

# In and out: Challenges and opportunities to use favorable genes from different subgenomes in *Brassica Paradise*



Jinling Meng

Huazhong Agricultural University, Wuhan, China

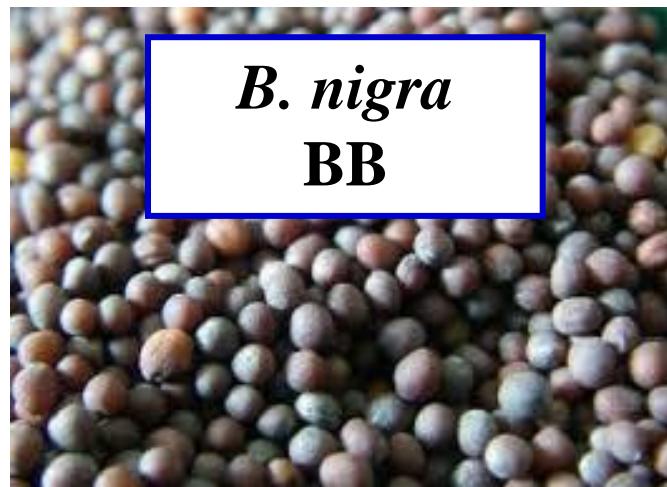


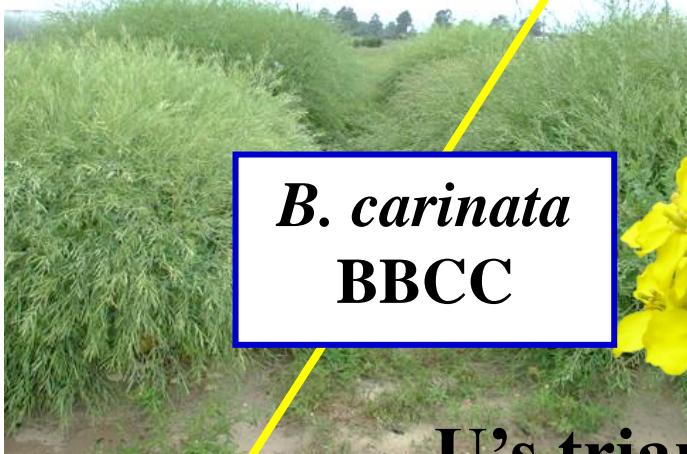
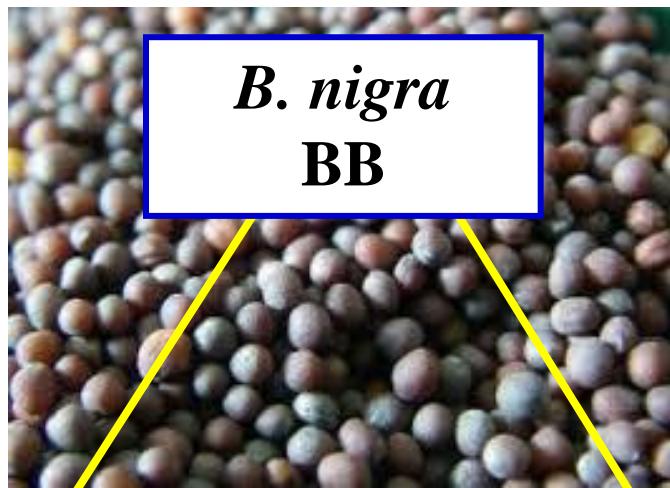
**U's triangle of *Brassica***



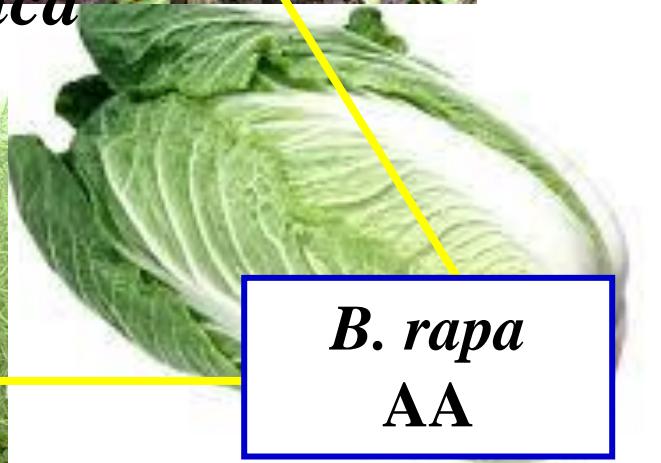
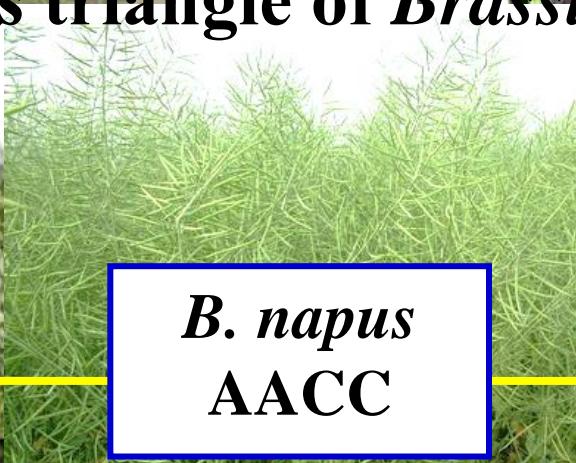
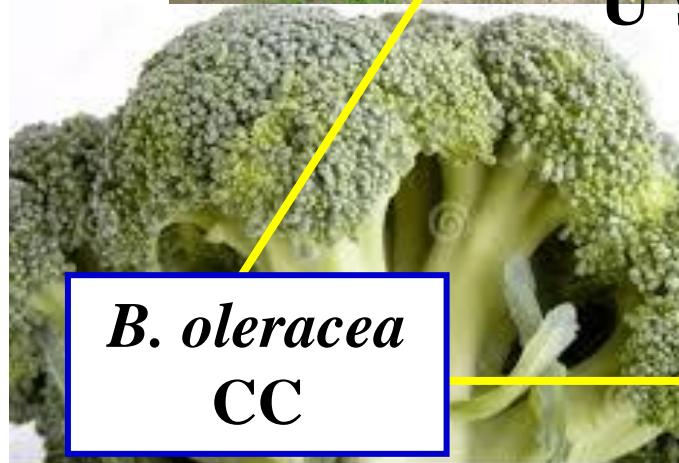
U's triangle of *Brassica*



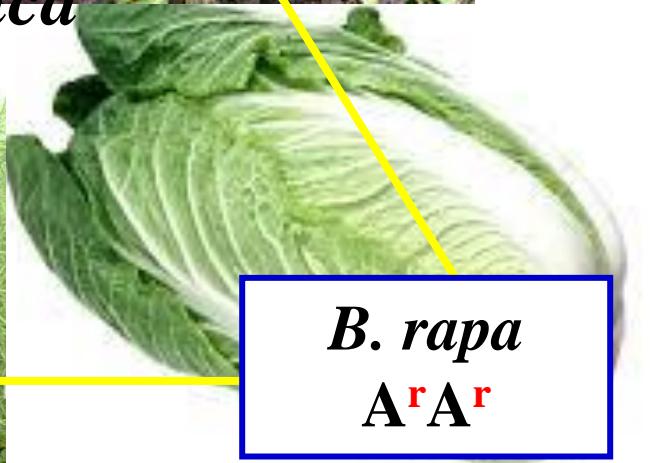
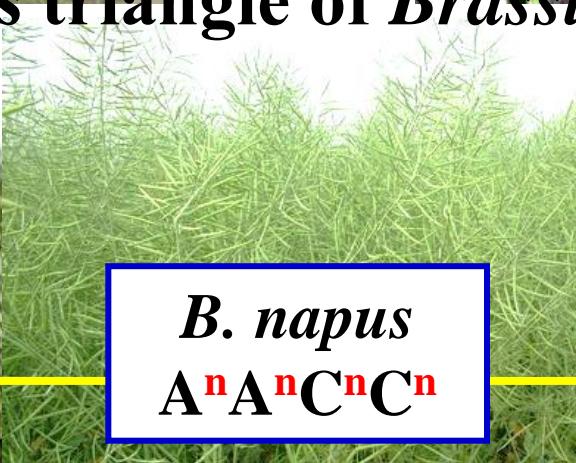
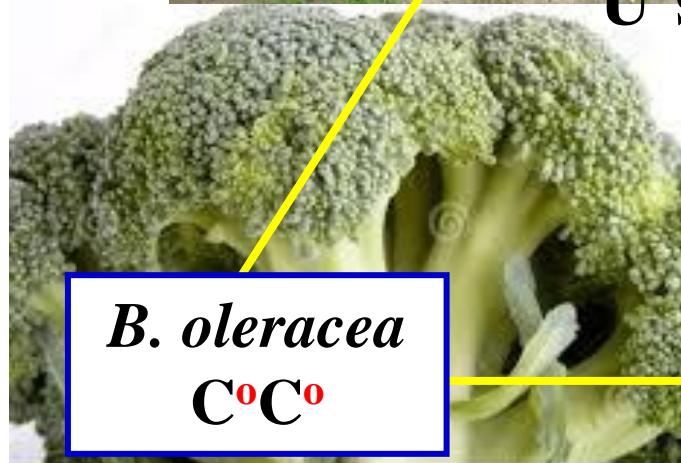
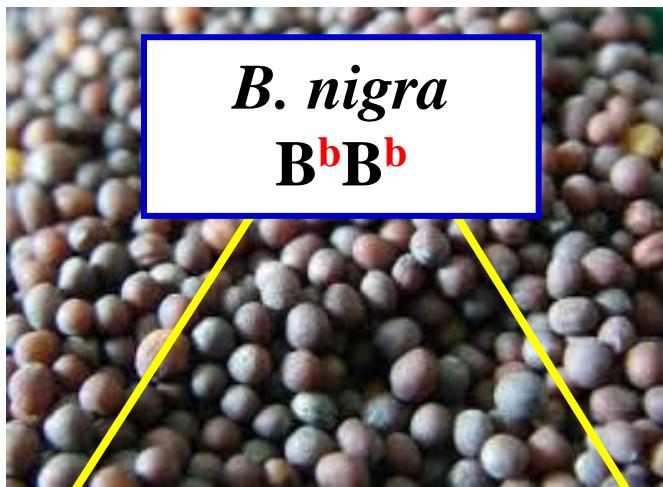




## U's triangle of *Brassica*



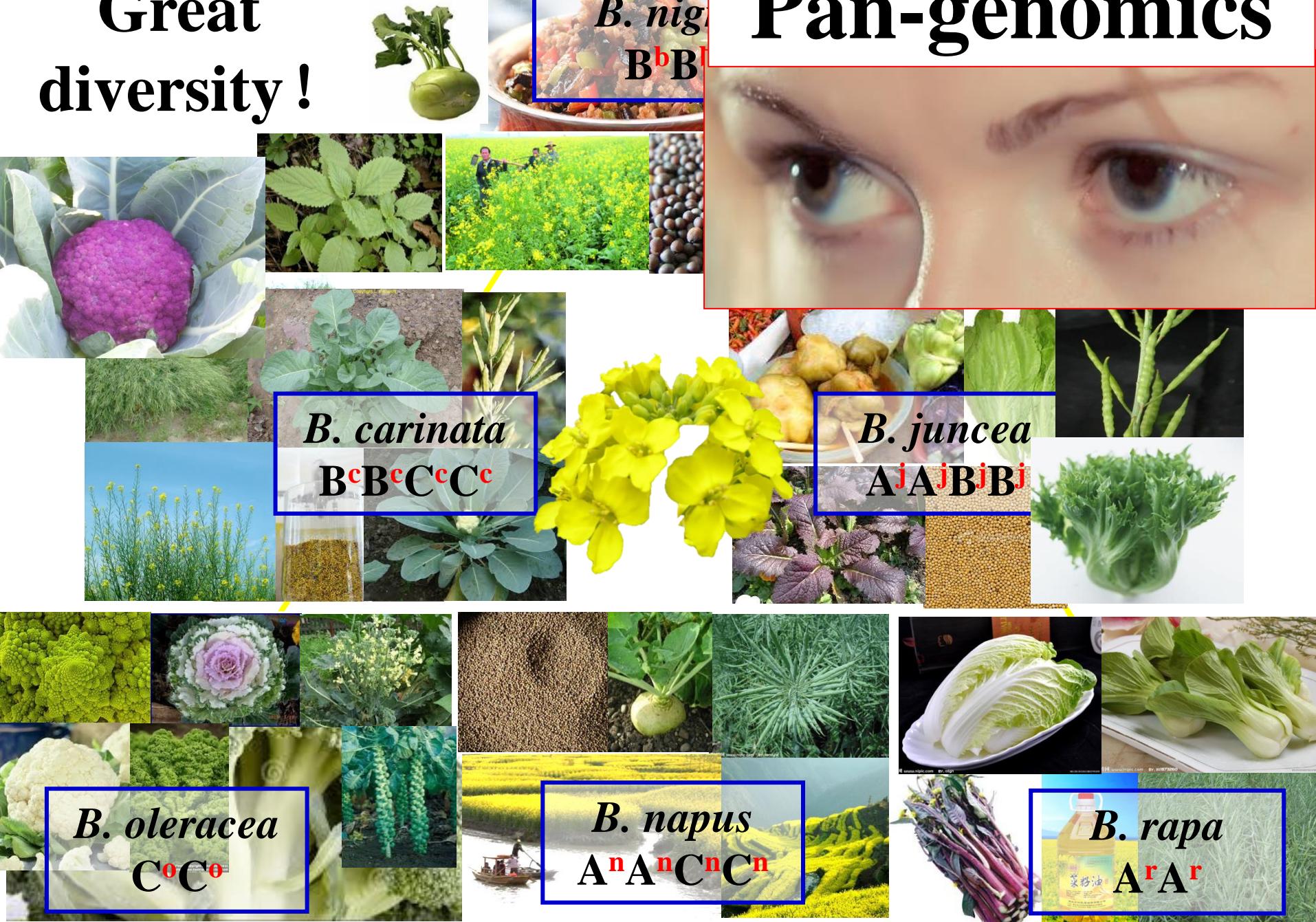
# Subgenomes



U's triangle of *Brassica*



# Great diversity !



# Pan-genomics

Thousands of  
different genes and  
numerous alleles  
there!

