Towards new *Brassica* crops:
Genetic improvement of *Brassica* hexaploids

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The U's Triangle of *Brassica* species

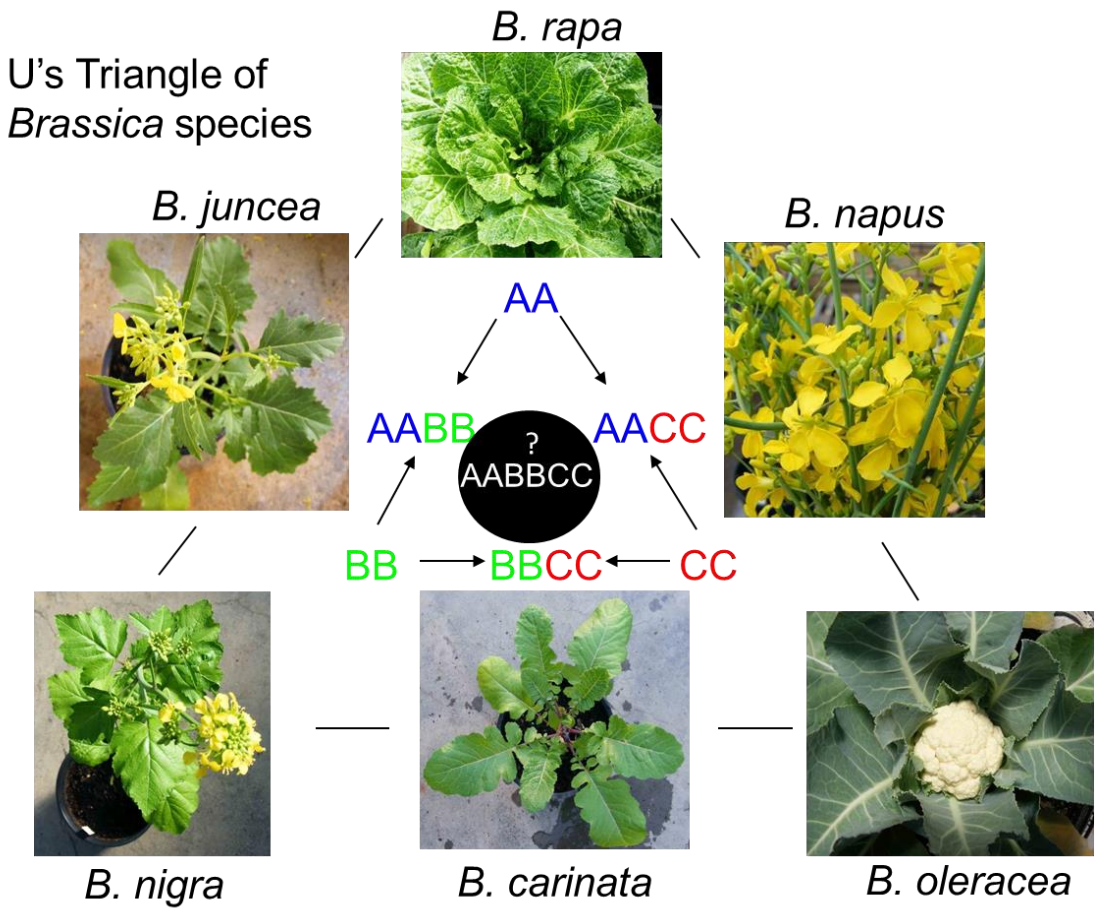


Fig. 1. Relationship of six natural *Brassica* species in the triangle of U (adapted from U 1935).

The U's Triangle of *Brassica* species

Desirable phenotypic traits exist in all six "U's Triangle" species:

B. rapa: oilseed, leaf, root vegetable types; photoperiod insensitivity, herbicide and *Verticillium* resistance, high genetic diversity

