



Exploration of *P nigra L.* genetic variation for partial resistance against the co-adapted pathogen *Melampsora larici-populina* Kleb.

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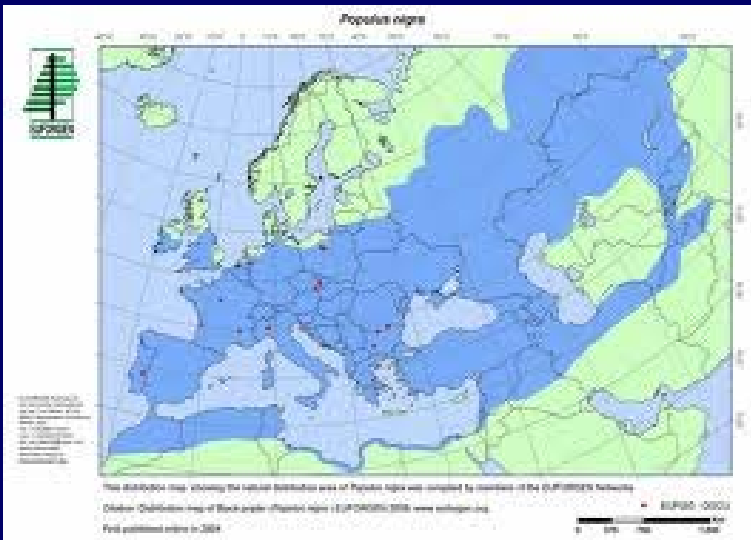
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Context



Populus nigra – *Melampsora larici-populina* a natural pathosystem in Europe



- High genetic diversity in host and pathogen natural populations
- High yield losses in plantations / small impact in natural ecosystem
- Selective pressures from cultivated clones are rapid and strong



Context

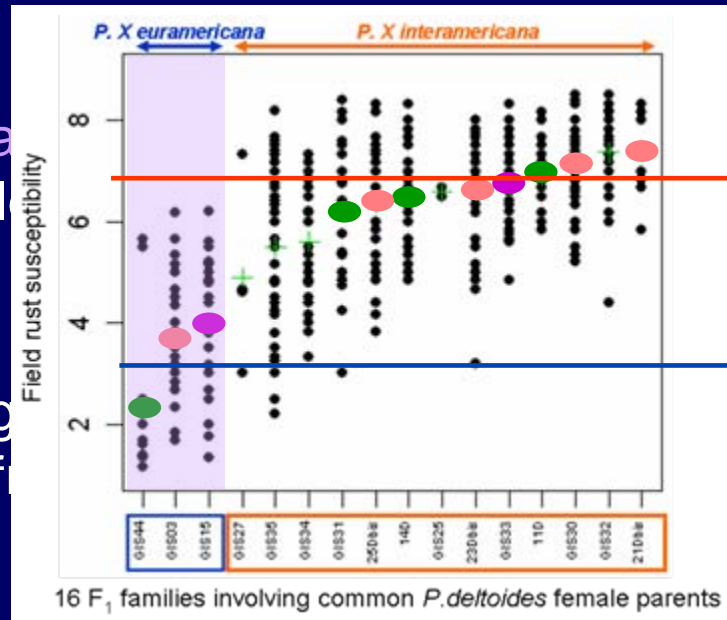


P. nigra, a parental species of interest for breeding

- Resistance : Less negative heterosis in DxN than in DxT hybrids

- Avoidance : large areas, more favorable

- Tolerance : significant independent



epidemics, DxT

DxN mass losses

- Higher durability of resistance level of DxN cultivars even deployed in large areas

Objectives & methods



Partial resistance components
and their strain-specificity
Field and laboratory tests



Breeding and
deployment
guidelines

Genetic control of
partial resistance
*Mating designs and
genetic mapping*



Selection pressure
on *Mlp* populations
*Characterization of
Mlp populations*



Genetic variation
in natural populations
*Phenotypic evaluation and
association analysis*



