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Harold Duruflé, Annabelle Déjardin, Véronique Jorge, Marie Pégard, Gilles Pilate, Odile Rogier, Leopoldo Sanchez, Vincent Segura

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Une approche de biologie des systèmes pour ➤ mieux comprendre le déterminisme génétique de la production et de la qualité du bois du peuplier

Durufilé H., Déjardin A., Jorge V., Pégard M., Pilate G., Rogier O., Sanchez L., Segura V.*



INRAE



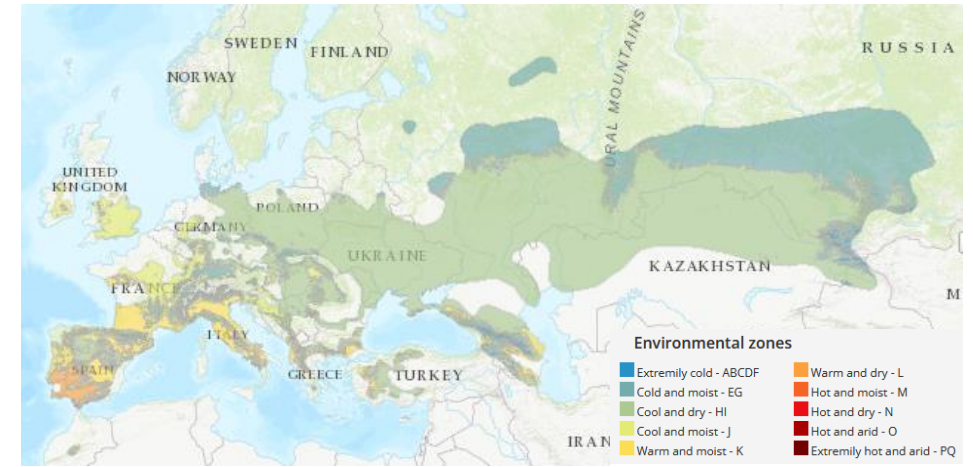
➤ Context : *Populus sp.*

- The model tree
 - Fast growth
 - Clonal propagation
 - High levels of genetic diversity
 - Ability to transform (transgenics)
 - First tree genome sequenced
 - Small genome (550 Mb)
 - Dioecious (Individual female and male)

Populus: A Model System for Plant Biology

Stefan Jansson¹ and Carl J. Douglas²

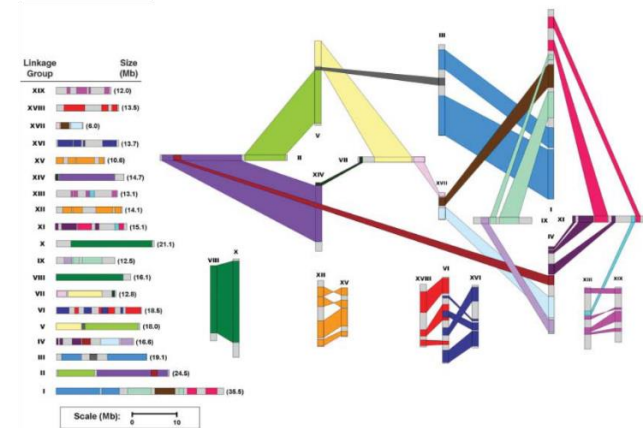
Annu. Rev. Plant Biol. 2007.58:435-458.



(EUFORGEN)

The Genome of Black Cottonwood, *Populus trichocarpa* (Torr. & Gray)

G. A. Tuskan, ^{1,3*} et al. 5 SEPTEMBER 2006 VOL 313 SCIENCE



➤ Context : *Populus sp.*

- The model tree
- Ecological importance
 - a pioneer species along rivers (riparian species)
 - indicator of biodiversity dynamics



➤ Context : *Populus sp.*

- The model tree
- Ecological importance
- Economic importance
 - Cultivated interspecific hybrids (*P. nigra* X *P. deltoides*)
 - 9,6 Million ha in the World (~ 200,000 ha in France)
 - High added-value wood production



