



HAL
open science

Collaborative research in forest genomics and tree breeding: mutual benefits and future contribution to adaptation of forests

Catherine Bastien

► To cite this version:

Catherine Bastien. Collaborative research in forest genomics and tree breeding: mutual benefits and future contribution to adaptation of forests. Doctor honoris causa ceremony, Swedish University of Agricultural Sciences (SLU). SWE., 2012, Uppsala, Sweden. <hal-02803576>

HAL Id: hal-02803576

<https://hal.inrae.fr/hal-02803576v1>

Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



HAL Authorization



Collaborative Research in forest genomics and tree breeding :

*Mutual benefits and future contribution
to adaptation of forests*

Catherine Bastien

*INRA UR588, AGPF, Orléans, France
Catherine.bastien@orleans.inra.fr*

ALIMENTATION
AGRICULTURE
ENVIRONNEMENT



Outline

- Why accelerated artificial selection from Forest Tree Breeding could assist adaptation of forests to climate change ?
- Dissection of genetic variation a common interest in tree breeding and genomics
- Results from 'Phenotype-Genotype' collaborative research
- New perspectives from high throughput tree genome sequencing

• Forest Tree Breeding contributes to Competitiveness of forest sector

“... We estimate that landowners can realize net present values of \$125 to over \$750/ha across a range of productivity and silvicultural management regimes simply by planting the best genotypes that are currently available from commercial nurseries...”

2006. Journal of Forestry 104:352-358



Breeding programs

Improved forest Material

Deployment

• Forest Tree Breeding is facing new challenges

Maintain genetic gain for wood production



Assist adaptation of forest to climate changes

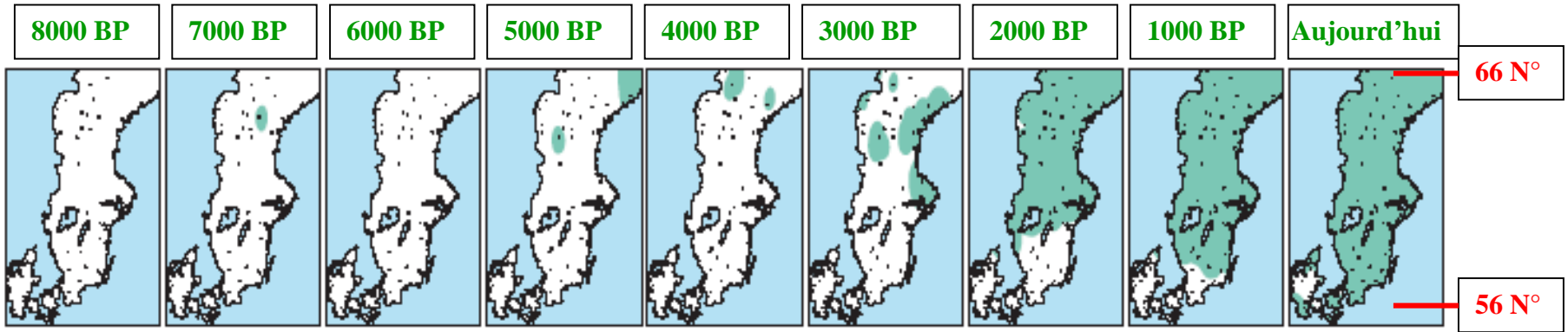


- **Forests have already experienced climatic changes**

Migration = an evolutionary force at species level favoured by important gene flow



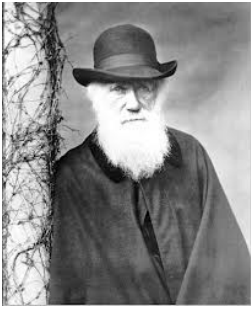
20 to 50 km per century !