B. nigra: condiment types; resistance to blackleg/phoma disease

B. oleracea: leaf and floral vegetable types; *Verticillium* resistance, high genetic and phenotypic diversity

B. carinata: oilseed and leaf vegetable types; salt tolerance, pod shatter resistance

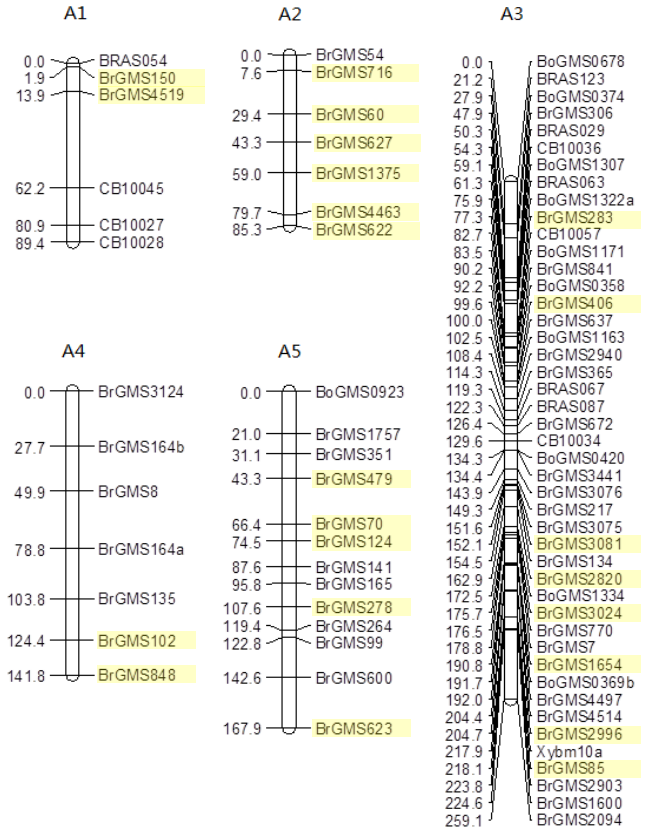
B. napus: oilseed, root and leaf vegetable types, salt tolerance, high seed yields

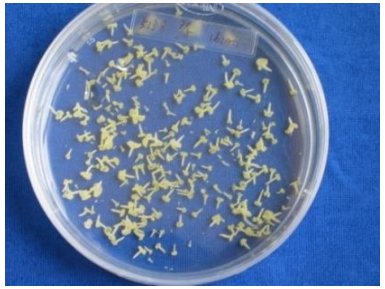
B. juncea: oilseed, stem and leaf vegetable types, yellow-seededness, resistance to blackleg/phoma disease

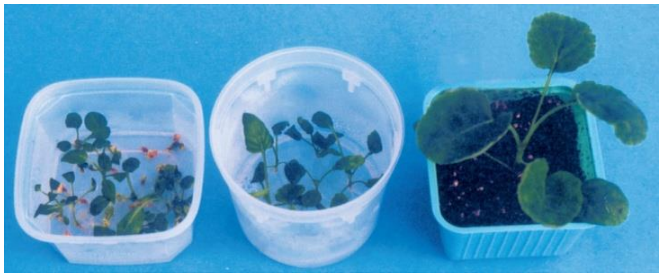
Fig. 2. Examples of agronomic cultivars and useful traits present in each of six *Brassica* "U's Triangle" species.

Research achievements

- We created artificially synthesized Rapeseed by wide hybridization among various *Brassica* species.
- We selected elite *B. napus* germplasms with superior quality, high yield and various stresses resistance / tolerance as well as colorful flowers.
- We first developed novel hexaploid *Brassica* (with A, B and C genomes) via microspore culture and DH populations, constructed genetic linkage maps, and measured several important phenotypic traits for QTL mapping.







Yang et al., Theor Appl Genet, 2016

Research achievements

ARTICLES

nature genetics
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Yang et al., Nature Genetics, 2016

The genome sequence of allopolyploid *Brassica juncea* and analysis of differential homoeolog gene expression influencing selection

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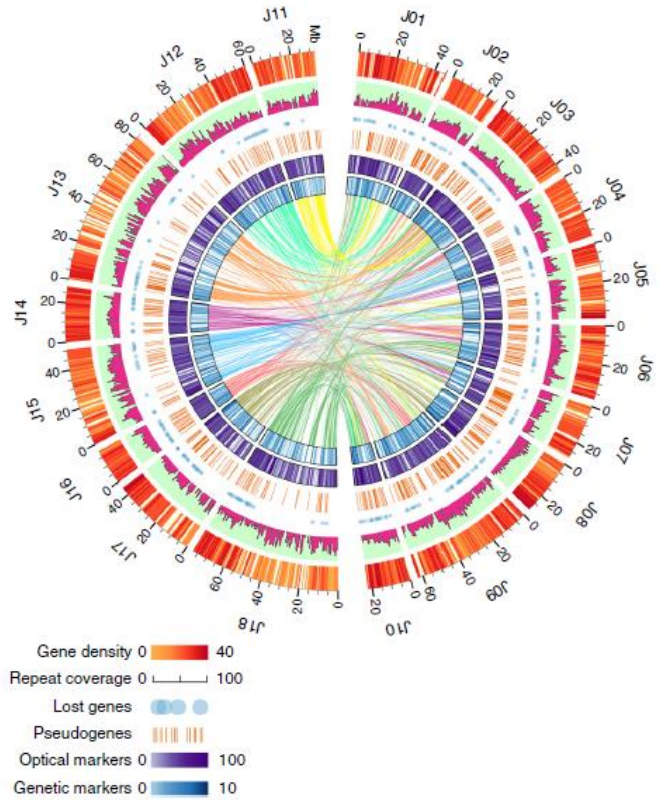


