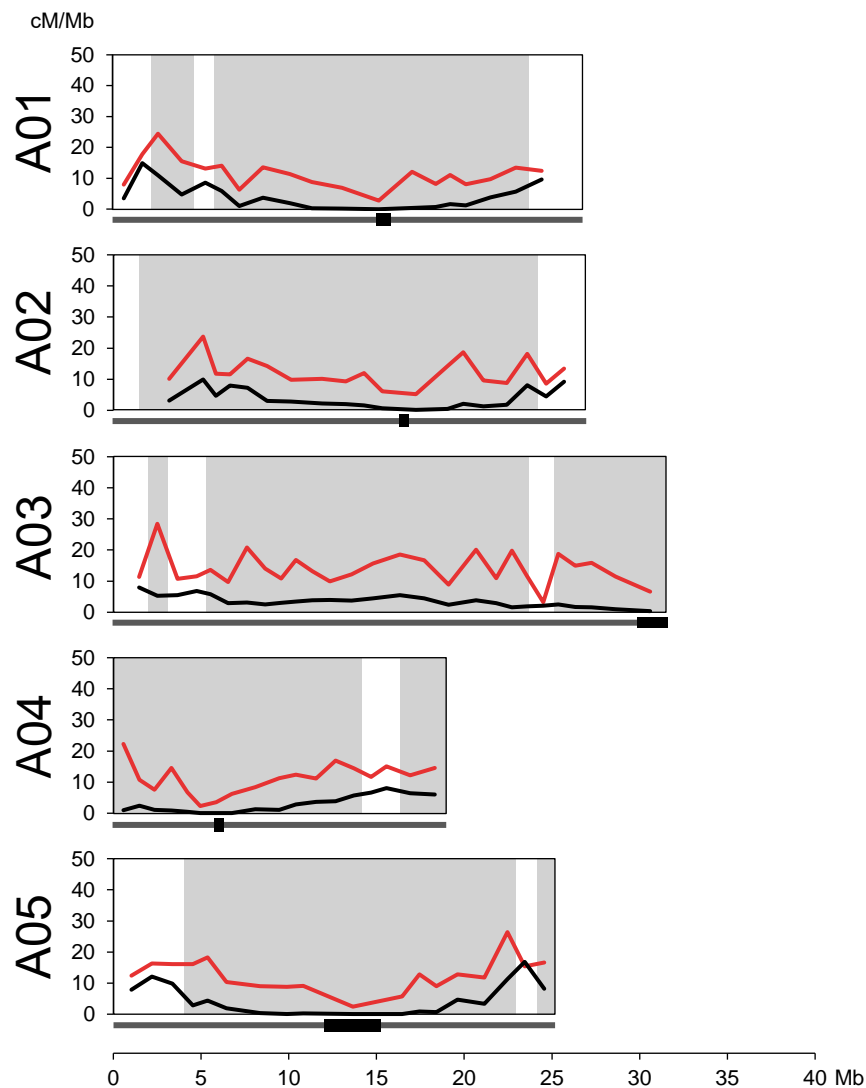
**CAPTION**  
 $A_n A_r$  (2x)  
 $A_n A_r C_n$  (3x)



# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## COs distribution along the A chromosomes in the AAC hybrid

