

# Brassica Genetics & Genomics

## Research Program at INRA

Michel RENARD

INRA Research Program, Saskatoon, December 10th, 2009



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## Brassica Group

- Anne-Marie Chèvre
  - Anne Laperche
  - M. Renard
  - Régine Delourme
  - Maria Manzanarès
  - Antoine Gravot
  - Alain Bouchereau
  - Nathalie Nesi
  - Mathilde Orsel
  - Françoise Le Cahérec
  - .....
- 40 persons from**  
**- INRA**  
**- Agrocampus Ouest**  
**- University of Rennes**

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## Actors & Partnership

- Arabidopsis group in Versailles
- Other INRA Divisions
- Universities, CNRS, ....
- Biogenouest core facilities
- Promosol, Sofiprotéol
- Cetiom, Onidol
- GIE Colza & Procolza
- Génoplante & Biogemma
- Geves
- Ademe, ...



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# Genetic Resources

Anne Laperche & M. Renard

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## National Center for Brassica Genetic Resources



### National Collection

*B. oleracea* : 563 accessions  
*B. napus* 58 accessions

Evaluation and multiplication

### Network Collection

*B. napus* : 18 accessions

### INRA Collection

*B. oleracea* : 479 accessions  
*B. napus* : 726 accessions  
*B. carinata* : 57 accessions  
*B. nigra* : 3 accessions  
*B. juncea* : 130 accessions

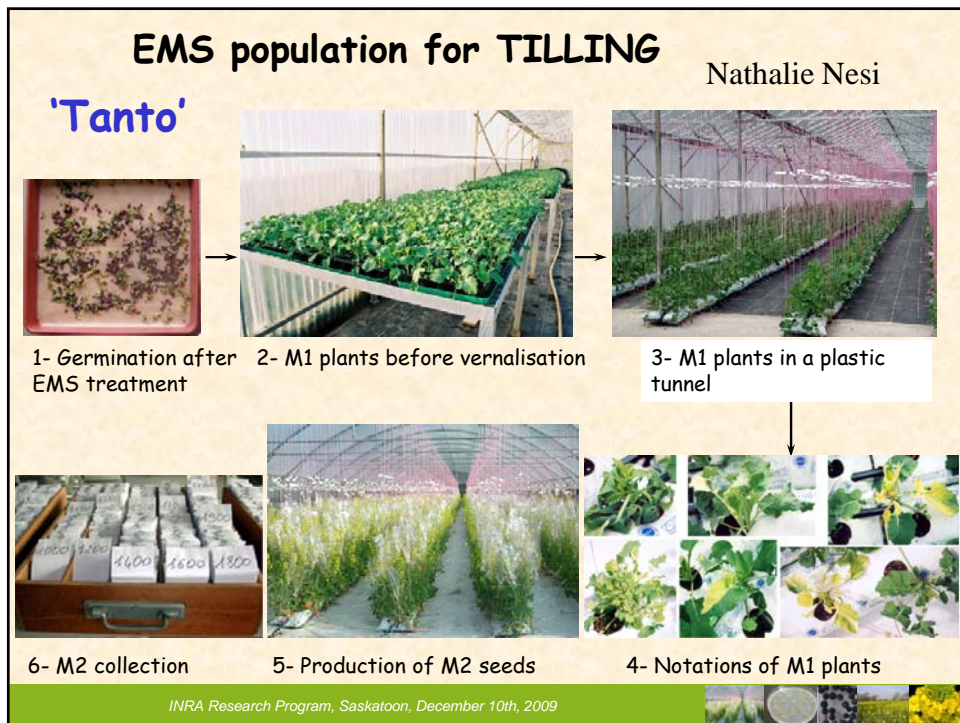
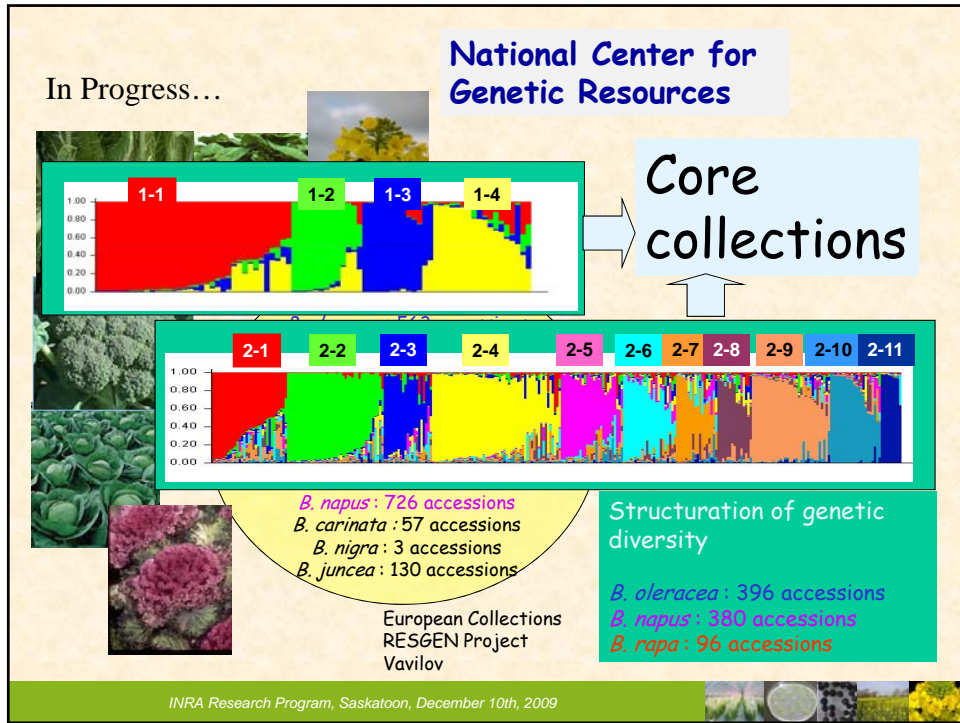
### Structuration of genetic diversity