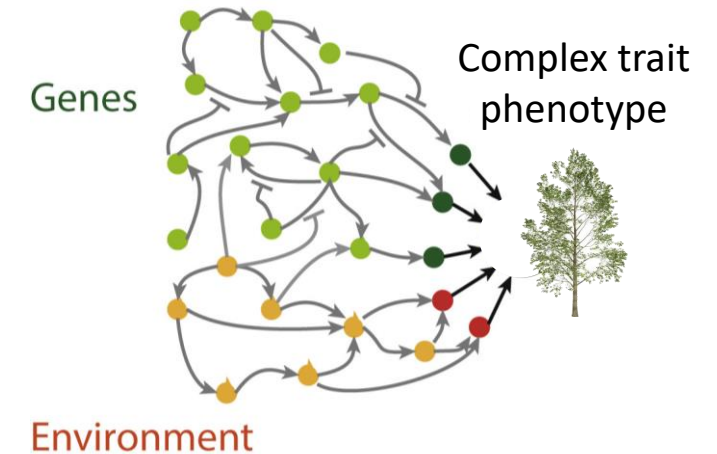
➤ Research question

Understand traits of interest such as wood production and quality

➔ Genetic architecture and its underlying determinism

But ... complex traits ➔ Polygenic architecture possibly with:

- Epistatic interactions
- GxE interactions
- Rare alleles

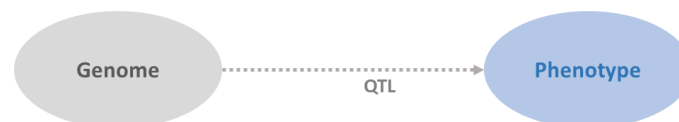


Adapted to Mathieson 2021

Despite a fairly high heritability

(part of phenotype variability which is due to genetic differences between individuals of a population)

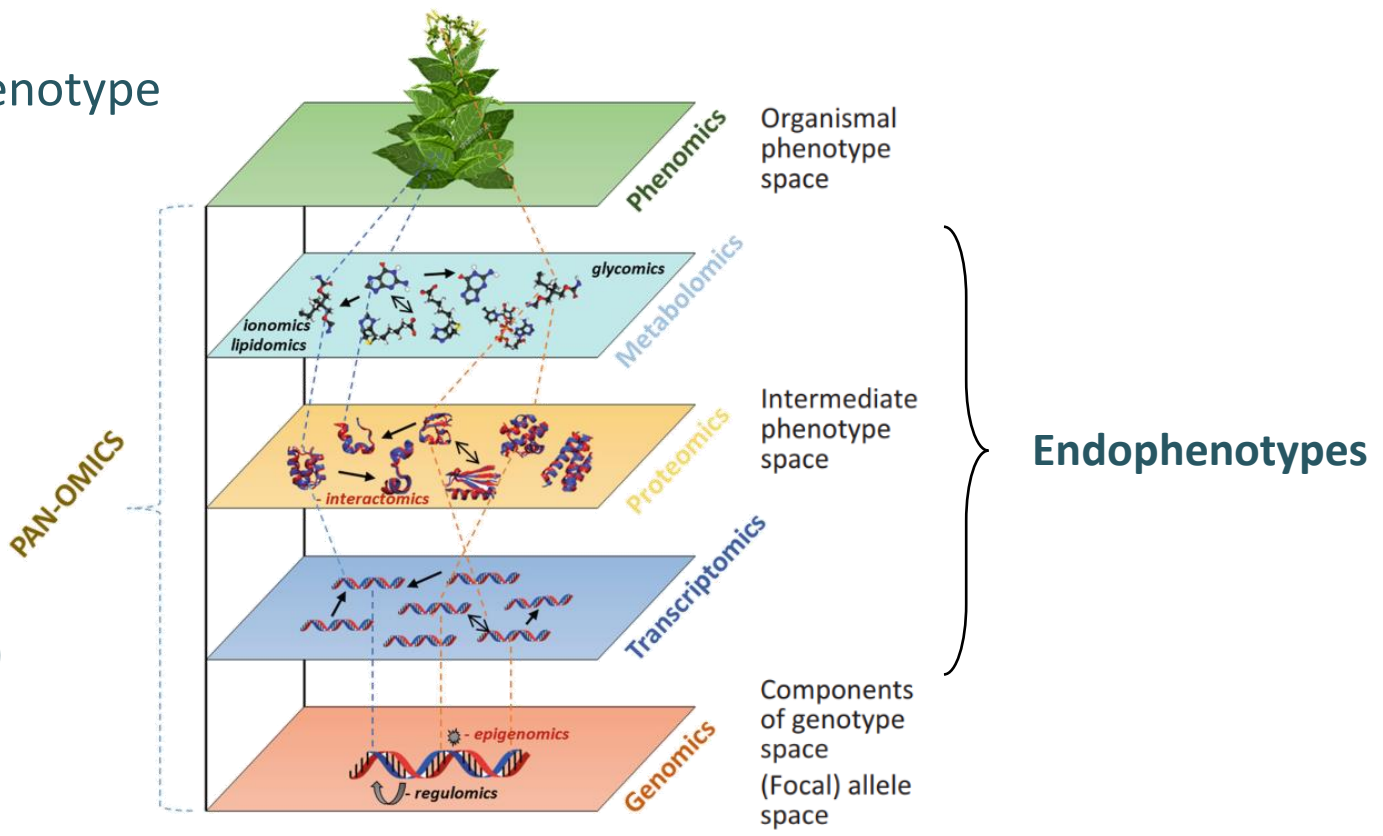
QTLs overall explain only a small proportion of genetic variability