❖ CO rates increase significantly in most intervals compared to the AA hybrid

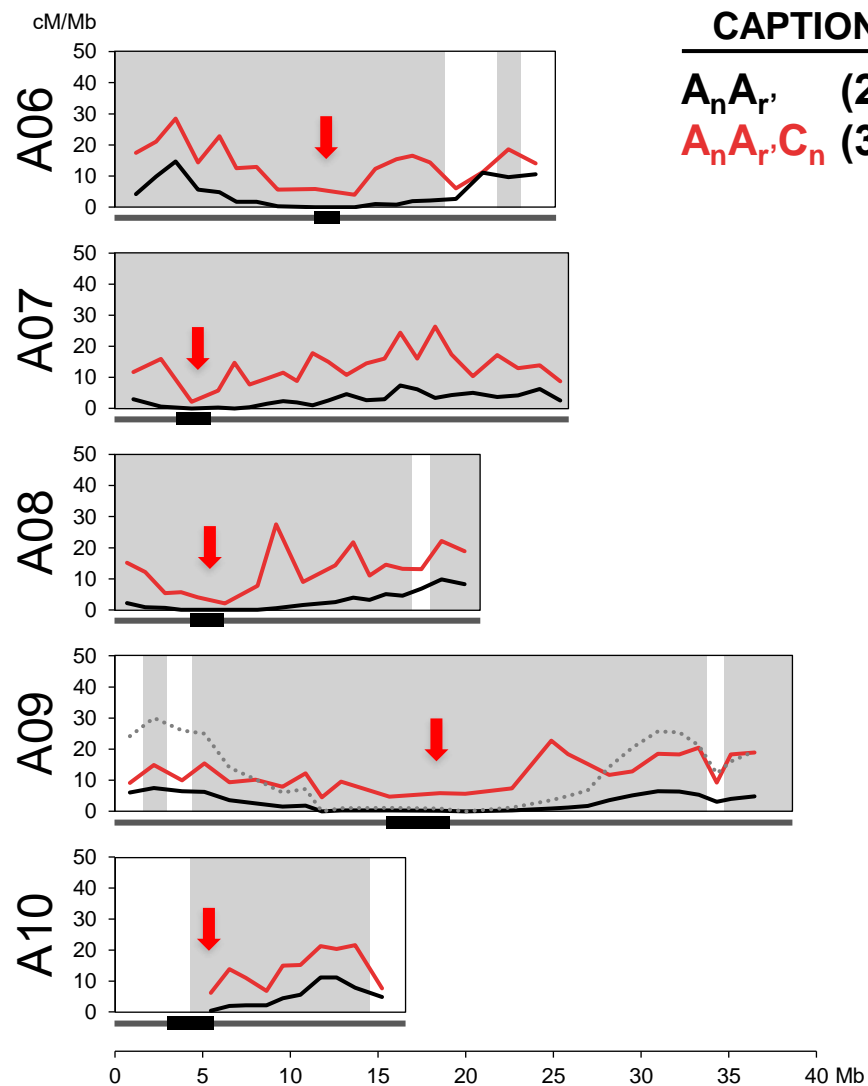
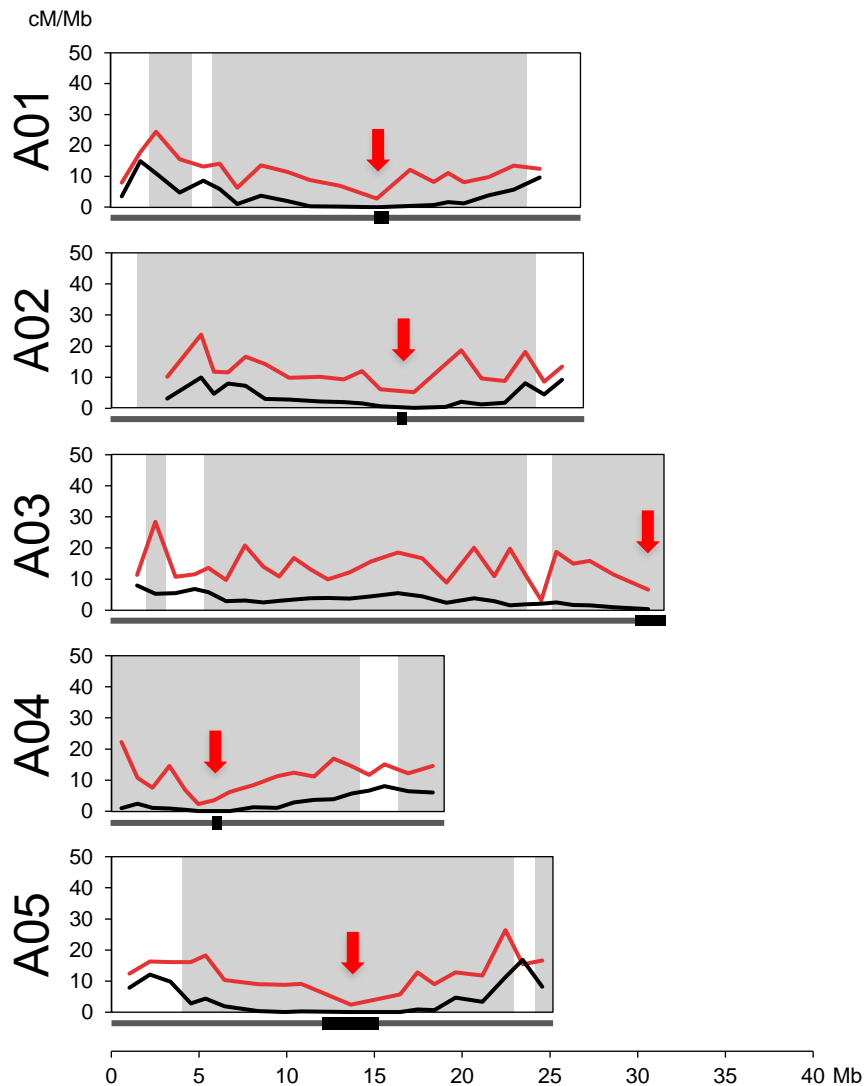


