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.

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**

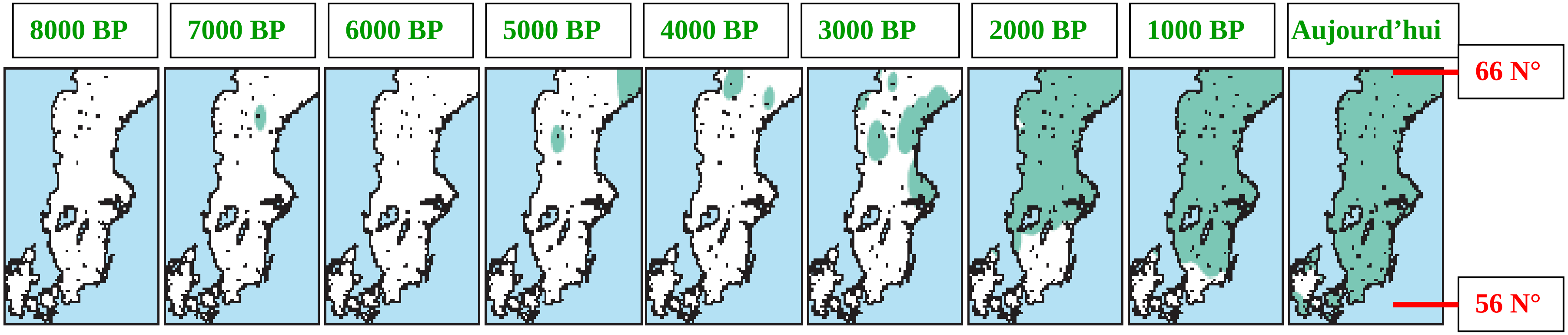
Maintain genetic gain for wood production

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

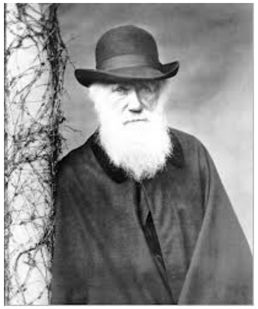
20 to 50 km per century !



Post quaternary glaciation migration of Spruce in Scandinavia

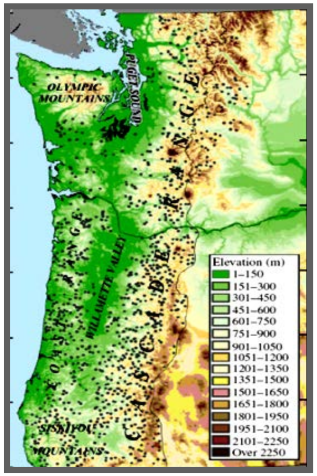
Hannerz et al 2000

- **Forests have already experienced climatic changes**



Selection = an evolutionary force at population level

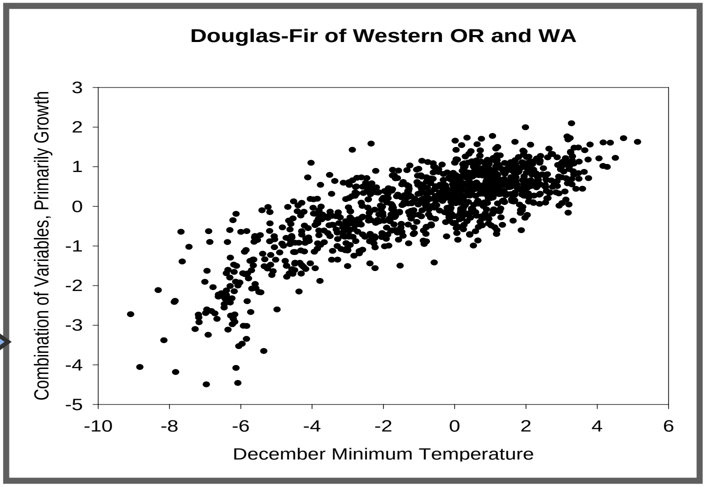
Large collection of natural populations



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

⬇

thanks to high genetic diversity present in forest tree populations

Genetic variation

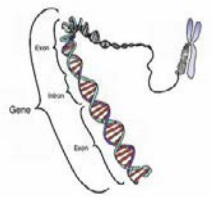
intensively investigated in tree breeding and in genomics

