Influence of nitrogen constraint on quantitative resistance to clubroot in *Brassica napus*

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Context

Use of quantitative resistance (QR) to construct resistant varieties

- ❑ Quantitative variation is more abundant in nature
- ❑ QR is more difficult to overcome by pathogen populations
- ❑ Diversity of (cellular and physiological) mechanisms underlying QTL

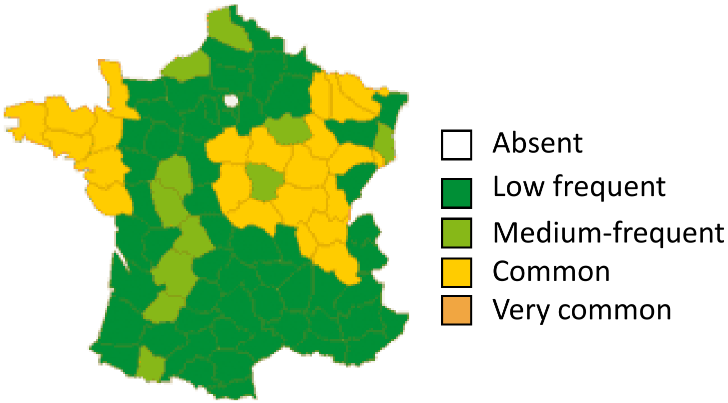
However QR is difficult to use:

- ❖ Many genetic factors having weak effect
- ❖ Expression of QR depending on biotic and abiotic environments

How biotic (microbiota**) and abiotic factors (**water availability, temperature, nutritional-nitrogen constraints**)**
can modulate the effect / expression of clubroot quantitative resistance?

Pathosystem Clubroot - *Brassicaceae*

Disease distribution in France



Genetics of quantitative resistance to clubroot

Different sources of clubroot QR

Complex genetic architecture of QR (QTL and epiQTL)

Weak to strong QTL effects

according to both host genotype and *P. brassicae* isolate

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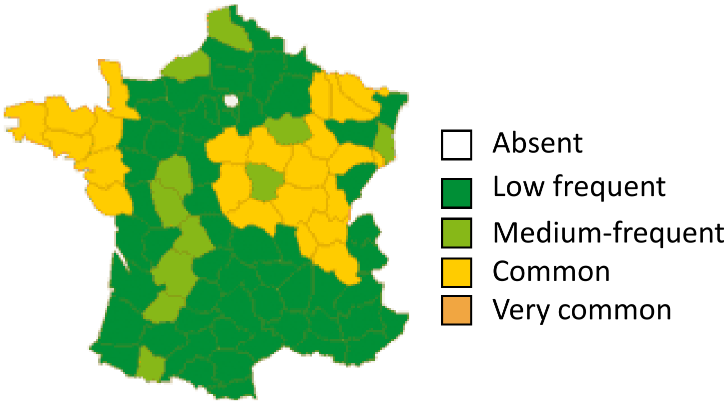

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Environmental factors favouring clubroot development

- Soil pH
- Soil calcium content
- **Temperature**
- **Soil moisture**
- **Fertilization** (nitrogen fertilization)

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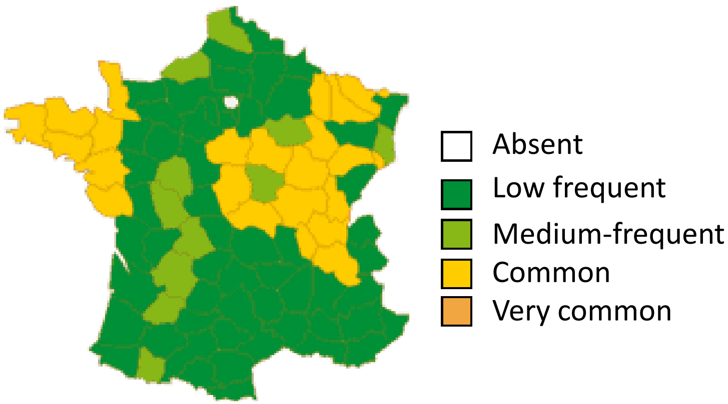

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Impact of Nitrogen on disease development

- Nitrogen deficiency or over fertilization not only influences plant growth and development, but also disease development

- Low / high-nitrogen supply can boost… or repress plant diseases

- Many ways in which nitrogen can positively or negatively influence plant diseases

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What about the *Brassica napus* / *P. brassicae* pathosystem?