Figure 1 The genome of *B. juncea* vegetable-use variety T84-66. The *B. juncea* genome comprises 10 chromosomes belonging to BjuA (J01–J10; right semicircle) and 8 chromosomes belonging to BjuB (J11–J18; left semicircle), scaled on the basis of their assembled length. Homeologous relationships between BjuA and BjuB chromosomes are displayed with connecting lines colored according to the BjuB subgenome. The tracks, from outer to inner, show gene density (non-overlapping, window size = 500 kb), repetitive sequence density (window size = 500 kb), the location of gene loss (blue solid point for gene loss), the location of pseudogenes (solid line for pseudogenes), genome (optical) marker density (window size = 500 kb) and genetic marker density (window size = 500 kb).

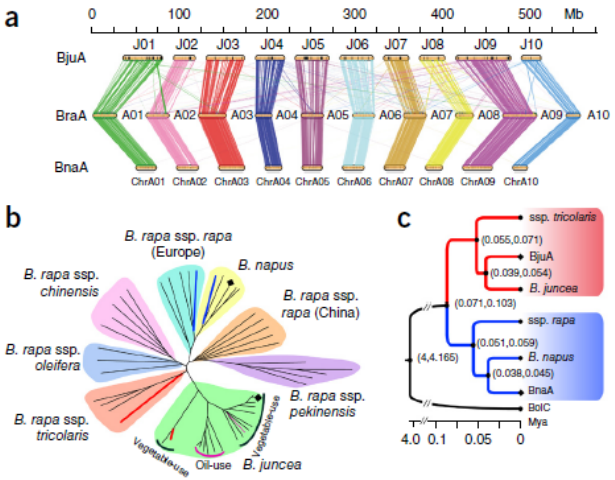
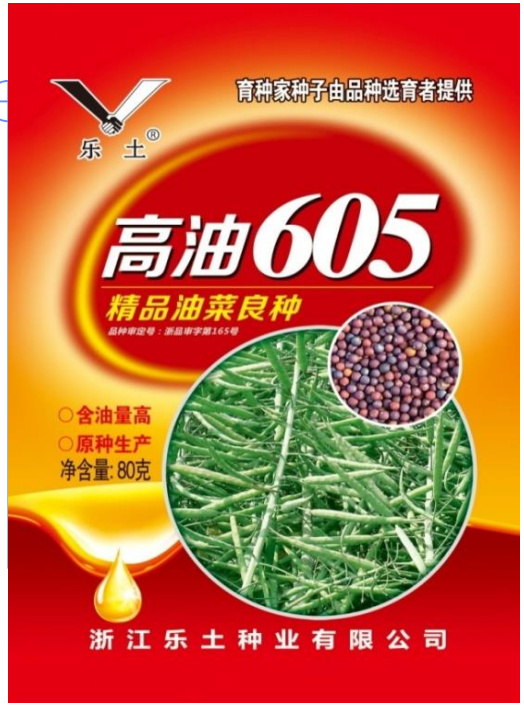


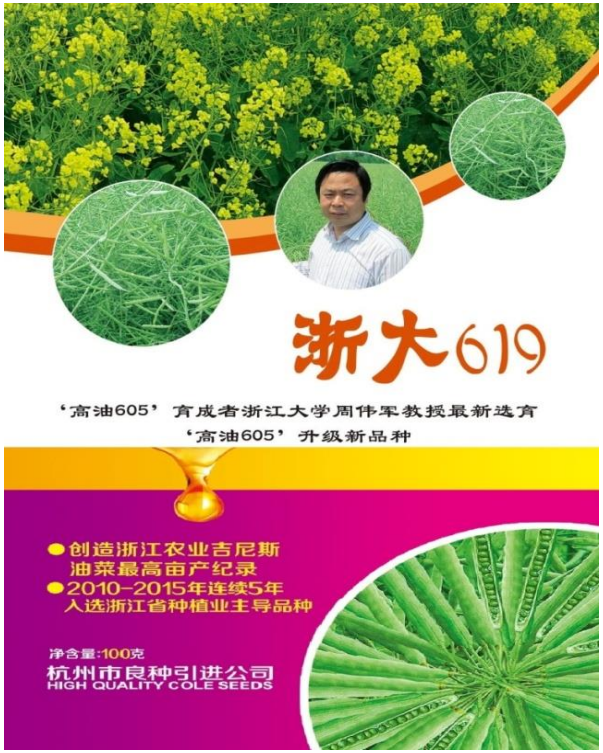
Figure 2 Synteny and phylogenetic evolution analysis of three A-subgenome in *Brassica* species. (**a**) Schematic representation of synteny among *B. rapa* (BraA), A subgenome of *B. juncea* (BjuA) and *B. napus* (BnaA). Each line connects a pair of orthologous genes between genomes or subgenomes. (**b**) A phylogenetic neighbor-joining tree constructed from BjuA, BnaA, and resequencing of A subgenomes of 17 *B. juncea*, 5 *B. napus* and 27 *B. rapa* accessions. Vegetable- and oil-use subvarieties of *B. juncea* are marked with black and rose lines. (**c**) An ultrametric tree constructed from A subgenomes of *B. juncea* (BjuA) and *B. napus* (BnaA); two A subgenomes from the resequencing of *B. juncea* (BjuA_R16) and *B. rapa* ssp. *tricolaris*; and two A subgenomes from the resequencing of *B. napus* (BnaA) and *B. rapa* ssp. *rapa* (Europe). *B. oleracea* (BolC) is considered as an outgroup. Numbers in parentheses indicate the divergence time interval (Mya). The two A subgenomes from the resequencing of *B. juncea* (BjuA) and *B. rapa* (ssp. *tricolaris*) correspond to the two red and bold branches in **b**. The two A subgenomes from the resequencing of *B. napus* (BnaA_R1) and *B. rapa* ssp. *rapa* (Europe) correspond to the two blue bold branches in **b**.