Post quaternary glaciation migration of Spruce in Scandinavia

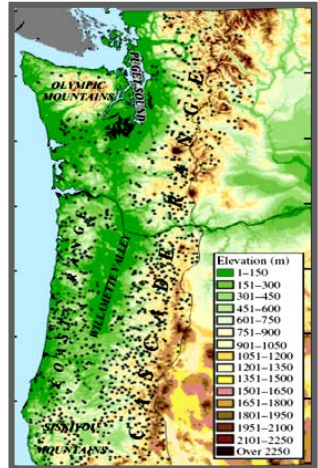
Hannerz et al 2000

• Forests have already experienced climatic changes



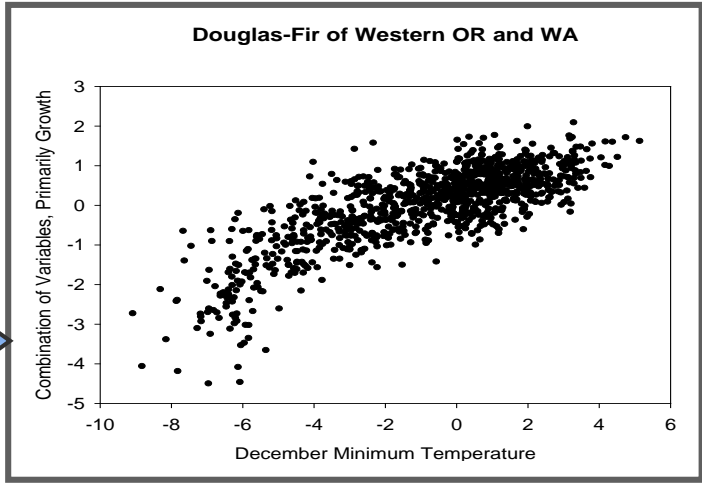
Selection = an evolutionary force at **population** level

Large collection of natural populations



Douglas-fir
St Clair et al 2005

Studies in common gardens



Clinal variation along temperature gradients

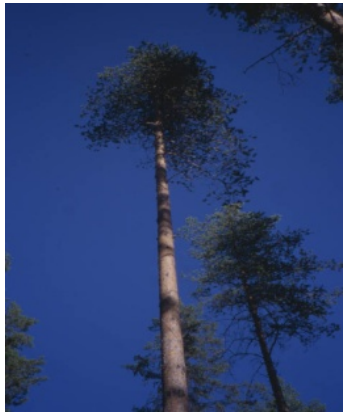
**Tree breeders could combine
assisted migration and
accelerated artificial selection
to assist adaptation of forests**



Genetic variation

intensively investigated in tree breeding and in genomics

Up to now mainly through Phenotype in tree breeding



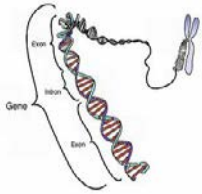
- Resemblance of phenotypes of related individuals is a proxy of **Breeding Value**
- Variation of phenotype of a given individual across environments describes **phenotypic plasticity**
- Breeding values allow prediction of **adaptive and economical gains** from selection



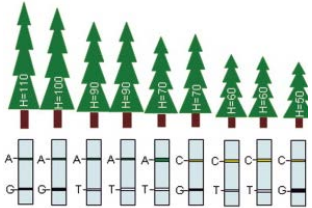
Genetic variation

intensively investigated in tree breeding and in genomics

Up to now mainly through Genotype in genomics



- DNA sequences of genes and individual genomes

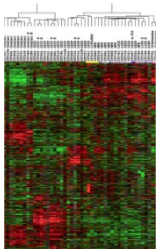


- Nucleotide variation and Structural variants

- Nb of genes involved in traits of interest, their effects and their position on genome

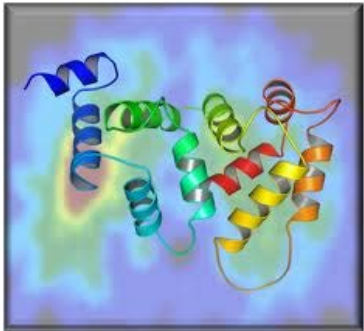


- Gene expression and gene function



To improve long term breeding efficiency, forest tree breeders need :

- to increase **precision** of genetic evaluation
- to reduce **selection age**
- to increase **selection intensity**
- to develop more **multi-trait selection**
- to better monitor **genetic diversity**



Molecular markers ($h^2=1$) tightly linked to genes involved in control of target traits can help them !