**CAPTION**  
 $A_n A_r$  (2x)  
 $A_n A_r C_n$  (3x)

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## COs distribution along the A chromosomes in the AAC hybrid

❖ Even in intervals close or including the **centromeres**, where **new recombining regions** are formed

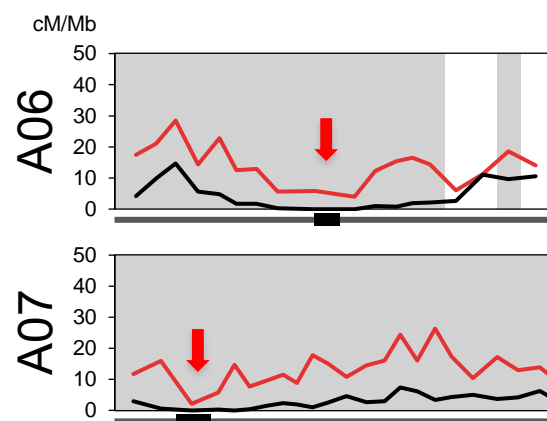
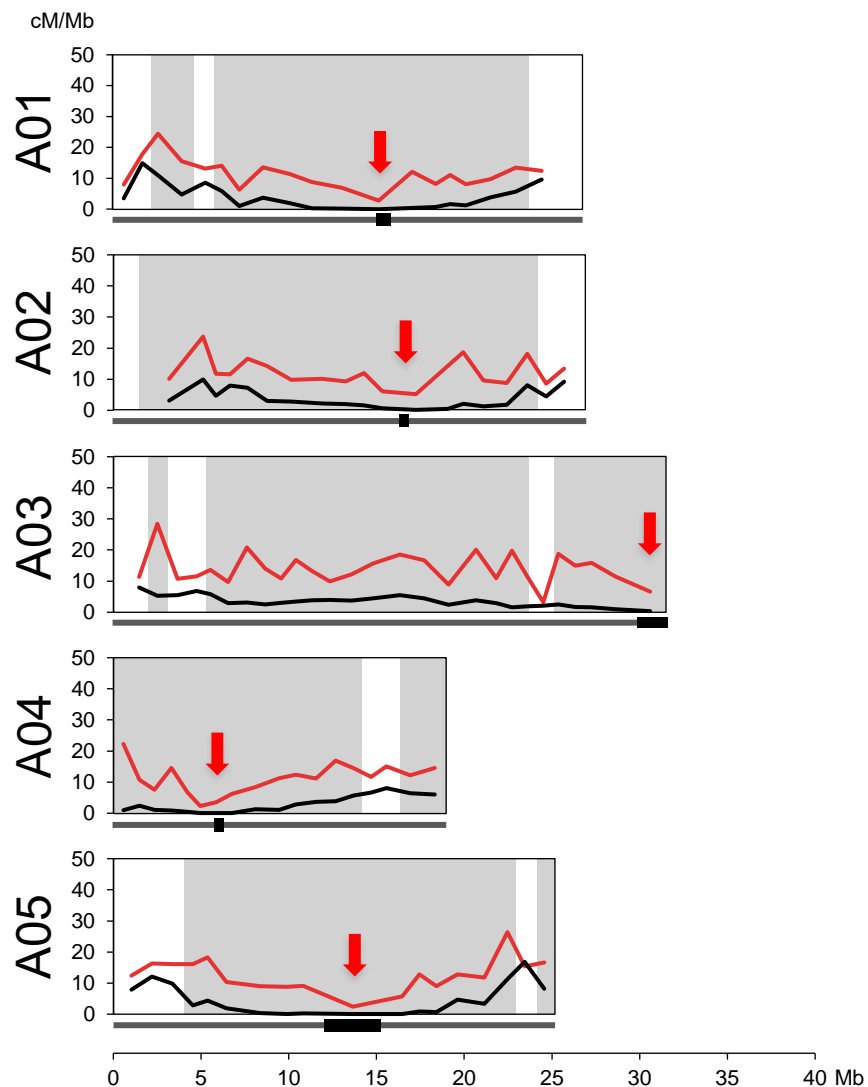