The case of the missing heritability
(Maher, Nature 2008)

➤ Interest of 'omics' and the systems biology approach

- NGS have revolutionized biology:
 - Providing large omics datasets
 - Constitutes simpler endophenotypes
 - Intermediate between the genome and a phenotype



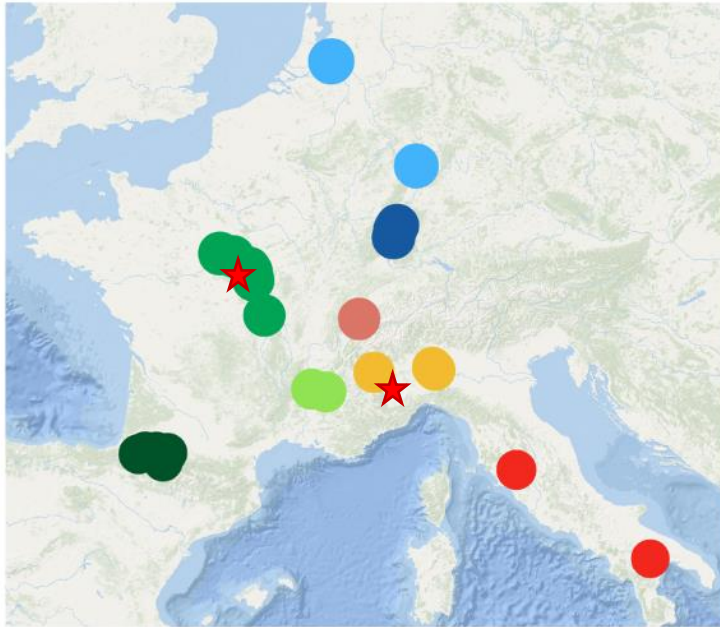
Typically the case of gene expression (RNAseq)

➤ Data from the SYBIOPOP project

241 genotypes of *P. nigra*

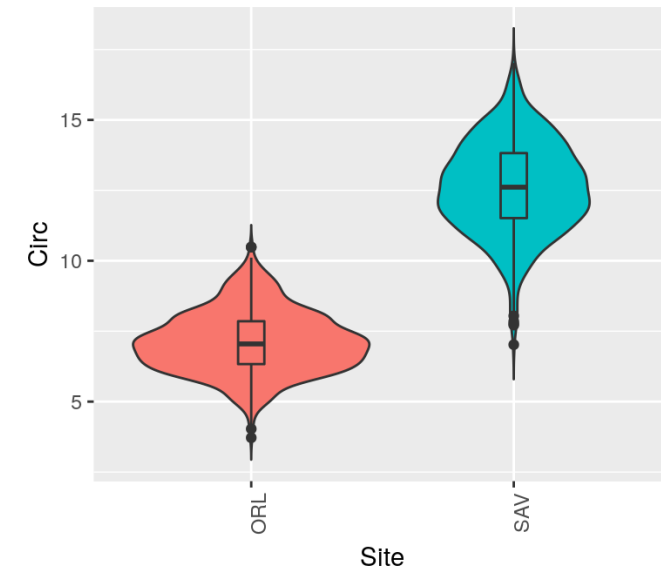
- Large natural diversity of the Western Europe
- From **11 natural populations**
 - 8 biogeographic zones

- Neth_Kuh
- Rhin
- Dranse
- Loire_Allier
- Ramieres
- Adour
- Ticino
- Pag_basen



• Phenotypic data

- Growth & wood properties (NIRS)
- 11 traits × 2 sites
 - Orléans (France) & Savigliano (Italy)
- **Contrasted growth conditions**