*B. oleracea* : 396 accessions  
*B. napus* : 380 accessions  
*B. napus* : 96 accessions

European Collections  
RESGEN Project  
Vavilov

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In Progress...

➤ **Development of genetic materials**

*e.g.* Populations for Nested Association Mapping

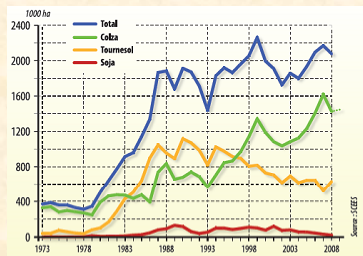
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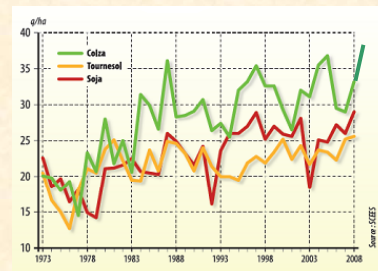
**Oilseed rape : an increasing economic importance**

WOSR production in France:

**Evolution of acreage**



**Evolution of yield**



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## Main traits of interest

- **Oil Yield**
- **Abiotic stress resistance: nitrogen, water**
- **Disease Resistance: blackleg, clubroot, broomrape**

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## Three Brassica teams

- Genome organisation
- Oil yield under nitrogen and water limitations
- Disease resistance

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# Genome Organisation team

Anne-Marie Chèvre

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# Genome Organisation

## 1) Homologous & Homoeologous Recombination

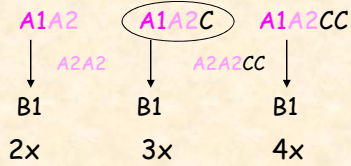
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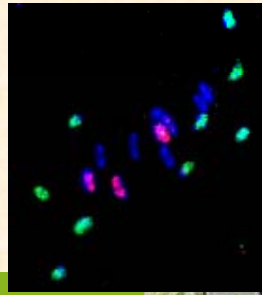
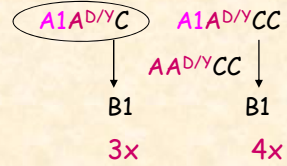
## Homologous recombination: analysis of A genome

Analysis of the A genome : Production of F1 hybrids at different ploidy levels (2x/3x/4x) between the same genotypes and analyses of the homologous recombination rates.

Effect of the ploidy level (*B.rapa*)

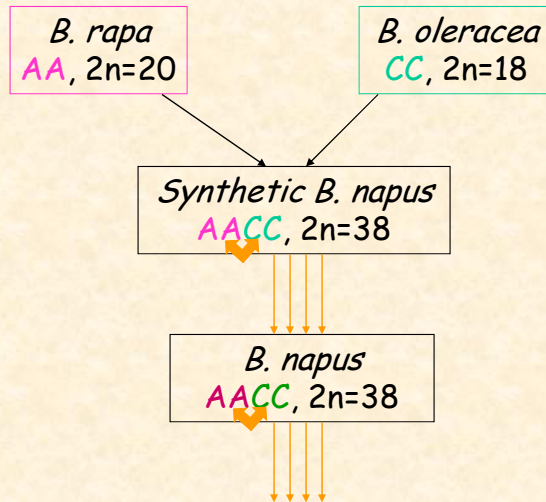


Effect of the genotype (*B.rapa*/*B.napus*)



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## Homoeologous recombination



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## Results & Perspectives

Homologous recombination between A genome : AA<AAC<<AAC  


-> introgression can be restricted to the genes of interest

- Impact of number and nature of the C chromosomes?
- What about CCA hybrids?

Homoeologous recombination between A and C genomes:

during stabilisation of synthetic oilseed rape

-> homeologous recombination plays a key role

-> its level depends on genotype, cytoplasm and gametes

- Nature and frequency of structural rearrangements?
- Impact of functional regulation?

between A and C genomes in *B.napus*

-> control by *PrBn* and a network of genes

-> NRT are induced on different chromosomes

- Genes implied in homoeologous recombination control?