Up to now mainly through <u>Phenotype</u> 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

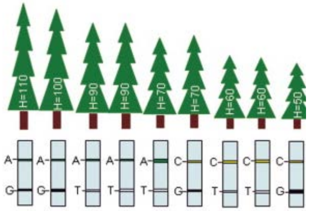
Genetic variation

intensively investigated in tree breeding and in genomics

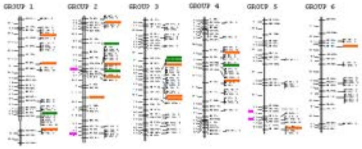


Up to now mainly through Genotype in genomics

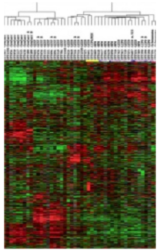
- DNA sequences of genes and individual genomes



- Nucleotide variation and Structural variants



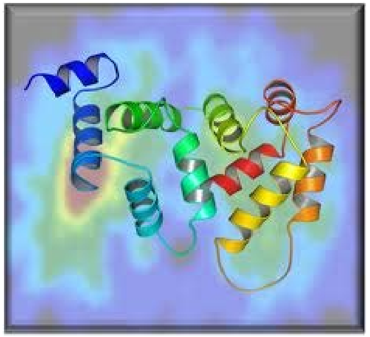
- Nb of genes involved in traits of interest, their effects and their position on genome



- 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 :

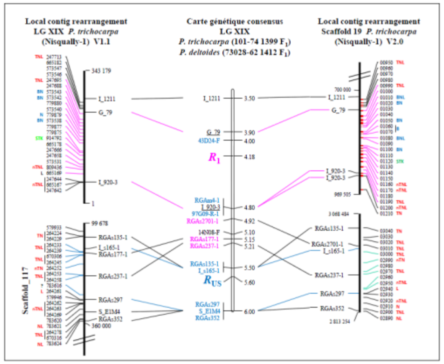
- Phenotypic information for a wide range of traits

Molecular Geneticists provided :

- Molecular markers

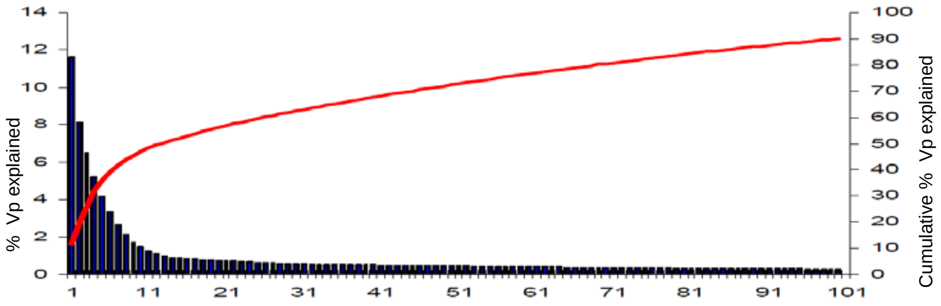
RAPD, SSR, SNP,…

- Genetic maps



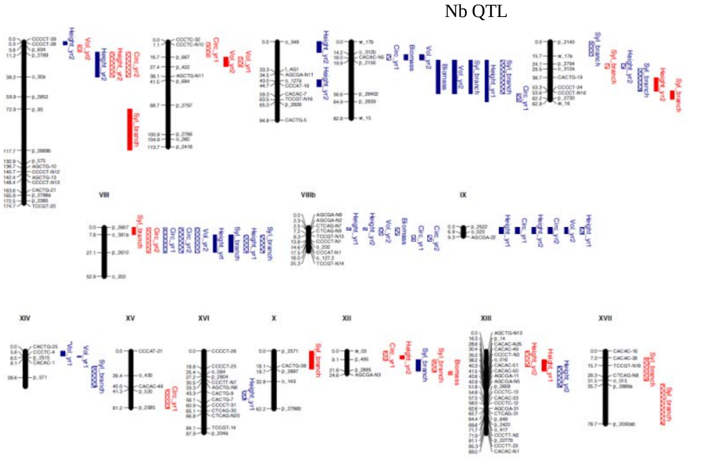
ALIMENTATION
AGRICULTURE
ENVIRONNEMENT

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)