*B. nigra*  
 $B^bB^b$

*B. carinata*  
 $B^cB^cC^cC^c$

*B. juncea*  
 $A^jA^jB^jB^j$

*B. napus*  
 $A^nA^nC^nC^n$

*B. rapa*  
 $A^rA^r$

?



Can we put different subgenomes from various species into **one** along with their specific genes?

*B. carinata*  
 $B^cB^cC^cC^c$

*B. nigra*  
 $B^bB^b$

*B. juncea*  
 $A^jA^jB^jB^j$

*Brassica hexaploid*  
 $A^jA^jB^jB^jC^oC^o$

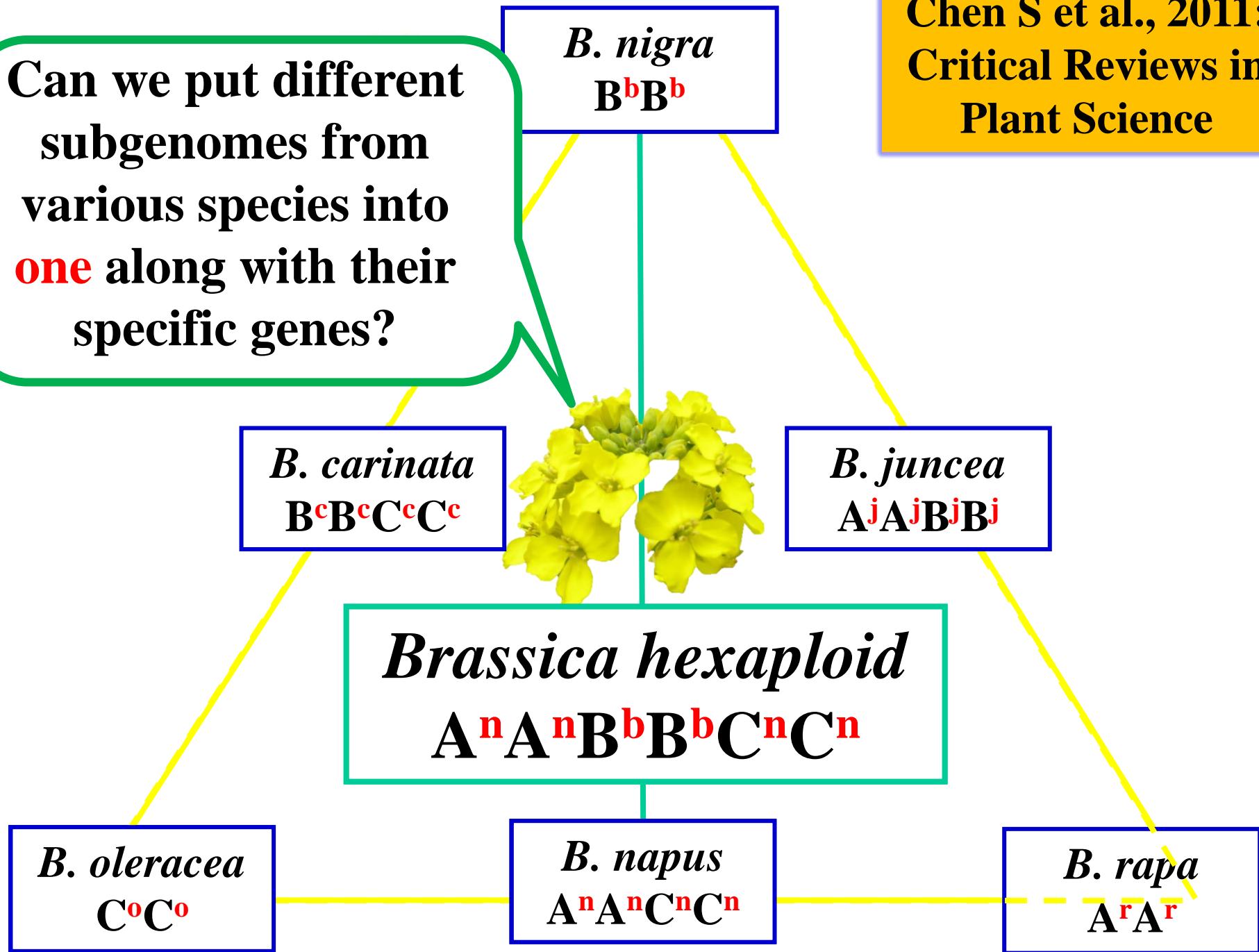
*B. oleracea*  
 $C^oC^o$

*B. napus*  
 $A^nA^nC^nC^n$

*B. rapa*  
 $A^rA^r$



Can we put different subgenomes from various species into **one** along with their specific genes?



Can we put different subgenomes from various species into **one** along with their specific genes?

*B. carinata*  
 $B^cB^cC^cC^c$

*B. nigra*  
 $B^bB^b$

*B. juncea*  
 $A^jA^jB^jB^j$

*Brassica hexaploid*  
 $A^rA^rB^cB^cC^cC^c$

*B. oleracea*  
 $C^oC^o$

*B. napus*  
 $A^nA^nC^nC^n$

*B. rapa*  
 $A^rA^r$



Jiang et al., 2007; Tian et al., 2010

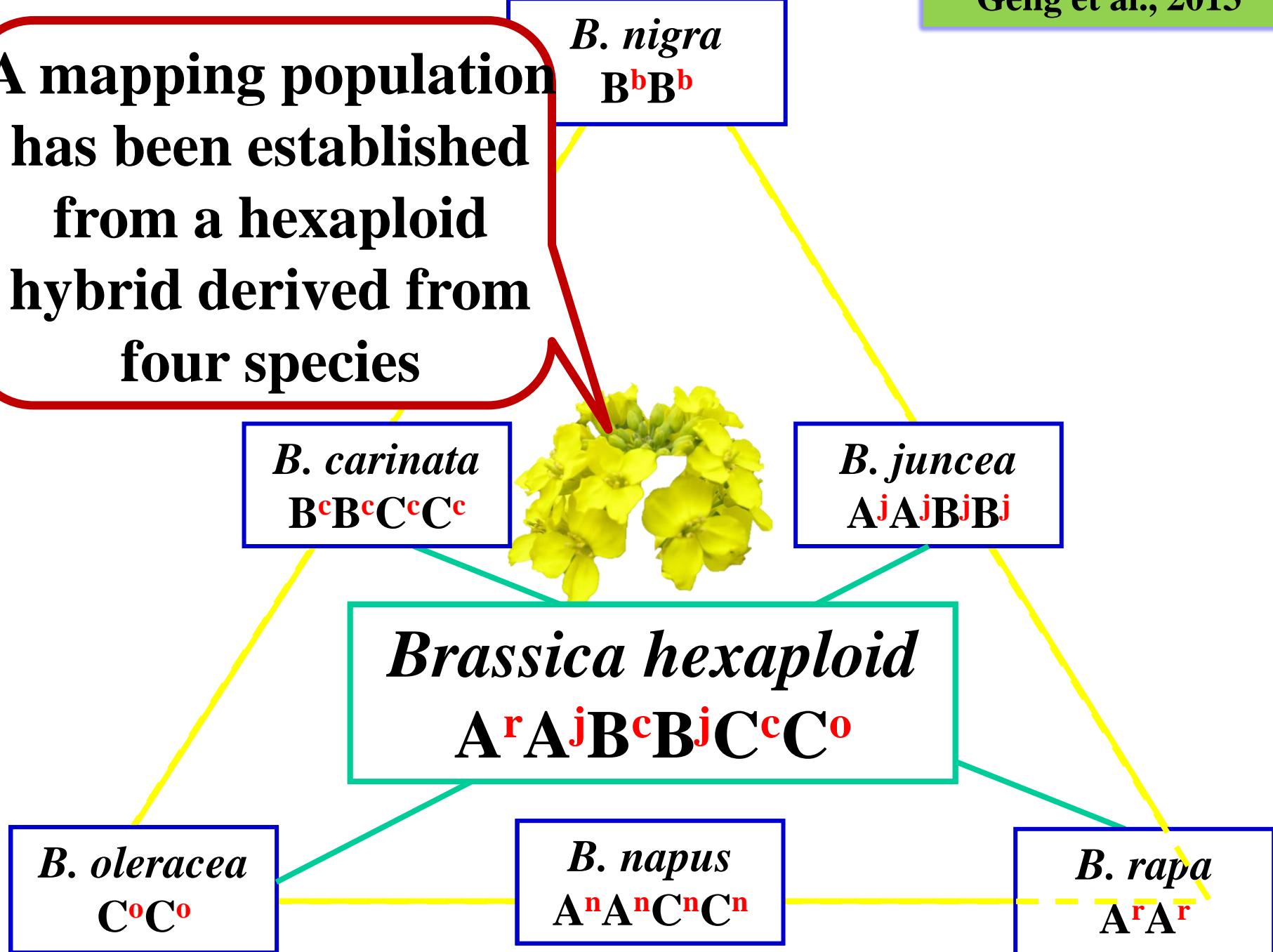


*B. rapa*  
 $A^rA^r$

*B. carinata*  
 $B^cB^cC^cC^c$

Hexaploid  
 $A^rA^rB^cB^cC^cC^c$

A mapping population has been established from a hexaploid hybrid derived from four species



