# The concept of phenomic selection: using Near InfraRed Spectroscopy (NIRS) to predict quantitative phenotypes

Vincent Segura<sup>1</sup>, Jean-Paul Charpentier<sup>1,2</sup>, Kévin Ader<sup>1,2</sup>, Redouane El Malki<sup>1</sup>, Justine Guet<sup>1,3</sup>, Véronique Jorge<sup>1</sup>, Patrick Poursat<sup>4</sup>, Jean-Charles Bastien<sup>1</sup>, Patricia Faivre-Rampant<sup>5</sup> and Catherine Bastien<sup>1</sup>

> INRA, Orléans, France <sup>1</sup>UR0588 AGPF, <sup>2</sup>Génobois, <sup>3</sup>USC 1328 LBLGC, <sup>4</sup>UE0995 GBFOR INRA, Evry, France <sup>5</sup>UMR1165 URGV

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# Near Infrared Spectroscopy (NIRS)

- NIRS is a high-throughput phenotyping technique traditionally used for evaluating the physical and chemical properties of biological samples
- In forest research, it has mainly and successfully been applied to the prediction of **wood properties**, incl. **chemical composition** and **physical properties** (reviewed by Tsuchikawa, 2007)
- More anecdotically, the discrimination potential of NIRS has been explored, through the identification of species and provenances of wood and leaf samples (Richardson *et al.*, 2003; Tsuchikawa, 2007; Sandak *et al.*, 2011; O'Reilly-Wapstra *et al.*, 2013)
  - $\Rightarrow$  NIRS is able to capture some genetic information

### NIRS is an interesting biological marker?

- Few recent studies have more directly confirmed this point, by estimating the **broad sense heritability** of NIRS and/or **mapping** corresponding **loci** (Posada *et al.*, 2009; O'Reilly-Wapstra *et al.*, 2013)
- These results suggest that NIRS signature is potentially an interesting biological marker, which could be used to predict the heritable variation of quantitative traits
- We aimed at testing such hypotheses in natural populations of *P. nigra*

### **Experimental design**

• 223 P. nigra cloned genotypes organized in 6 metapopulations



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### **Experimental design**

- 223 P. nigra cloned genotypes organized in 6 metapopulations
- Randomized Complete Block Design (6 Blocks) located at INRA Orléans



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### Genotypic and phenotypic data

ullet Genotyping: 12k SNP Chip yielding  $\sim$  8,000 high quality SNPs



# Genotypic and phenotypic data

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- Phenotyping over 2 successive rounds of coppicing (2008 2009 & 2010 2011)



### Collection and preparation of wood samples



- $\approx$  50 cm stem sections, 3 blocks  $\Rightarrow$  610 samples (171  $\times$  3 + 45  $\times$  2 + 7  $\times$  1)
- Milling  $\Rightarrow$  610 wood powders ( $\leq 1mm$ )



# NIRS acquisition and preprocessing

 NIRS (10,000 - 4,000 cm<sup>-1</sup>) collection in rotating cups with a spectrum 400 Perkin Elmer spectrophotometer



- Restriction to  $8,000 4,000 \ cm^{-1}$  wave number range
- Statistical pre-treatments (normalization, detrend, 1<sup>st</sup> & 2<sup>nd</sup> derivatives), yielding 7 spectra modalities: raw, norm, dt, der1, der2, norm\_der1, norm\_der2

#### Genetic variability of quantitative traits



Results & Discussion

# Genetic variability along NIRS



V. Segura (INRA)

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Results & Discussion

# Genetic variability along NIRS



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#### Predictions of Quantitative Traits clonal means

**G**-BLUP

4-fold Cross-Validation repeated 500 times



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#### Relationships between predictions and heritability



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# Conclusions / Future work

#### • Conclusions:

- NIRS is a powerful **high-throughput** technique that can **capture** a substantial amount of **genetic variation**
- NIRS signature is thus an interesting marker which can be used to efficiently predict the genetic variation of quantitative traits *Phenomic prediction*
- Future work:
  - NIRS from **wood** *vs.* NIRS from **leaves** collected with a portable spectrometer in the field!



# **Contributions / Acknowledgements**

- Genotyping
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