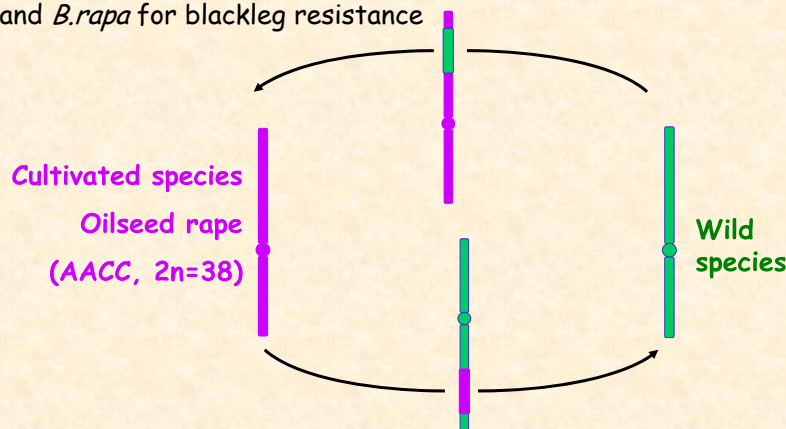
- Use of the genetic control to generate a diversity in *B.napus*

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## Use of results on homologous and homeologous control

Gene introgression from *B.nigra* (BB, 2n=16), *B.juncea* (AABB, 2n=36) and *B.rapa* for blackleg resistance



Gene flow from transgenic oilseed rape to wild radish

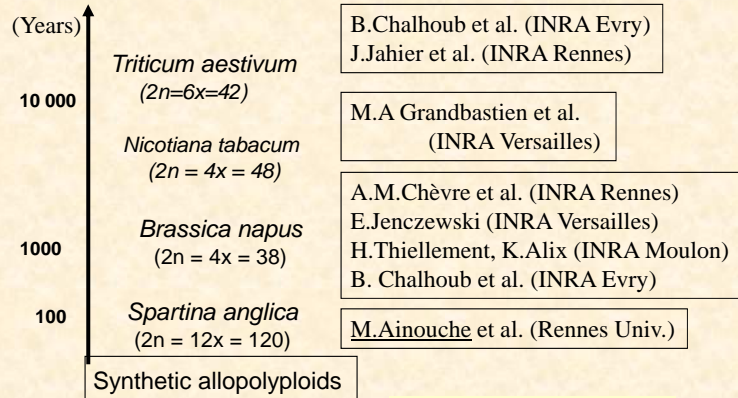
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**French polyploidy network (ANR)  
How do these mechanisms arise at different time scales?**



**LONG TERM EVOLUTION, DIVERGENCE**



**NEOPOLYPLOIDS**

-> in project:  
European network

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2) Sequencing of the highly duplicated *B. napus* genome

(ANR: 2010-2013)

Boulos Chalhoub



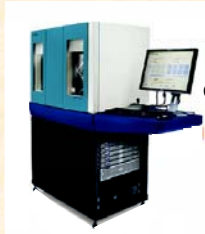
Coordination with national efforts:  
-French Brassica Network



Coordination with international efforts:  
-Multinational *Brassica* Genome Project consortium  
-EU coordination and collaboration (I. Bancroft, Guy Barker)  
-US and Canada coordination and collaboration (C. Town, Chris Pires, Isobel Parkin)  
*B. Rapa* and *B. oleracea*

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## Sequencing of a winter *B. napus* cv. (strategy and timeline)



Genome Sequencer FLX



Roche / 454

Sequencing (50X;  
Solexa) of 72 pb  
reads & pair-ends

20X (400) bp reads

- 1- Sequencing and sequence assembly Year 1 (2010)
- 2- Alignment to *B. rapa* and *B. oleracea* genome sequences Year 1 (2010)

Collaborations    *B. rapa* cv Chiifu: 5X genome sequencing  
                          *B. oleracea* cv B0001 5X genome sequencing

- 3- Anchoring on dense genetic maps: Years 1, 2 and 3

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## Dense genetic maps

Resequencing of 7-8 other genotypes (P1, P3: Régine Delourme  
P4: Brunel) (year 1, 2 and 3): Solexa paired ends



Illumina / Solexa  
Genetic Analyzer

(Parents of 4 segregating populations)

Develop and Map more than 10000  
SNPs that will help in anchoring of  
sequence contigs on genetic maps  
as well as their wide use in oilseed  
rape breeding programs.