- Few studies have suggested that a high-nitrogen supply tends to reduce the damage caused by *P. brassicae* infection
- Winter oilseed rape is usually considered to have a high requirement for nitrogen
- …But increasing demands for adaptation to low-input agricultural practices (especially low nitrogen input)

Diversity, genetics and molecular mechanisms involved in N x clubroot quantitative resistance responses

Experimental design

92 winter oilseed rape inbred lines
Diversity set

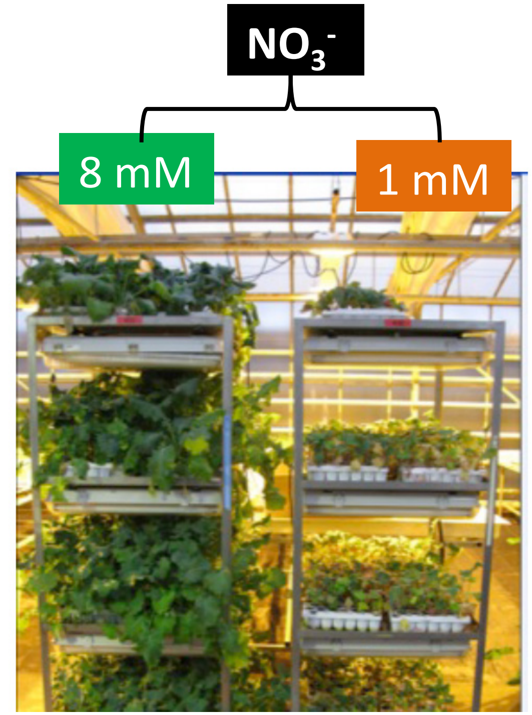
108 doubled haploids
('Darmor-*bzh*' x 'Yudal')
Segregating population

2 isolates (Europe)
eH
K92-16

6 winter oilseed rape inbred lines

3 spring oilseed rape inbred lines

5 isolates (Canada)
SACAN-ss3
SACAN-ss1
ORCA-ss4
AbotJE-ss1
L-G1 + L-G2 + L-G3

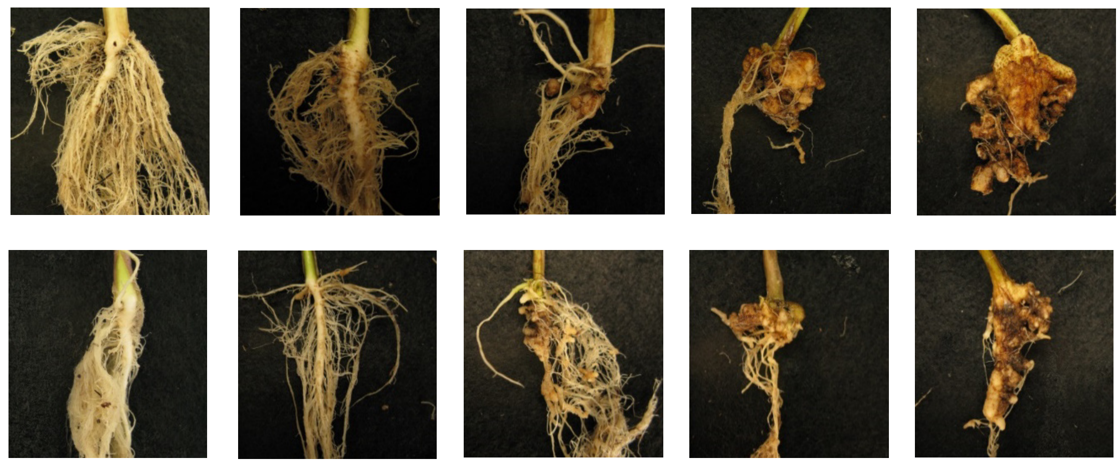


Fully developed clubs and important symptoms are observed under both low and high-nitrogen supply…