*B. nigra*  
 $B^bB^b$

*B. carinata*  
 $B^cB^cC^cC^c$

Different  
subgenomes could  
be also put into a  
existed species



*B. juncea*  
 $A^jA^jB^jB^j$

*B. napus*  
 $A^nA^nC^nC^n$

*B. oleracea*  
 $C^oC^o$

*B. rapa*  
 $A^rA^r$

Different  
subgenomes could  
be also put into a  
existed species

*B. nigra*  
 $B^bB^b$

*B. carinata*  
 $B^cB^cC^cC^c$



*B. juncea*  
 $A^jA^jB^jB^j$

*B. napus*  
 $A^nA^nC^nC^n$

*B. oleracea*  
 $C^oC^o$

*B. rapa*  
 $A^rA^r$

*B. nigra*  
 $B^bB^b$

Different  
subgenomes could  
be also put into a  
existed species

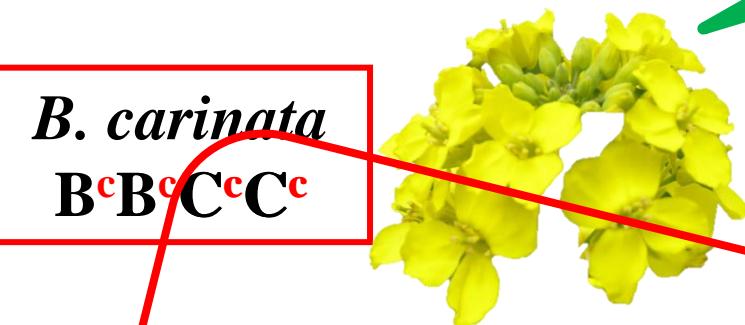
*B. carinata*  
 $B^cB^cC^cC^c$

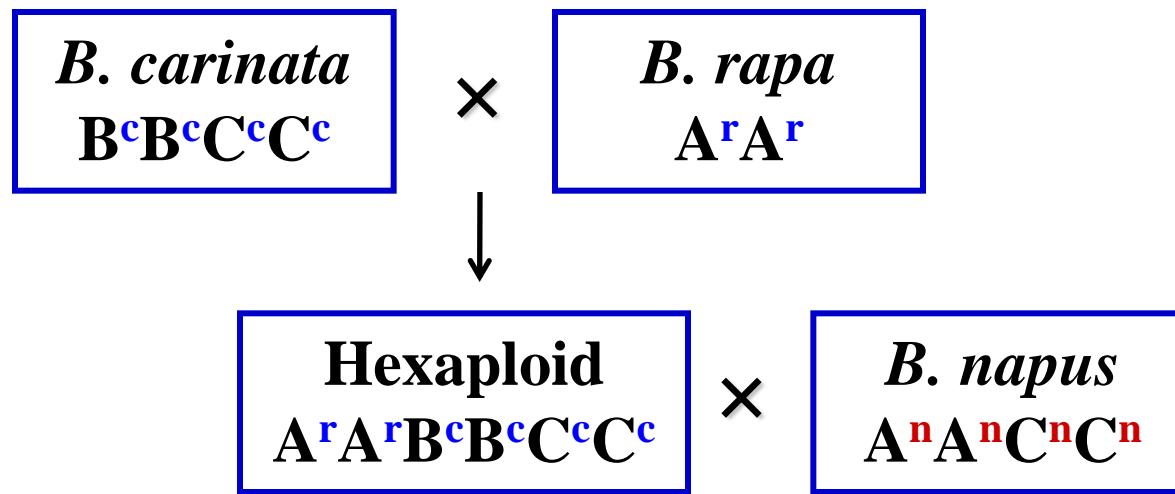
*B. juncea*  
 $A^jA^jB^jB^j$

*B. oleracea*  
 $C^oC^o$

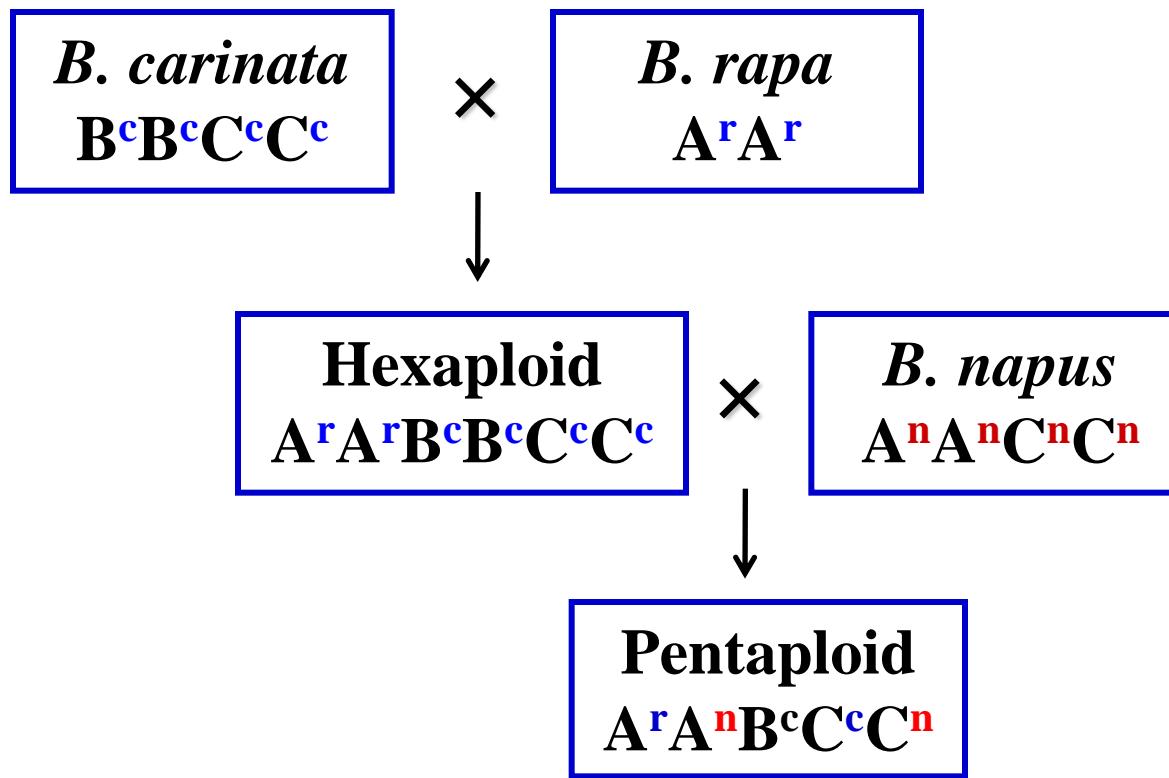
*B. napus*  
 $A^nA^nC^nC^n$   
 $A^rA^rC^rC^r$

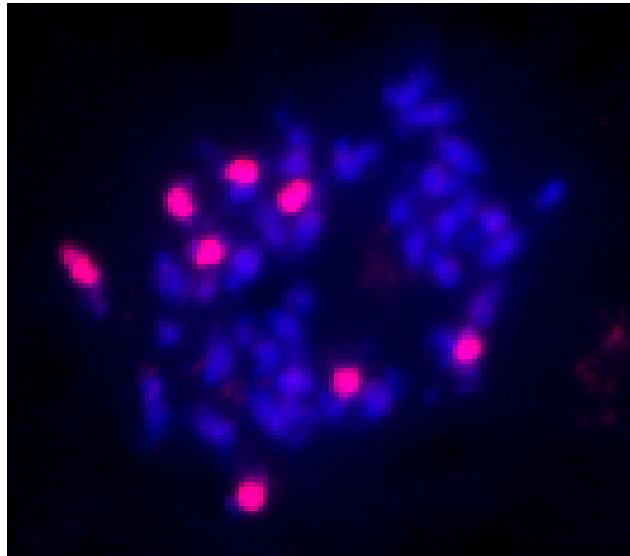
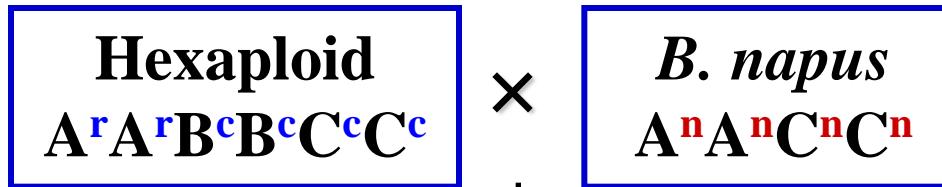
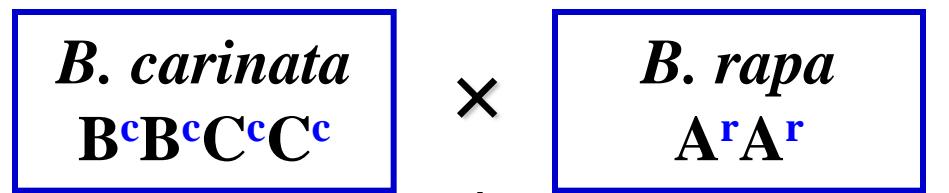
*B. rapa*  
 $A^rA^r$



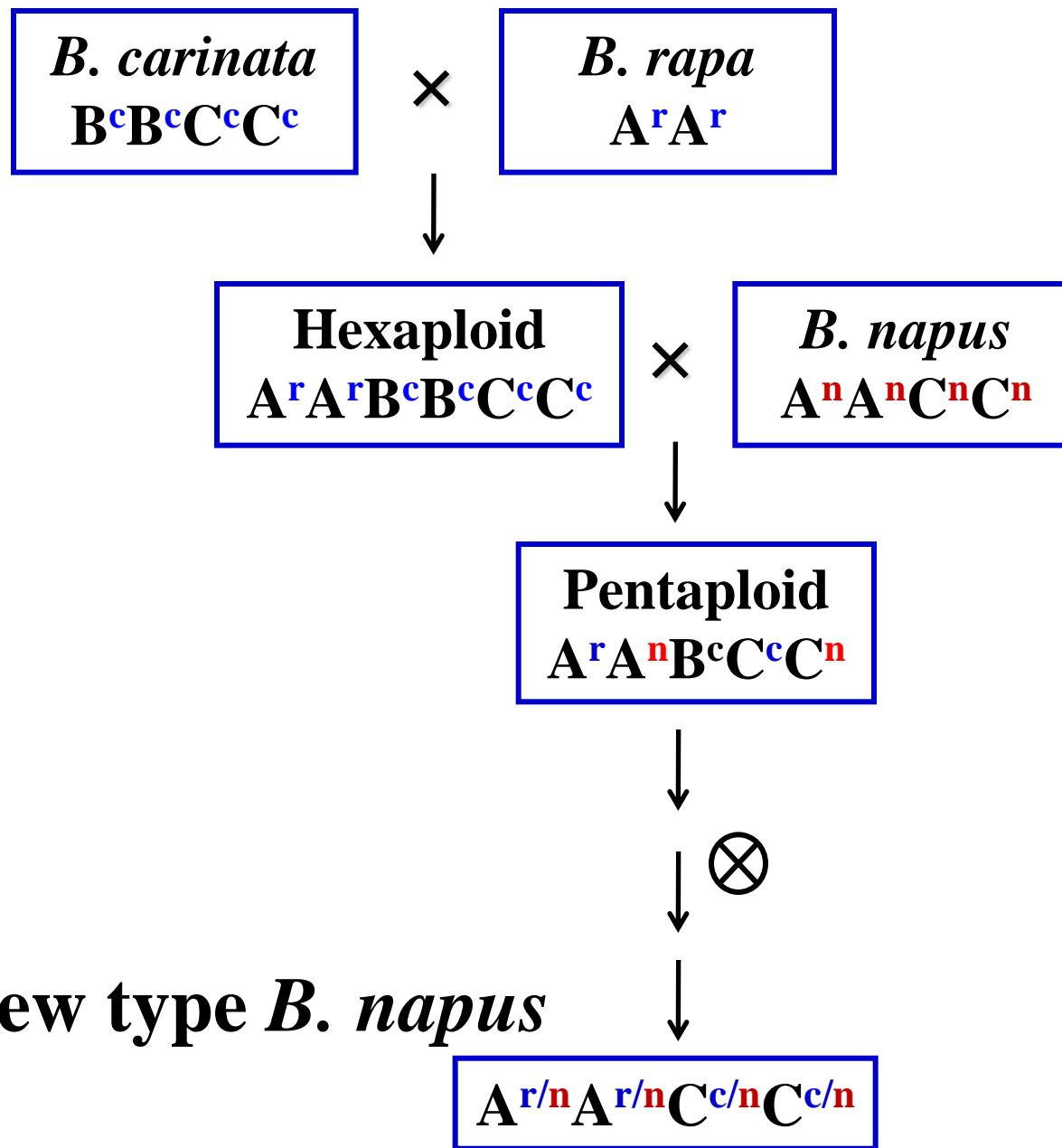


Hybrid  $B. rapa$   $B. carinata$

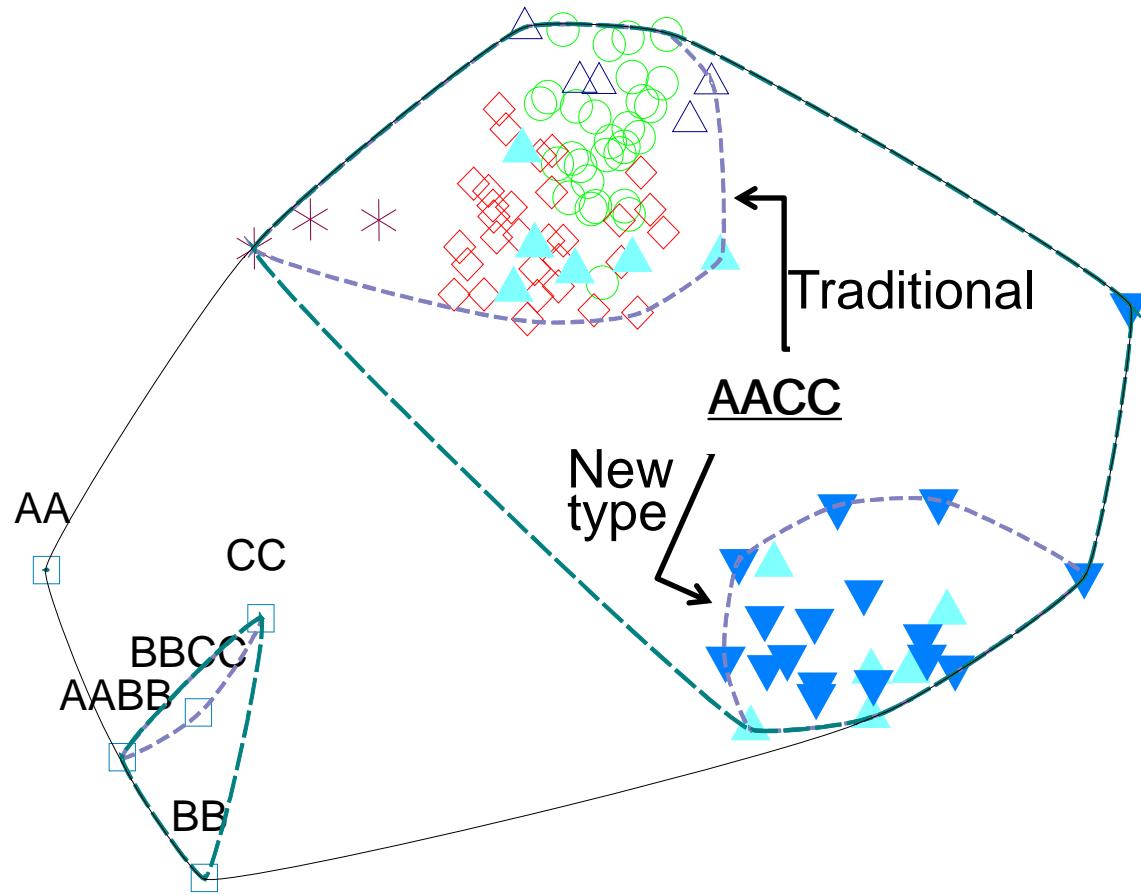




8 red chromosomes  
were from B genome



Li et al., 2004



New type *B. napus*:



Traditional *B. napus*:

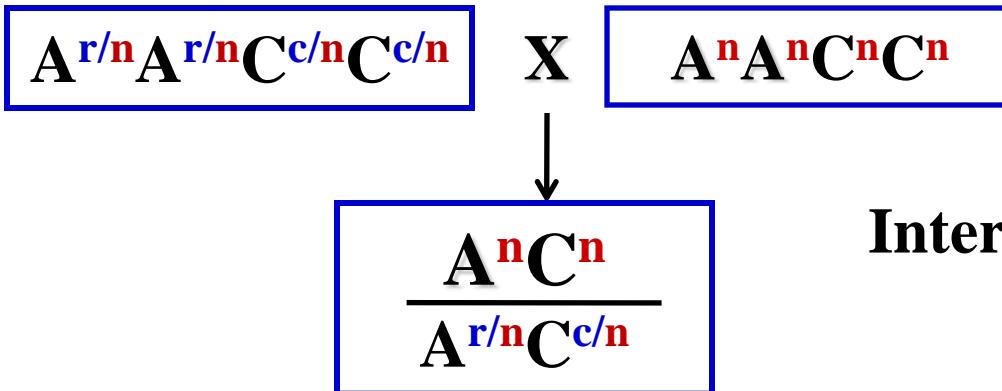
- Australia
- ◇ China
- △ Europe
- \* India

Other species:



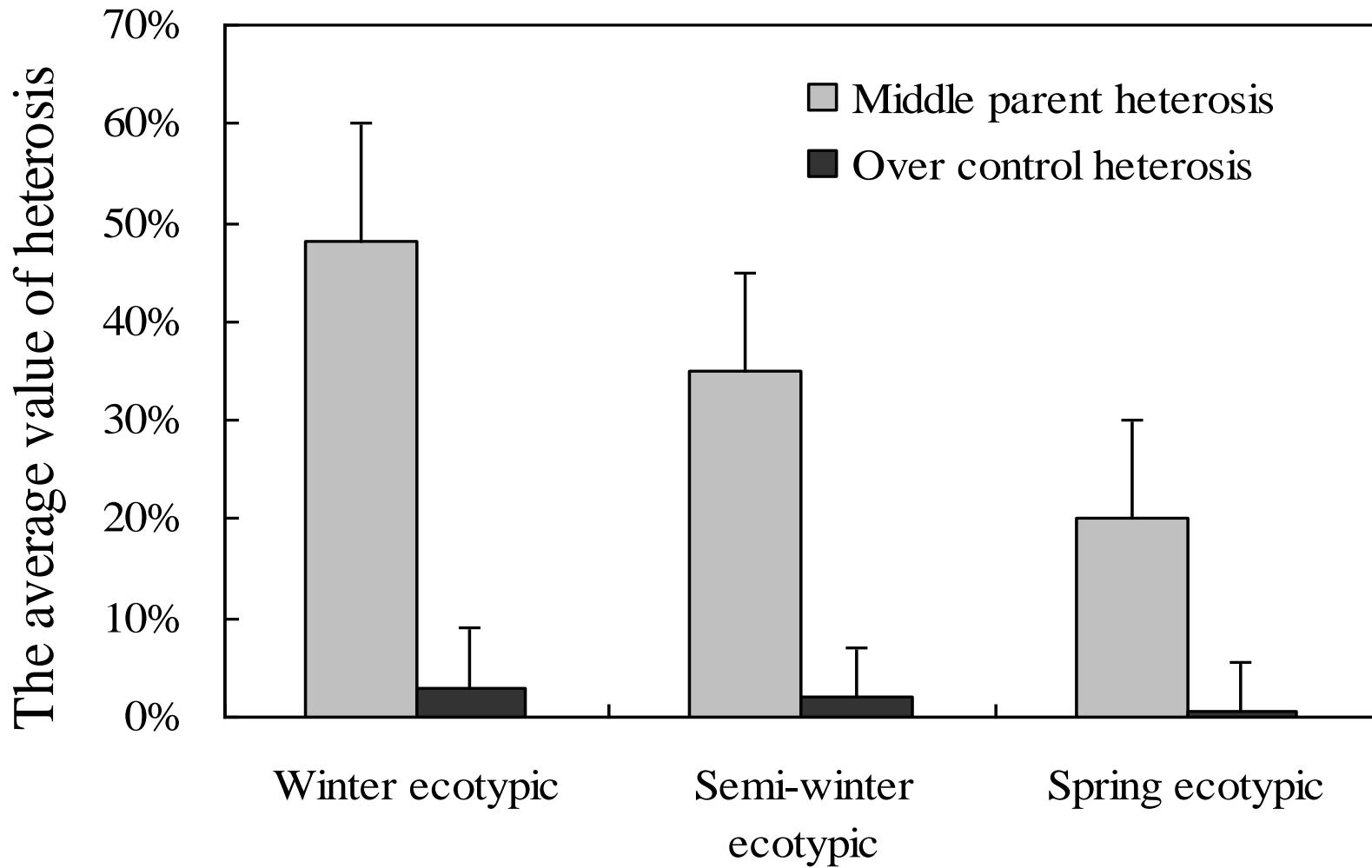
## Analysis on genetic diversity on *B. napus* accessions and other Brassica species

# Partial new type *B. napus*



Intersubgenomic hybrids



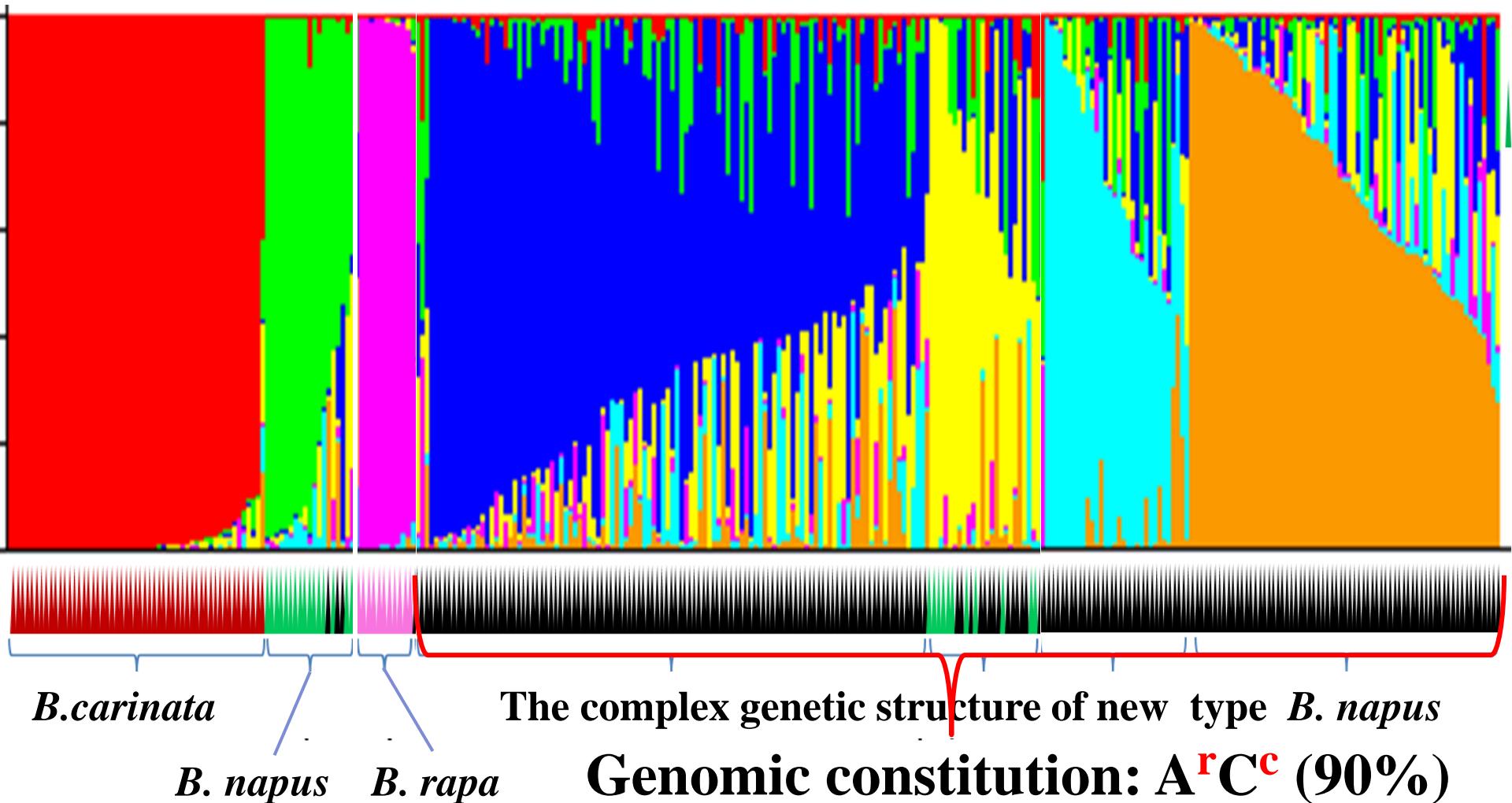


## Heterosis overview on partial intersubgenomic hybrids in three ecotypic regions of rapeseed production

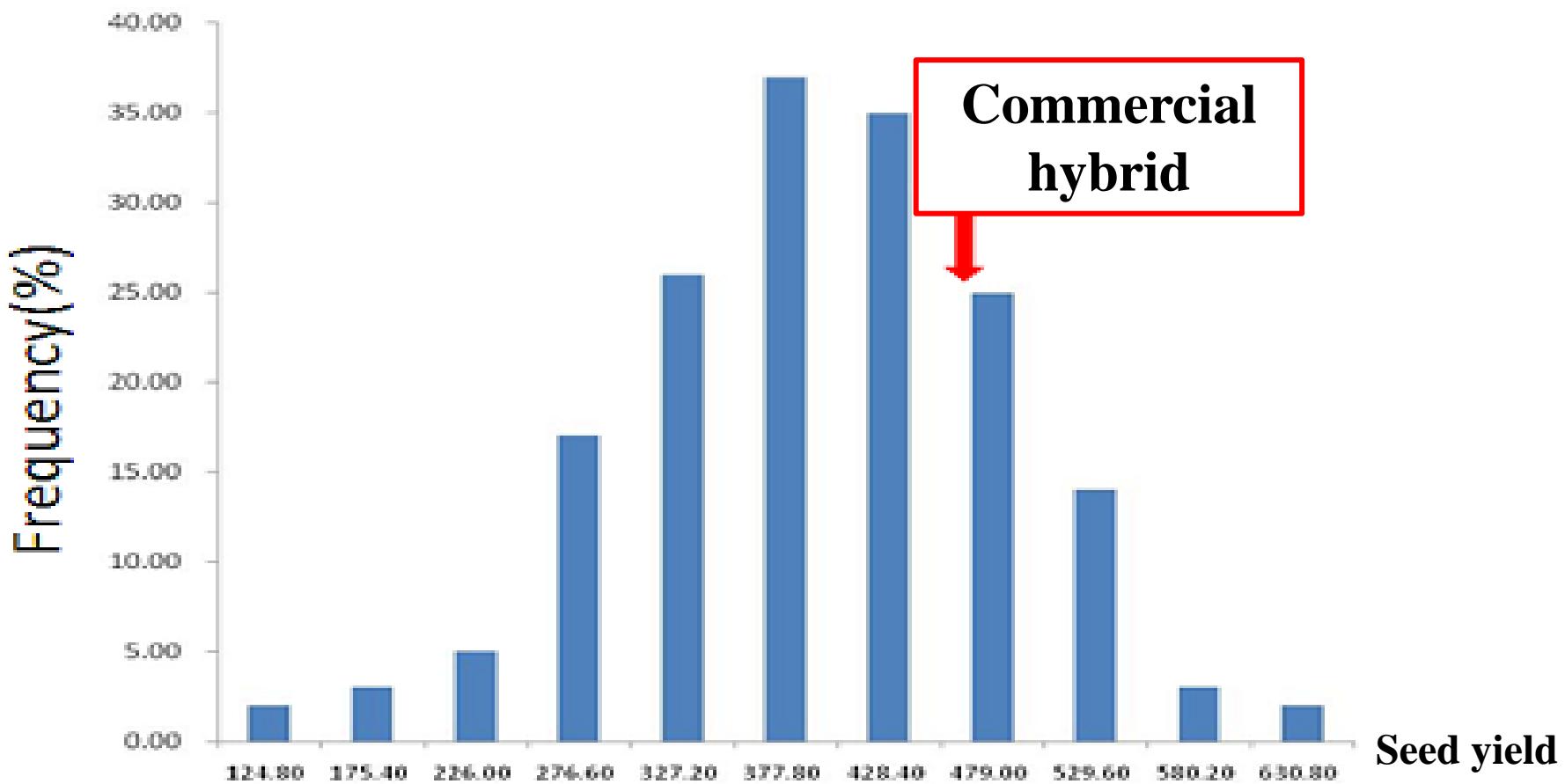
# Construct a A<sup>r</sup>/C<sup>c</sup> genepool of new type *B. napus*