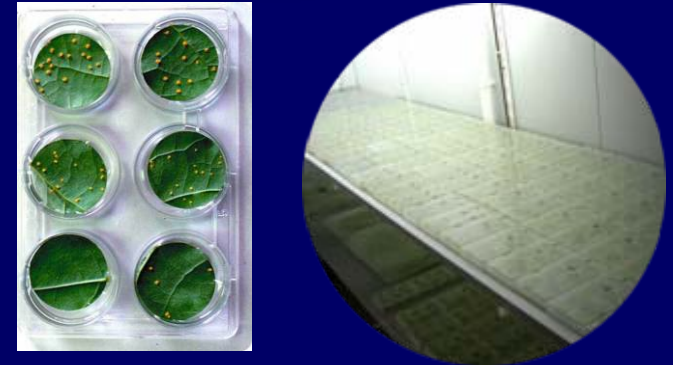
Evaluation of rust resistance



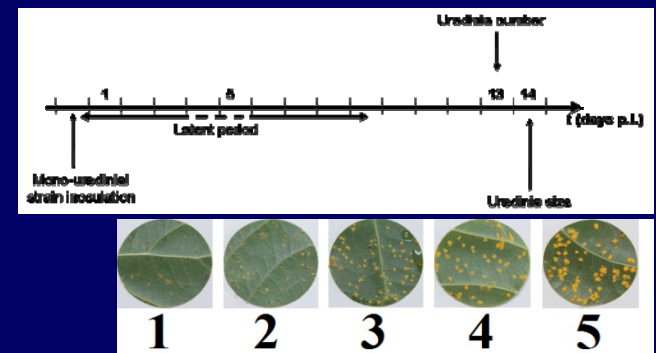
Natural infection in field test



Artificial infection in laboratory test



1-8 Rust score on the most infected leaf



Characterization of *Mlp* populations
(virulence, aggressivity)

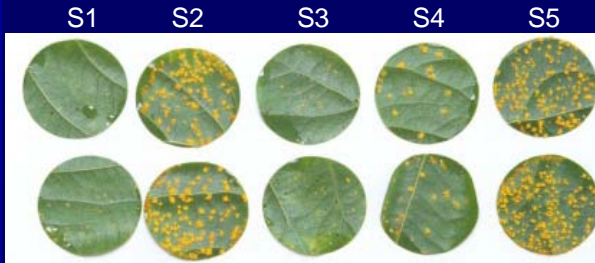
Strains collected in natural
populations and in cultivated areas

Specificity of rust resistance

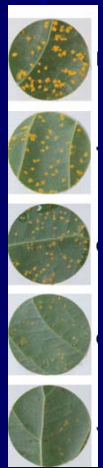


830 clones x (3-20 mono-uredinial strains)

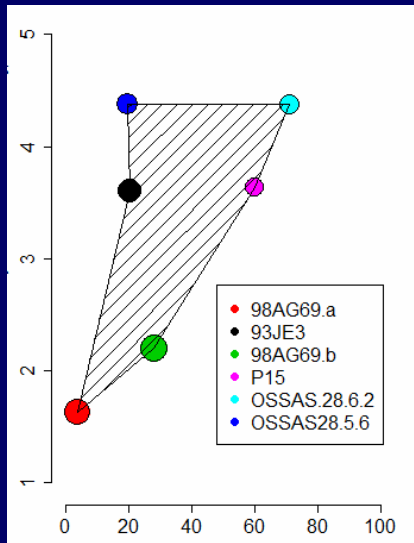
Clone BDG



- Partial Resistance in *P. nigra* is as high strain-specific as in interspecific hybrids with qualitative defeated resistances



Average uredinia size



Nb uredinia /disk

$$V_{G \times S} / V_G$$

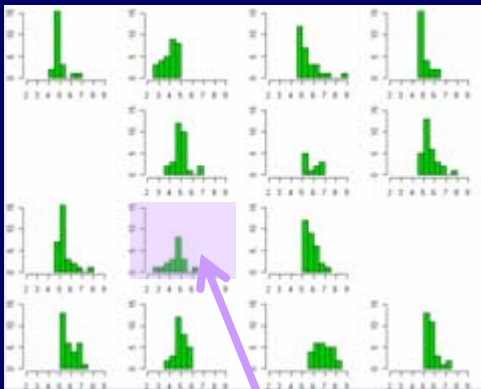
Latent period	0.75
Average uredinia size	1.05