Clubroot class symptoms 0 1 2 2+ 3

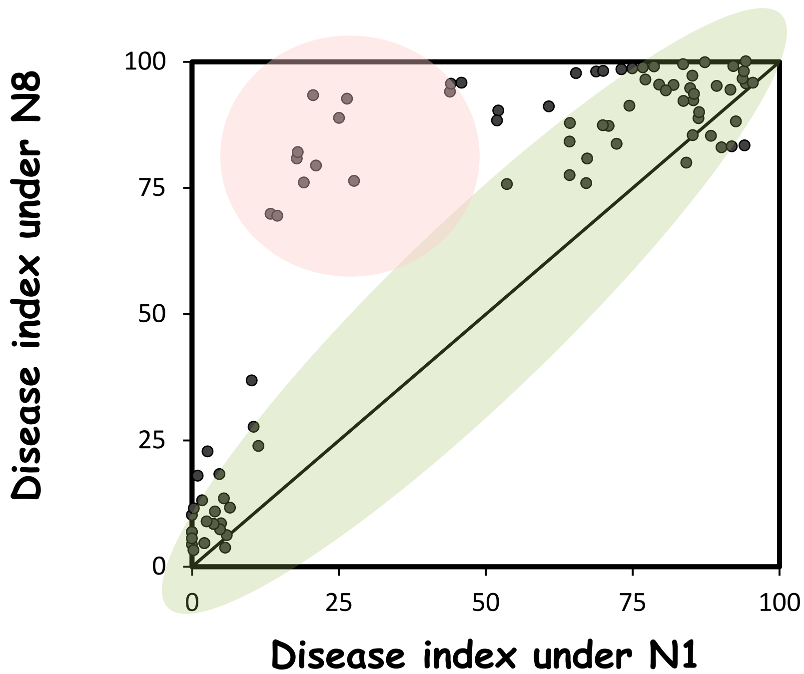
under N8 supply

under N1 supply



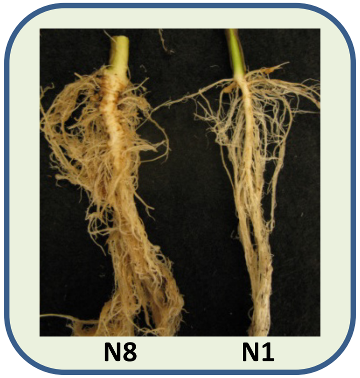
Laperche et al. 2017

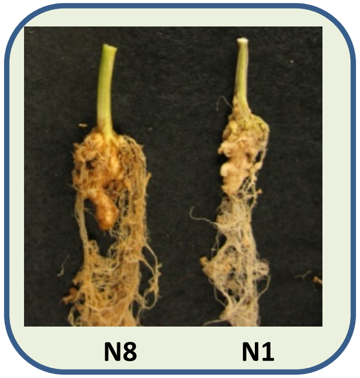
Genotype-dependent modulation of the clubroot response triggered by nitrogen



Diversity of clubroot responses among 92 oilseed rape genotypes against infection by eH isolate under high and low-nitrogen supply