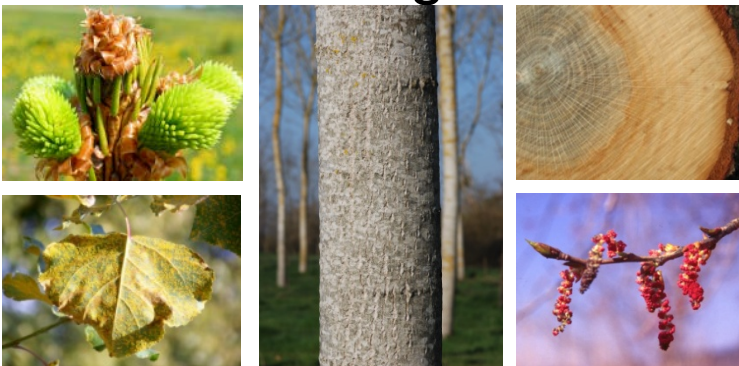
QTL Research

20 Years of QTL detection in forest trees

Quantitative Trait Loci

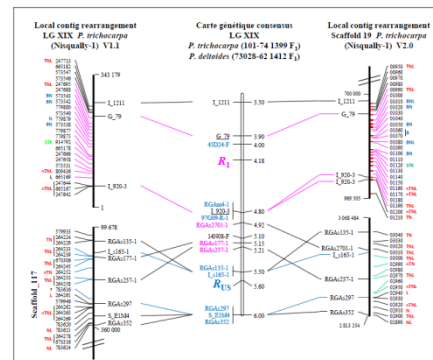
Breeders provided :

- Pedigrees :
- Phenotypic information for a wide range of traits

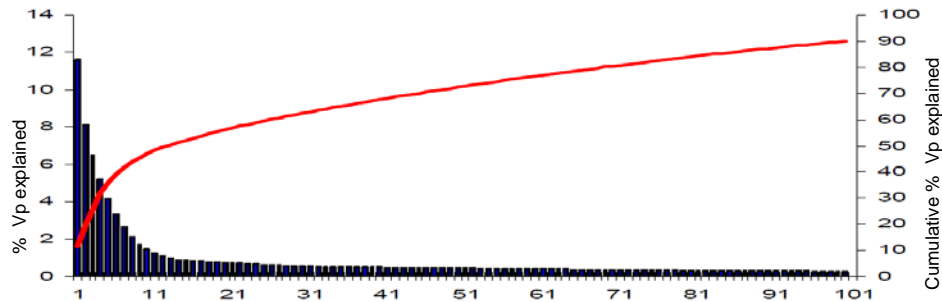


Molecular Geneticists provided :

- Molecular markers
RAPD, SSR, SNP,...
- Genetic maps

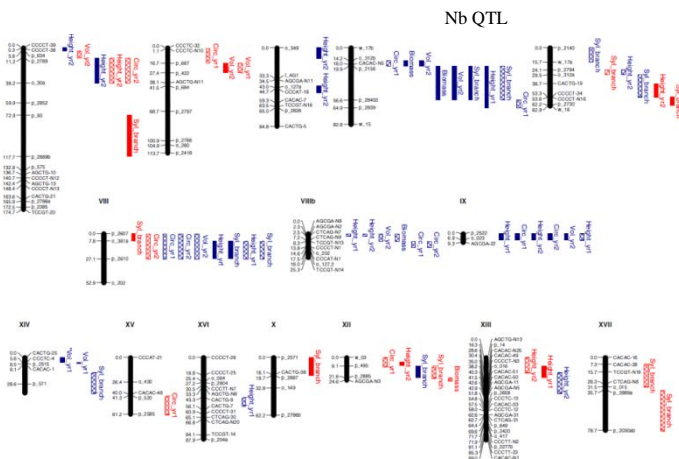


Results from 20 Years of QTL detection in forest trees



➤ Few loci with **high** effects (>25% Vp explained)