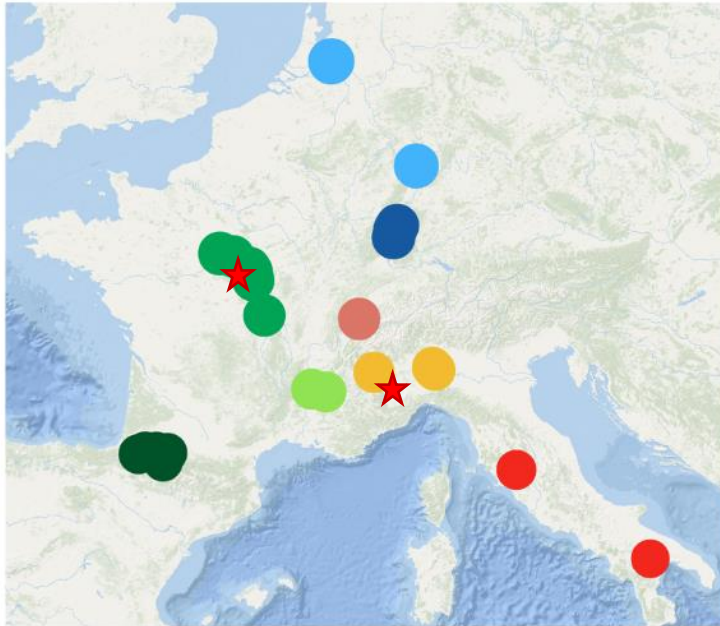


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- 11 traits × 2 sites
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• Original climates (~100 variables)

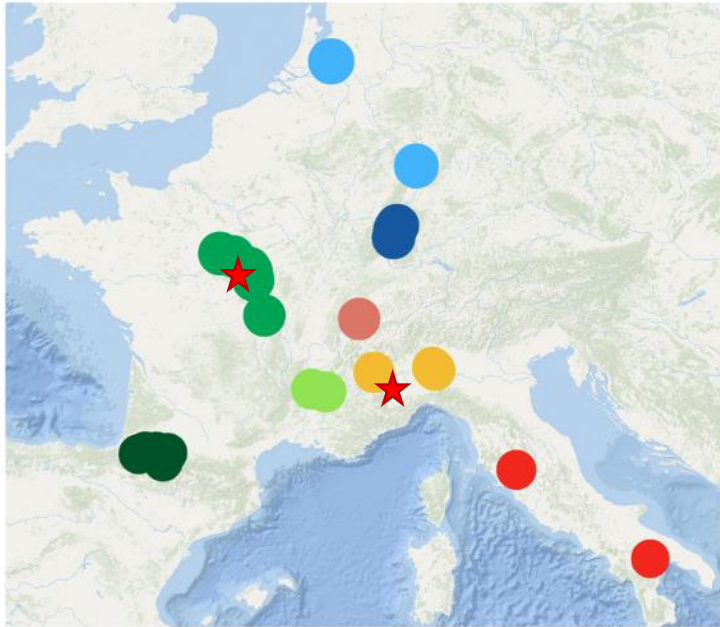


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• Omics Data

- Transcriptomic (wood RNAseq)
 - Cambium and Xylem
 - ~41k transcripts

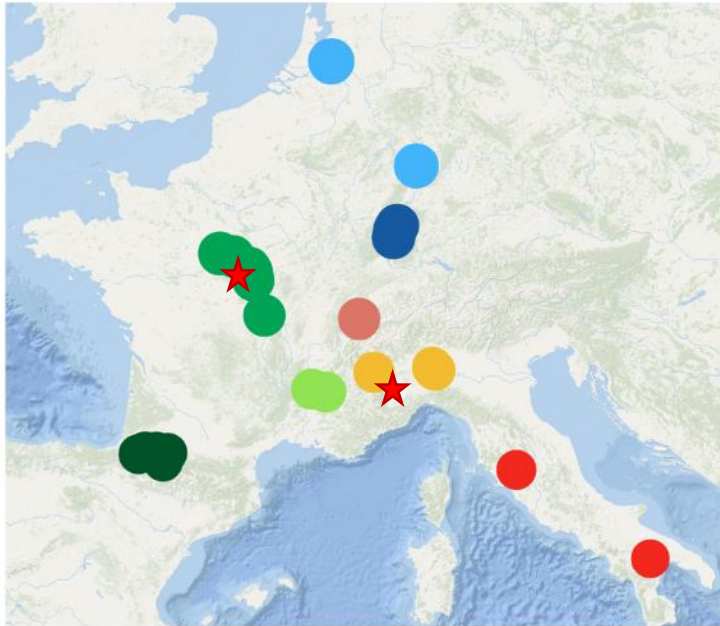


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• Phenotypic data

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• Omics Data

- Transcriptomic (wood RNAseq)
 - Cambium and Xylem
 - ~41k transcripts
- Genomic
 - 800k SNPs