# Genetic structure of the population is distinguished from traditional *B. napus* and its parental species

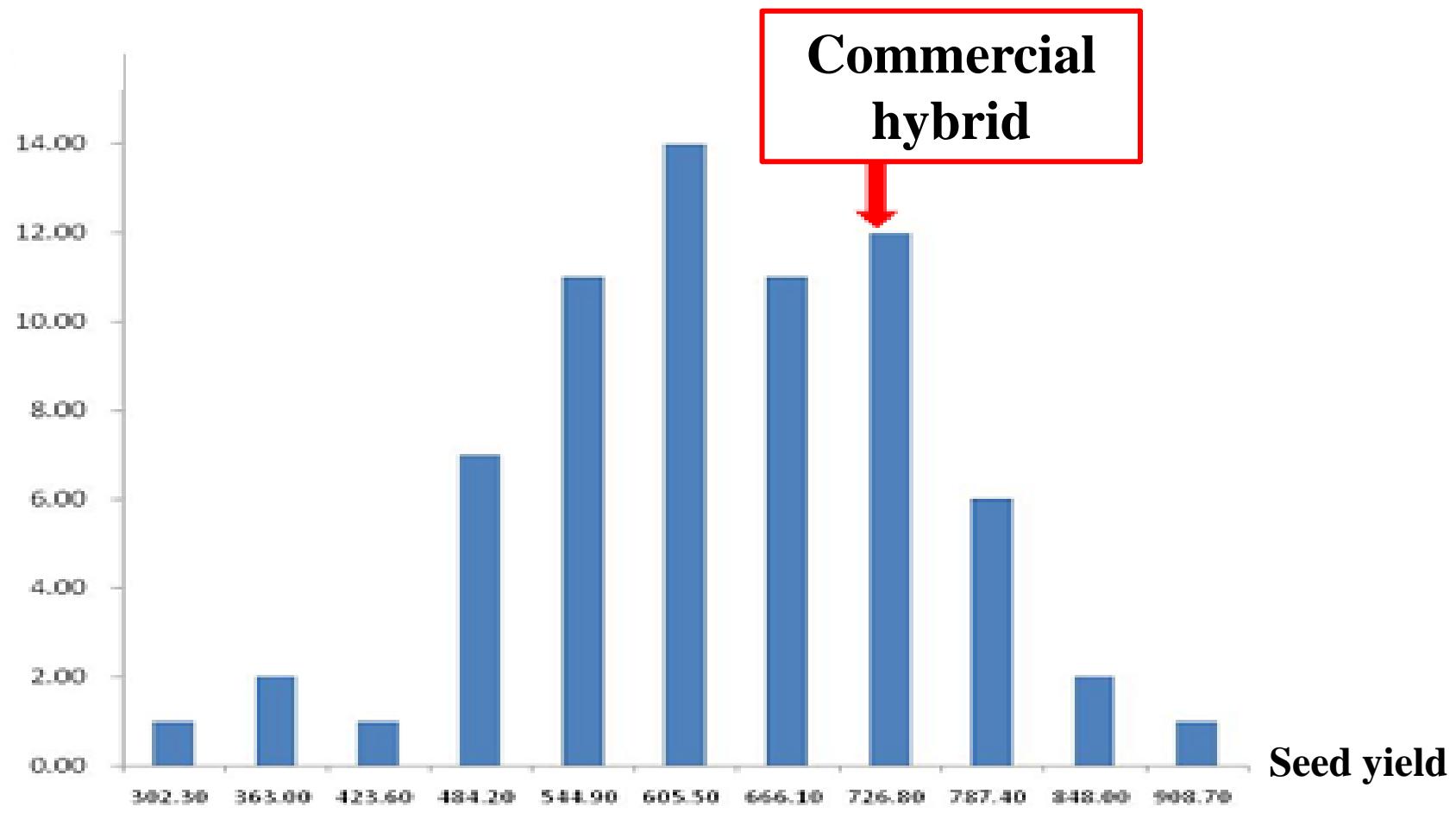


The heterosis potential of selected inbred lines of new type *B. napus* was evaluated with four testers



Grown in Wuhan, 2012

The heterosis potential of selected inbred lines of new type *B. napus* was evaluated with four testers



Grown in south-east of Wuhan, 2012

# Construct a A<sup>r</sup>/C<sup>c</sup> genepool of new type *B. napus*

Founder parents:

**78 cultivars**

*B. carinata* (B<sup>c</sup>B<sup>c</sup>C<sup>c</sup>C<sup>c</sup>)

**135 cultivars**

*B. rapa* (A<sup>r</sup>A<sup>r</sup>)

Introduce  
Dominant genic  
male sterility

Selected lines  
of new type  
*B. napus*

Hexaploid  
(A<sup>r</sup>A<sup>r</sup>B<sup>c</sup>B<sup>c</sup>C<sup>c</sup>C<sup>c</sup>)

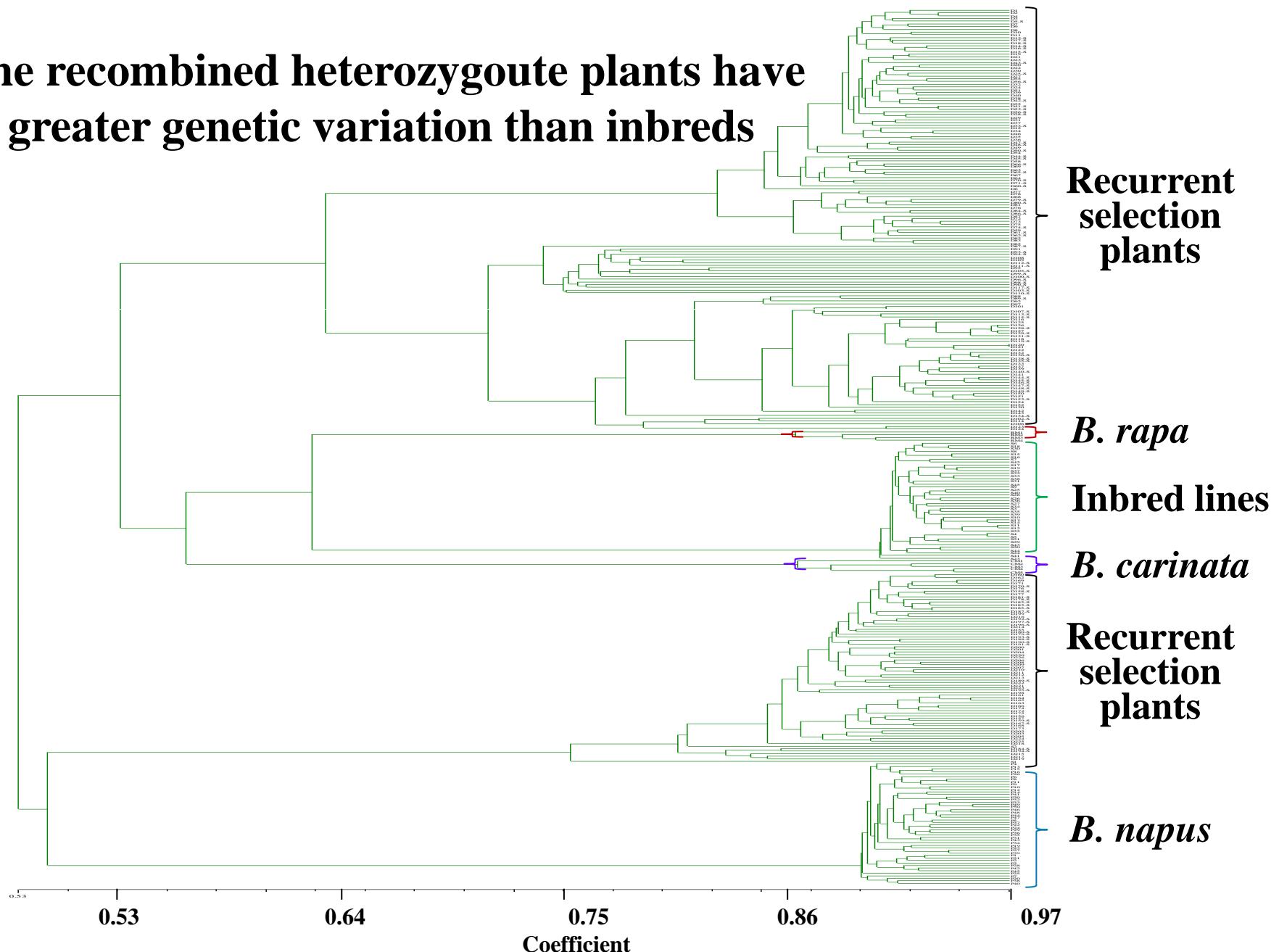
**A<sup>r</sup>/C<sup>c</sup> genepool of new type *B. napus***  
**~10,000 plants**