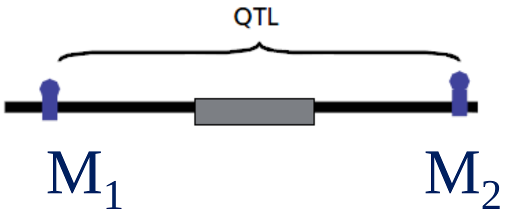
From Rae *et al. Tree Genetics and Genomes*, 2008

- Loci of interest are widespread on all chromosomes

- epistatic interactions exist

Potential of Marker Assisted Selection in forest trees

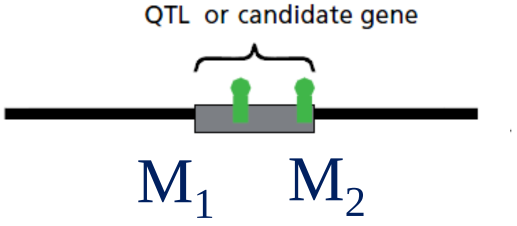
Flanking markers

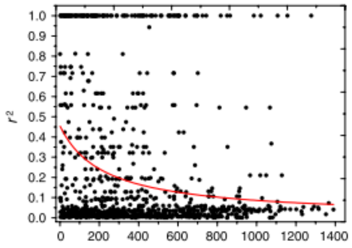


- Request fine mapping & validation
- a small part of phenotypic variation explained

Markers in high LD

with QTL or underlying gene



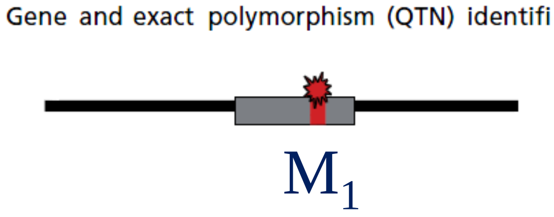


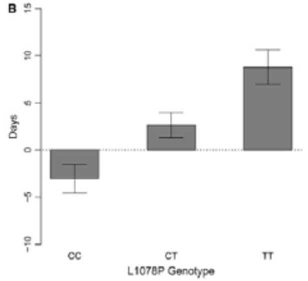
From Chu *et al.* *Genetica*, 2009

- Request high density of SNP markers

Causal mutation

in underlying gene





From Ingvarsson *et al*., Genetics 2008

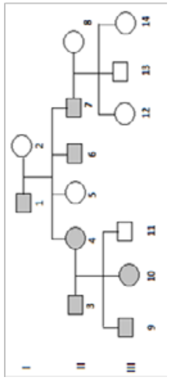
- Alleles with high additive effects are rare

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



Average relationship
Coefficients from Pedigree

$$\mathbf{A}=\begin{bmatrix} 1 & 0 & 0.5 & 0 & 0.5 \\ 0 & 1 & 0 & 0.5 & 0 \\ 0.5 & 0 & 1 & 0 & 0.25 \\ 0 & 0.5 & 0 & 1 & 0 \\ 0.5 & 0 & 0.25 & 0 & 1 \end{bmatrix}$$