RESEARCH ARTICLE

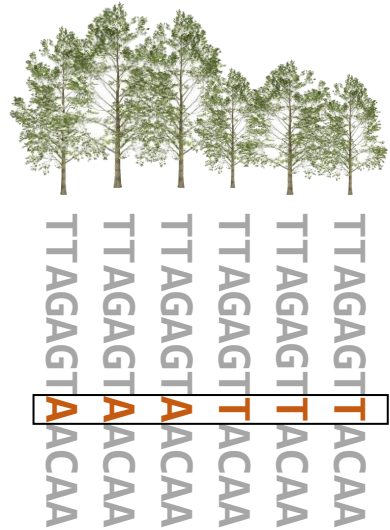
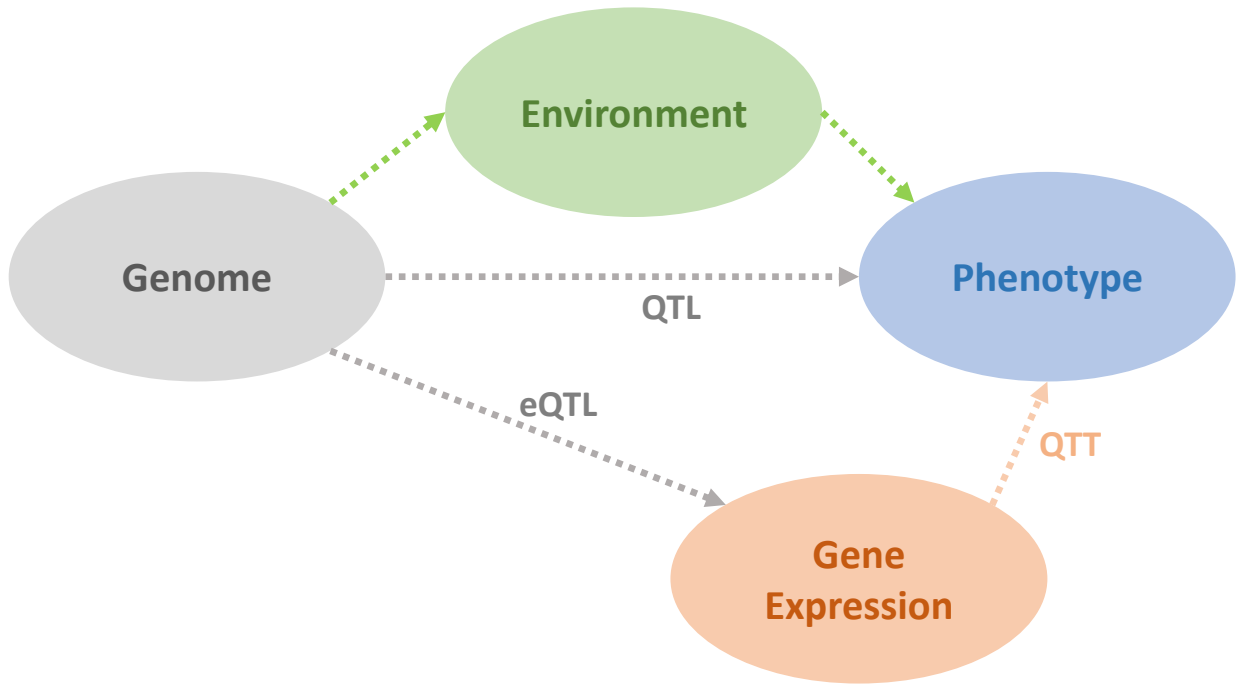
Open Access

Accuracy of RNAseq based SNP discovery and genotyping in *Populus nigra*



Odile Rogier¹, Aurélien Chateigner¹, Souhila Amanzougarene¹, Marie-Claude Lesage-Descauses¹, Sandrine Balzergue^{2,3}, Véronique Brunaud², José Caius², Ludivine Soubigou-Taconnat², Véronique Jorge¹ and Vincent Segura^{1*}