Inbred  
lines



Recombined  
heterozygote plants for  
recurrent selection

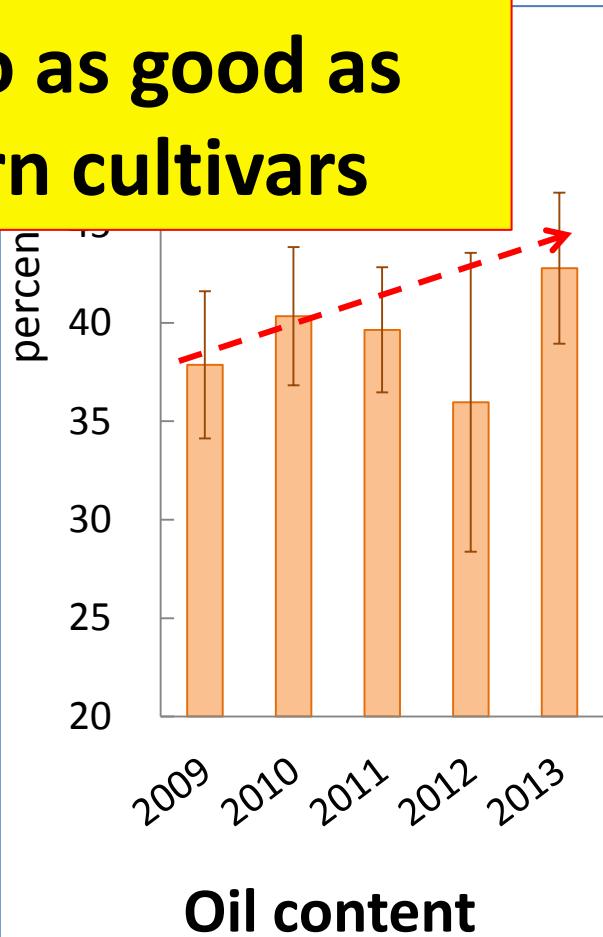
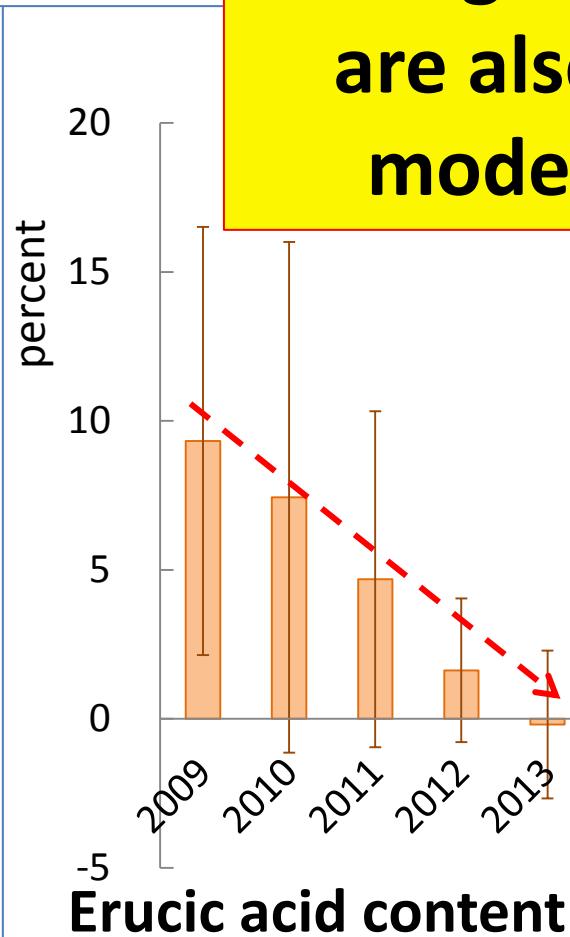
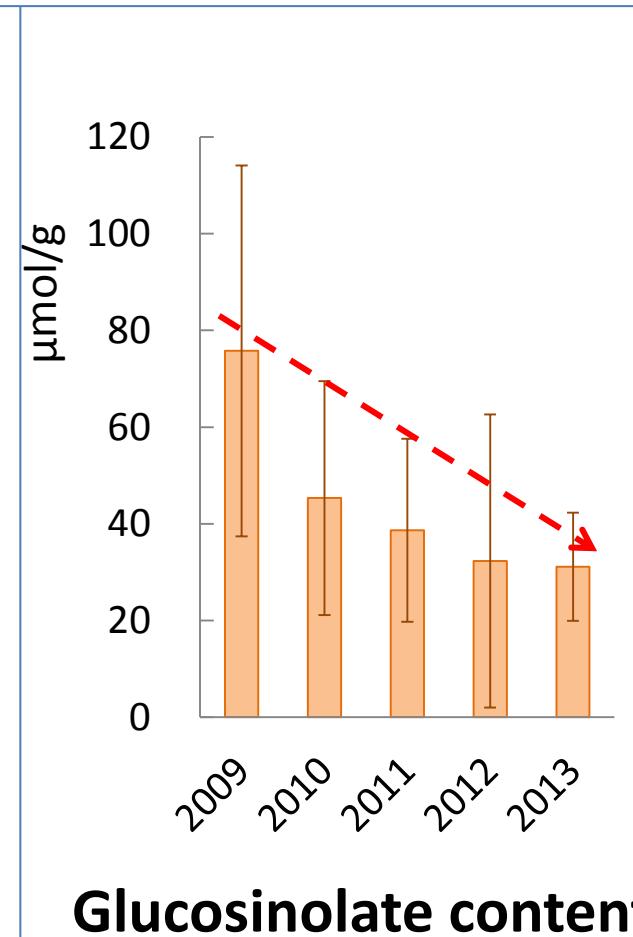
# The recombined heterozygote plants have greater genetic variation than inbreds



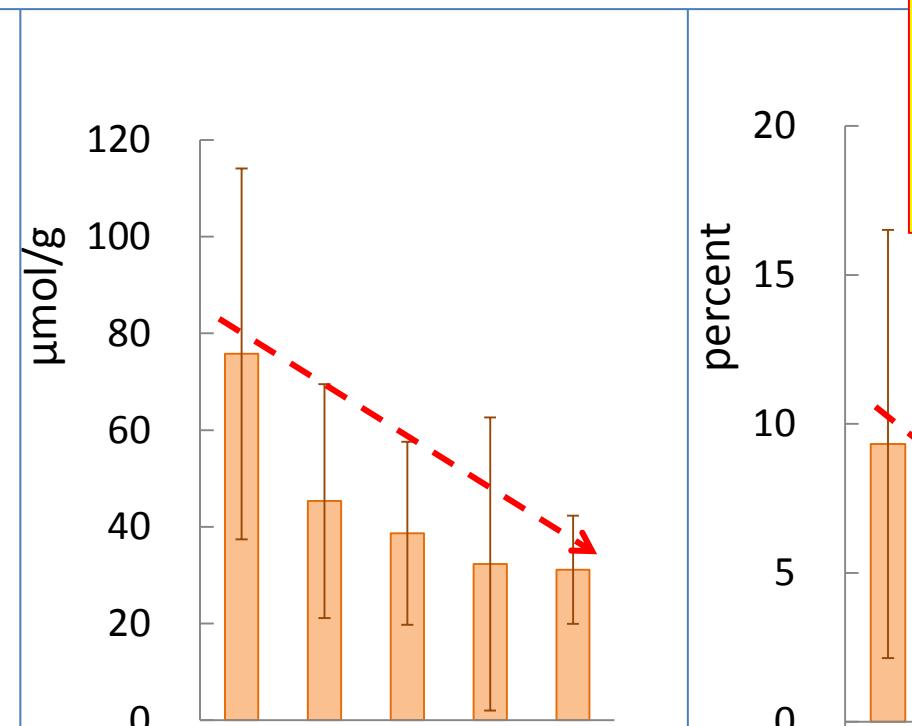
Genetic similarity in lines of new type *B. napus* and their parental species

# Traits in the population have been greatly improved by recurrent selection

The agronomical traits are also as good as modern cultivars

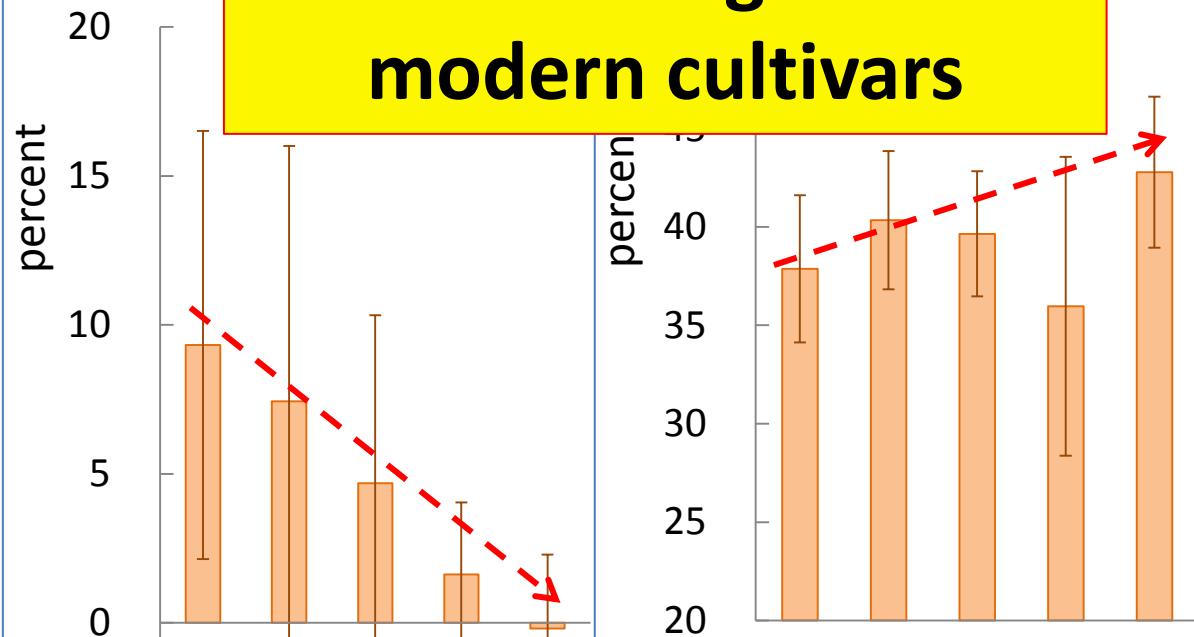


# Traits in the population have been greatly improved by recurrent selection



Bring A<sup>r</sup>/C<sup>c</sup> subgenomes  
in *B. napus*

The agronomical traits  
are also as good as  
modern cultivars



Shift-out the dross by  
recurrent selection

去粗取精

# In and out:

Bring A/C subgenomes from all of Brassica oilseed crops **in one**

Shift-**out** the dross by recurrent selection

去粗取精

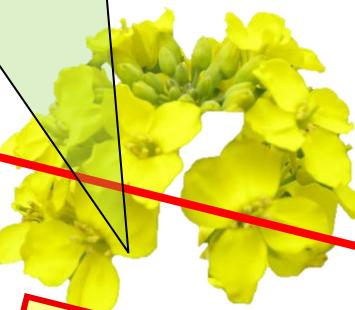
*B. carinata*  
 $B^cB^c/C^cC^c$

*B. juncea*  
 $AjAjRjRjBjBj$

*B. oleracea*  
 $C^oC^o$

*B. napus*  
 $A^nA^nC^nC^n$

*B. rapa*  
 $A^rA^r$



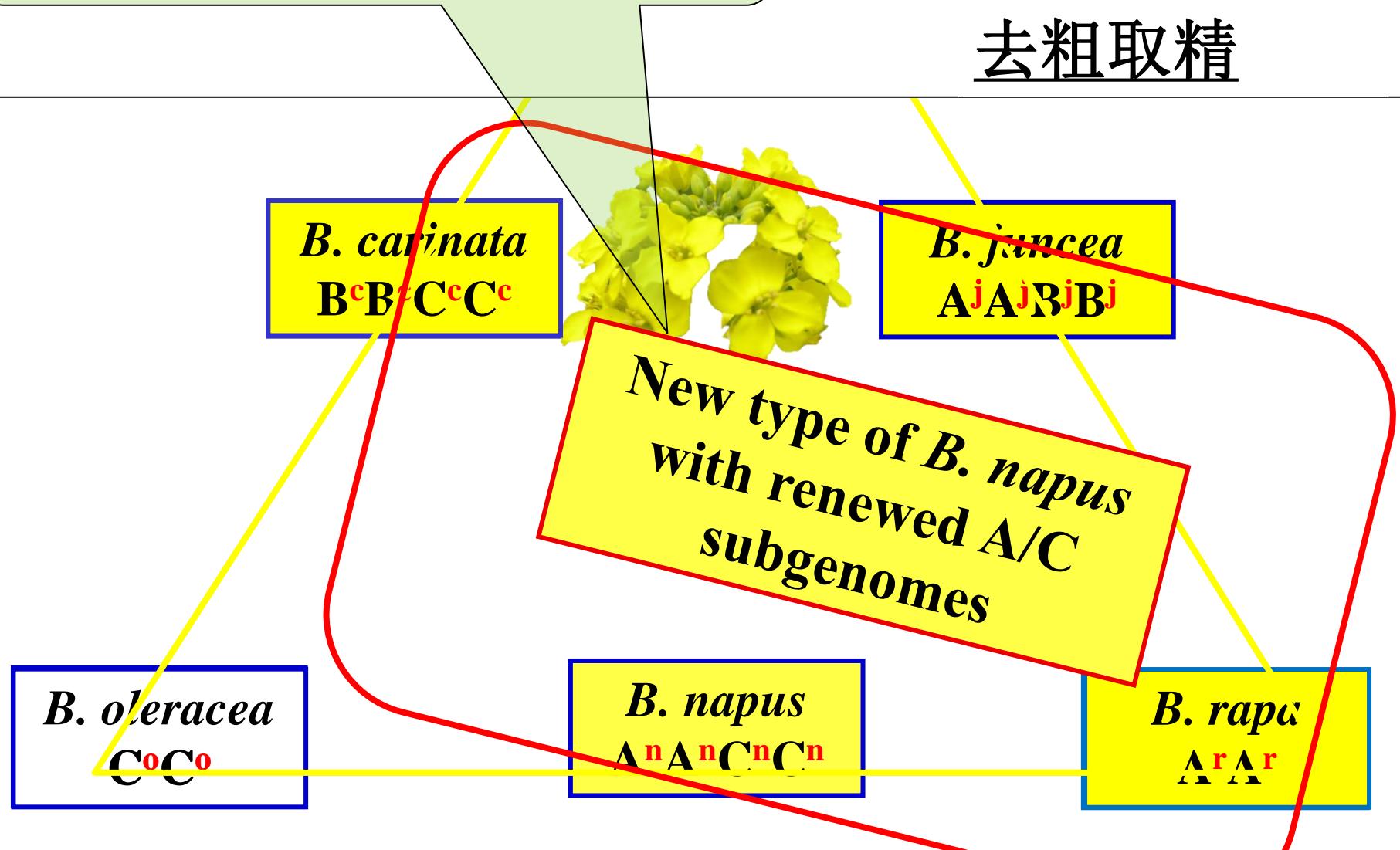
New type of *B. napus*  
 $A^rA^rC^cC^c$