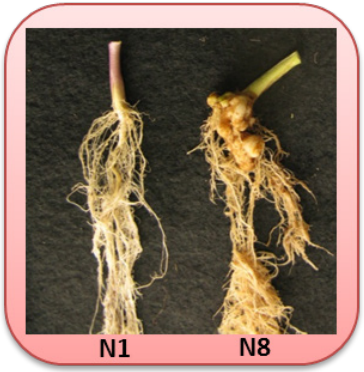
Non N-responsive genotypes





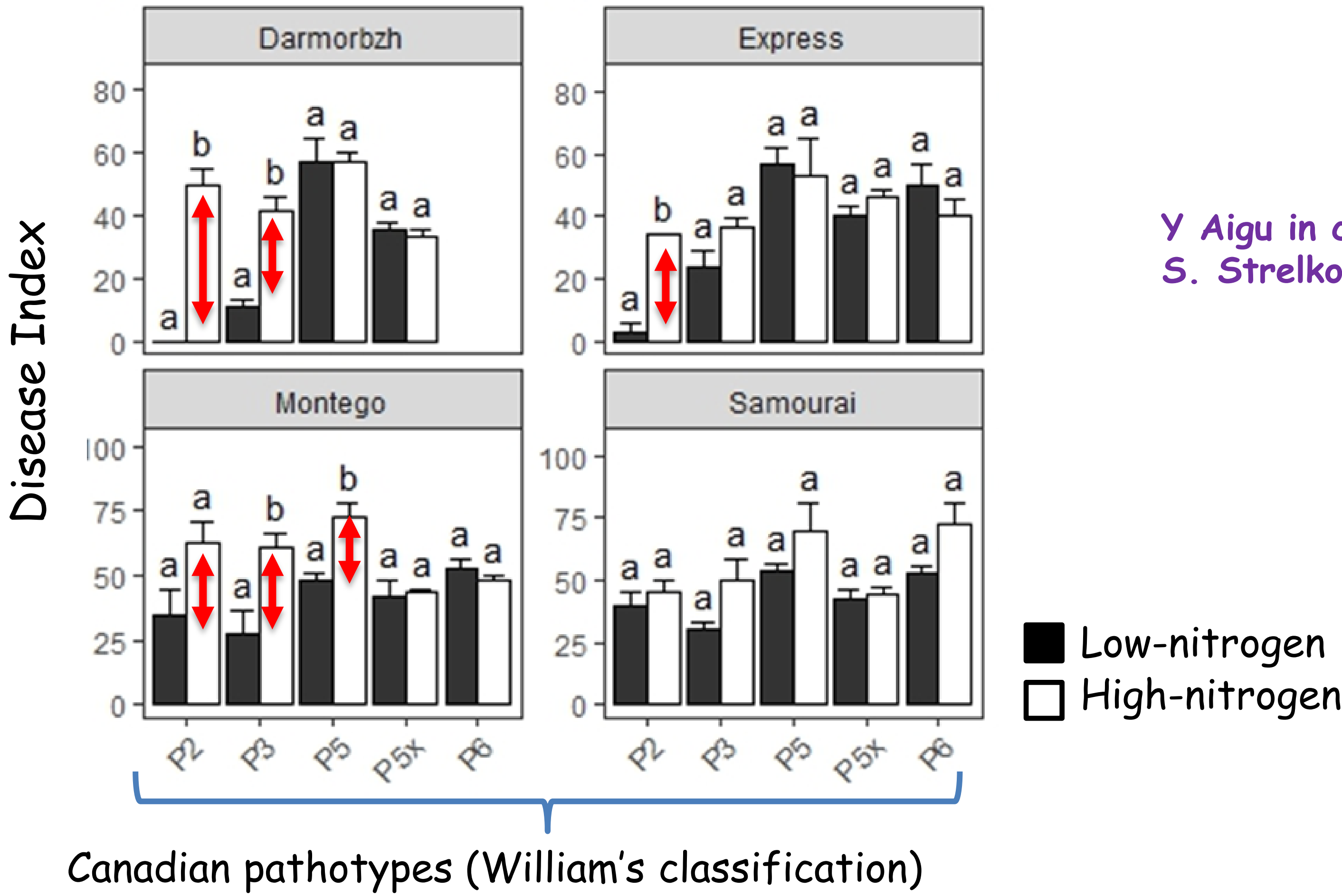
N-responsive genotypes

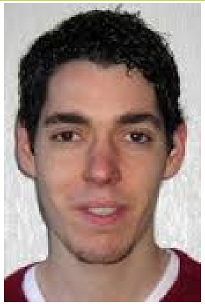
Yudal



Laperche et al. 2017; Aigu, 2017

The influence of nitrogen supply on host clubroot response depends on both plant and pathogen genotypes



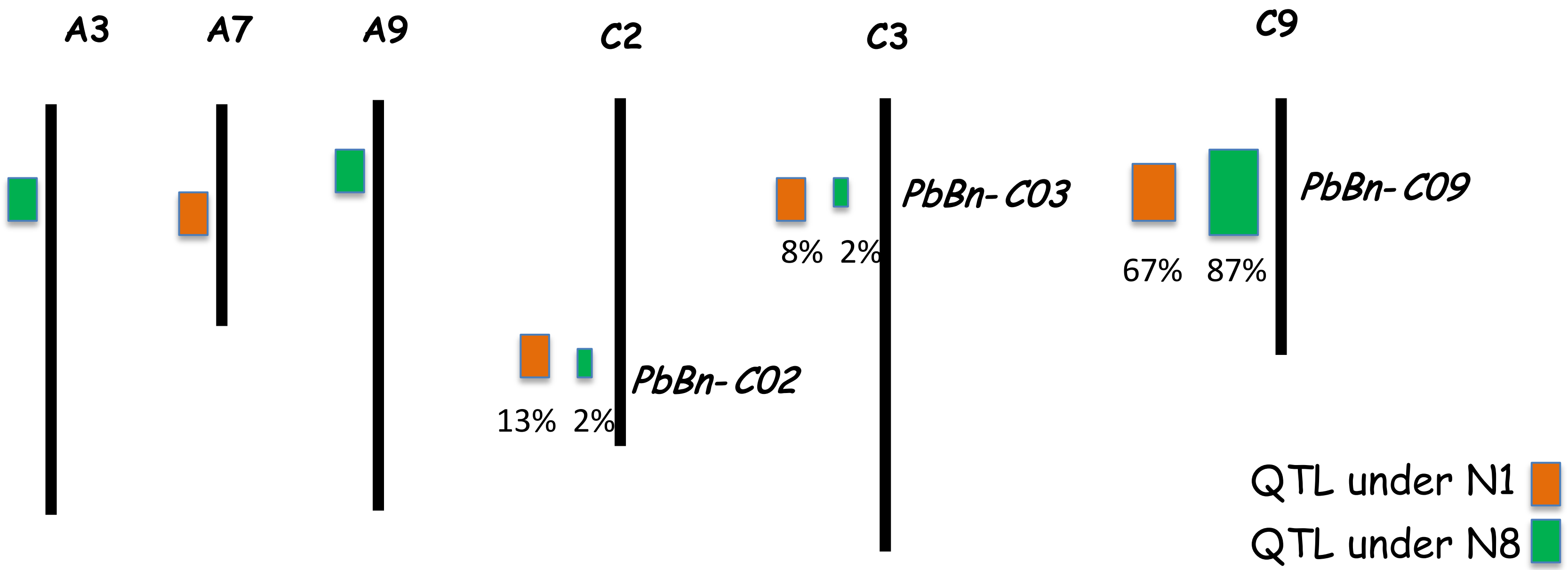


Y Aigu in collaboration with S. Strelkov (Univ. Alberta)

Aigu et al. in prep

Genetic architecture of N-dependent clubroot resistance

108 DH progeny from the cross Darmor-*bzh* x Yudal / isolate eH of *P. brassicae*



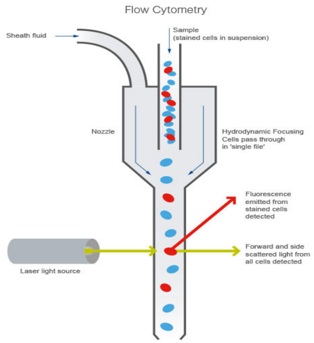
QTL architecture is similar under N1 & N8