Research achievements



Released 5 new Rapeseed varieties with high oil content & high yield:

- Zhenongda 601
- Zhenongda 605 (Gaoyou 605)
- Zheda 619 (best disease resistance, top ten varieties in Zhejiang in 2016)
- Zheda 622 (oil content reached up to 49.13%)
- Zheda 630 (oil content reached up to 49.82%, highest oil in Zhejiang, ranked 1st among China national conventional varieties)



Meanwhile, we developed a high yielding and high efficiency commercial protection system accordingly for our new rapeseed cultivars, thus made a great contribution to the healthy and sustainable production of rapeseed industry.

Trigenomic bridges for *Brassica* improvement

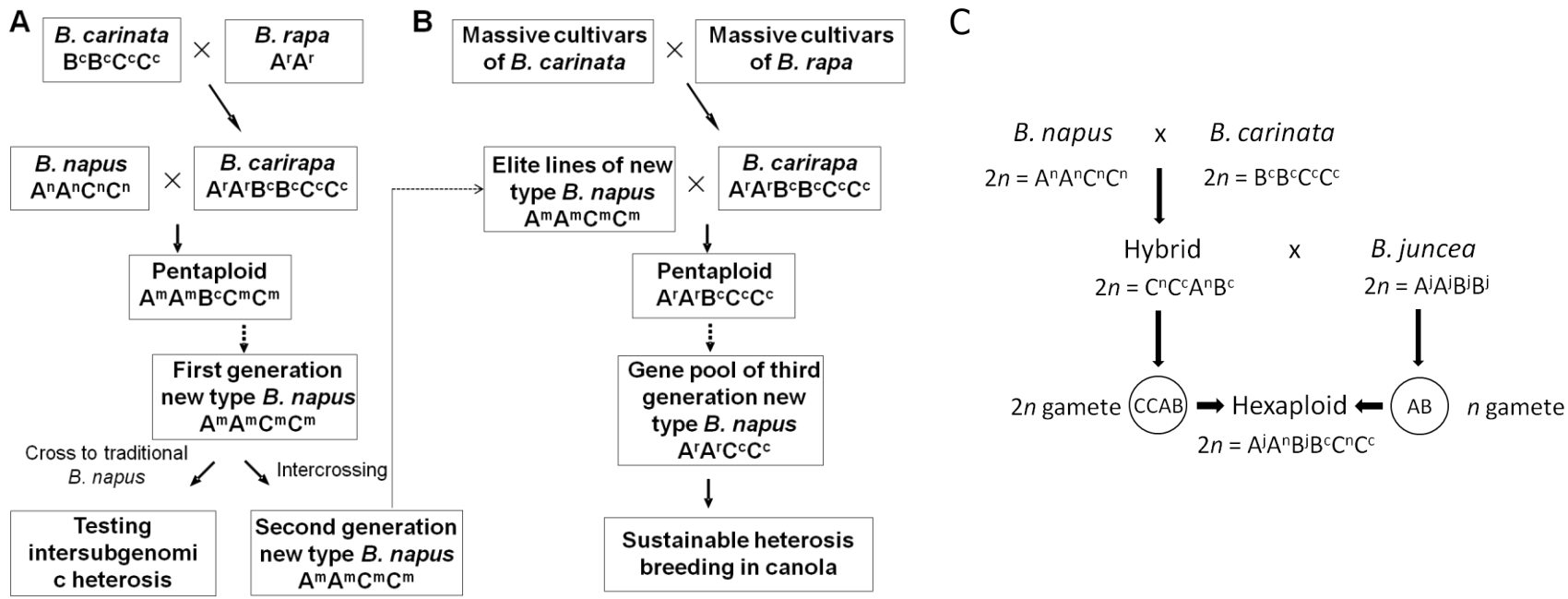


Fig. 3. Production of 'new type' *B. napus* and allohexaploid *Brassica* (2*n* = AABBCC). Mixed genome contributions (from more than one species) are indicated with a superscript 'm'. A: First generation new type *B. napus* is produced by crossing *B. rapa* and *B. carinata*, colchicine doubling of the resulting $A^rB^cC^c$ hybrids to produce *'B. carirapa',* followed by backcrossing to *B. napus* cultivars and repeated selfing. B: Multiple cultivars of *B. carinata* and *B. rapa* are crossed, creating a new genetically-diverse '*B. carirapa*' pool. C.Crossing design to utilize unreduced gamete production by interspecific hybrids to produce allohexaploid *Brassica* (2*n* = AABBCC) from the allotetraploid species *B. juncea* (2*n* = AABB), *B. napus* (2*n* = AACC) and *B. carinata* (2*n* = BBCC).

Chen et al., Crit Rev Plant Sci, 2011

Challenges and opportunities

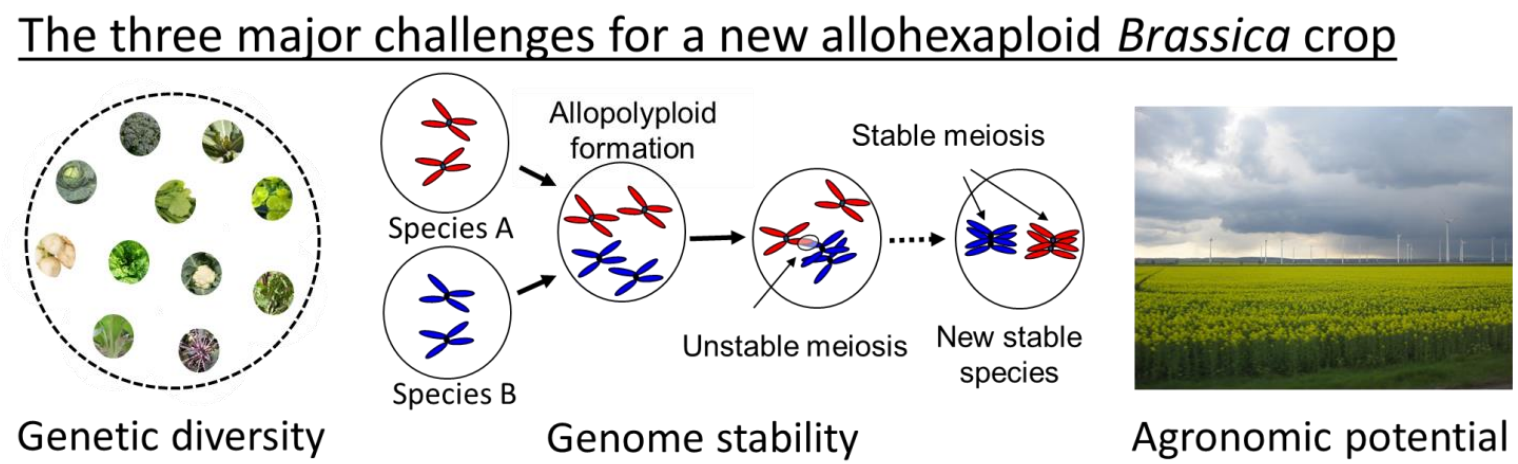


Fig. 4. The three major challenges facing establishment of *Brassica* allohexaploid germplasm as a new crop type:

- Generation of sufficient genetic diversity to establish a solid basis for selective breeding
- Restoration of genome stability
- Eventual proof of agronomic potential and superiority to current rapeseed cultivars