➤ A systems biology approach



➤ Summary

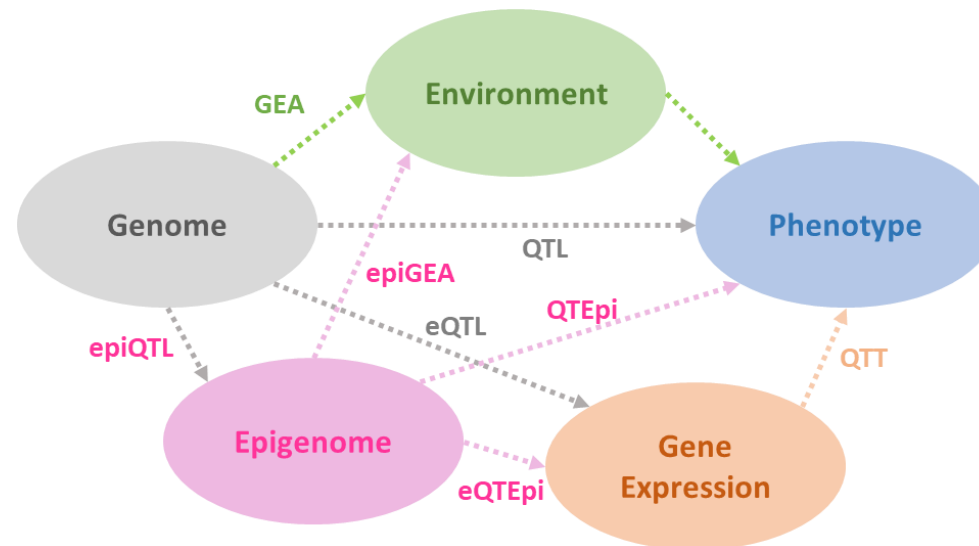
- A very significant association for the circumference
- The association is located in the previously identified
 - Poplar Biomass Locus #3” (Rae *et al.*, 2009)
- The association appears to be mediated by gene expression
- The correlation between gene expression and growth is negative
 - which would be consistent with a compromise between growth and defense.
- The association shows traces of divergent selection

➤ Perspectives

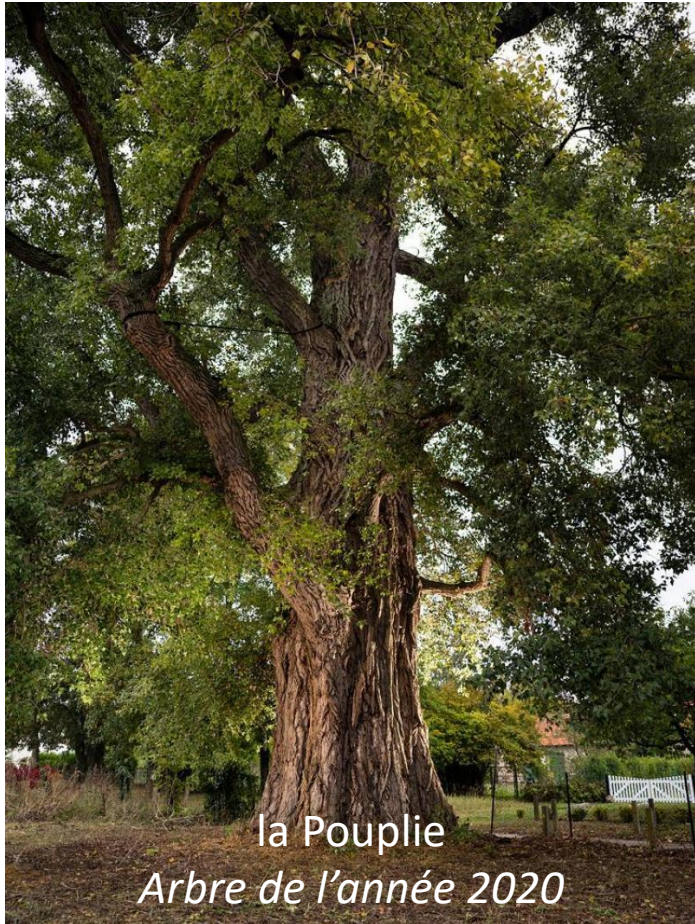
- Functional validation of the gene effect
 - Better understanding of the underlying mechanism
- Many other associations detected for biochemical traits (~20 loci)
 - eQTLs analyzes carried out for 34,226 transcripts (Wade *et al.*, 2022)
- Improved knowledge and pan-genomic prediction of complex phenotypes by an integrative multi-omics approach



Alexandre Duplan
(PhD 2022-2025)



Thanks to all people involved...



...and thank you for your attention

INRAE


BioForA


GBFOR
Génétique et Biomasse Forestières
Unité Expérimentale
ORléans

AGENCE NATIONALE DE LA RECHERCHE
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