Sustaining rapeseed production in the era of plant genomics and molecular biotechnologies

EU-China expert seminaron identifying potential joint priorities for research and innovation in food, agriculture and biotechnology***, Brussels, Oct 27-28, 2016***

Presented by

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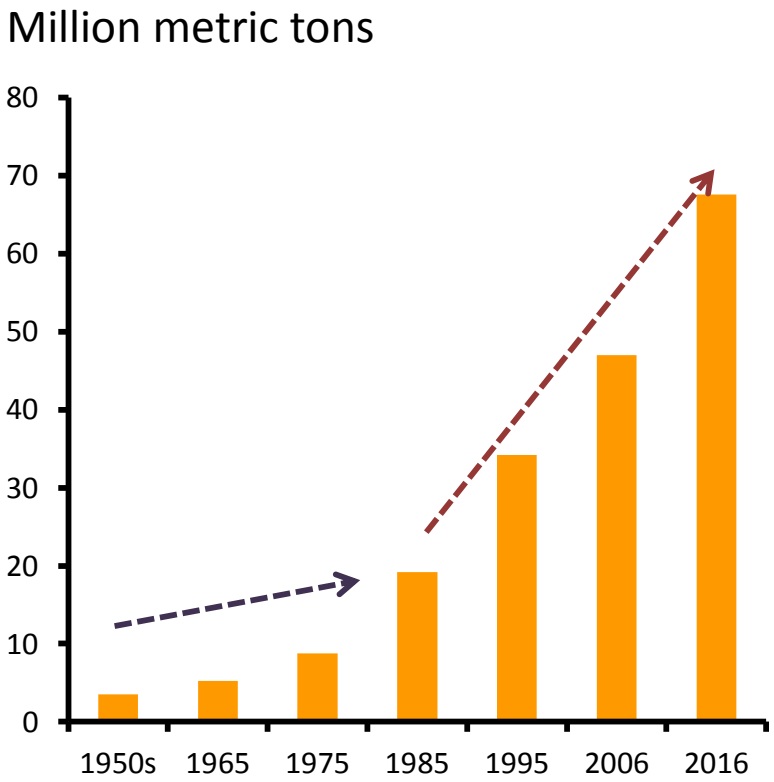
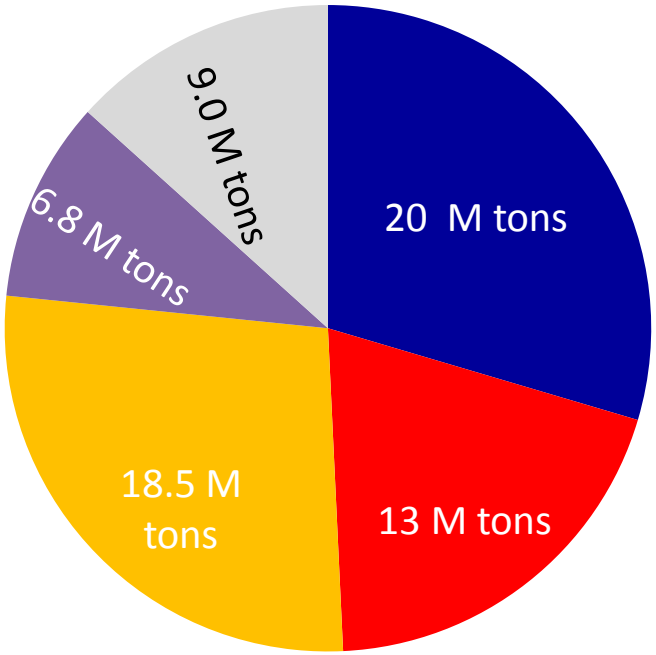
The cooperation between Europe and China on rapeseed, and challenges that both European and Chinese scientists are facing to sustain rapeseed production in the background of global climate change.

Importance of oilseed rape in EU and China



The World Rapeseed Production



The World Rapeseed Production 2015/2016
www.worldrapeseedproduction.com

The world rapeseed production has been increasing rapidly since 1950s, especially after the breakthrough of double low quality breeding in 1970s . Europe and China stand for about 30% and 20% of the world total production

History of EU-CN Cooperation in Rapeseed Research

1980s

The cooperation of Europe and China on rapeseed began in early 1980s, when China sent scholars to Europe to learn quality breeding.

1990s

The first Europe-China joint project on rapeseed was launched in 1996. Prof. Heiko Becker was the coordinator of this joint project that involved 3 European and 3 Chinese institutions.

2000s

The next decade witnessed the cooperation of the European and Chinese scientists in drawing QTL maps of rapeseed.

2010s

Genome *Br* was sequenced by Chinese scientists (wang et al., 2011, Nat. Genet.) with cooperation of European scientists.
Genome *Bn* was sequenced by French scientists (Chalhoub et al., 2014, Science) with cooperation of Chinese scientists.
Genome Bj was sequenced by scienctists in Zhejiang University (Yang et al., 2016, Nat. Genet.)

The First EU-CN Project on Rapeseed

1996-2000

History of EU-CN Cooperation in Rapeseed Research

1980s

The cooperation of EU and China in rapeseed research began in early 1980s, when China sent scholars to Germany, France, UK, Poland, to learn breeding towards double low seed quality.