➤ Many loci with **small** effects (age, environment)



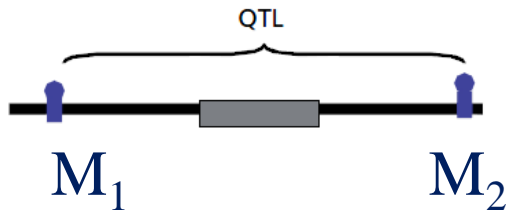
➤ Loci of interest are **widespread** on all chromosomes

➤ **epistatic** interactions exist

From Rae *et al.* *Tree Genetics and Genomes*, 2008

Potential of Marker Assisted Selection in forest trees

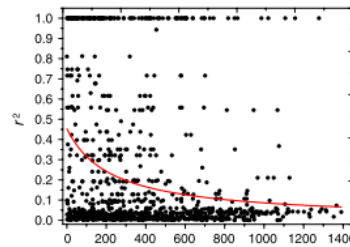
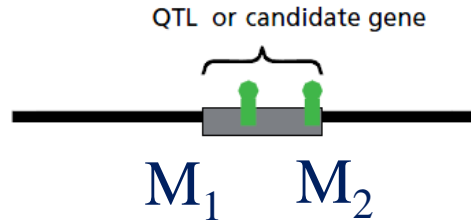
Flanking markers



- Request fine mapping & validation

- a small part of phenotypic variation explained

Markers in high LD with QTL or underlying gene

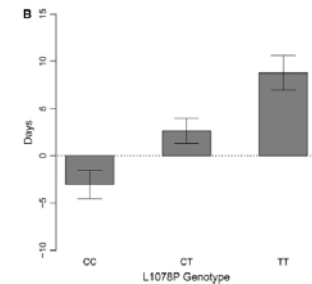
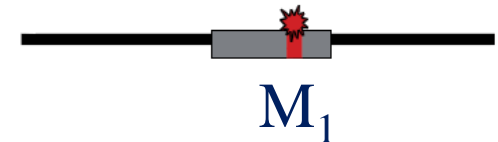


From Chu *et al. Genetica*, 2009

- Request high density of SNP markers

Causal mutation in underlying gene

Gene and exact polymorphism (QTN) identified



From Ingvarsson *et al., Genetics* 2008

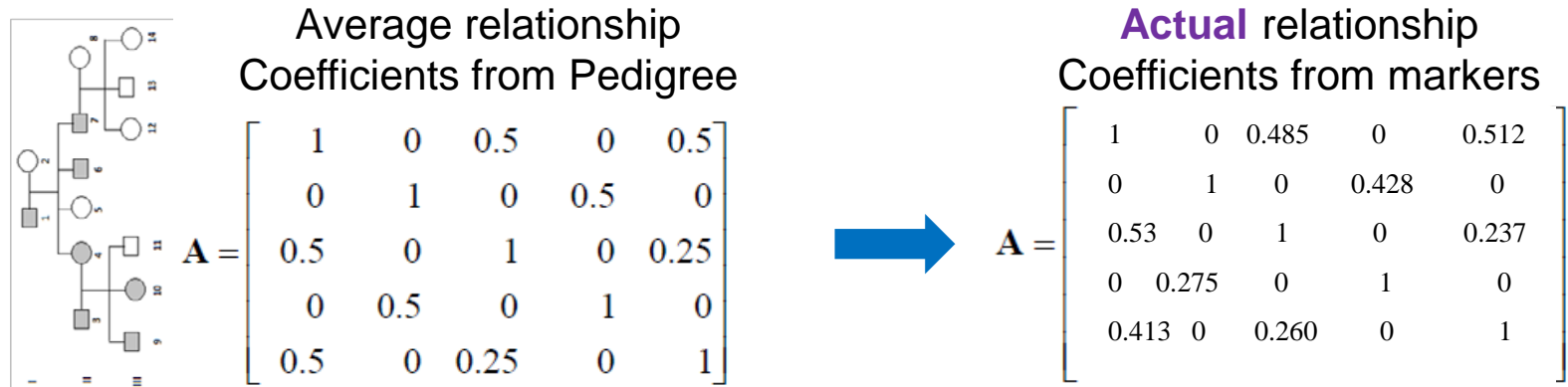
- Alleles with high additive effects are rare