Challenges and opportunities

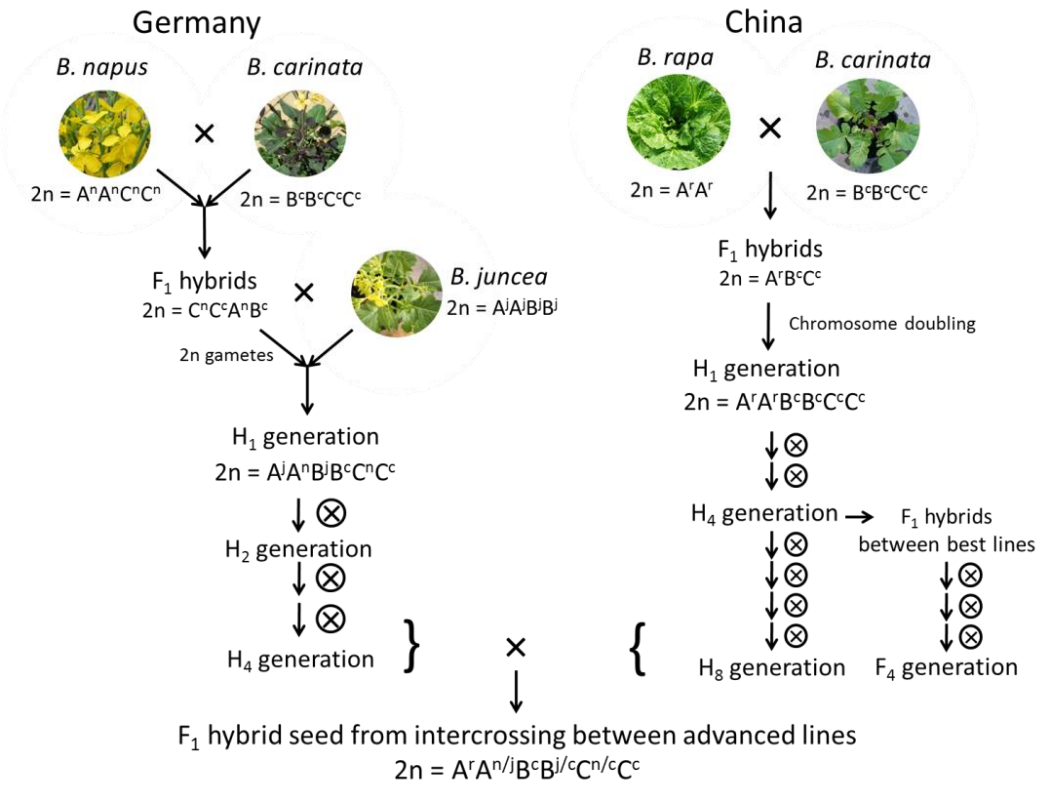


Fig. 5. Intercrossing between advanced generations of allohexaploid germplasm generated by the research groups involved in this collaboration has already been undertaken. Selection for high fertility was undertaken in every generation in both experimental groups, as well as selection for 2n = 54 chromosome complements in the Chinese germplasm and marker-based selection for complete A and C genome complements in the first generation of the German germplasm.

Challenges and opportunities

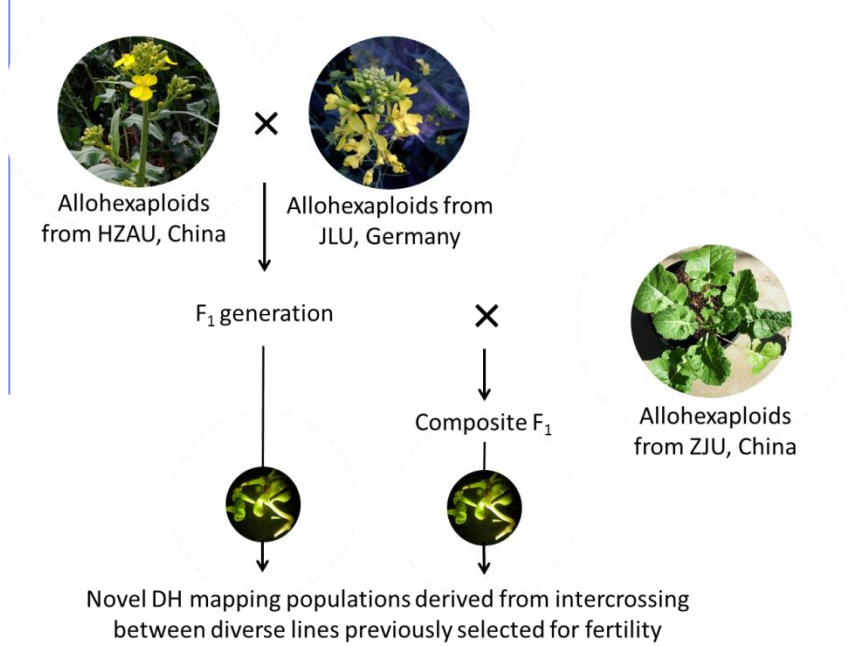


Fig. 6. Planned production of novel DH mapping populations through microspore culture from F_1 hybrids between advanced lines of different germplasm types selected for fertility and genome stability.