1990s

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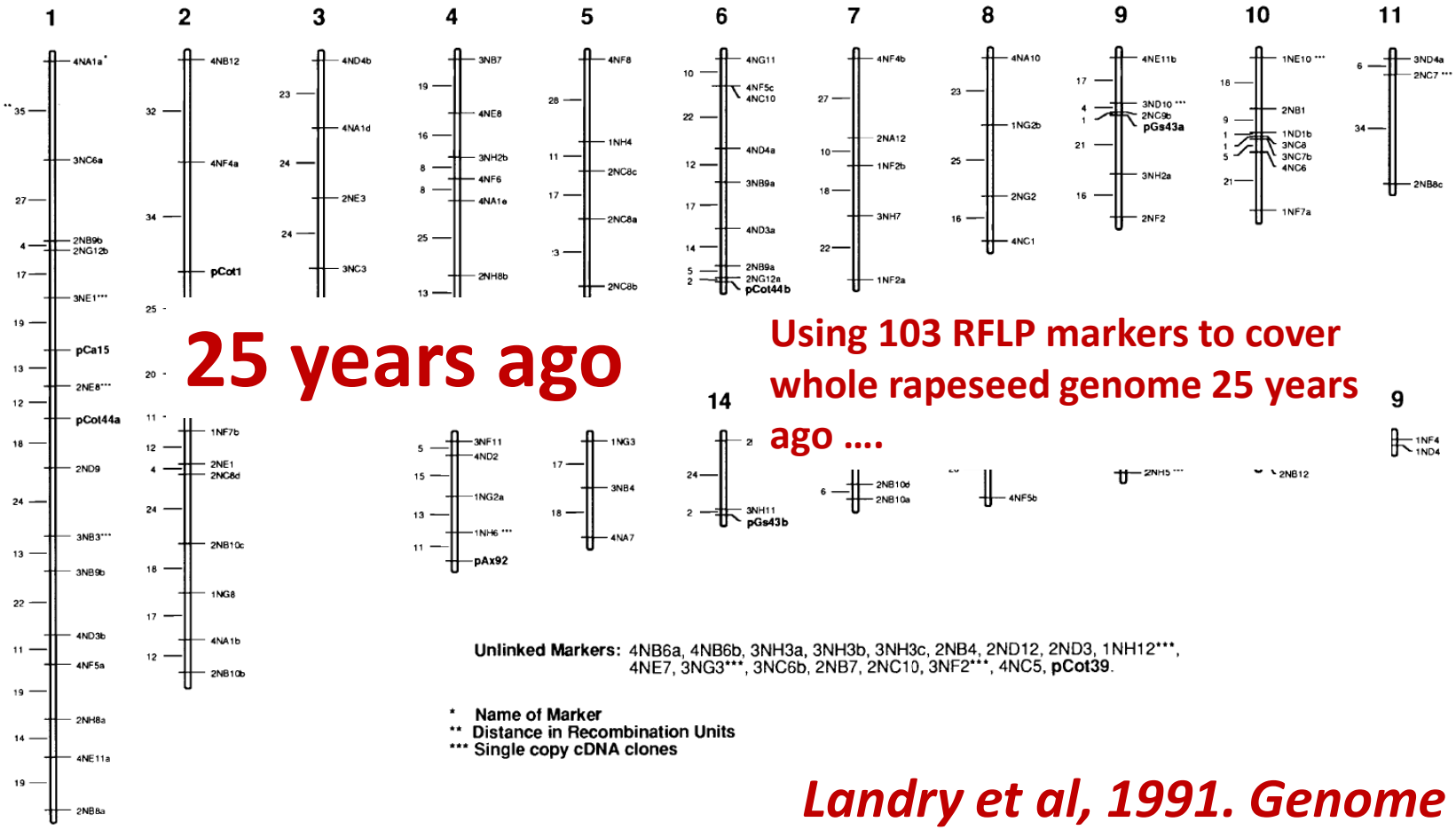
Cooperation Between EU-CN Scientists to Develop Rapeseed QTLs Maps



25 years ago

Using 103 RFLP markers to cover whole rapeseed genome 25 years ago ….

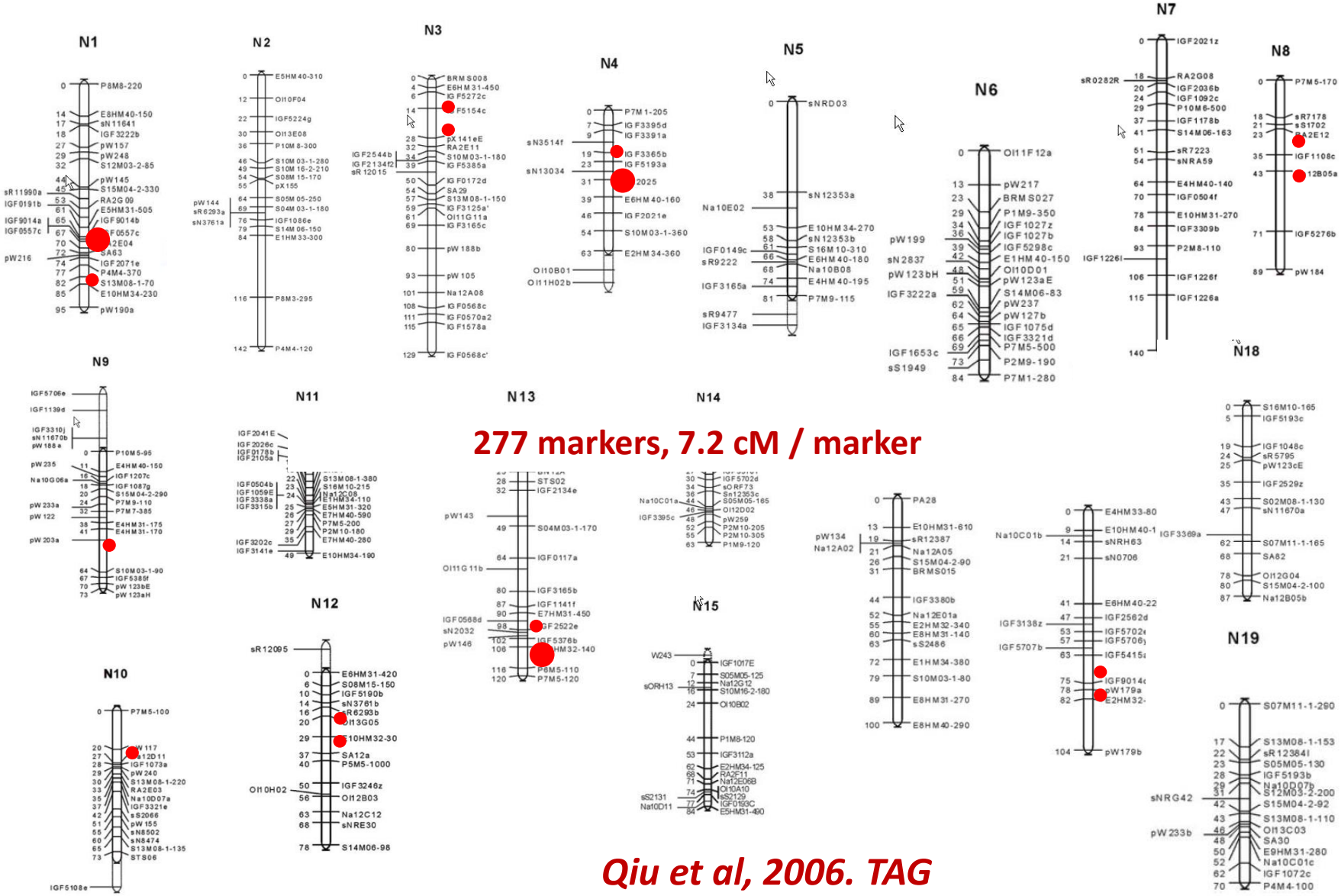
Unlinked Markers: 4NB6a, 4NB6b, 3NH3a, 3NH3b, 3NH3c, 2NB4, 2ND12, 2ND3, 1NH12***, 4NE7, 3NG3***, 3NC6b, 2NB7, 2NC10, 3NF2***, 4NC5, **pCot39**.