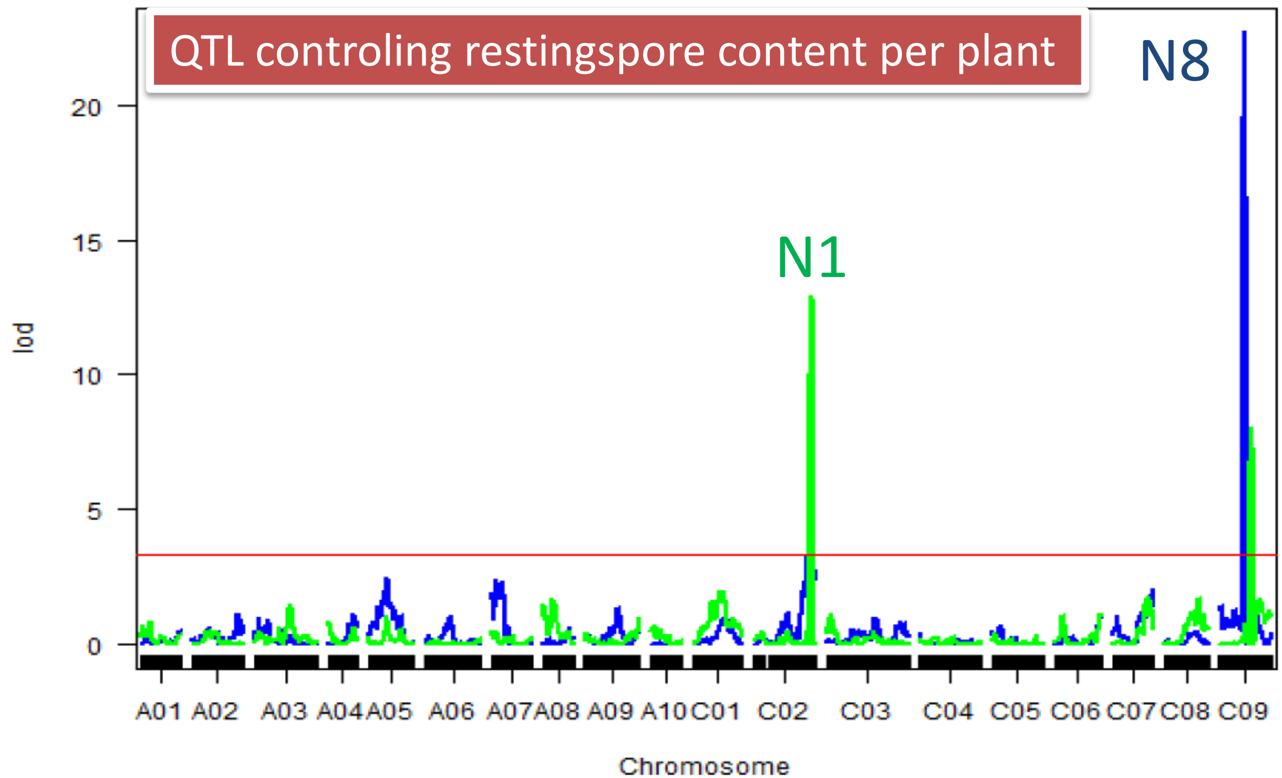
The magnitude of the QTL effect is dependant on the fertilization level