Genetic control of rust resistance



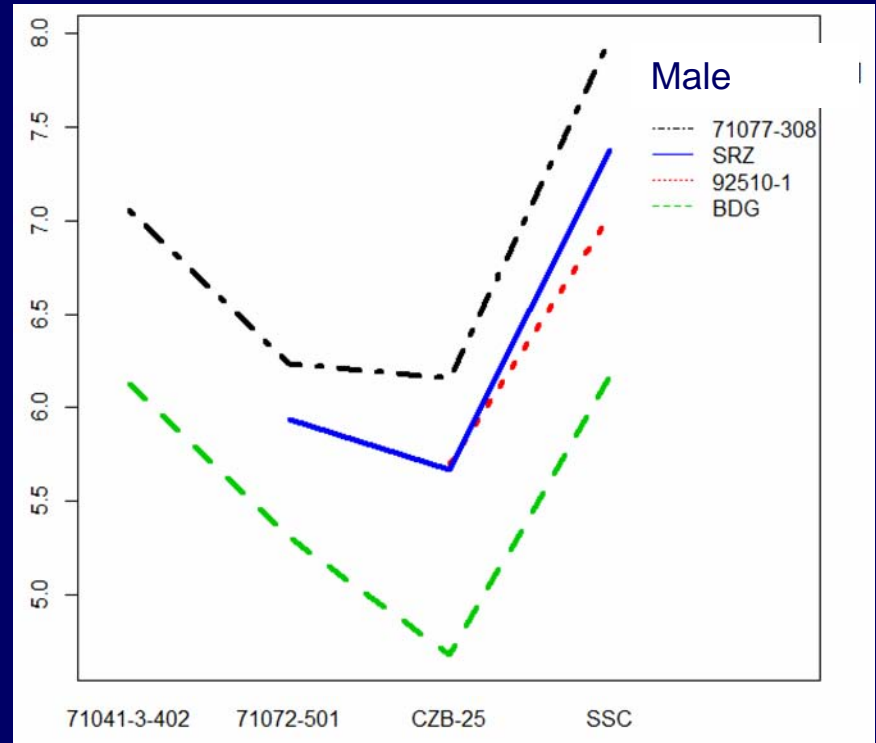
Field Resistance

Factorial mating design 4x4
(660 + 308 sup. clones 1311B)



Fam. 1311B
F1 mapping pedigree
Laboratory tests
2 strains

Field maximum rust score



Female parent

Parental additive effects explains 80% of family variation
But still an important within-family genetic variation