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# Rapeseed yield under nitrogen and water limitations

## team

Alain Bouchereau  
Nathalie Nési ; Françoise Le Cahérec

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## Objectives

**Goals : Improvement of the energetic yield of rapeseed production**

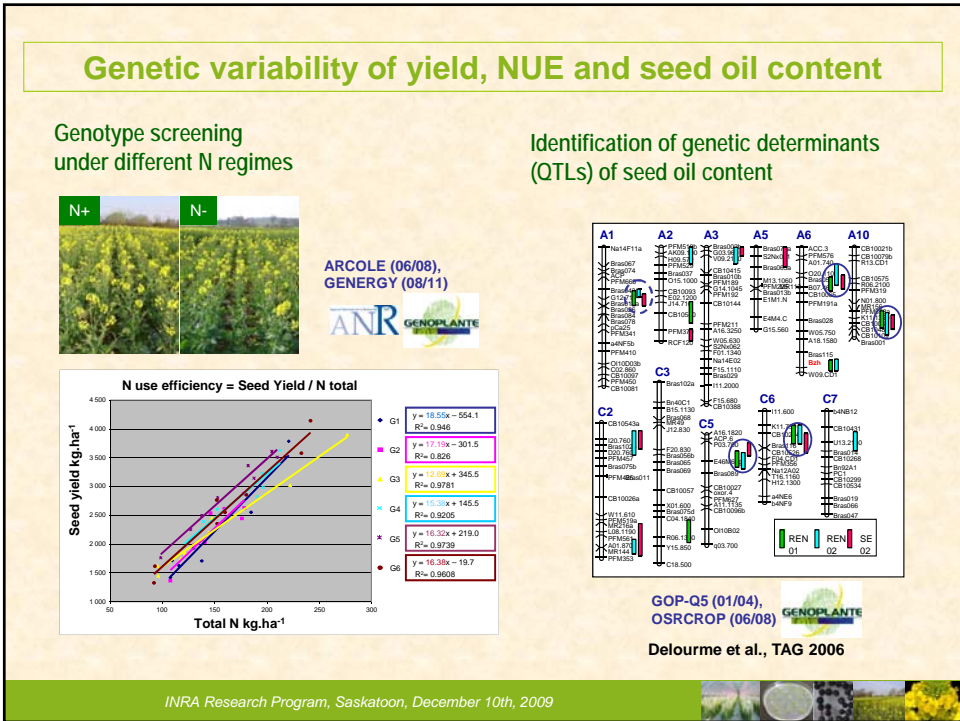
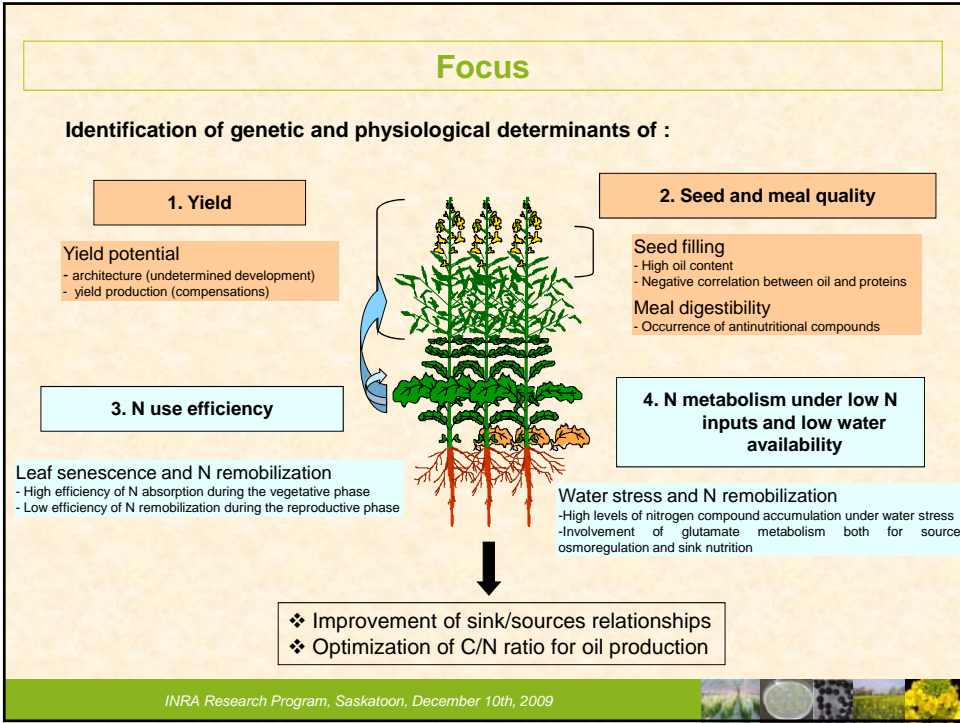
- ❖ Increasing oil production
- ❖ Decreasing nitrogen and water inputs
- ❖ Reducing energetic cost of oil extraction
- ❖ Preserving quality of co-products

**Global objective :**

**To optimize oil yield under limited nitrogen and water regimes and to ensure co-products quality**

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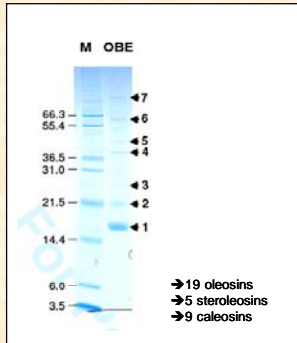