**CAPTION**  
 $A_n A_r$  (2x)  
 $A_n A_r C_n$  (3x)

# RATE AND DISTRIBUTION OF COs IN AA vs AAC HYBRIDS

## COs distribution along the A chromosomes in the AAC hybrid

- ❖ Even in intervals close or including the **centromeres**, where **new recombining regions** are formed



### CAPTION

$A_n A_r$  (2x)  
 $A_n A_r C_n$  (3x)

### In AAC hybrid

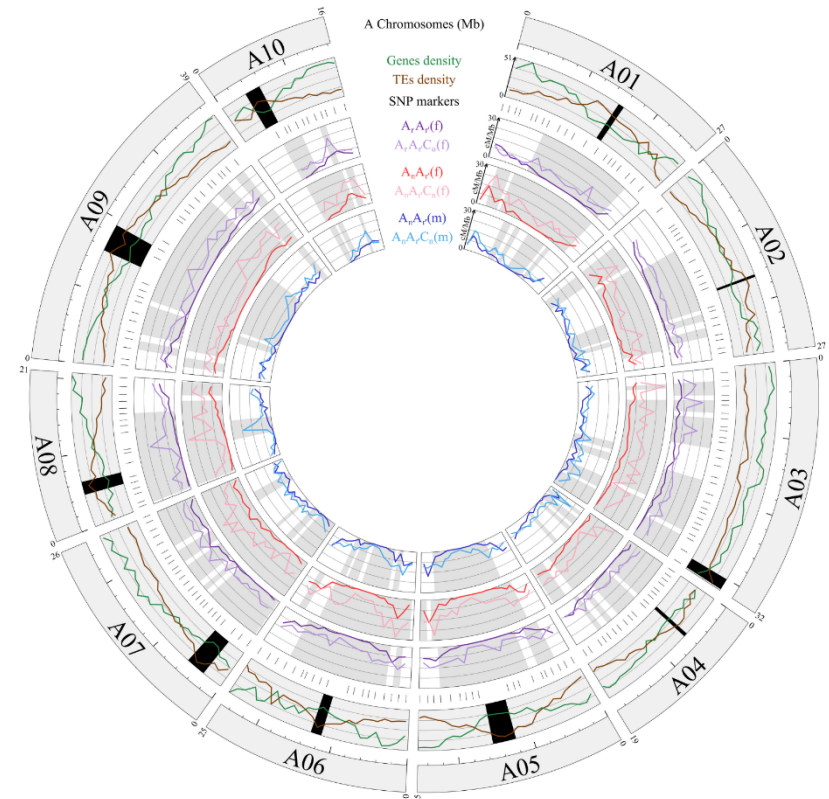
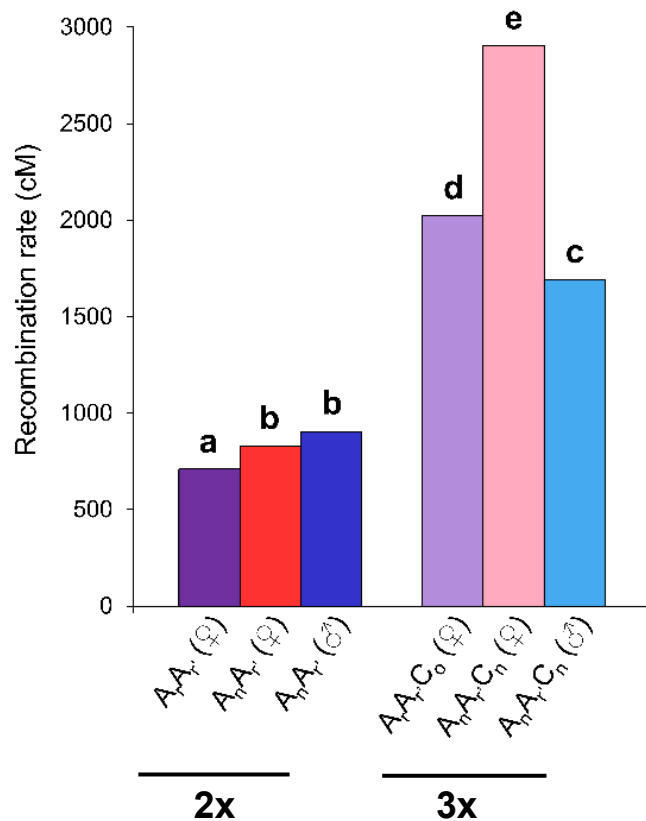
Recombination landscapes along each of the A chromosomes are  $\neq$  AA hybrid