* Name of Marker
** Distance in Recombination Units
*** Single copy cDNA clones

Landry et al, 1991. Genome

The rapeseed QTL maps began with only around 100 markers covering the whole genome 25 years ago.

From QTLs to Genome Sequencing

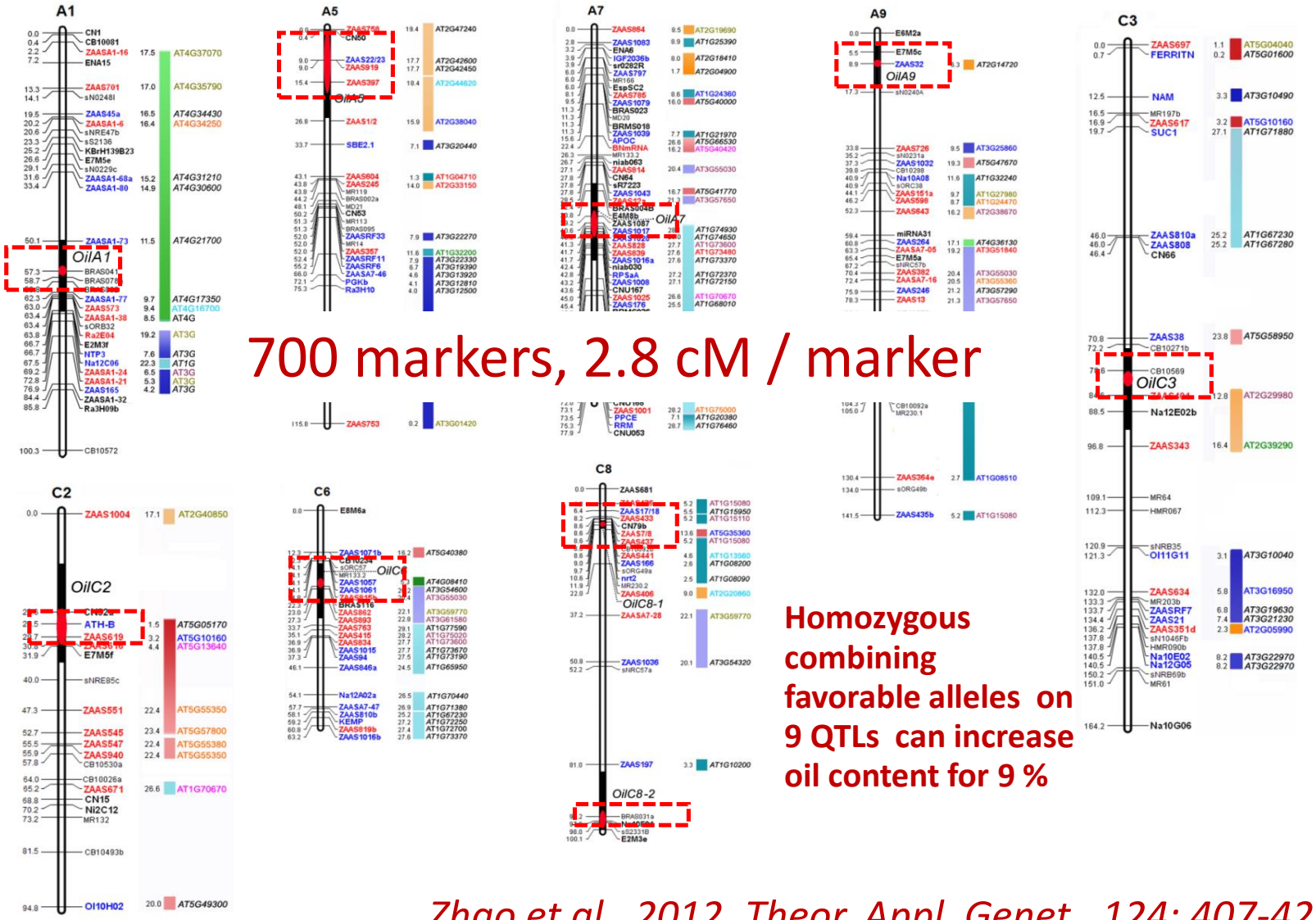


277 markers, 7.2 cM / marker

Qiu et al, 2006. TAG

To a very much advanced and densified T-N map, which was developed 10 years ago.