## Seed and meal quality

Oil extractability (APBV, CB, CETIOM)

Proteomic description of oleosome composition in rapeseed

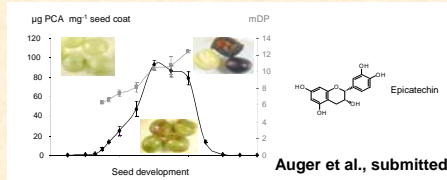


GENOBODIFER  
ANR GENOPLANTE

Jolivet et al., Proteomics 2009

Valorisation of co-products (APBV, URC, IJPB)

Identification of flavonoids in seed coats (LC-ESI-MS<sup>n</sup>)



Auger et al., submitted

Cloning of candidate genes involved in seed flavonoid metabolism

Orthologues BnTT (12 clones)			
Locus AtTT	Produit	Gènes BnTT	
PART. AUTOMATIQUE	TT1	WIP zinc-finger family	4
	TT4	CHS	> 10
	TT5	CHI	4
	TT6	F3H	2
	TT7	F3'H	1
PART. MANUELLE	TT3	DFR	2
	BAN	ANR	4
	TT10	laccase	> 3
	TT12	MATE-transporter	2
	TT2	MYB transcription factor	2
	TT16	MADS transcription factor	2
	TT8	bHLH transcription factor	2

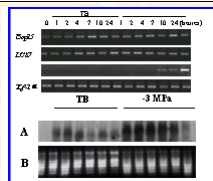
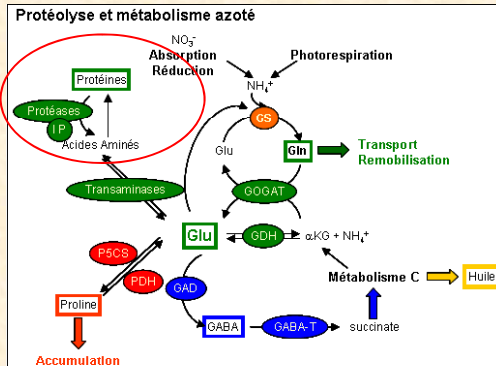
Nesi et al., Plant Cell Rep. 2009  
Auger et al., Planta 2009

CompGen (04/05)

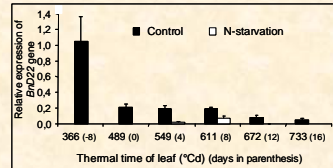
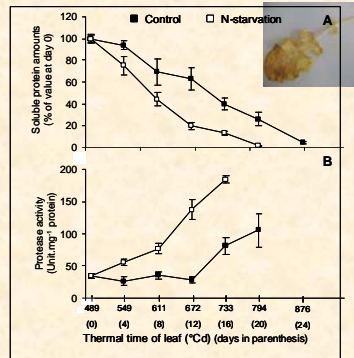
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## N remobilization during leaf senescence

Regulation of proteolysis (APBV, EVA)



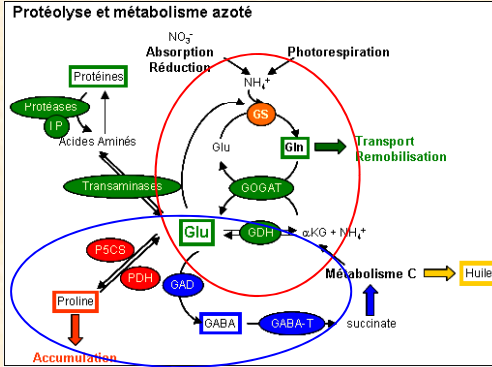
Desclos et al., Plant Physiol., 2008 ; Desclos et al., 2009, in prep.



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## N remobilization during leaf senescence

### Regulation of genes involved in glutamate metabolism



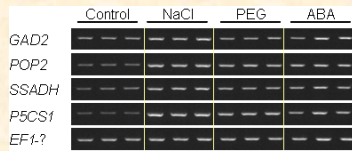
#### Glutamine synthetase BnGS1 :

> 5 genes AtGS → more than 15 genes BnGS1 identified

Anova (p < 0.0001)

	Low N	Old leaves	Flowering time
BnGSR1-2_Y12459			
BnGSR1-1_X76736			
BnGSL2_Y12458			
BnGSL1_X72751			
BnGS1_5			
BnGS1_2		+	
BnGS1_1		+	Transient +
BnGS1_4		+	Transient +
BnGSR2-2_Y12460		+	
BnGSR2-1_X82997		+	
BnGS1_7	+		+
BnGS1_6	+		Transient +