→

Actual relationship
Coefficients from markers

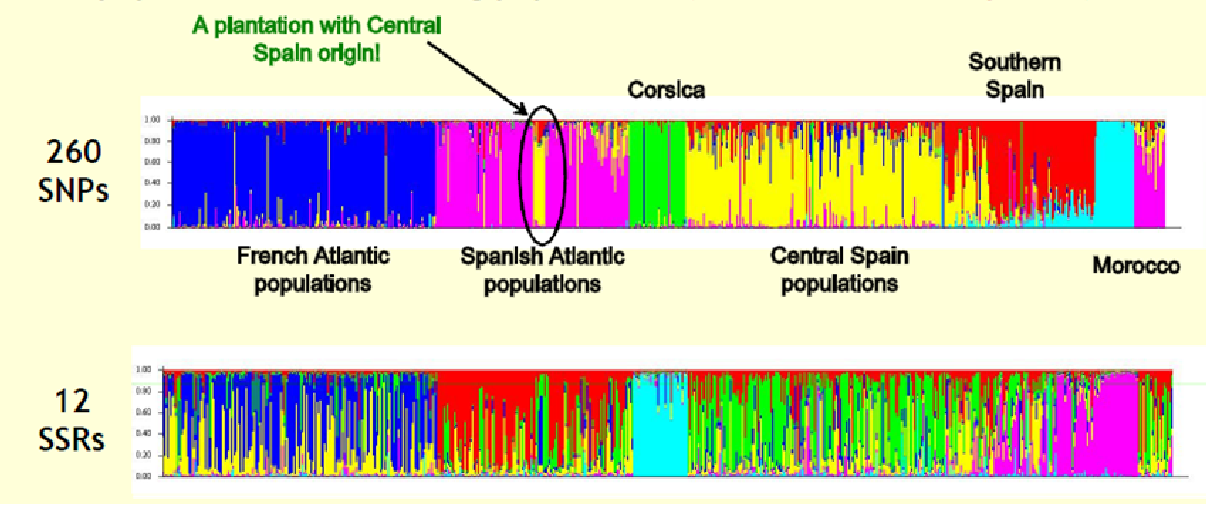
$$\mathbf{A}=\begin{bmatrix} 1 & 0 & 0.485 & 0 & 0.512 \\ 0 & 1 & 0 & 0.428 & 0 \\ 0.53 & 0 & 1 & 0 & 0.237 \\ 0 & 0.275 & 0 & 1 & 0 \\ 0.413 & 0 & 0.260 & 0 & 1 \end{bmatrix}$$

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

Potential of Marker Assisted Selection in forest trees

Other perspectives offered by molecular markers

Maritime pine



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

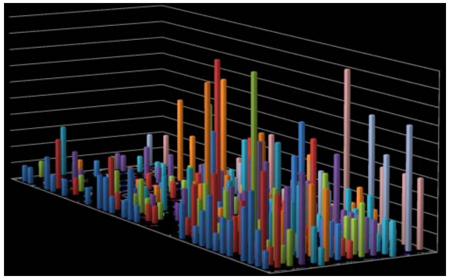
Polymix Breeding

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

Reference Genome Sequence

2006

2011

Under work in Sweden

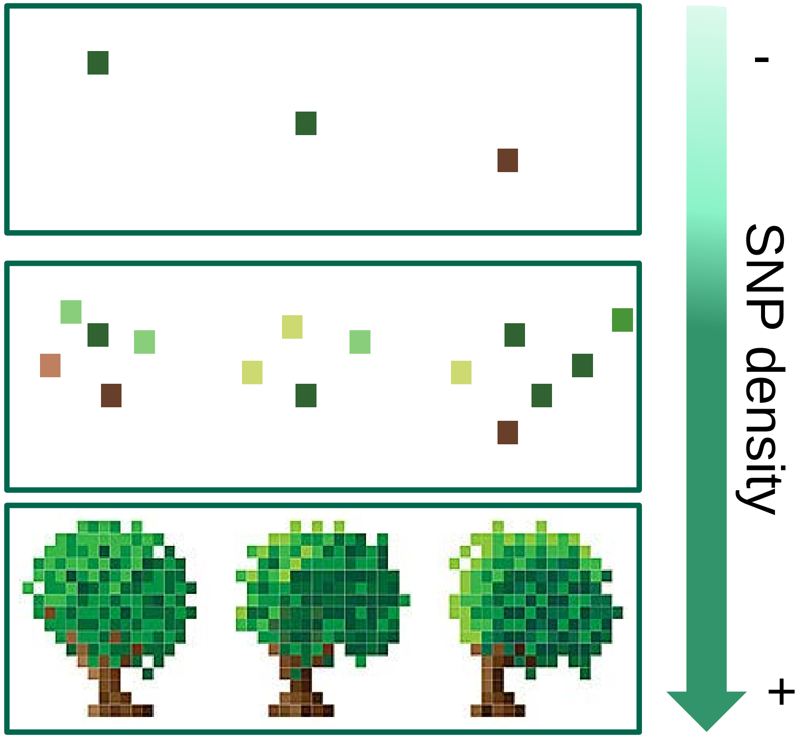
Genome re-sequencing identifies today millions of SNPs

(3 Millions SNP from a resequencing panel of 52 Populus nigra)

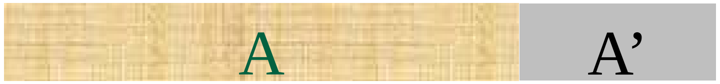
New perspectives from high throughput tree genome sequencing