From QTLs to Genome Sequencing



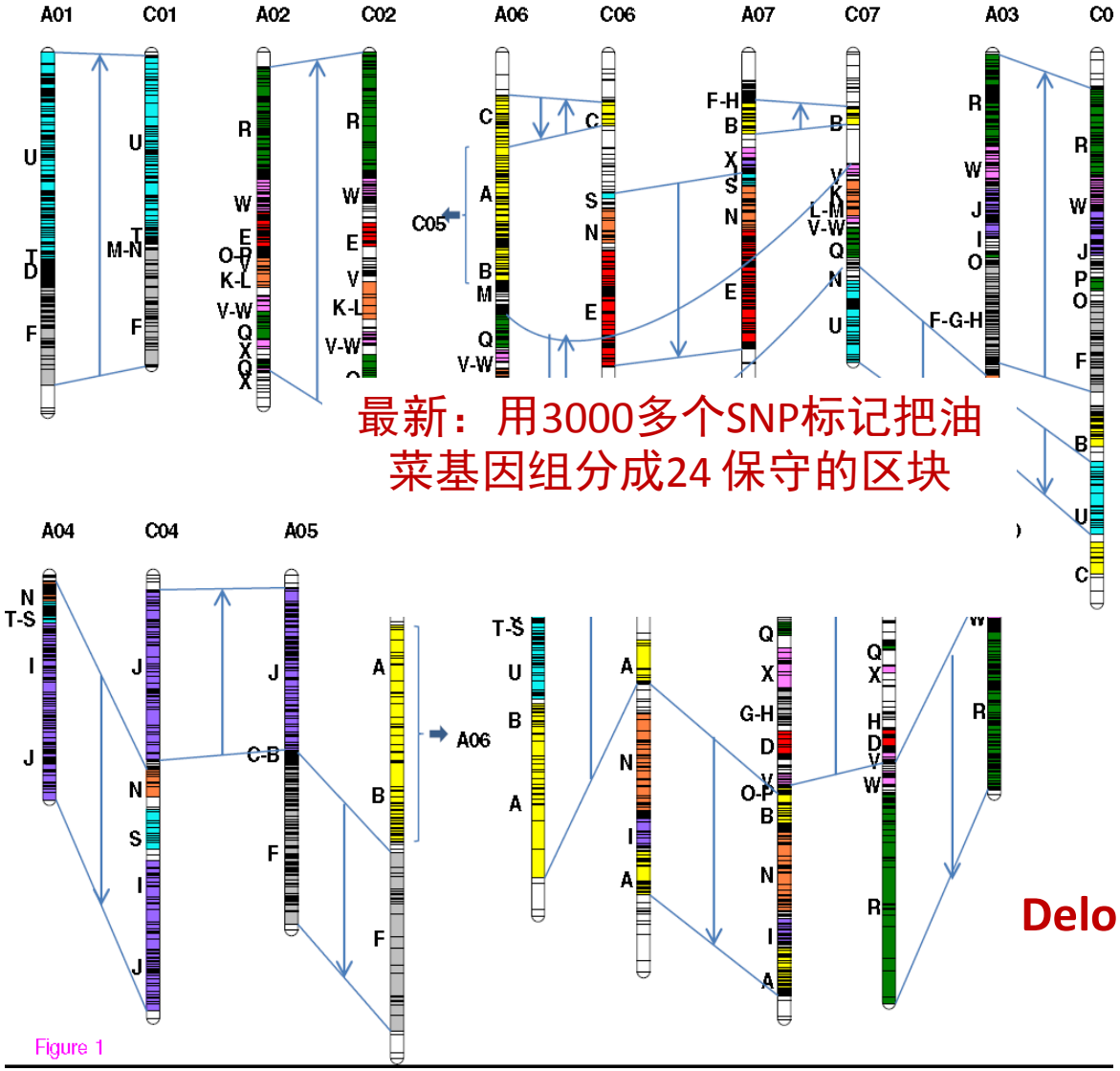
700 markers, 2.8 cM / marker

Homozygous combining favorable alleles on 9 QTLs can increase oil content for 9 %

Zhao et al., 2012. Theor. Appl. Genet., 124: 407-421

To the SG map with more than 700 markers that was reported in 2012.

From QTLs to Genome Sequencing



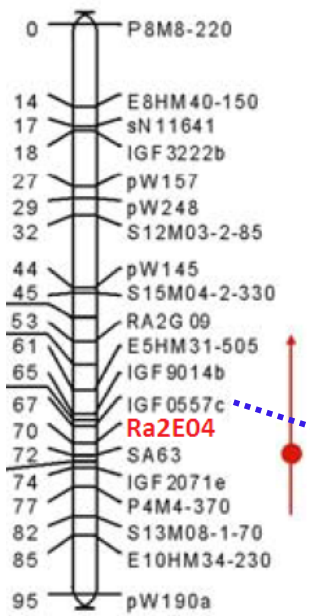
最新：用3000多个SNP标记把油菜基因组分成24 保守的区块

Delourme et al., 2013

To a more recent map with more than 3000 thousands SNPs that was published just a few years ago.

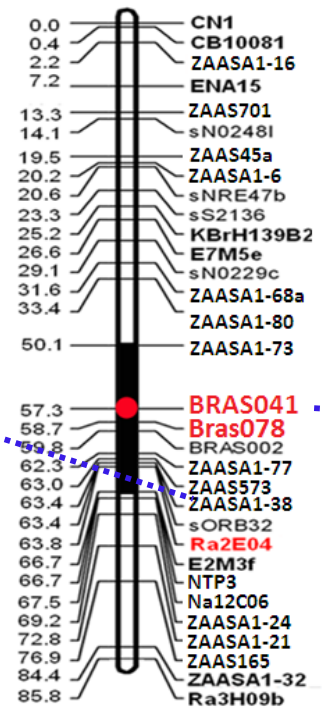
From QTLs to Genome Sequencing

TN-map (UK-CN)



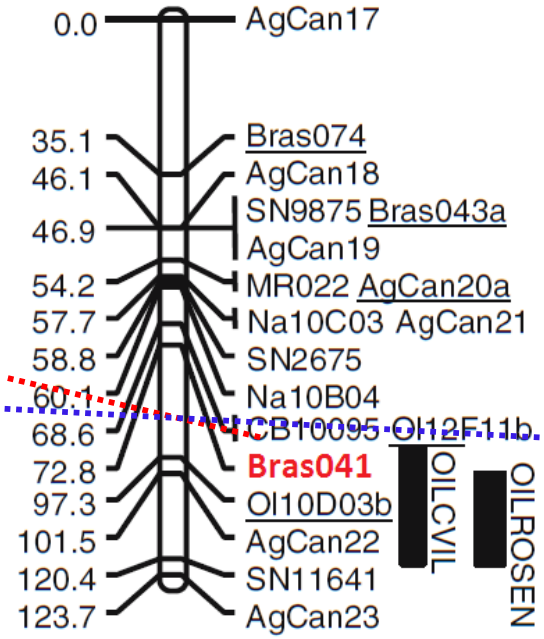
Qiu et al., 2006.
Theor. Appl. Genet.

SG-map (GM-CN)



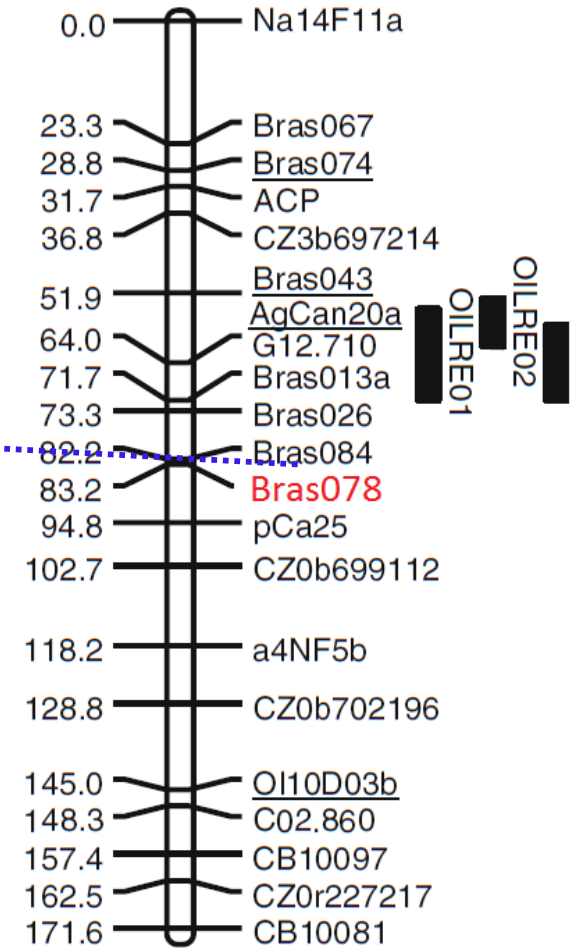
Zhao et al., 2012.
Theor. Appl. Genet.