Potential of Marker Assisted Selection in forest trees

➔ A **limited efficiency** to predict breeding values of traits of interest

BUT

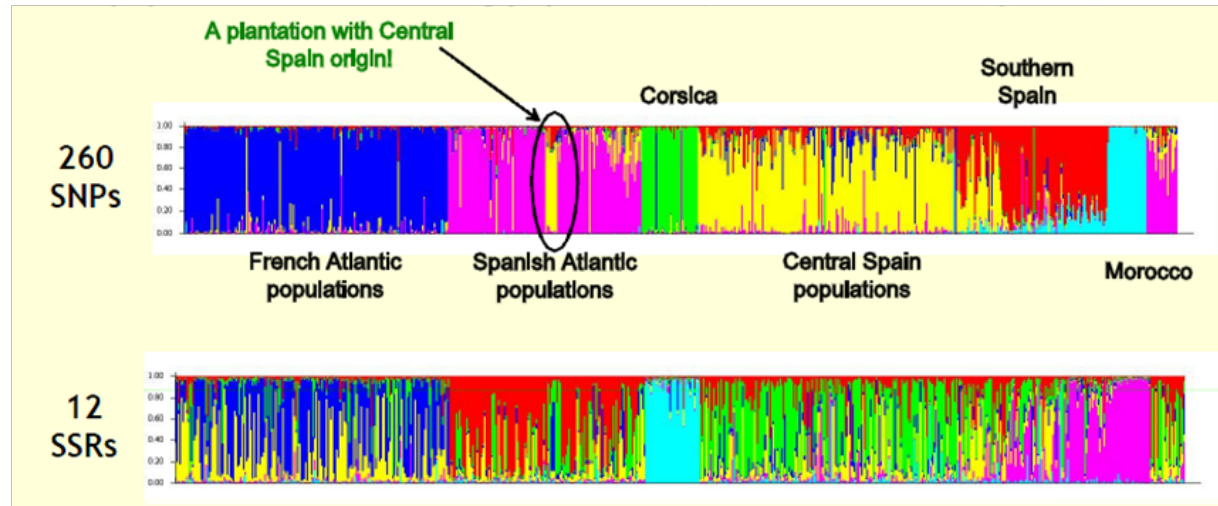
other perspectives are offered by molecular markers



- **Predict more precisely breeding values**
- **Allow better control of inbreeding**

Potential of Marker Assisted Selection in forest trees

Other perspectives offered by molecular markers



Gonzales-Martinez et al, NovelTree 2011

- High discrimination power for **certification** and **fingerprinting**

Potential of Marker Assisted Selection in forest trees

Other perspectives offered by molecular markers

Polymix Breeding

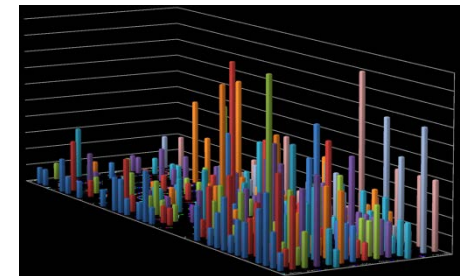
(Wheeler et al 2006)