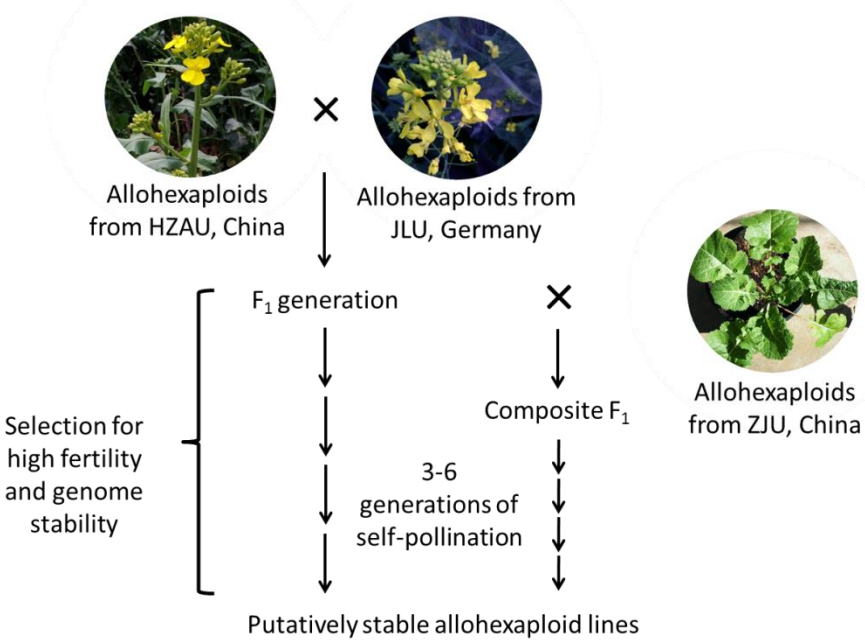


Fig. 7. We hypothesise that stable allohexaploids will result from intercrossing between diverse advanced lines after several generations of selection for fertility and genome stability.

Challenges and opportunities

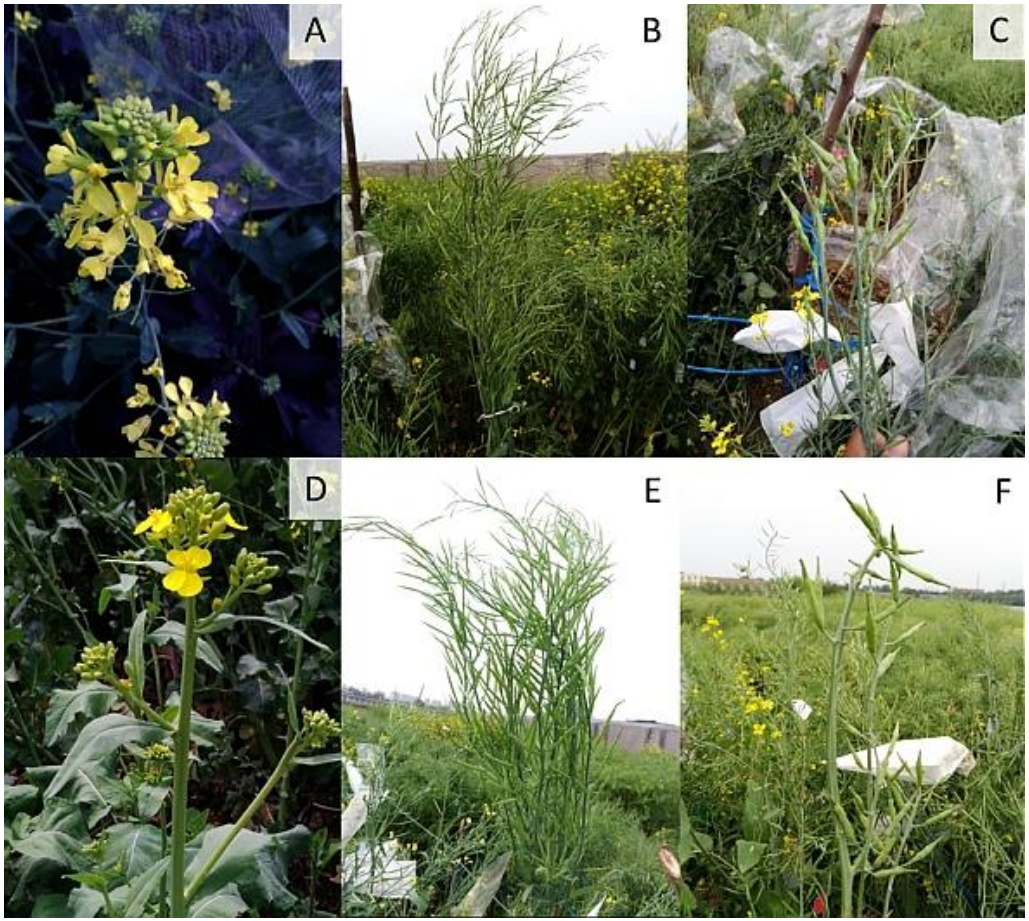


Fig. 8. German allohexaploid germplasm showing A) flowering; B) self-pollinated seed production; and C) seed setting after crossing as the female parent to a Chinese allohexaploid. Chinese allohexaploid germplasm showing D) flowering; E) self-pollinated seed production; and F) seed setting after crossing as the female parent to a German allohexaploid.

Proposal for collaboration

A multi-faceted approach will be used to:

- Investigate the relationship between chromosome rearrangements and meiotic behavior in advanced, putatively stable allohexaploid lines from different sources using high throughput genotyping and cytogenetics.