Laperche et al. 2017

Genetic architecture of N-dependent clubroot resistance

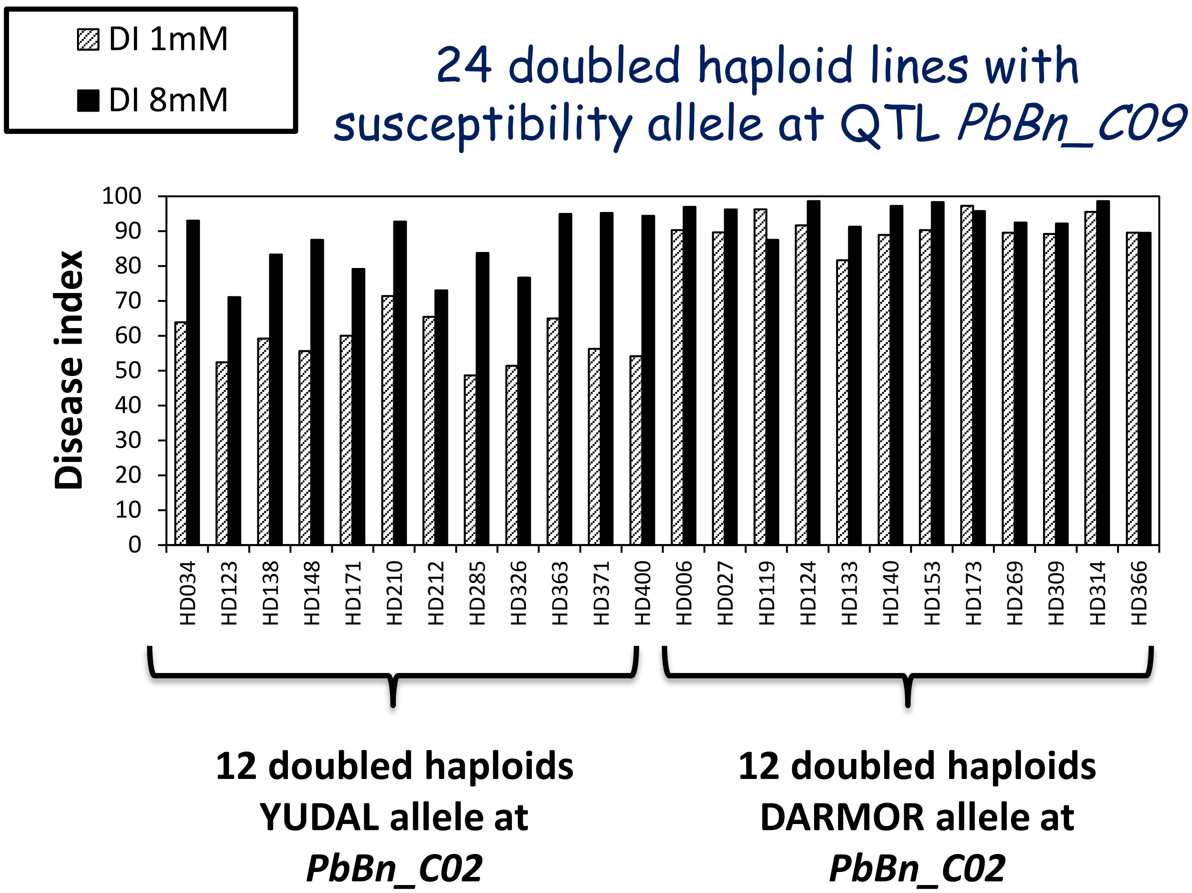
Variation of nitrogen supply exerts a switch on the effects of the two QTL controlling resting spore content





Aigu et al. 2018

PbBn_C02 is the main genetic factor implied in the N1-driven resistance to isolate eH

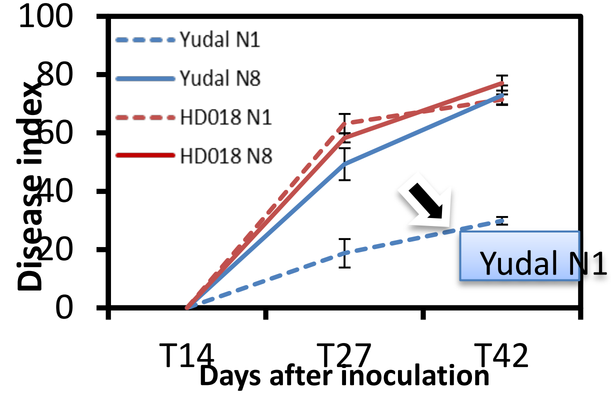


Molecular mechanisms involved in N-dependent clubroot resistance

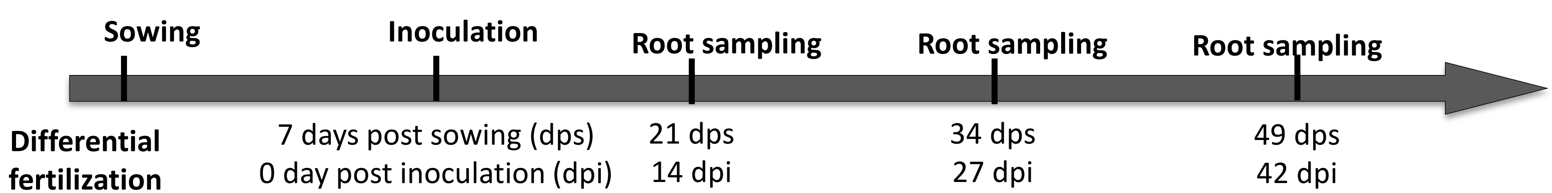
- ✓ Choice of contrasted genotypes to be compared…

'Yudal' HD018

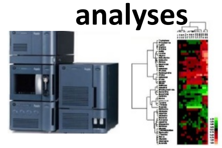
N8 N1 N8 N1



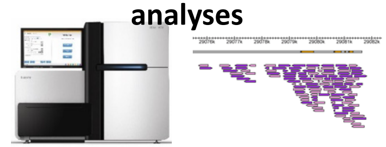
- ✓ Comparing dynamics of cellular responses to clubroot infection…