# In and out:

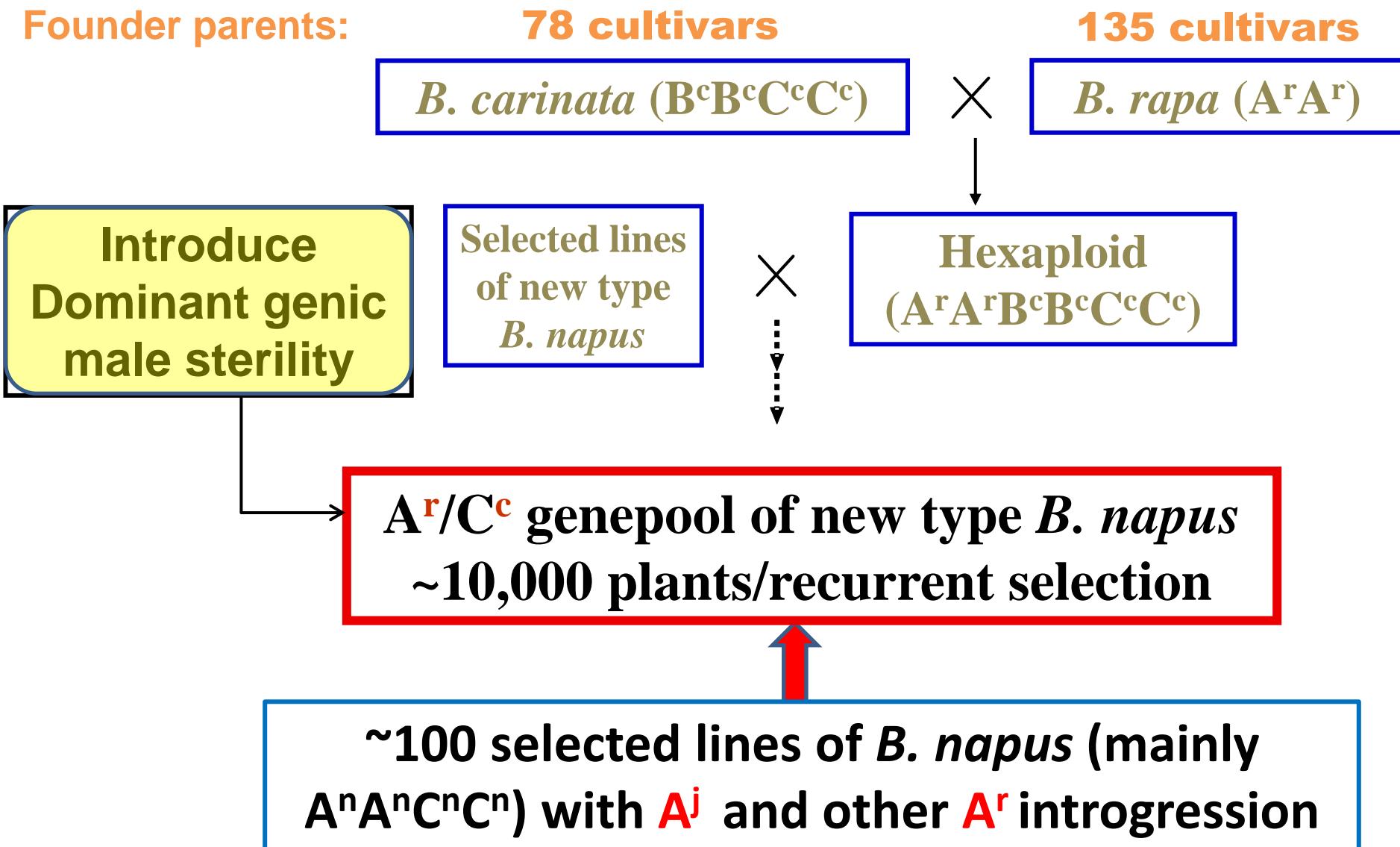
Bring A/C subgenomes from all of Brassica oilseed crops **in one**

Shift-**out** the dross by recurrent selection

去粗取精

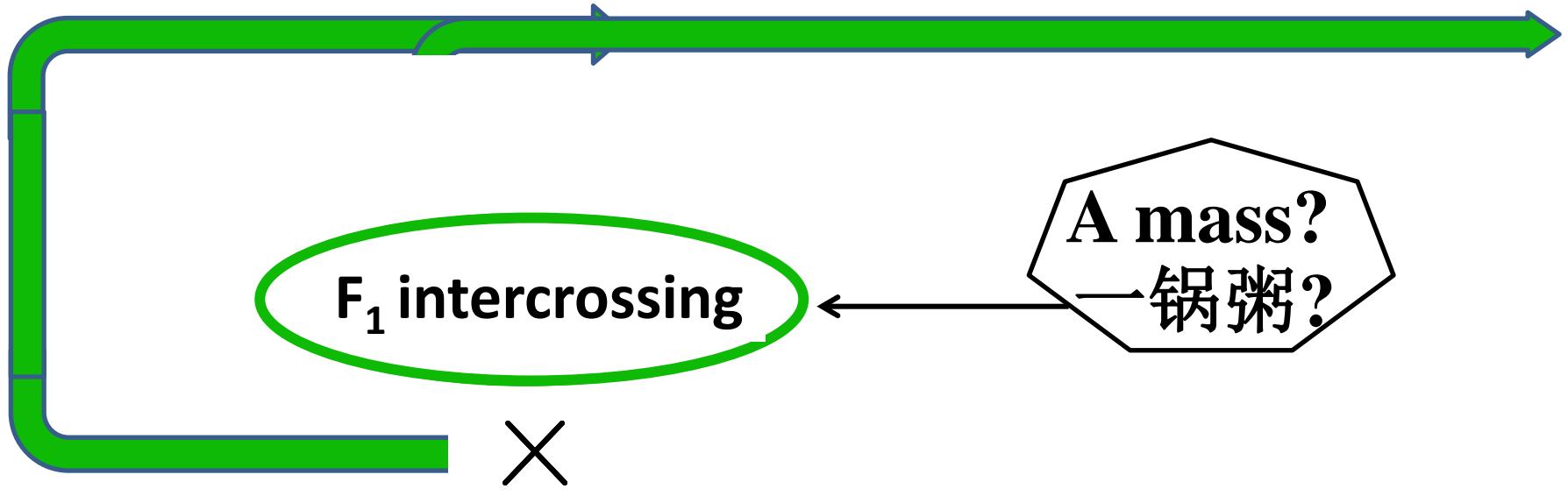


# Construct a A<sup>r</sup>/C<sup>c</sup> genepool of new type *B. napus*



**Shift-out the dross by  
recurrent selection**

**and by genomic selection  
with genomic knowledge**

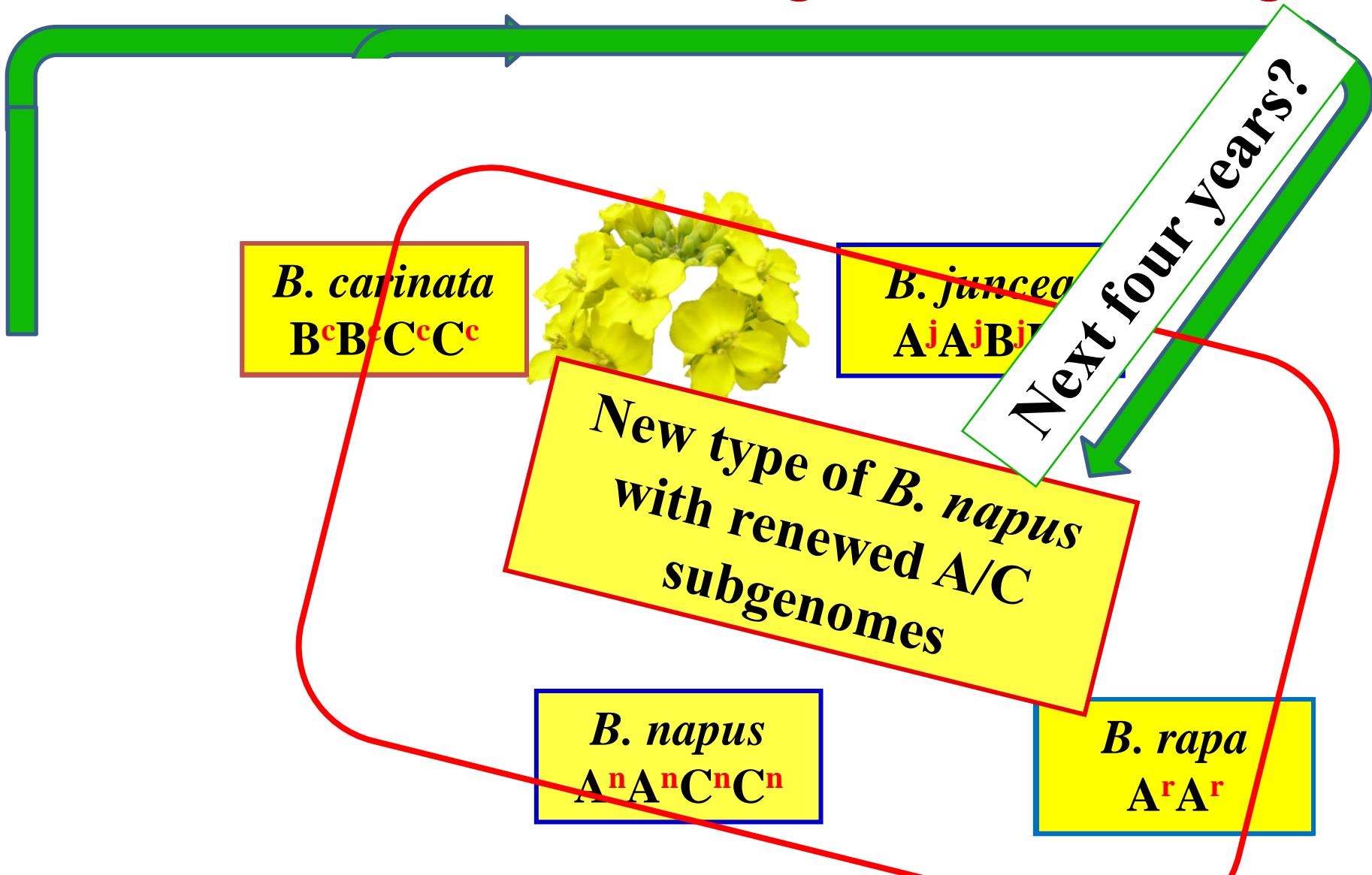


**A<sup>r</sup>/C<sup>c</sup> genepool of new type *B. napus*  
~10,000 plants/recurrent selection**

**~100 selected lines of *B. napus* (mainly  
A<sup>n</sup>A<sup>n</sup>C<sup>n</sup>C<sup>n</sup>) with A<sup>j</sup> and other A<sup>r</sup> introgression**

