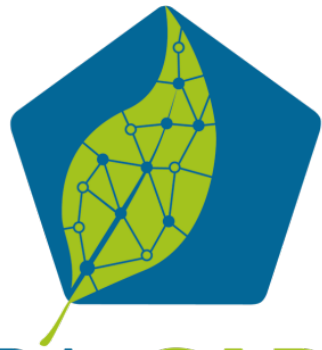


The ERA-CAPS “ABCEED” CONSORTIUM

- Michael Bevan, John Innes Centre, UK
- Loic Lepiniec, INRA Versailles, FR
- Michael Lenhard, Univ. Potsdam, DE



ERA-CAPS

ERA-NET for Coordinating
Action in Plant Sciences



Project Summary

The project integrates work in *Arabidopsis thaliana*, *Capsella sp.*, *Camelina sativa* and *Brassica napus*, aiming to identify genetic variation and genes controlling seed number, seed size, and seed quality traits.

Work Packages

1. Control of organ and seed size in *Arabidopsis* and *B. napus*
2. Control of ovule number in *Capsella* and *Arabidopsis*
3. Seed composition and quality in *Arabidopsis*, *Camelina* and *B. napus*

Deliverables

Identification of genetic variation and candidate genes controlling seed number, size and composition in *B. napus*

Integrated multi-scale phenotyping of seed maturation in Brassicaceae

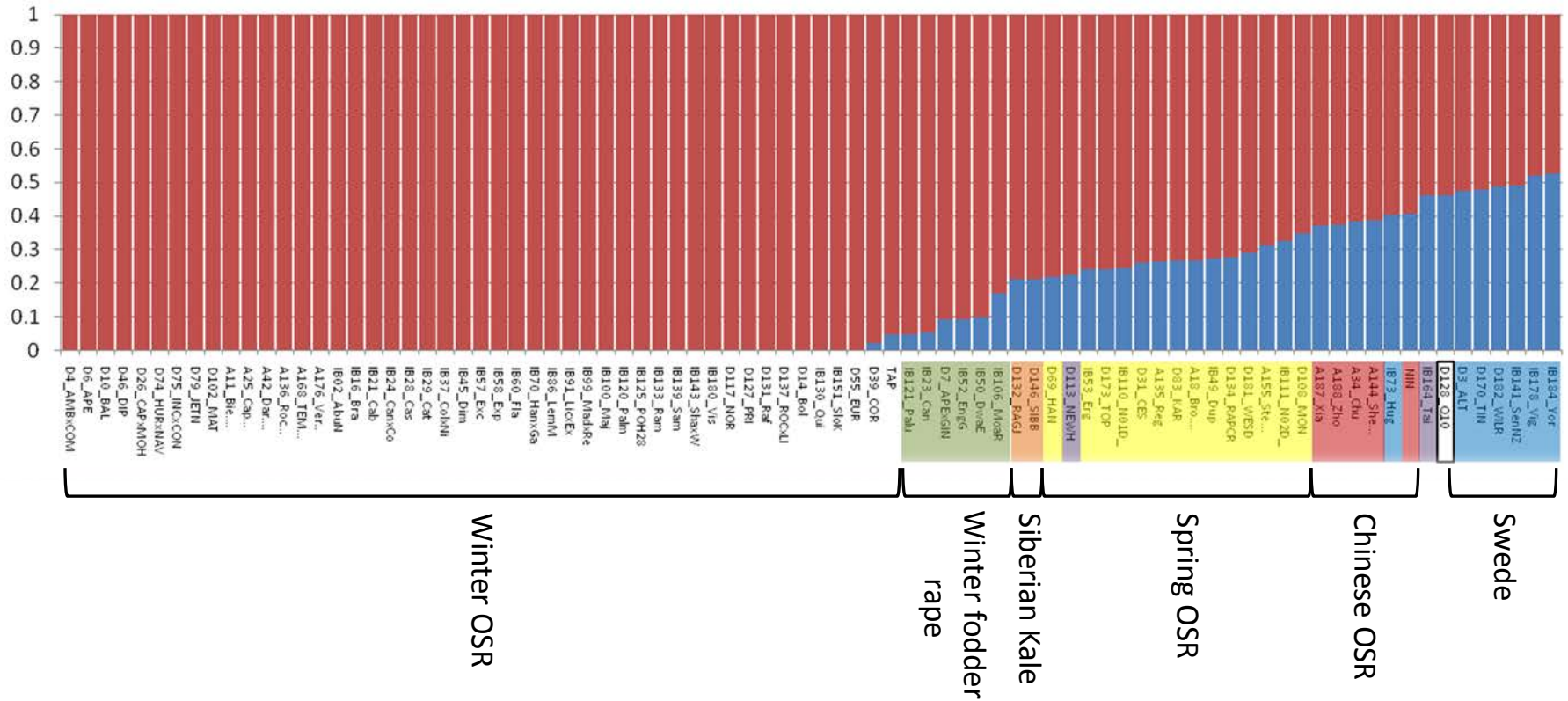
Comparative analyses of gene function in seed formation in Brassicaceae