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 = Sum of all marker effects

Advices for forest tree breeders

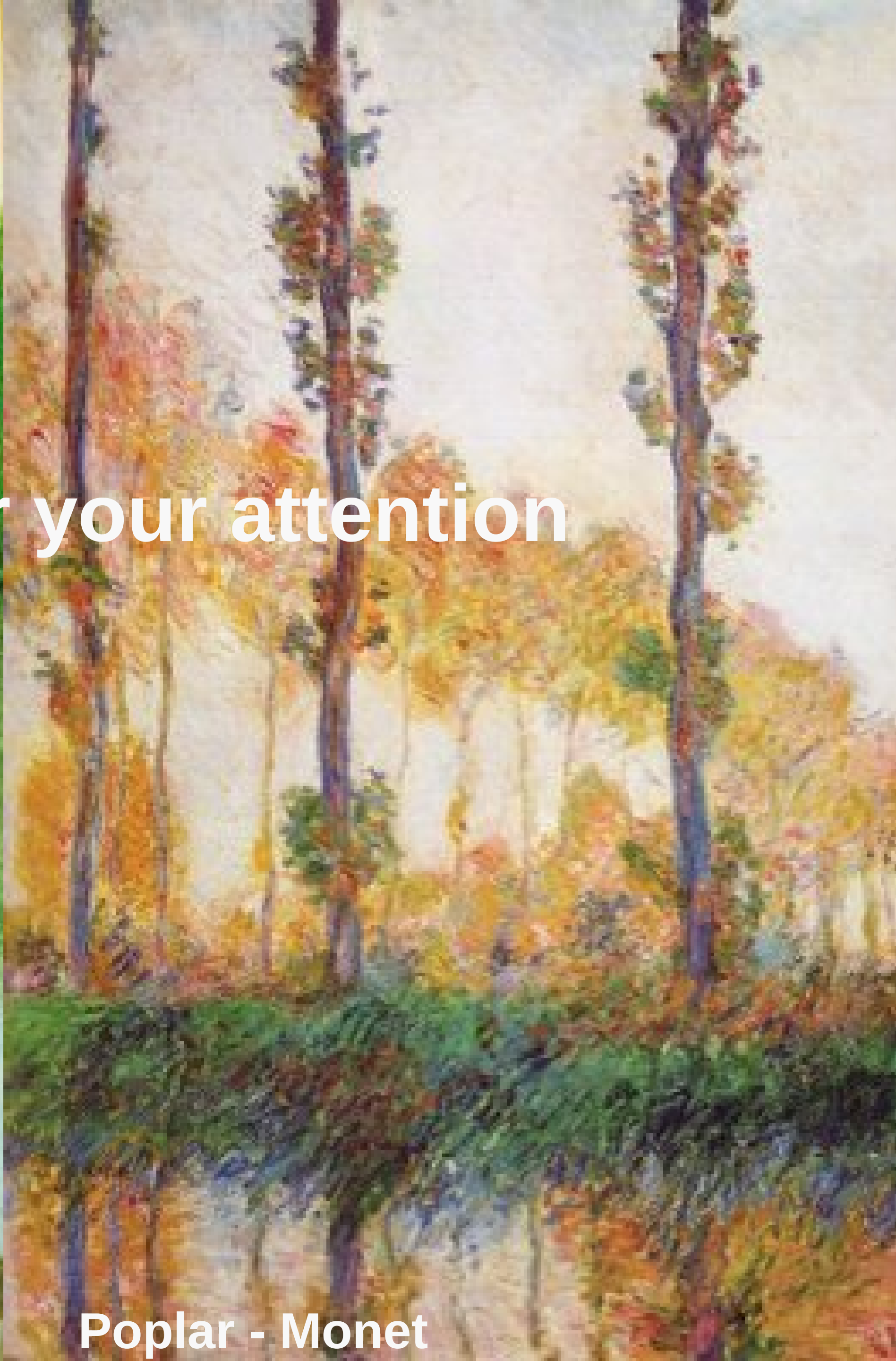
- Don't forget **high quality phenotyping** !!!
  - ✓ for good **association genetics**
  - ✓ for good **prediction** in MAS or GWS
  - ✓ for an optimized multi-trait **selection strategy**

- 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