	M1	M2	M3	M4	MixPol
F1	X	X	X	X	O
F2	X	X	X	X	O
F3	X	X	X	X	O

16 crosses

3 crosses



- Reduce crossing costs thanks to pedigree reconstruction in polymix families

New perspectives from high throughput tree genome sequencing

Large genomes for forest trees

Organisms	Genome size (bp)	% repetitive
<i>E. coli</i>	4.6 millions	
<i>Drosophila</i>	150 millions	
<i>Humans</i>	3 billions	43%
<i>A. thaliana</i>	130 millions (2n=10)	10%
<i>Poplar</i>	550 millions (2n=38)	40%
<i>Eucalyptus</i>	600 millions (2n=22)	6% ?
<i>Picea</i>	18-22 billions (2n=24)	70-75%
<i>Pinus</i>	25 billions (2n=24)	-

Reference Genome
Sequence

2006

2011



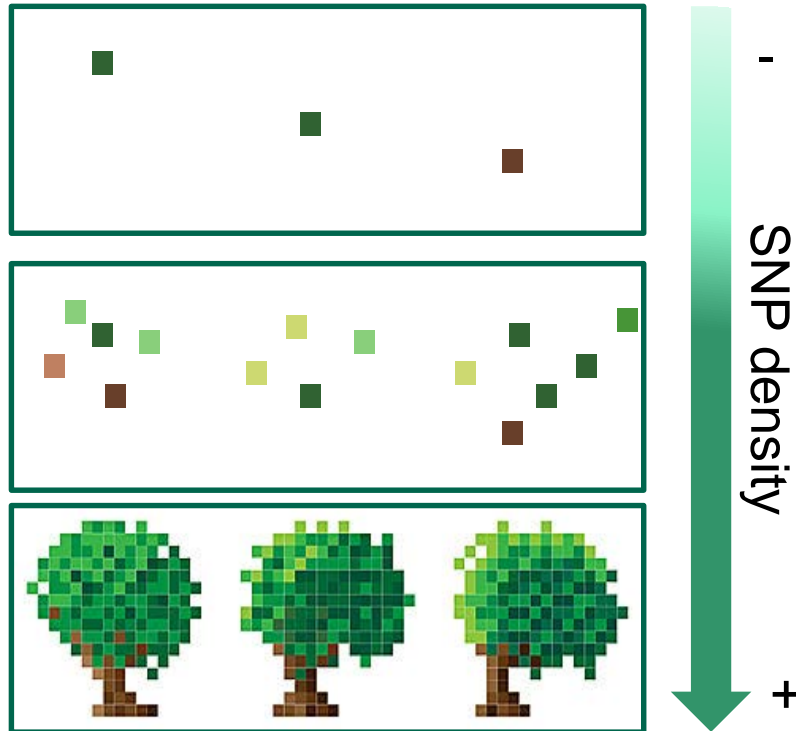
Under work in Sweden

Genome re-sequencing identifies today millions of SNPs
(3 Millions SNP from a resequencing panel of 52 *Populus nigra*)

New perspectives from high throughput tree genome sequencing

Genomic or Genome-wide selection

Meuwissen, 2001



A Reference or training population



A validation population

HT genotyping technologies
(50 000 – 300 000 SNPs)
and HT phénotyping

*There is no a priori on number or
position of underlying genes
It's a purely statistical approach*