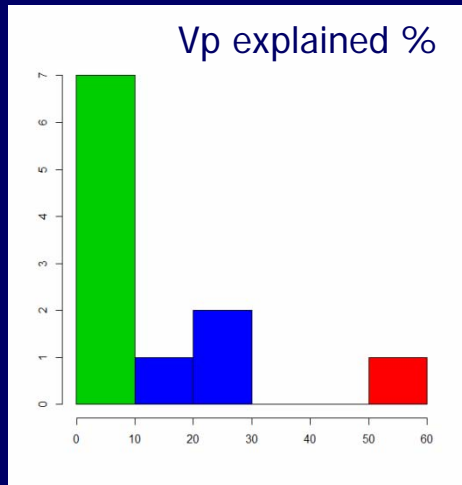
Genetic control of rust resistance



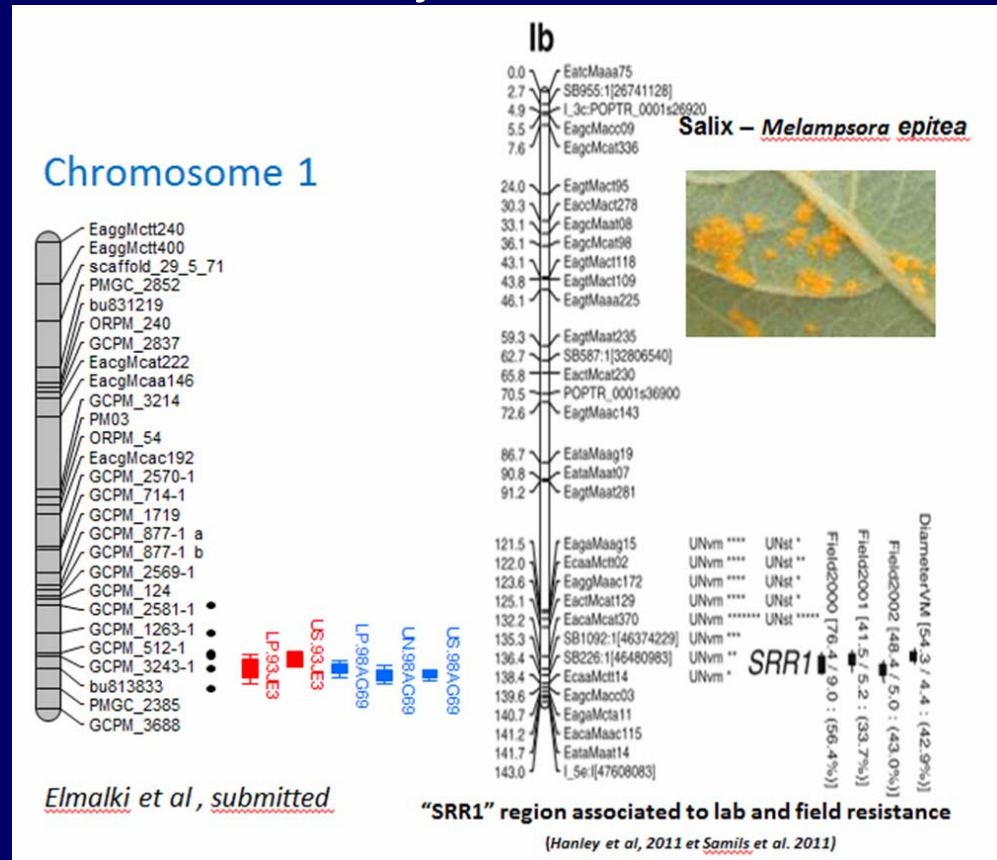
Fam. 1311B - 71072-501 x BDG – 308 F1 clones – 2 strains

- 11 QTLs on 7 chrom.