RNSL (French)



Delourme et al., 2006.
Theor. Appl. Genet.

DY-map (French)



Joint efforts also have been made to integrate QTLs from different maps onto one map.

History of EU-CN Cooperation in Rapeseed Research

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2000s

The next decade witnessed the cooperation of EU-CN scientists in drawing QTL maps and densifying molecular markers on the QTL maps of rapeseed.

2010s

And then comes the cooperation on genome sequencing and evolution analysis of the U-tringle *Brassica* species.

From QTLs to Genome Sequencing

PLANT GENETICS

Early allopolyploid evolution in the post-Neolithic *Brassica napus* oilseed genome

Boulos Chalhoub,[1*†] France Denoeud,[2,3,4*] Shengyi Liu,[5*] Isobel A. P. Parkin,[6†] Haibao Tang,[7,8] Xiyin Wang,[9,10] Julien Chiquet,[11] Harry Belcram,[1] Chaobo Tong,[5] Birgit Samans,[12] Margot Corréa,[2] Corinne Da Silva,[2] Jérémy Just,[1] Cyril Falentin,[13] Chu Shin Koh,[14] Isabelle Le Clainche,[1] Maria Bernard,[2] Pascal Bento,[2] Benjamin Noel,[1] Karine Labadie,[2] Adriana Alberti,[2] Mathieu Charles,[15] Dominique Arnaud,[1] Hui Guo,[9] Christian Daviaud,[16] Salman Alamery,[17] Kamel Jabbari,[1,18] Meixia Zhao,[19] Patrick P. Edger,[20] Houda Chelaifa,[1] David Tack,[21] Gilles Lassalle,[13] Imen Mestiri,[1] Nicolas Schnel,[13] Marie-Christine Le Paslier,[15] Guangyi Fan,[22] Victor Renault,[23] Philipp E. Bayer,[17] Agnieszka A. Golicz,[17] Sahana Manoli,[17] Tae-Ho Lee,[9] Vinh Ha Dinh Thi,[1] Smahane Chalabi,[1] Qiong Hu,[5] Chuchuan Fan,[24] Reece Tollenaere,[17] Yunhai Lu,[1] Christophe Battail,[2] Jinxiong Shen,[24] Christine H. D. Sidebottom,[14] Xinfa Wang,[5] Aurélie Canaguier,[1] Aurélie Chauveau,[15] Aurélie Bérard,[15] Gwenaëlle Deniot,[13] Mei Guan,[25] Zhongsong Liu,[25] Fengming Sun,[22] Yong Pyo Lim,[26] Eric Lyons,[27] Christopher D. Town,[7] Ian Bancroft,[28] Xiaowu Wang,[29] Jinling Meng,[24] Jianxin Ma,[19] J. Chris Pires,[30] Graham J. King,[31] Dominique Brunel,[15] Régine Delourme,[13] Michel Renard,[13] Jean-Marc Aury,[2] Keith L. Adams,[21] Jacqueline Batley,[17,32] Rod J. Snowdon,[12] Jorg Tost,[16] David Edwards,[17,32]† Yongming Zhou,[24]† Wei Hua,[5]† Andrew G. Sharpe,[14]† Andrew H. Paterson,[9]† Chunyun Guan,[25]† Patrick Wincker[2,3,4]†

Oilseed rape (*Brassica napus* L.) was formed ~7500 years ago by hybridization between *B. rapa* and *B. oleracea*, followed by chromosome doubling, a process known as allopolyploidy. Together with more ancient polyploidizations, this conferred an aggregate 72× genome multiplication since the origin of angiosperms and high gene content. We examined the *B. napus* genome and the consequences of its recent duplication. The constituent A_n and C_n subgenomes are engaged in subtle structural, functional, and epigenetic cross-talk, with abundant homeologous exchanges. Incipient gene loss and expression divergence have begun. Selection in *B. napus* oilseed types has accelerated the loss of glucosinolate genes, while

Chalhoub et al., 2014, Science

The genome of the mesopolyploid crop species *Brassica rapa*

The *Brassica rapa* Genome Sequencing Project Consortium

We report the annotation and analysis of the draft genome sequence of *Brassica rapa* accession Chiifu-401-42, a Chinese cabbage. We mapped 41,174 protein coding genes in the *B. rapa* genome, which has undergone genome triplication. We used *Arabidopsis thaliana* as an outgroup for investigating the consequences of genome triplication, such as structural and functional evolution. The extent of gene loss (fractionation) among triplicated genome segments varies, with one of the three copies consistently retaining a disproportionately large fraction of the genes expected to have been present in its

Brassica nigra (B genome) and *B. oleracea* (C genome) having formed the amphidiploid species *B. juncea* (A and B genomes), *B. napus* (A and C genomes) and *B. carinata* (B and C genomes) by hybridization. Comparative physical mapping studies have confirmed genome triplication in a common ancestor of *B. oleracea*[11] and *B. rapa*[12] since its divergence from the *A. thaliana* lineage at least 13–17 MYA[6,7,13].