> Differential transcription during senescence



Biosynthesis and catabolism of proline

Biosynthesis and degradation of GABA

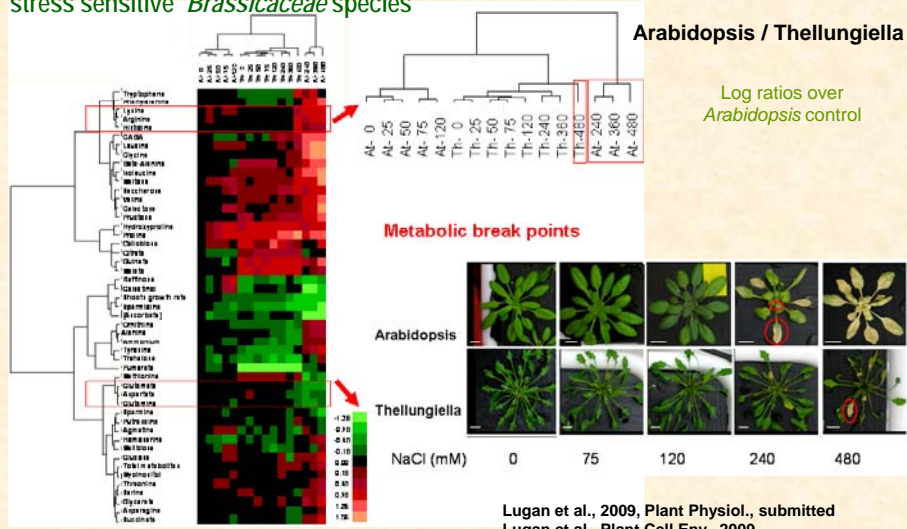
Renault et al., submitted

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## N remobilization during leaf senescence

### Comparative metabolic profiling between water and nitrogen stress tolerant and stress sensitive *Brassicaceae* species



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# Disease resistance team

Régine Delourme & Maria Manzanarès

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## ► Main OSR diseases in France



**Stem canker**  
*Leptosphaeria maculans*  
anamorph *Phoma lingam*



**Alternaria**  
*Alternaria brassicae*



**Sclerotinia**  
*Sclerotinia sclerotiorum*



**Verticillium wilt**  
*Verticillium longisporum*



**Light leaf spot**  
*Pyrenopeziza brassicae*



**Clubroot**  
*Plasmodiophora brassicae*



**Powdery mildew**  
*Erisiphe polygoni*



**Broomrape**  
*Phelipanche ramosa*



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**Clubroot**  
*Plasmodiophora brassicae*



**Powdery mildew**  
*Erysiphe polygoni*



**Broomrape**  
*Phelipanche ramosa*



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## ► Stem canker (*Leptosphaeria maculans*)



Photo R. Delourme  
 Leaf spots

- One of the most important disease worldwide (Europe, Canada, Australia)



Photo B. Delourme  
 Crown necrosis

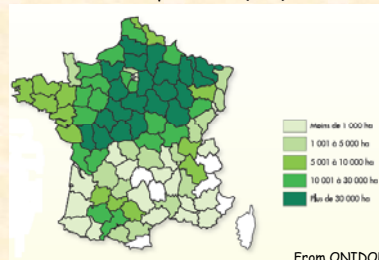
- 5 to 20 % yield losses in France



(photo CETIOM)

- Disease incidence and severity could increase in relation with climatic changes (Evans et al., 2008)

Oilseed rape in France (2008)



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## Genetic resistance to *L. maculans*

- **Qualitative resistance: from seedling stage**

→ in *B. napus*



in related species  
(*B. rapa*, *B. juncea*, *B. nigra*)

many *R/m* genes

Specific: R-Avr inter.  
Easy to overcome

- **Quantitative resistance: at adult stage**

→ in *B. napus* (Jet Neuf...)



Polygenic: many QTL

Partial, not specific?  
Durable

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## Durable management of blackleg resistance

What are & how to associate resistance factors for a durable management of resistance faced to a highly variable pathogen population ?

- Organisation of the resistance genetic factors ?  
Relation specific resistance genes/ quantitative resistance ?
- Evolution of pathogen populations depending on the type of resistance used ?

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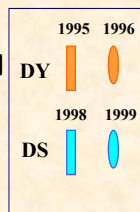
## Genetic analysis of the quantitative resistance



Resistance QTL :  
two progenies

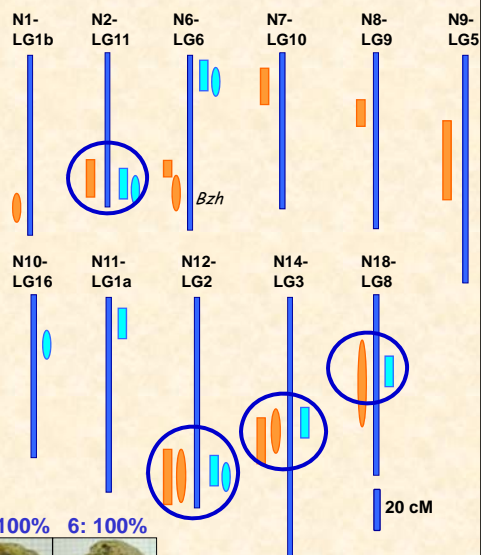
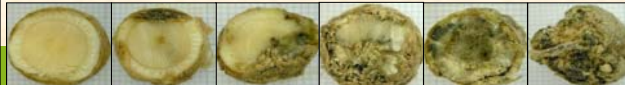
Darmor-bzh x Yudal  
Darmor x Samourai