- One major QTL



- Other minor QTLs are trait- and strain-specific



Genetic control of rust resistance

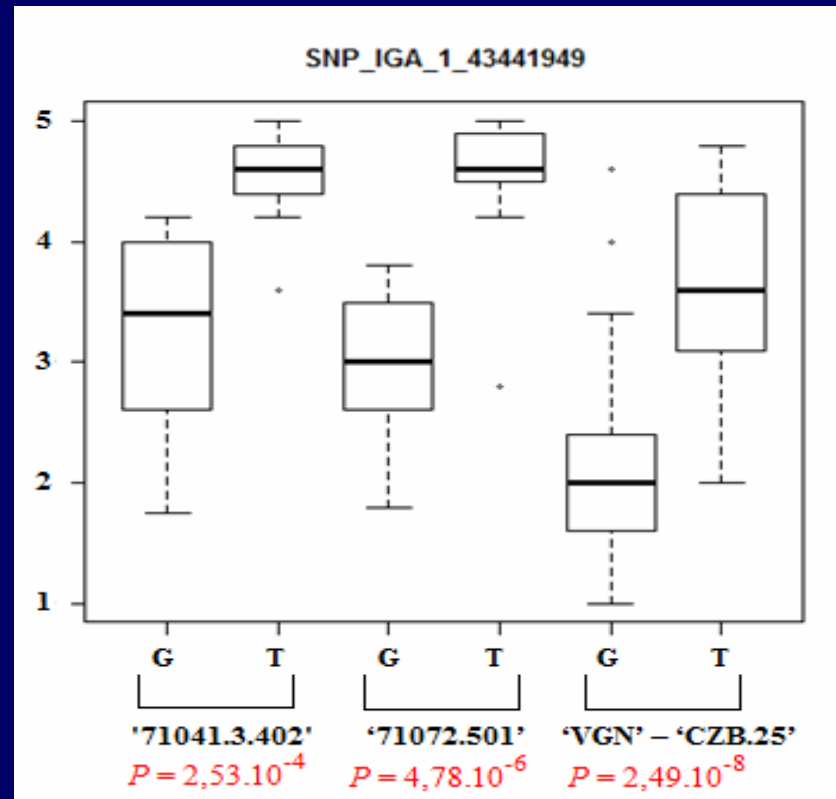


Validation of the major QTL on chromosome I in two other families

Factorial mating design 5x4

		♂			
		SRZ	BDG	71077.308	92510.1
♀	VGN - CZB.25	•	•	•	•
	71071.3.402		•	•	•
	71072.501	•	•	•	
	SSC	•	•	•	•

Average uredinia size



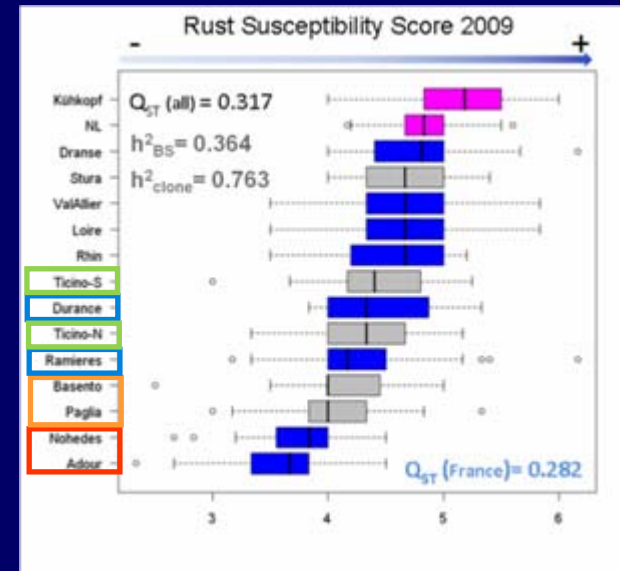
Vp %: **46%** **68%** **33%**

Natural genetic variation

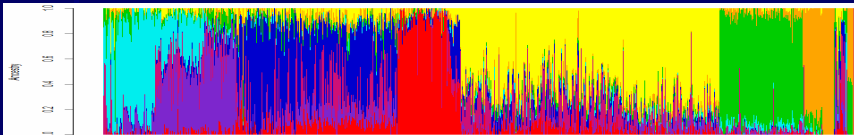
14 natural populations
1141 clones
Clonal test in Orleans



Field Resistance (2009, 2010)



8192 SNP
K=8

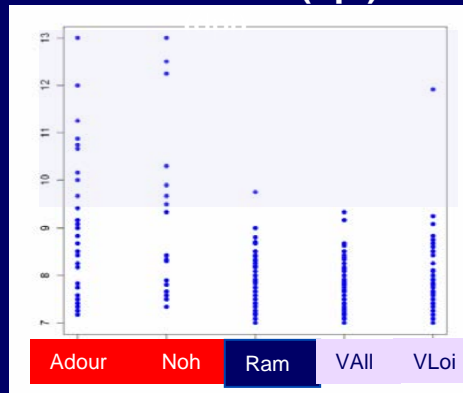


A geographical pattern for resistance to *Mlp* in *P.nigra* with large individual variation within population

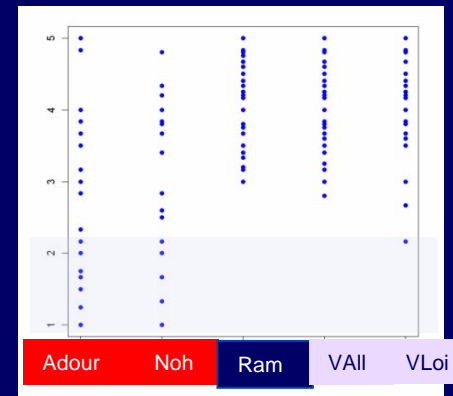
Natural genetic variation

Same geographical pattern for components of partial resistance evaluated in laboratory tests (5 strains)