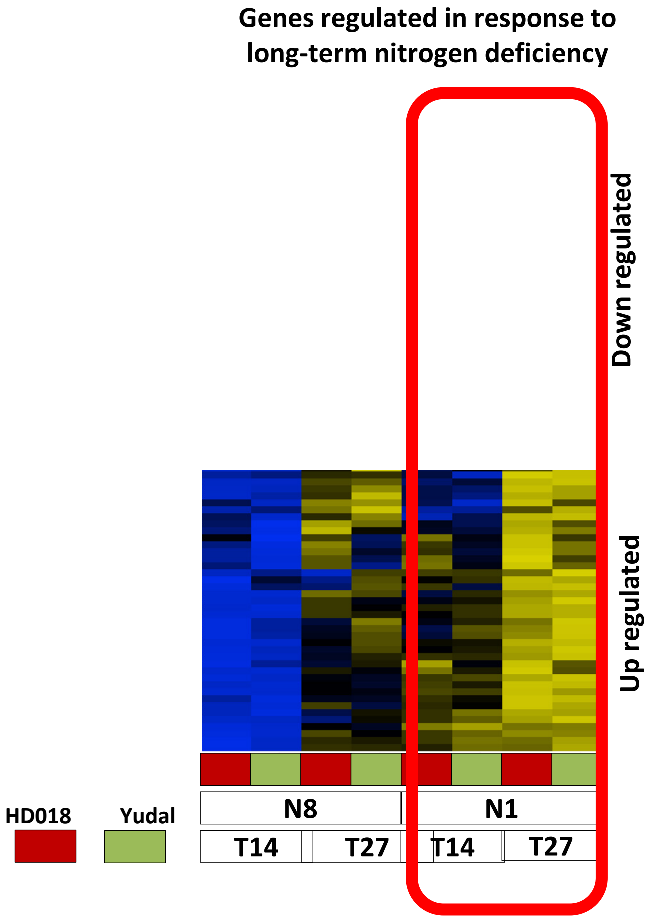
Metabolomic analyses

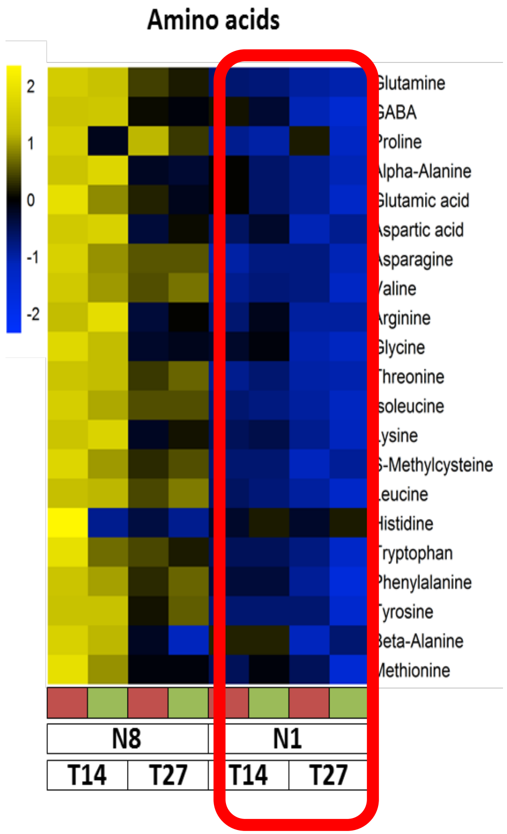


Transcriptomic analyses



Both genotypes display similar metabolic and transcriptomic responses to nitrogen deficiency in non-inoculated conditions





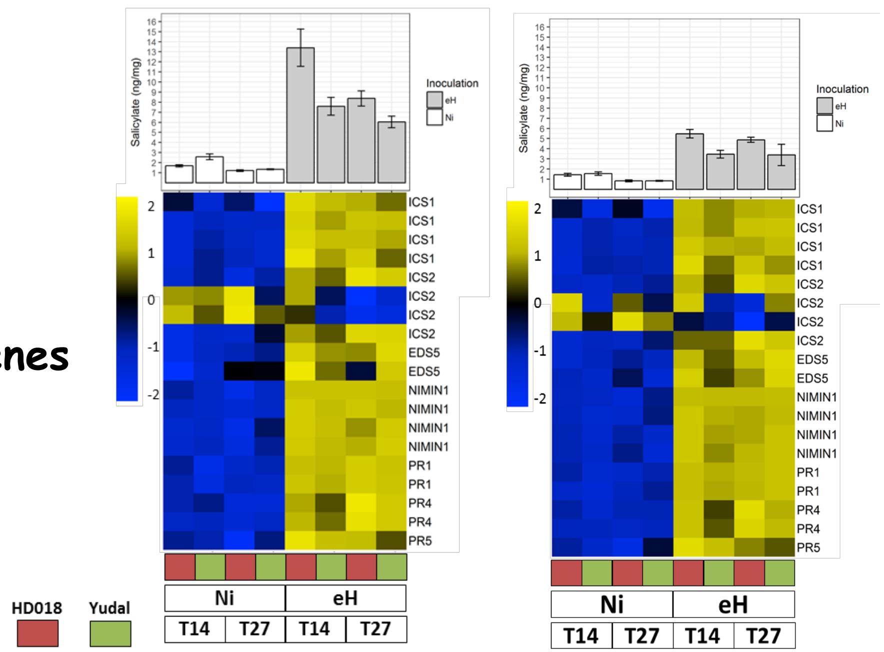
Aigu et al. (in prep)