(Pilet et al, 1998, 2001)



Classes G2 index

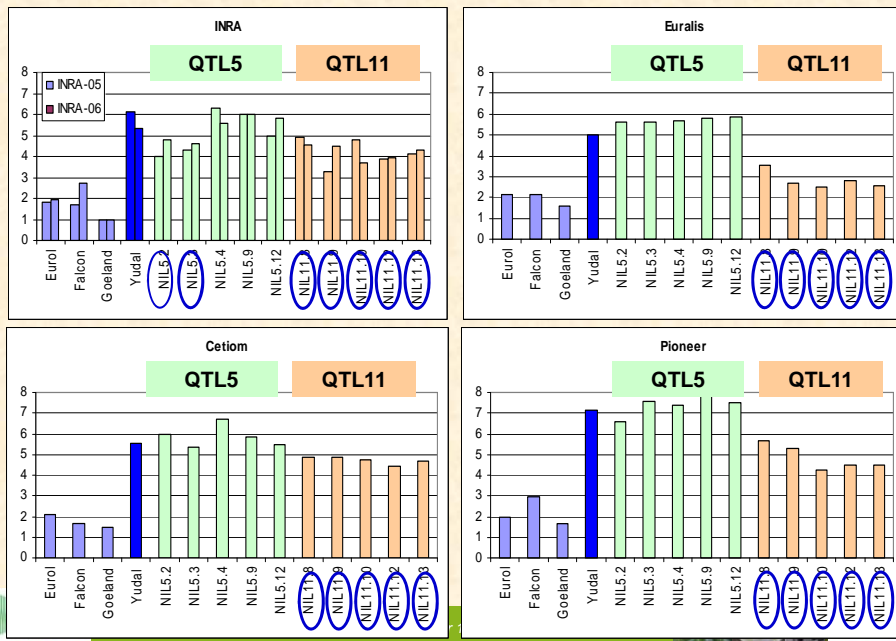
1: 0% 2: <25% 3: <50% 4: <75% 5: <100% 6: 100%



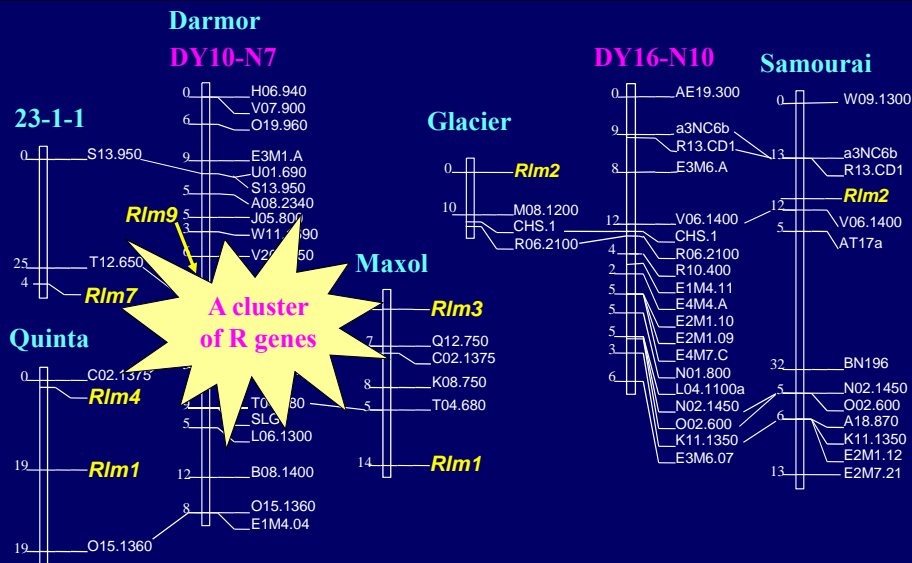
Photos J.N. Aubertot

## Trials in H2005-06: G2 index

(Delourme et al, 2008)



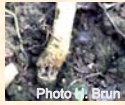
## Localization of *B. napus* *Rlm* genes



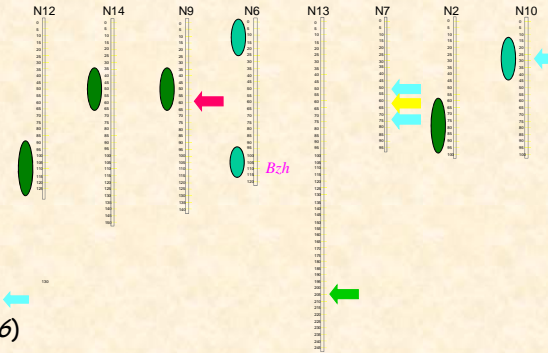
Delourme et al. 2004; 2006

## Localization of *Rlm* genes / QTL for adult resistance (DI)

### Quantitative resistance



QTL



### Specific resistance genes

\* From oilseed rape  
(Delourme et al. 2006)



\* From related species  
*B. nigra*: *Rlm10*

*B. juncea*: *Rlm6*

*B. rapa*: *Rlm1, 7*

(Leflon et al. 2007)

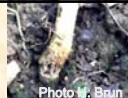
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What are & how to associate resistance factors for a durable management of resistance faced to a highly variable pathogen population ?