- ✓ COs are formed all along the A genome, even in the vicinity of the centromeres
- ✓ No Gradient for CO rates along chromosome arms

# RATE AND DISTRIBUTION OF COs IN AA VS AAC HYBRIDS

In conclusion:

- ➔ The additional C genome allows to change the rate and distribution of COs between the homologous A chromosomes in AAC allotriploids
- ➔ Whatever the sex of meiosis and C genome origin, but with slight variations for COs rate



# RATE AND DISTRIBUTION OF COs IN CC vs CCA HYBRIDS

Rate and distribution of COs are also modified along the C homologs in **CCA** hybrids



*B. napus* AAC**C**,  
 $2n=4x=38$

(Chalhoub *et al.*, 2014)

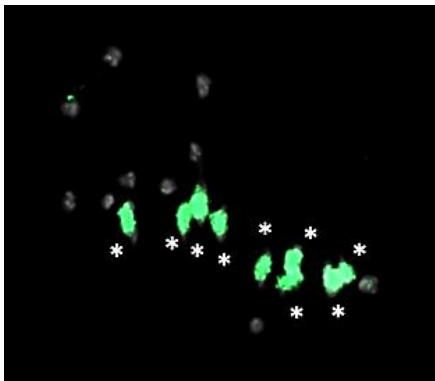
X



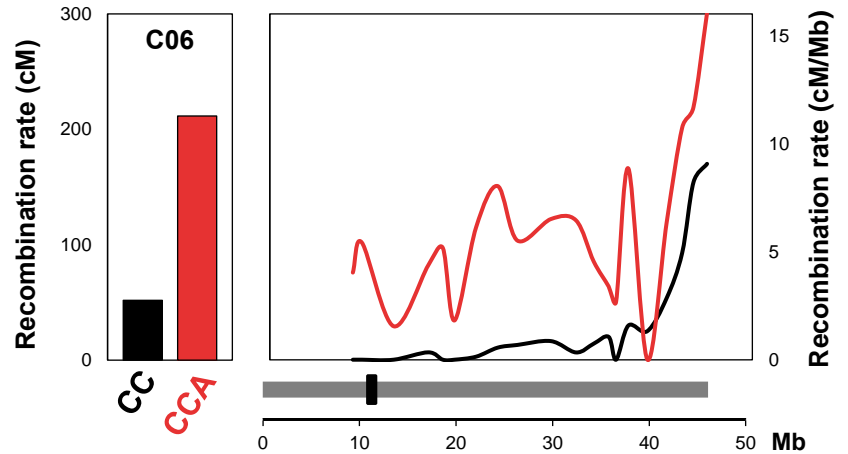
*B. oleracea* **CC**,  
 $2n=2x=20$

(Wang *et al.*, 2011)

**CCA**  
 $2n=3x=28$



e.g. C06 homologs pair:

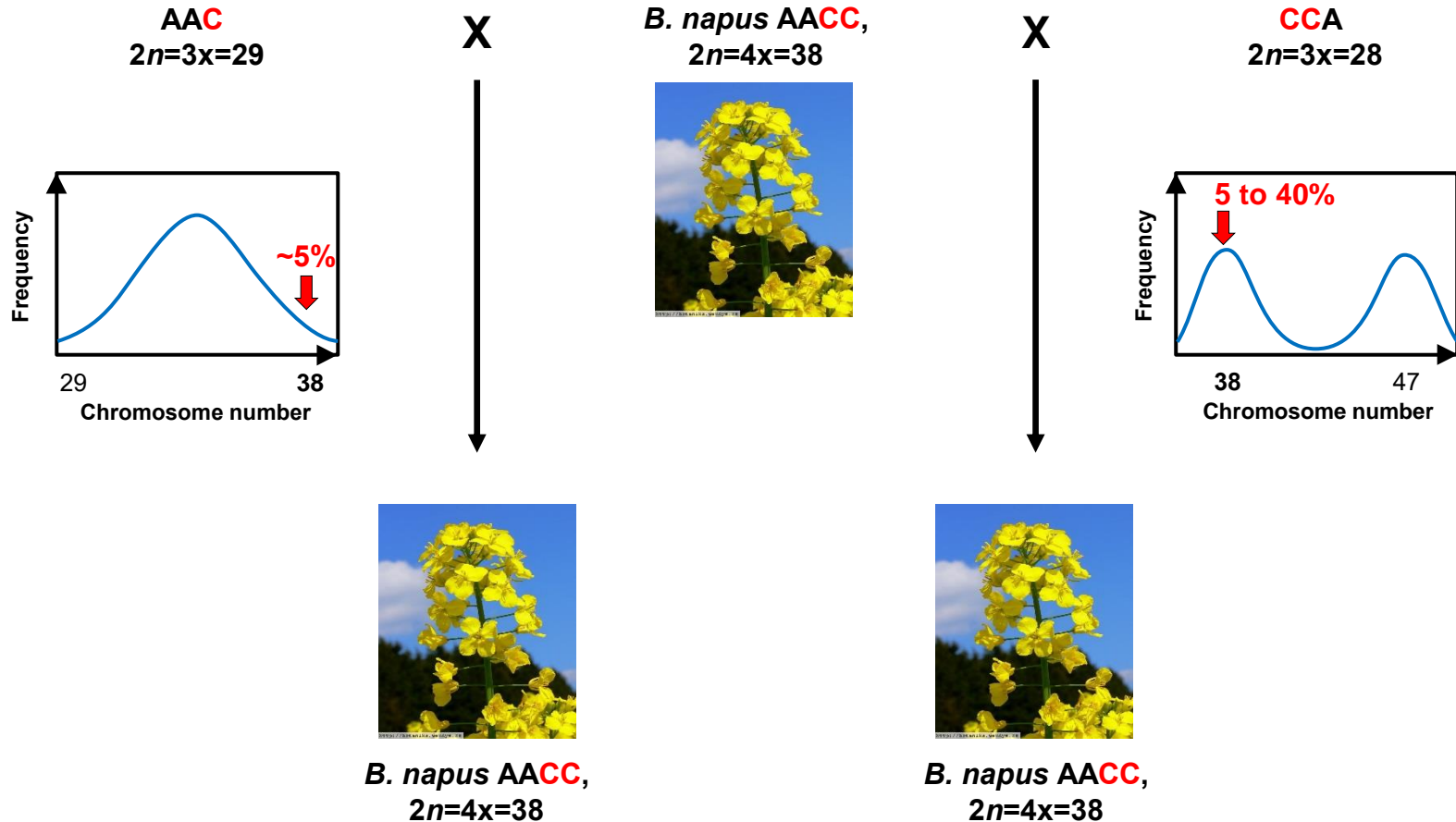


In *Brassica*, it is possible to enhance recombination both between A and C homologs, by using AAC and CCA allotriploid hybrids, respectively

# CONCLUSIONS

## Interest for rapeseed breeding programs

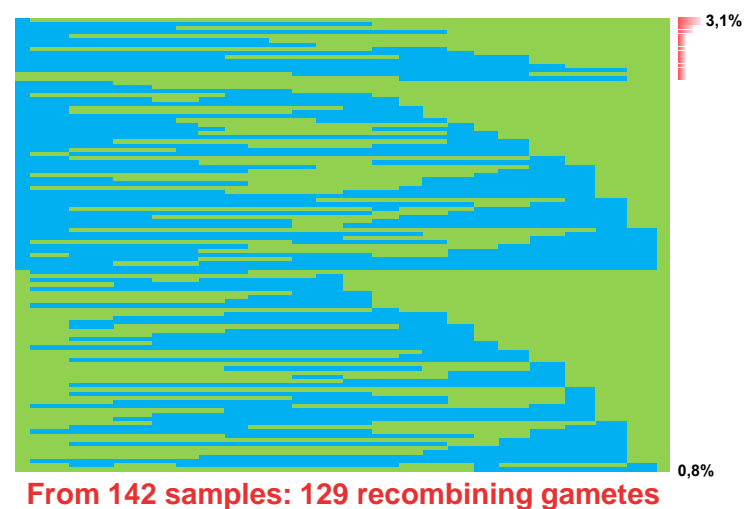