In inoculated roots, SA-responses are the major features in both genotypes and in both nitrogen conditions

SA content

SA-related genes

Salicylic acid response under N8 | Salicylic acid response under N1

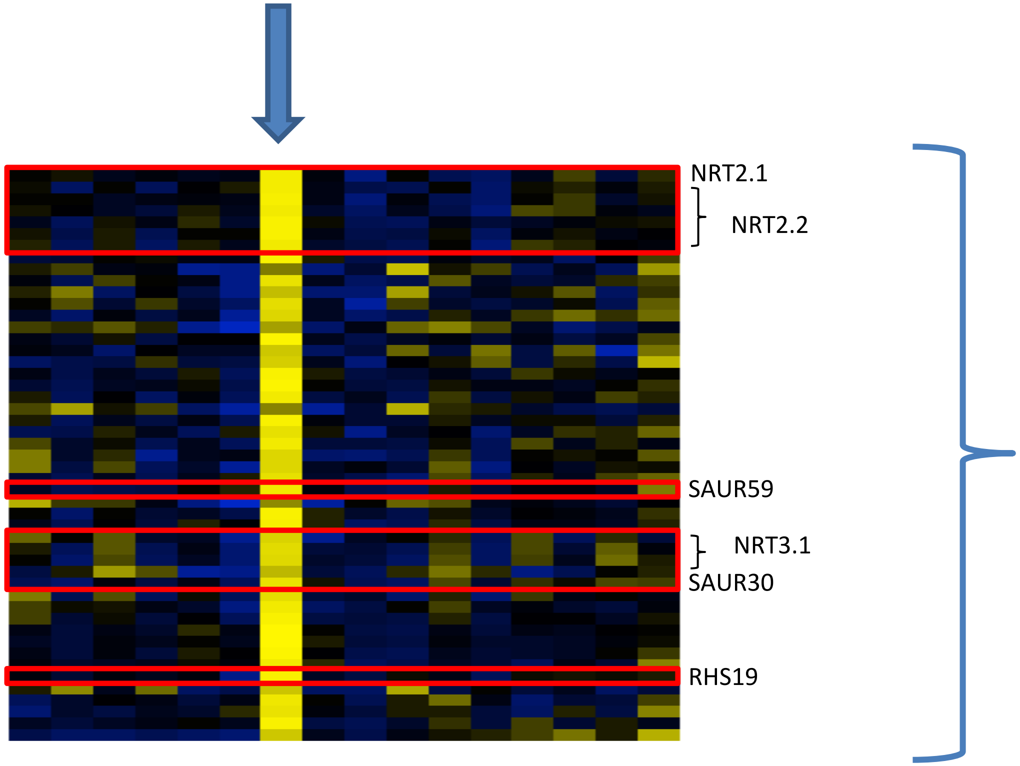


SA-responses to infection are not sufficient to explain the low-nitrogen clubroot resistance in Yudal

Aigu et al. (in prep)

Very few transcriptomic regulations are specific to 'Yudal x N1'

The expression of 80 genes is specifically induced in infected roots of Yudal under low-nitrogen condition



NRT genes and auxin responsive genes

Aigu et al. (in prep)

Summary

- ✓ Oilseed rape response to clubroot can be modulated by nitrogen supply
- ✓ Modulation of clubroot response triggered by nitrogen depends on both plant genotype and pathogen isolate
- ✓ QTL *PbBn-C02* controls partial resistance under low nitrogen supply
- ✓ Resistance harbored by Yudal in low-nitrogen conditions
  - Does not involve massive transcriptional or metabolome reprogramming
  - Is not associated to SA-related responses

➢ Current work to clone QTL *PbBn-C02*

Summary

Similar results were obtained in Arabidopsis:

- ✓ **Modulation of the effect of clubroot resistance QTL by flooding (water availability during the secondary phase of the *P. brassicae* life-cycle) (Gravot et al, 2016)**

- ✓ **Modulation of the effect of clubroot resistance epigenetic QTL by temperature (Liégard et al, under revision)**

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Similar results were obtained in Arabidopsis:

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Importance of linking physiological and genetic analysis for the study of abiotic-biotic stress interactions and predict the modulation of resistance in various environments

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