Using 72× coverage of paired short read sequences generated by Illumina GA II technology and stringent assembly parameters, we assembled the genome of the *B. rapa* ssp. *pekinensis* line Chiifu-401-42 and analyzed the assembly (Online Methods and Supplementary Note)

Wang et al., 2011, Nat Genet

Subgenome parallel selection is associated with morphotype diversification and convergent crop domestication in *Brassica rapa* and *Brassica oleracea*

Feng Cheng[1,7], Rifei Sun[1,7], Xilin Hou[2,7], Hongkun Zheng[3,7], Fenglan Zhang[4,7], Yangyong Zhang[1], Bo Liu[1], Jianli Liang[1], Mu Zhuang[1], Yunxia Liu[1], Dongyuan Liu[3], Xiaobo Wang[1], Pingxia Li[1], Yumei Liu[1], Ke Lin[5], Johan Bucher[5], Ningwen Zhang[5], Yan Wang[1], Hui Wang[1], Jie Deng[1], Yongcui Liao[1], Keyun Wei[1], Xueming Zhang[1], Lixia Fu[1], Yunxiao Zhu[1], Baleng Li[1], Chenchenng Cai[1], Shujiang Zhang[1], Chifen Zhang[1], Fei Li[1], Hui Zhang[1], Jiyang Zhang[1], Qing Guo[1], Zhiyuan Liu[1], Jin Liu[1], Chao Sun[1], Yuan Ma[1], Haijiao Zhang[1], Yang Cui[1], Micheal R Freeling[6], Theo Borm[5], Guusje Bonnema[1,5], Jian Wu[1] & Xiaowu Wang[1]

Brassica species, including crops such as cabbage, turnip and oilseed, display enormous phenotypic variation. *Brassica* genomes have all undergone a whole-genome triplication (WGT) event with unknown effects on phenotype diversification. We resequenced 199 *Brassica rapa* and 119 *Brassica oleracea* accessions representing various morphotypes and identified signals of selection at the mesohexaploid subgenome level. For cabbage morphotypes with their typical leaf-heading trait, we identified four subgenome loci that show signs of parallel selection among subgenomes within *B. rapa*, as well as four such loci within *B. oleracea*. Fifteen subgenome loci are under selection and are shared by these two species. We also detected strong subgenome

Cheng et al., 2016, Nat Genet

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

Jinghua Yang[1–3,11], Dongyuan Liu[4,11], Xiaowu Wang[5,11], Changmian Ji[4,11], Feng Cheng[5,11], Baoning Liu[4], Zhongyuan Hu[1–3], Sheng Chen[6], Deepak Pental[7], Youhui Ju[4], Pu Yao[4], Xuming Li[4], Kun Xie[4], Jianhui Zhang[4], Jianlin Wang[8], Fan Liu[9], Weiwei Ma[1], Jannat Shopan[1], Hongkun Zheng[4], Sally A Mackenzie[10] & Mingfang Zhang[1–3]

The *Brassica* genus encompasses three diploid and three allopolyploid genomes, but a clear understanding of the evolution of agriculturally important traits via polyploidy is lacking. We assembled an allopolyploid *Brassica juncea* genome by shotgun and single-molecule sequencing and integrated genomic and genetic maps. We discovered that the subgenomes of *B. juncea* and *Brassica napus* each had independent origins. Results suggested that subgenomes of *B. juncea* were of monophyletic origin and evolved into vegetable-use and oil-use subvarieties. Homoeolog expression dominance occurs between subgenomes of allopolyploid *B. juncea*, in which differentially expressed genes display more selection potential than neutral genes. Homoeolog expression dominance in *B. juncea* has facilitated selection of glucosinolate and lipid metabolism genes in subvarieties used as vegetables and for oil production. These homoeolog expression dominance relationships among Brassicaceae genomes have contributed to selection response, predicting the directional effects of selection in a polyploid crop genome.

Yang et al., 2016, Nat Genet

French scientists dominated the sequencing of *Brassica napus* genome, whilst Chinese scientists sequenced the genomes *Brassica oleracea, Brassica juncea* and *Brassica rape.* We can be very impressed by the author list showing the close and efficient cooperation between European and Chinese scientists.

The Challenges EU-CN Scientists Facing

The opportunities:

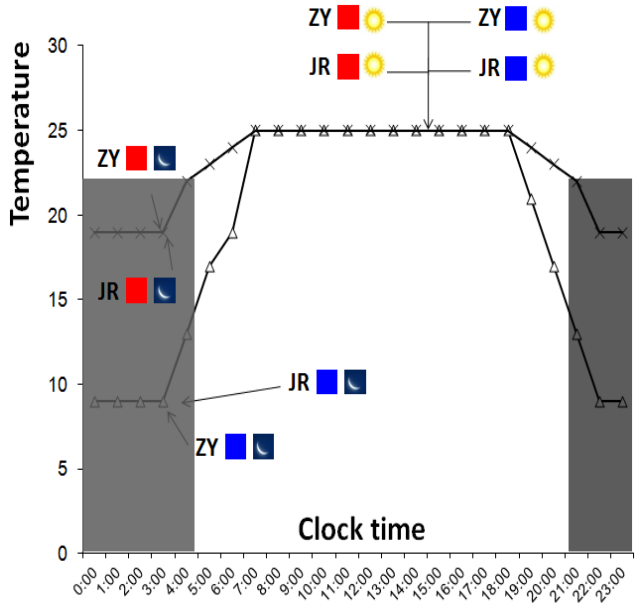
The advent of the new era of plant genomics brings along opportunities for the breakthrough of rapeseed improvement as well as for coping with a variety of challenges, which include

The challenges include :

- Global climate change,
- Narrowed genetic diversity,
- Degradation of arable land, deficiency of P and N , etc.

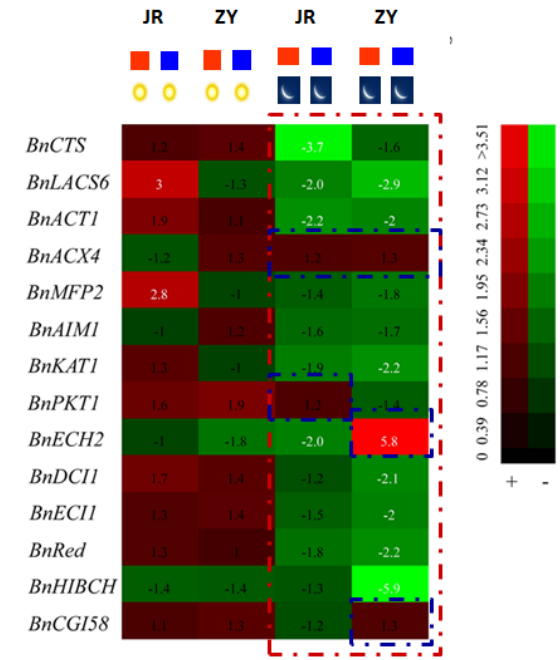
The challenges seriously demand for new strategies towards a sustainable development of rapeseed production in both CN and EU.