- Enlarge genetic diversity based on existing germplasms and in newly generated lines produced by intercrossing and recombination between diverse Chinese and European germplasms.

- Select and assess agronomic traits in the advanced germplasms using field-based phenotyping and QTL mapping.

Anticipated outcome

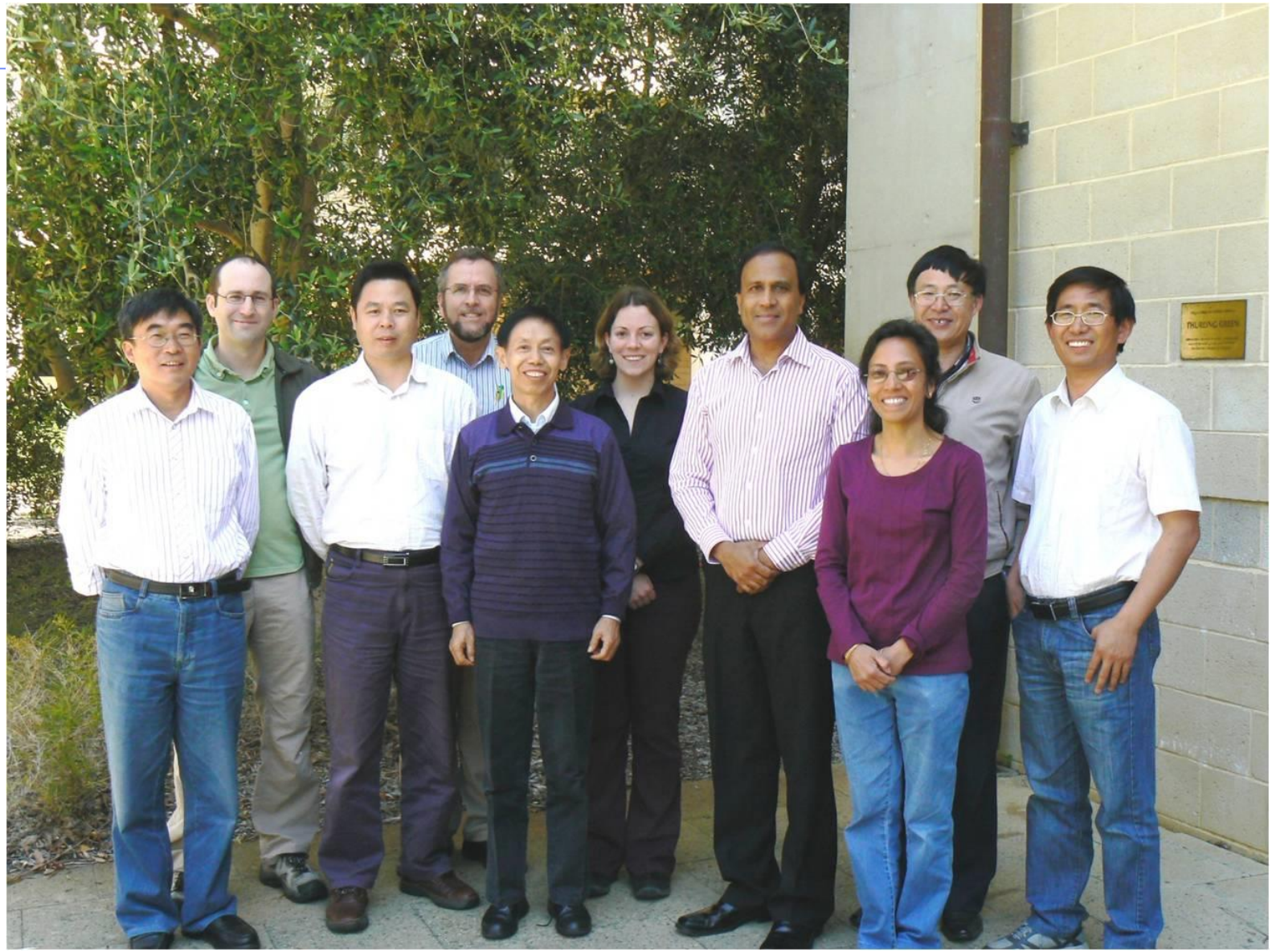
- Research will understand karyotype variation (chromosome rearrangements, duplication and deletion of chromosome segments) in advanced lines of allohexaploid germplasms.

- Identify genotype- and species-specific factors responsible for meiotic stability in diverse allohexaploid germplasms, and improve genome stability and agronomic trait performance.

- Results will facilitate the development of a new, high-yielding rapeseed crop species for oil, vegetable and biomass energy production in China, Europe and worldwide.

Acknowledgements

Colleagues including Univ. Giessen (German), HZAU (China) & UWA (Australia)



Acknowledgements

Group photo of my Lab

Thank you