**Diversity panel of 100 *B. napus* accessions screened for yield traits
(In collaboration with Rachel Wells, JIC)**

- * Seed weight
- * Number of pods
- * Seeds per pod
- * Pod length
- Seed quality traits



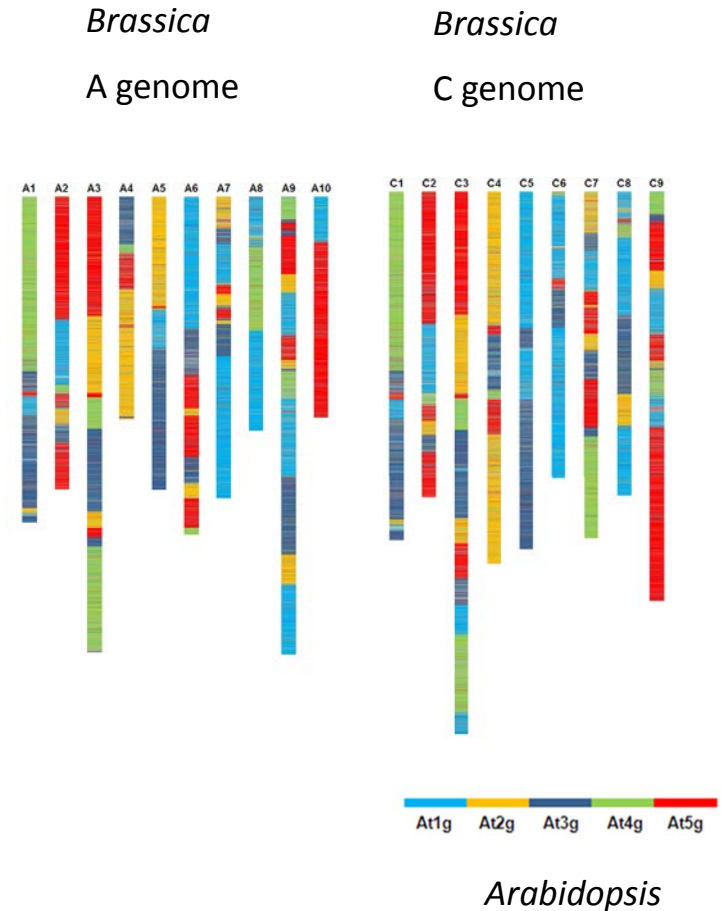
Natural variation in rapeseed – Association transcriptomics



Distribution of SNP alleles to show population structure and relatedness

Marker order

- Pseudomolecules
- Developed using *B. rapa* and *B. oleracea* genome sequences
- Genome assembly corrected via:
 - Unigene order in Tapidor x Ningyou7 high density transcriptome SNP map (9,169 unigenes)
 - Synteny with *A. thaliana*