**Shift-out the dross by  
recurrent selection**

**and by genomic selection  
with genomic knowledge**



*B. nigra*  
**B<sup>b</sup>B<sup>b</sup>**

*B. carinata*  
**B<sup>c</sup>B<sup>c</sup>C<sup>c</sup>C<sup>c</sup>**

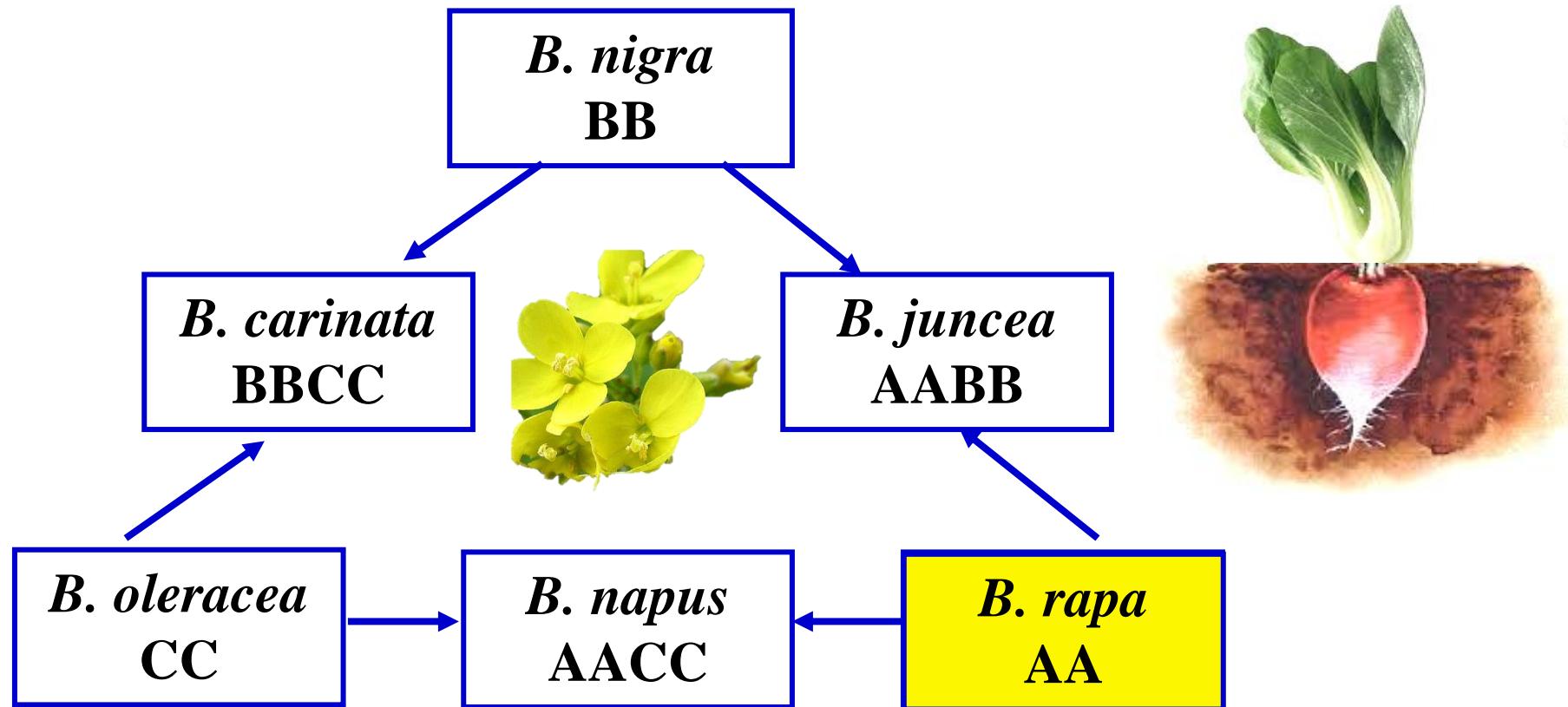
*B. juncea*  
**A<sup>j</sup>A<sup>j</sup>B<sup>j</sup>B<sup>j</sup>**



*B. napus*  
**A<sup>n</sup>A<sup>n</sup>C<sup>n</sup>C<sup>n</sup>**

*B. oleracea*  
**C<sup>o</sup>C<sup>o</sup>**

*B. rapa*  
**A<sup>r</sup>A<sup>r</sup>**



**Brassicaceae**

*Brassicaceae*

*Brassica*

芸薹科

芸薹族

芸苔属

*Crucifer*

十字花科





**Brassicales**

芸薹目

**Brassicaceae**

芸薹科

**Brassiceae**

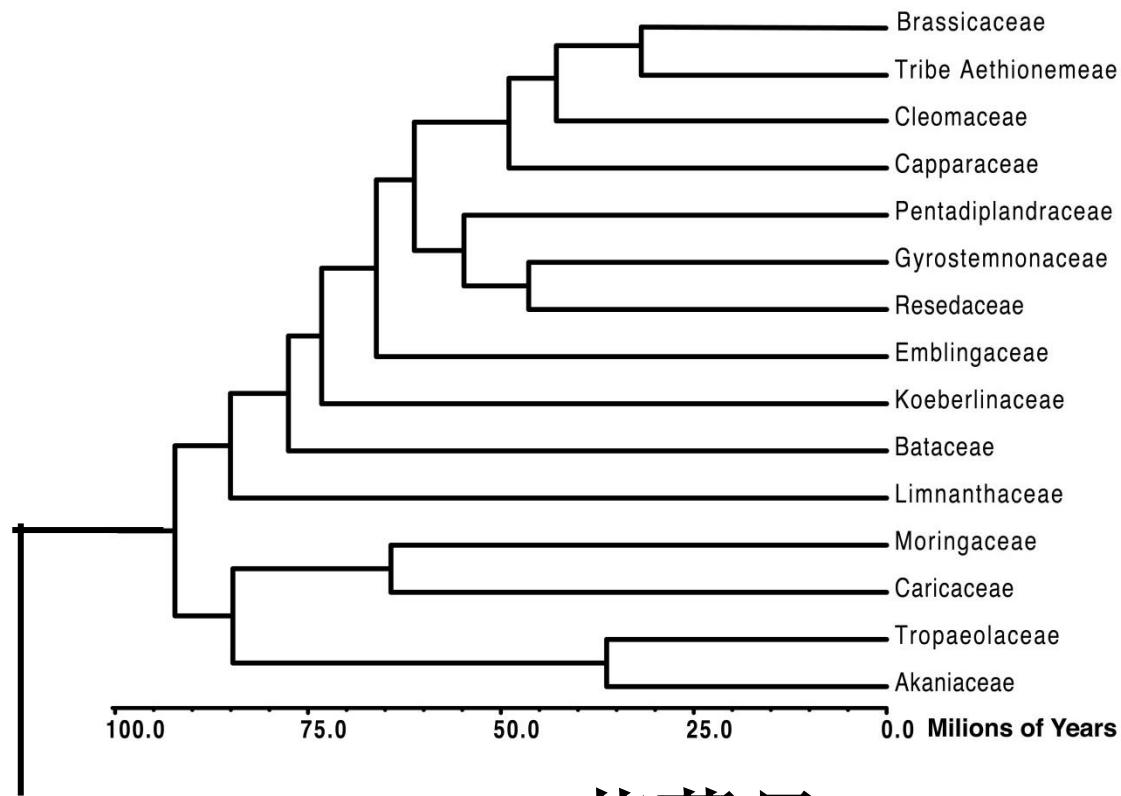
芸薹族

**Brassica**

芸苔属

*Camelina sativa*





**Brassicales**

芸薹目

**Brassicaceae**

芸薹科

*Brassicaceae*

芸薹族

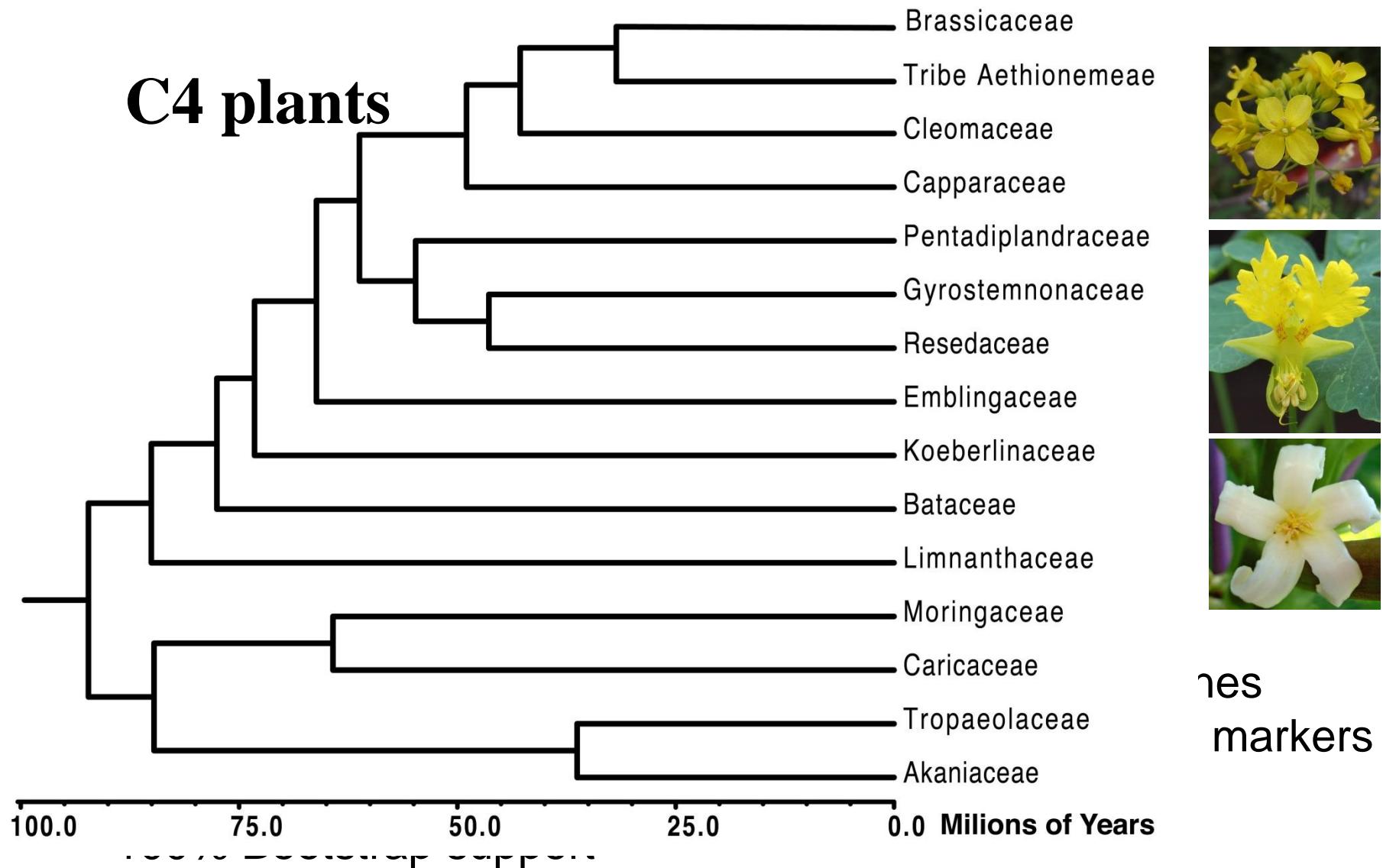
*Brassica*

芸苔属



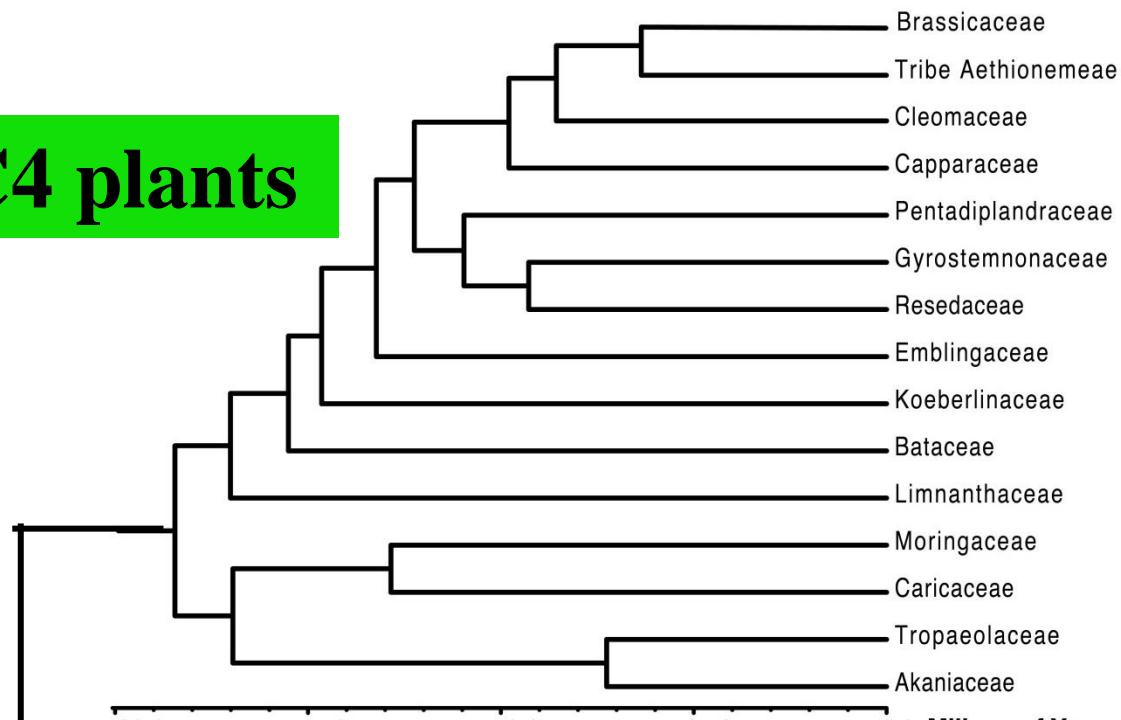
# Brassicaceae: 18 families (4765 species)

C<sub>4</sub> plants



Pat Edger et al. (Pires lab) unpublished data

## C4 plants



Brassicales

芸薹目

Brassicaceae

芸薹科

*Brassiceae*

芸薹族

*Brassica*

芸苔属



Brassica  
Paradise

# Acknowledgement:

Students and colleagues worked and working in my lab

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Internal & International companies

Friends



# Thanks !