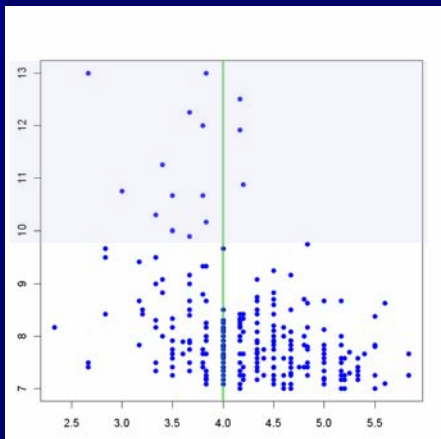
Latent Period (dpi)



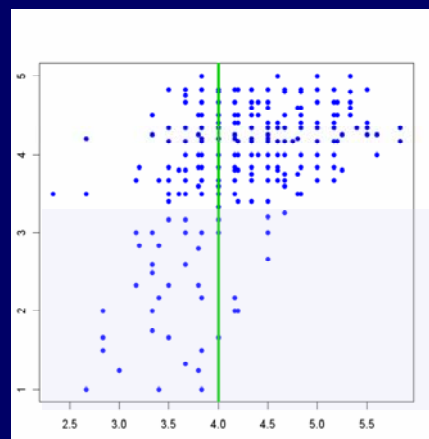
Uredinia size



Latent Period (dpi)



Uredinia size



2009 Field Rust score

- Latent period and uredinia size were the most relevant descriptors of resistance assessed in the field



Local adaptation of *Mlp*

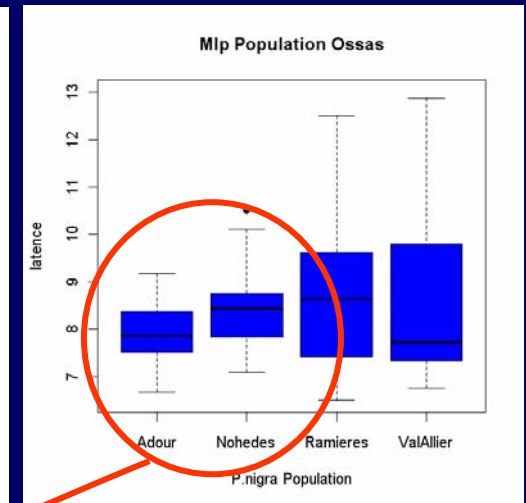
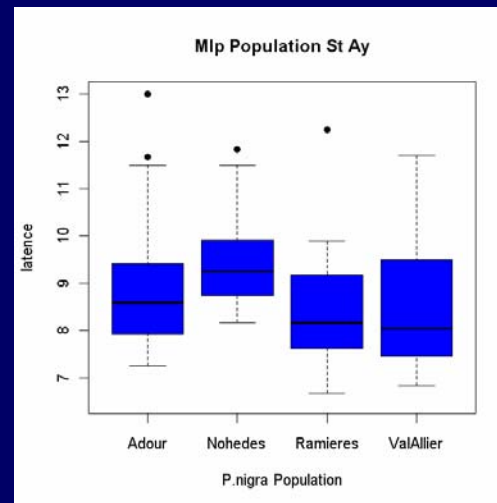
4 *P. nigra* host populations: 6 clones / population

3 *Mlp* populations: 6 strains / population



24 clones x 18 strains

Local adaptation of the pathogen may lead to higher susceptibility but also less GxS interactions





Conclusions



- *P.nigra* natural populations offer relevant genetic resources to breed for *Mlp* rust resistance
- Genetic control for field resistance is mostly additive and explained by increased latent period and reduced sporulation
- Major resistance factors with high strain-specificity and located in genomic regions rich in resistance gene clusters control are revealed in different genotypes
- Local adaptation of pathogen populations is observed and erosion of these resistance factors is expected



Breeding guidelines



- Identify the best provenances but explore also individual variation in other provenances for higher diversity of resistance factors to be cumulated in breeding stocks
- Use as early as possible recombination of the best *P.nigra* parental resources of different geographical origins
- Complete field resistance evaluation by laboratory tests with a collection of reference Mlp strains covering pathogen diversity
- Explore potential interest of molecular markers to screen genetic diversity of resistance sources and design more complex resistance
- To balance possible erosion of specific resistances, include tolerance evaluated in specific field tests and possible constitutive resistance



THANKS



MAPRAAT and GIS
Peuplier