Current work on seed weight per pod locus

- Sequencing the locus and flanking region in multiple variants



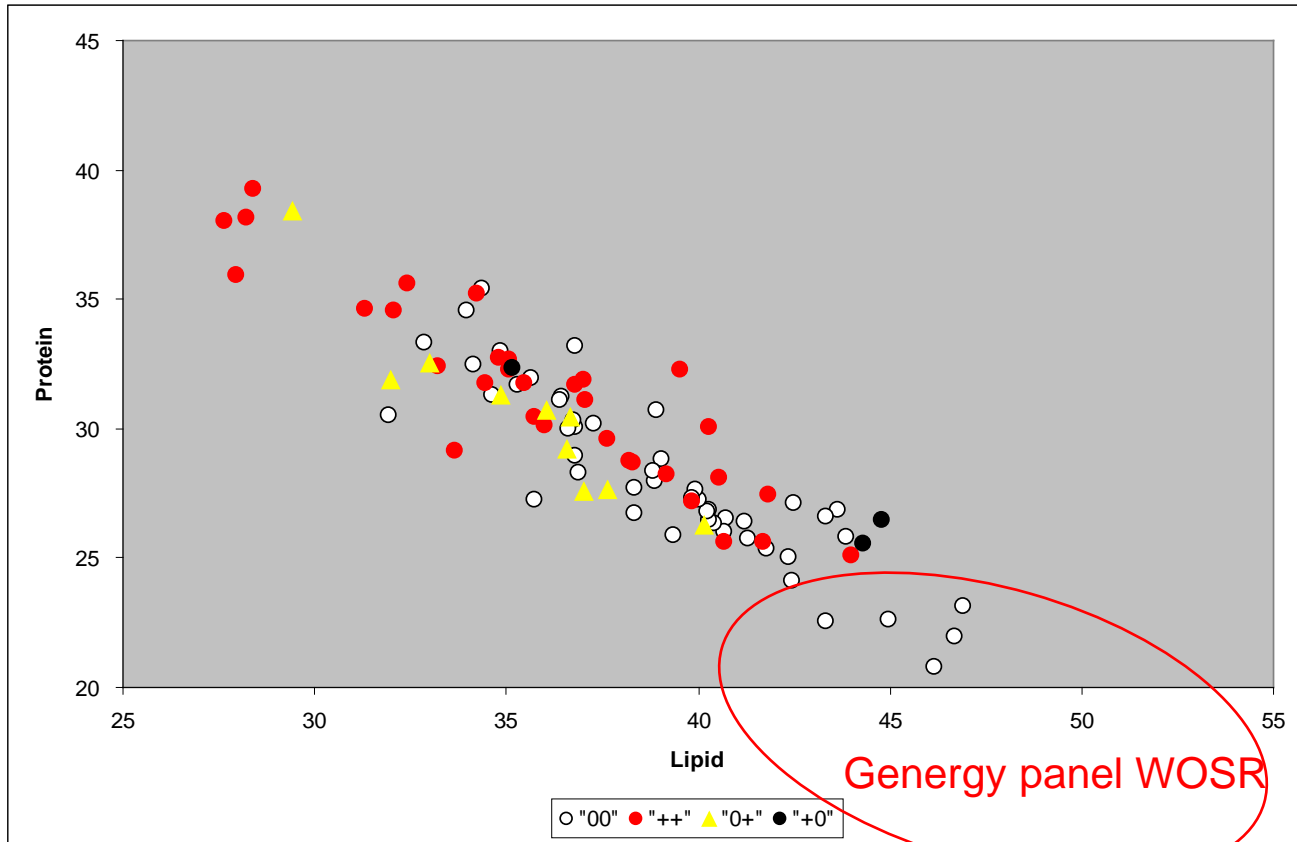
- Assessment of phenotypes in *Arabidopsis* knockout lines
- What happens when we drive the *Arabidopsis* gene with the proposed varying promoters of *B. napus*?
- RNAseq of developing seeds in multiple lines



NIRS analyses performed at INRA Rennes.

- **Humidity**
- **lipid content L (dry matter)**
- **protein content P (dry matter)**
- **glucosinolate content GLS**
- **erucic acid content 22:1**
- **Other fatty acids not reliable**

There is a negative correlation between seed lipid and protein content in the population



Protein x lipid correlation
Negative correlation between L and P contents ($r = 0.91$)
« 00 » exhibit the highest L content

Enhancing seed size and seed oil content in *Camelina sativa*, a promising oilseeds crop

Camelina (false flax) is an oilseed crop that requires genetic improvement to increase yield

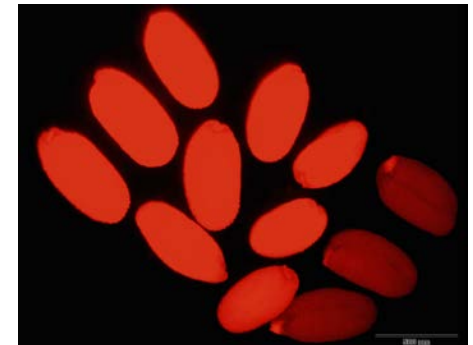
- Very high omega 3 fatty acids
- High tocopherol
- High polyunsaturated fatty acids
- Excellent cooking properties
- An excellent jet fuel!