$G = \text{Sum of all marker effects}$

Advices for forest tree breeders

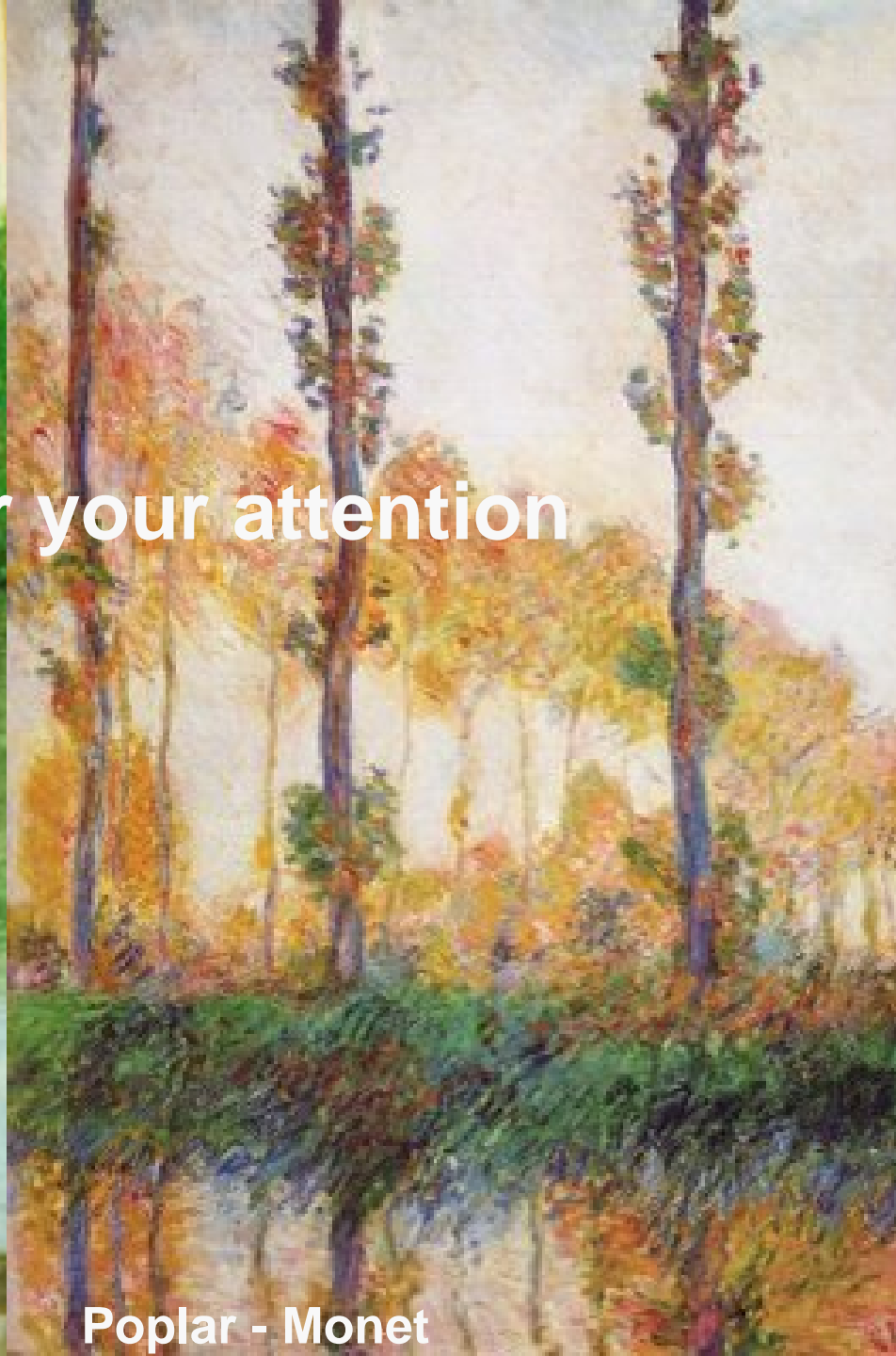


- Don't forget **high quality phenotyping !!!**
 - ✓ for good **association genetics**
 - ✓ for good **prediction** in MAS or GWS
 - ✓ for an optimized multi-trait **selection strategy**
- Genome sequences arise from **collaborative efforts**. But high quality **phenotyping** will also benefit of collaborative efforts (multi-environments, functional traits,...)
- It's time to prepare **breeding tools** which will be able to manage a huge quantity of phenotype + genotype data !!!

Thank you for your attention



Willow - Reigate Priory



Poplar - Monet