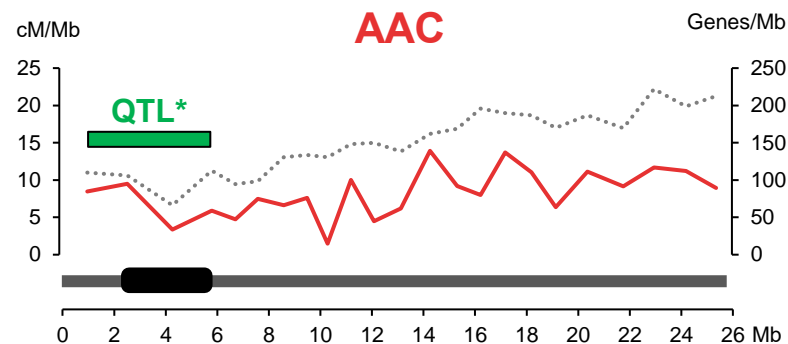
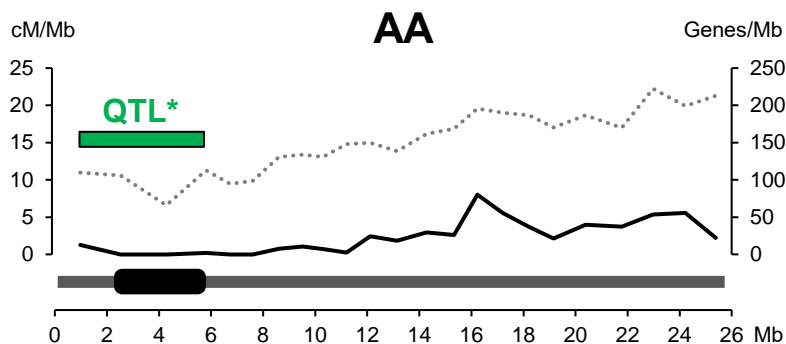
- ❖ AAC and CCA hybrids are fertile ( $\pm 10\%$  of *B. napus* fertility)
- ❖ Both can produce AACC plants through intercross with *B. napus*