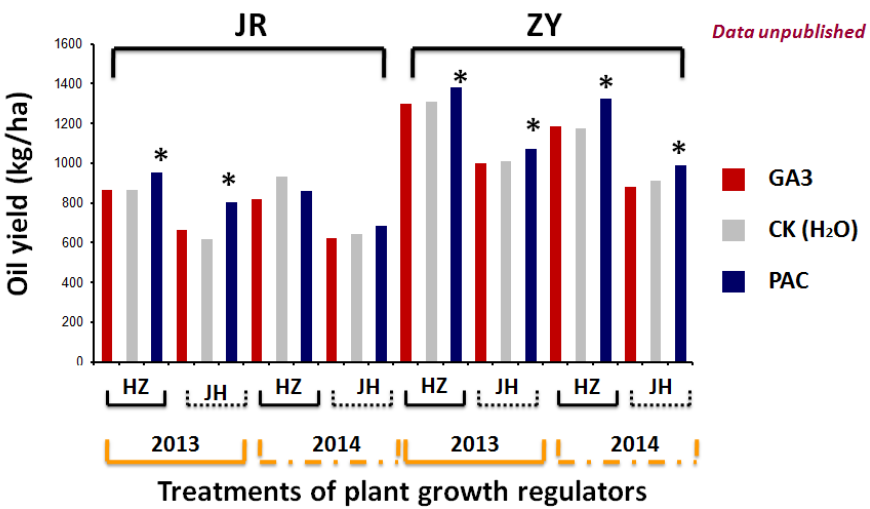
On-going Research in My Lab

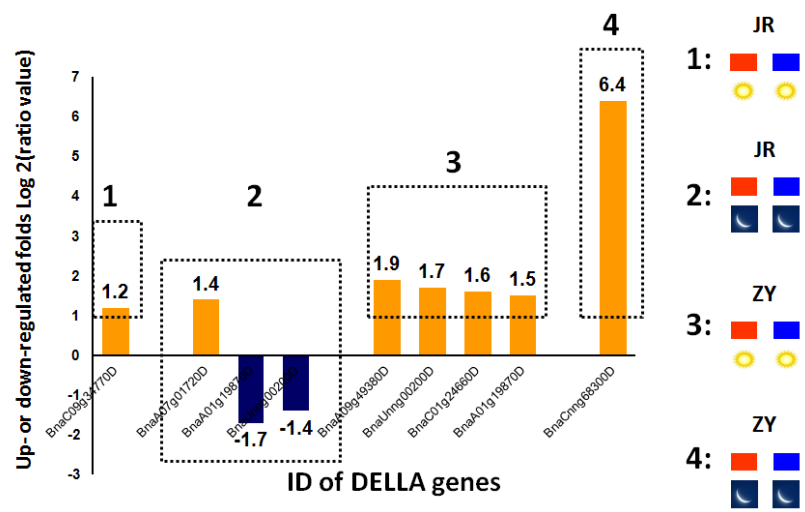


Reads coverage on rapeseed genome

	0%-80%	80%-90%	90%-100%
A1	23901(40.3%)	7089(11.9%)	28333(47.8%)
A2	22120(37.3%)	6920(11.6%)	30366(51.1%)
B1	22997(38.1%)	7147(11.9%)	30131(50.0%)
B2	22269(36.1%)	6958(11.3%)	32498(52.6%)
C1	22731(38.2%)	7039(11.8%)	29802(50.0%)
C2	23044(38.3%)	6912(11.5%)	30213(50.2%)
D1	21253(35.3%)	6694(11.1%)	32238(53.6%)
D2	25190(43.6%)	7070(12.2%)	25523(44.2%)
E1	23803(39.5%)	7129(11.9%)	29198(48.6%)
E2	23517(39.9%)	7177(12.2%)	28270(47.9%)
F1	21570(34.2%)	6835(10.8%)	34686(55.0%)
F2	25128(43.1%)	7094(12.2%)	26057(44.7%)
G1	21946(35.5%)	6880(11.2%)	32877(53.3%)
G2	23398(38.9%)	7010(11.7%)	29694(49.4%)
H1	22740(37.1%)	7287(11.9%)	31269(51.0%)
H2	22585(36.3%)	7189(11.6%)	32392(52.1%)