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## What about durability?

Overcoming under real cropping conditions (3 years) of :

- *Rlm1*, a *B.napus* specific gene in France (Rouxel et al 2003)
- *LepR3*, a *B.rapa* specific gene in Australia (Li et al 2003)

Experimental design to assess potential durability (Brun et al. 2000)

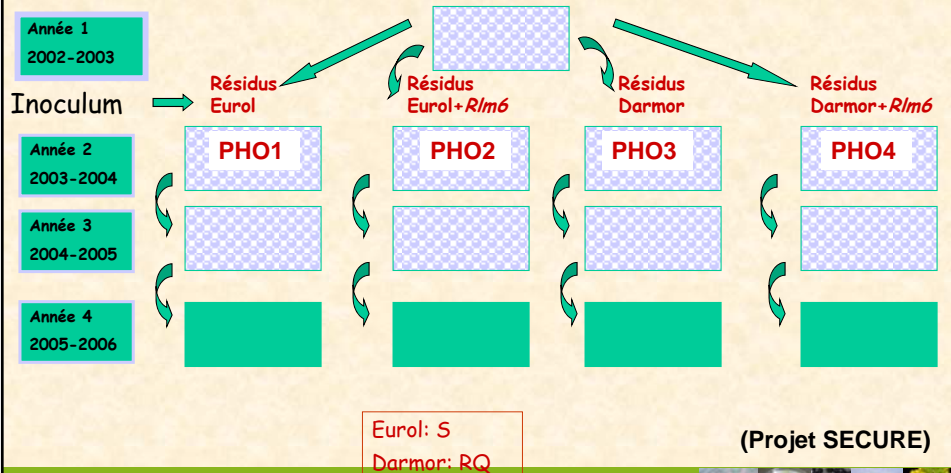
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## Recurrent Selection in the field

(Brun et al 2000)

Local Inoculum : Oilseed rape residues



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UMR BiO3P-Rennes

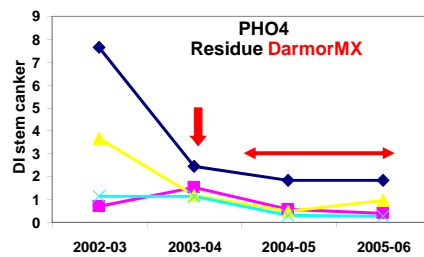
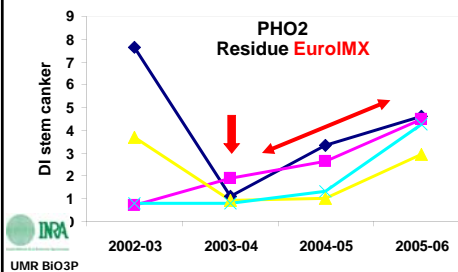
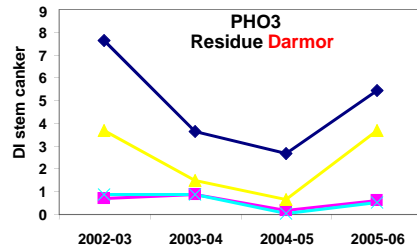
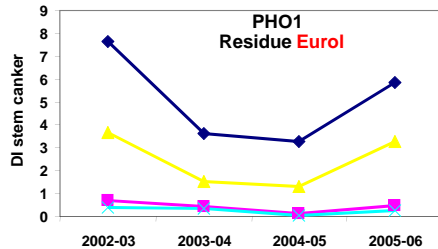
## Effect of genetic background?

### Stem base Canker over years

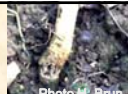
(Brun et al, 2007)

MX = *Rlm6*

◆ EuroI  
 ■ EuroIMX  
 ▲ Darmor  
 ◆ DarmorMX



INRA  
 UMR BIO3P



## What about durability?

Overcoming under real cropping conditions (3 years) of :

- *Rlm1*, a *B.napus* specific gene in France (Rouxel et al 2003)
- *LepR3*, a *B.rapa* specific gene in Australia (Li et al 2003)

Experimental design to assess potential durability (Brun et al. 2000)

- The results of the potential durability obtained experimentally for *Rlm6* were close to the results of the overcoming of *Rlm1* and *LepR3* resistances under commercial deployment
- Association of quantitative and qualitative resistance improved potential durability

In progress... Strategies for  
 Management in time and space

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## New targets for the future?

- Heterosis
- Multi-trait resistance
- Insect resistance?

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## THANK YOU



Conventional



Cleistogamous

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