# CONCLUSIONS

## Interest for rapeseed breeding programs

- ❖ AAC and CCA hybrids allow to generate a larger diversity of gametes
- ❖ Shuffle genomic regions usually deprived of COs, **where genes of agronomic interest have been detected**

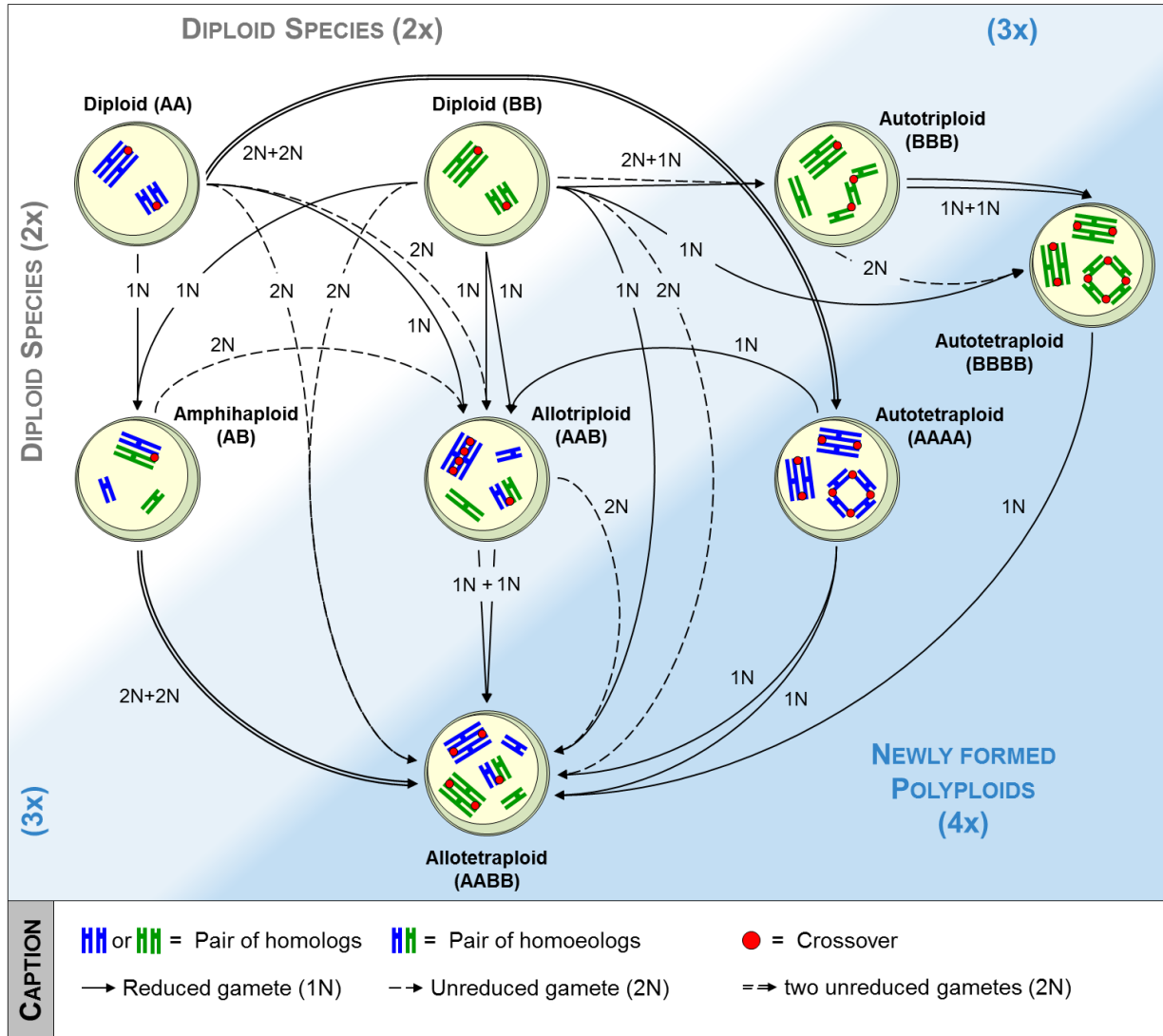


\*QTL of yield and seed quality (Bouchet *et al.*, 2016)

# CONCLUSIONS

## Concerning the speciation success of polyploidy plants

- ❖ *B. napus* may have been formed through a triploid-bridge 7,500 years ago





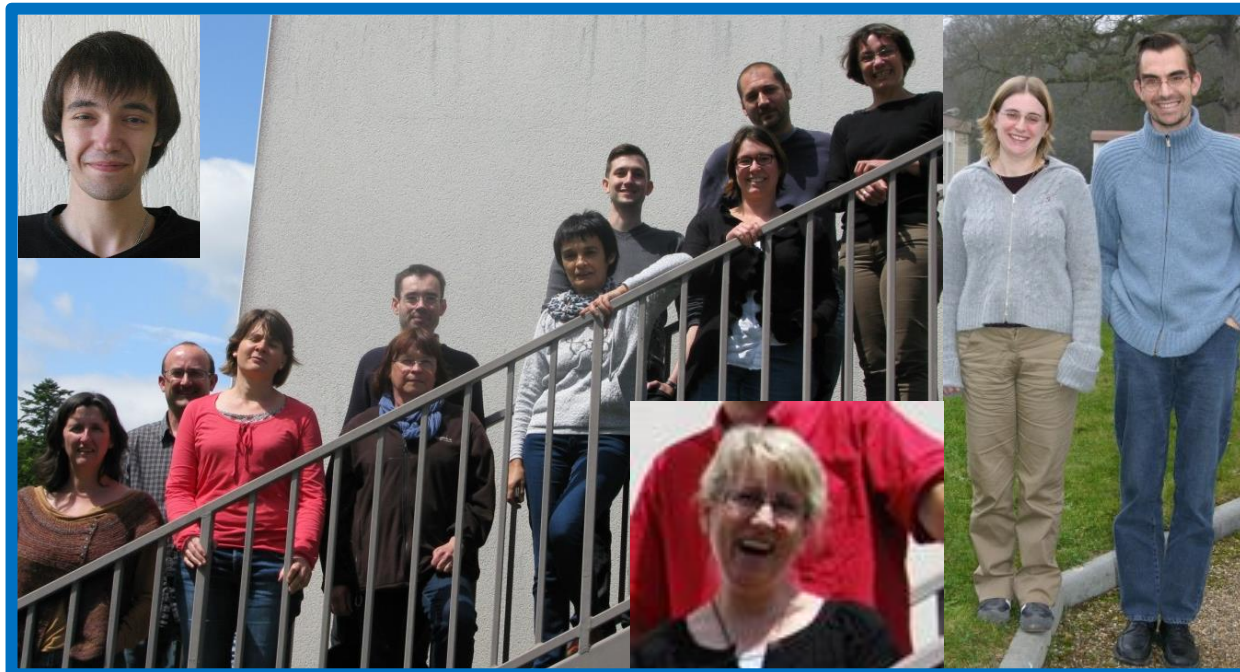
# AKNOWLEDGMENT

## INRA LE RHEU :

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# ...And thank you for your attention