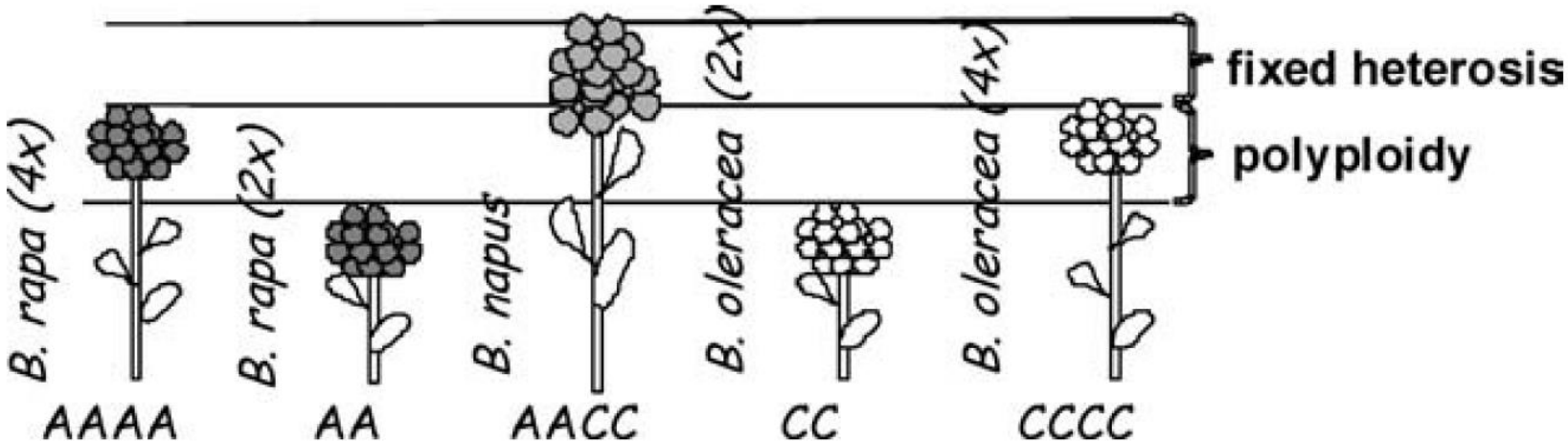




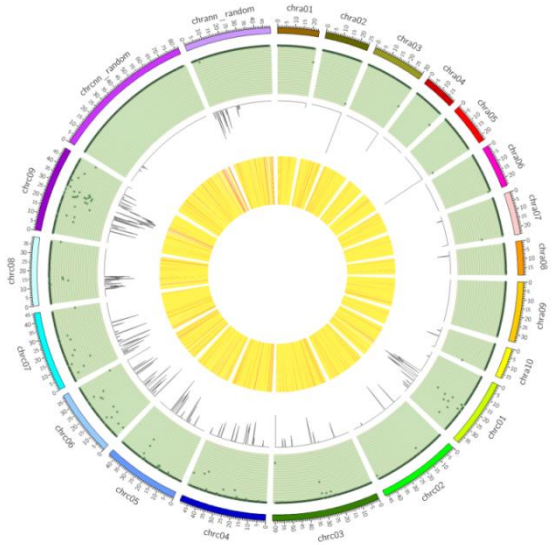
Zhou et al., 2016, data unpublished

In my lab, we are investigating the negative effect of high NT (caused by global warming) on the reduction of rapeseed SOC, and we are looking for effective solution to repress lipid decomposition arose from high NT.

On-going Cooperation with EU Scientists in My Lab

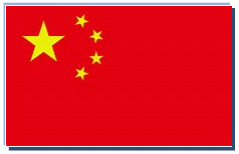


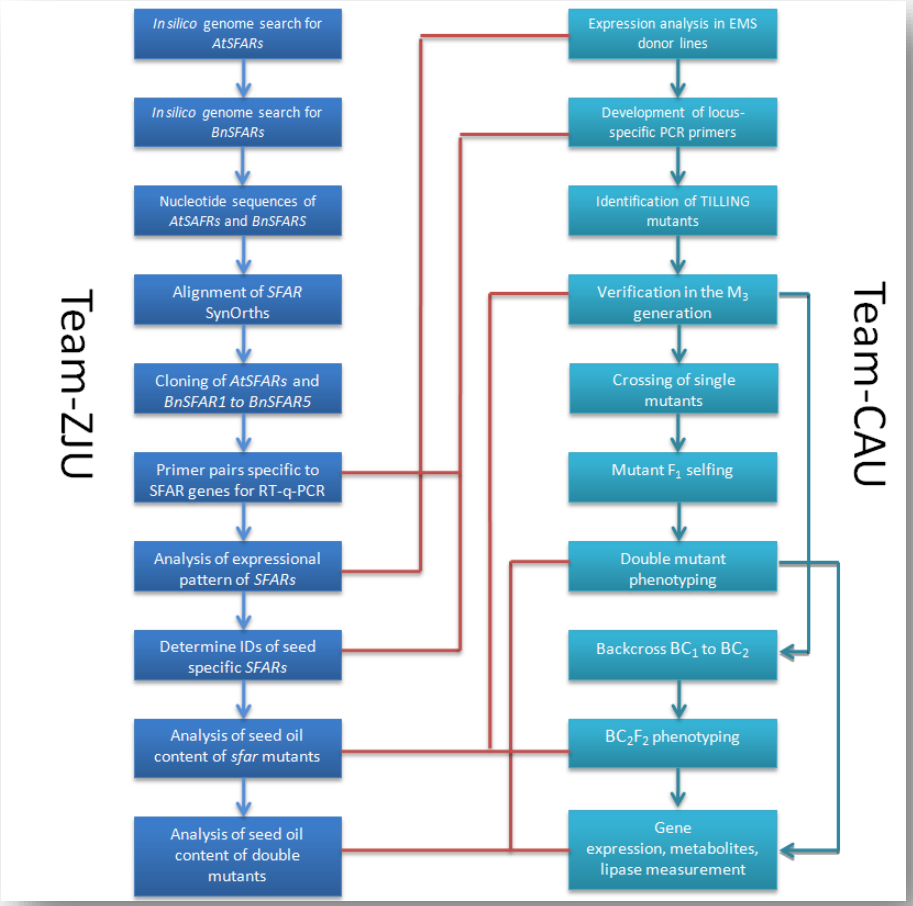
A2A2 (No.2) | A2A2C3C3 (No.15) | C3C3 (No.6)



We are also closely cooperating with University Goettingen to investigate fixed heterosis in artificially re-synthesized rapeseed at genomic, transcriptome and epigenetic levels.

On-going Cooperation with EU Scientists in My Lab





TILLING and Editing *SFARs* Genes

项目批准书
Bewilligungsschreiben

根据中德专家评审结果，浙江大学的蒋立希教授与德国 Christian-Albrechts-University Kiel 的 Christian Jung 教授提出的申请书已获批准。项目号为：GZ 1099。详见中德双方的批准信。

Aufgrund der Stellungnahme chinesischer und deutscher Gutachter ist der gemeinsame Antrag von Prof. Dr. Christian Jung, Christian-Albrechts-University Kiel, und Prof. Dr. Lixi Jiang, Zhejiang University, bewilligt worden. Geschäftszeichen: GZ 1099. Genaueres entnehmen Sie bitte dem chinesisch-deutschen Bewilligungsschreiben.

中德科学中心
2015 年 11 月 2 日
Chinesisch-Deutsches Zentrum
für Wissenschaftsförderung
02.11.2015

collaborating with University Kiel in TILLING and editing the genes which were named as *Seed Fatty Acid Reducers* (*SFARs*)

The Challenges EU-CN Scientists Facing

Hangzhou, China, April 3-7, 2013

As Chinese partner, I organized two rapeseed workshops between China and Germany, to figure out the challenges that we are facing.

The first workshop took place Hangzhou 3 years ago.

The Challenges EU-CN Scientists Facing

Kiel, Germany, May 22-25, 2016

And the second one was held in Kiel just a few months ago.

Conclusions of two Sino-German rapeseed meeting

After discussion on the workshops, Chinese and German scientists agreed to take actions to :

1. To establish a shared platform to exchange genotyping and phenotyping data from rapeseed populations, diversity sets and mutant collections, as well as tools for bioinformatics analysis.

2. To sustain rapeseed yield through hybrid development and basic research to investigate the functional and genomic bases of heterosis, including the fixed-heterosis in amphiploidy rapeseed.

3. To introduce new alleles from other Brassica species, in order to increase the genetic diversity in rapeseed (*Brassica napus*).

I would suggest these strategies to cope with the challenges for a sustainable rapeseed production, in the background of global climate change.

The campus of Zhejiang University

Thank you for your attention !