Identification of Arabidopsis seed development genes in Camelina

The candidate genes are: *LEC1* (at1g21970), *LEC2* (at1g28300), *ABI3* (at3g24650), *FUSCA3* (at3g26790), *NF-YC2* (at1g56170), *WRI1* (at3g54320) and *SHB1* (at4g25350), *IKU1* (at2g35230), *MEE* (at3g46330), *IKU2* (at3g19700) and *AP2* (at4g36920).

The identified AFL Camelina genes(*ABI3*, *FUS3*, *LEC1* and *LEC2*) will be first cloned (cDNA) into expression vectors and then tested in *Physcomitrella patens* using Oleosin promoter pOle1:::GFP for functionality (i.e. transcriptional activation of the promoter, ability of synergistic effect). Genes displaying activity in *Physcomitrella* will be used to complement Arabidopsis mutants and overexpressed in Camelina wild type.

The overexpression of Arabidopsis IKU2 results in 30% increase in seed size and total oil content in Arabidopsis transgenic seeds.



Selfing *Capsella* species have reduced flower size

Capsella grandiflora

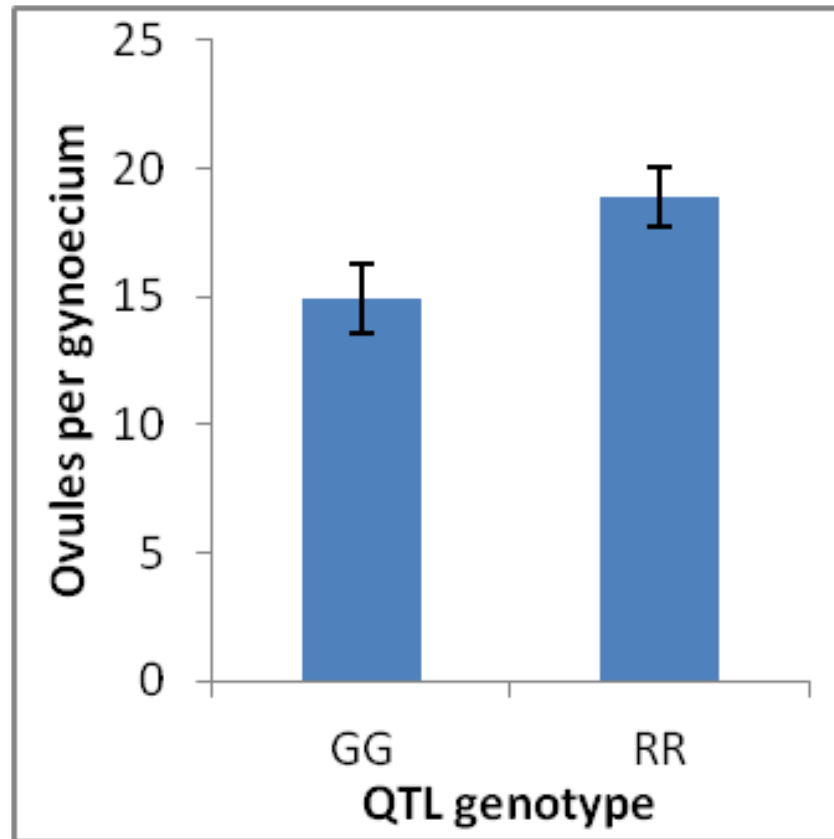
Capsella rubella

Capsella orientalis



Measurements of seed composition from subset of *C. grandiflora* x *C. rubella* recombinant inbred lines (Sicard et al., 2011) is ongoing at INRA Versailles.

Isolating genes for ovule number



Mendelization of QTL F, one of two QTL for ovule number (Slotte et al., 2012)

Consortia meetings

- April 2014 Versailles
- May 2015 Potsdam
- May- June 2016 London

Joint activities

- GWAS of *B. napus* lipid and protein composition
- RNAseq of developing seeds
- Detailed lipid and seed protein composition
- Regulatory network function in seed development