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

Catherine Bastien

HAL Id: hal-02803576
https://hal.inrae.fr/hal-02803576

Submitted on 5 Jun 2020

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

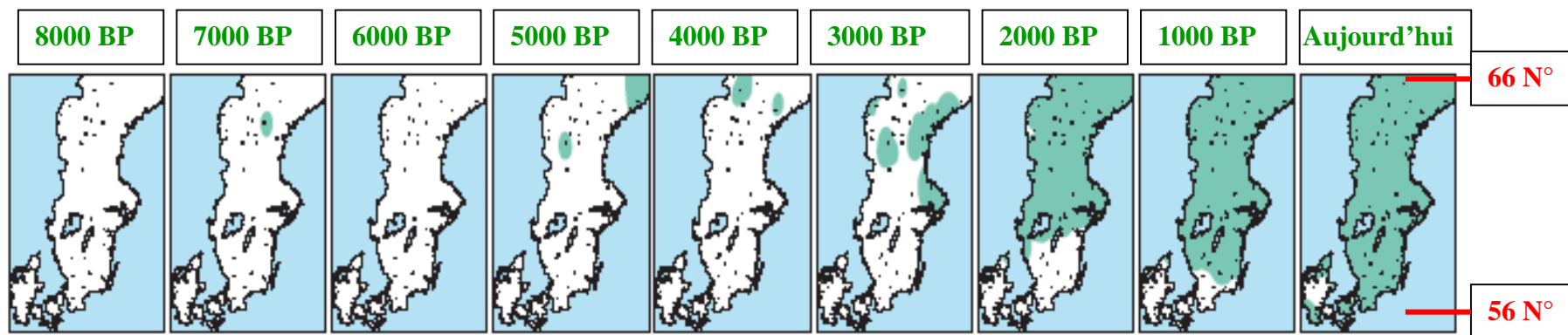Assist adaptation of forest
to climate changes

• Forests have already experienced climatic changes

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

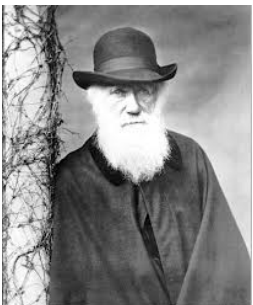20 to 50 km per century !

| 8000 BP | 7000 BP | 6000 BP | 5000 BP | 4000 BP | 3000 BP | 2000 BP | 1000 BP | Aujourd'hui |

66 N°

56 N°

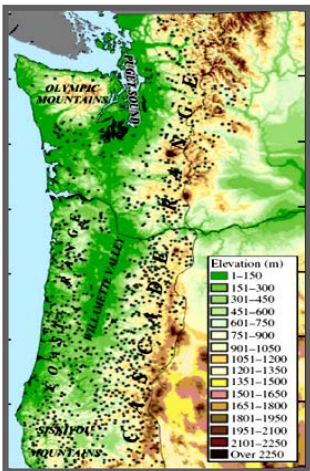Post quaternary glaciation migration of Spruce in Scandinavia

Hannerz et al 2000

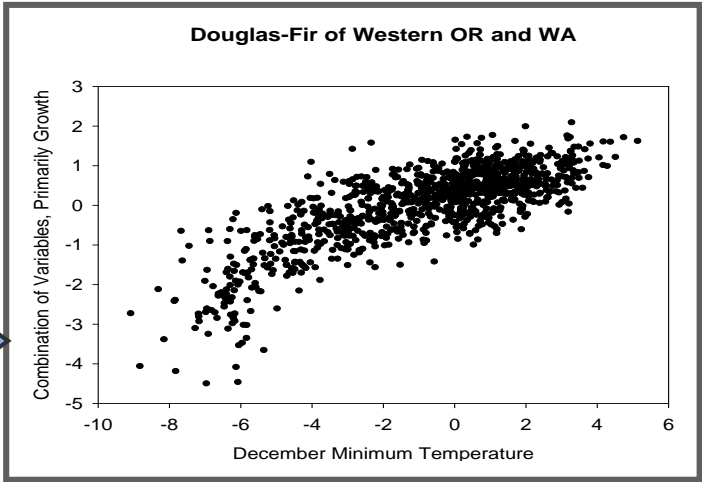# • **Forests have already experienced climatic changes**

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

Douglas-Fir of Western OR and WA

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
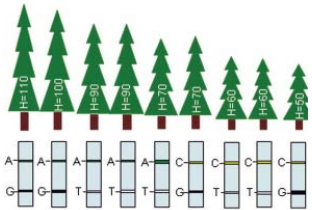
Genetic variation
intensively investigated in tree breeding and in genomics

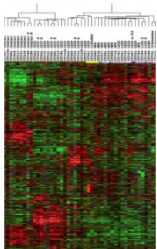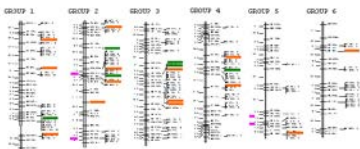**Up to now mainly through <u>Genotype</u> in genomics**
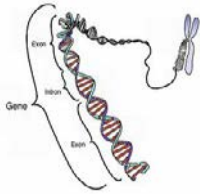
- DNA sequences of genes and individual genomes

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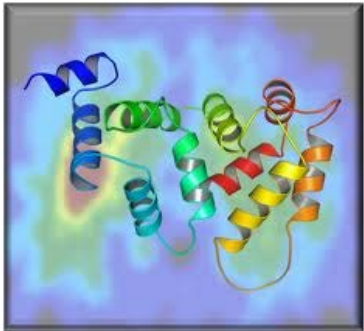
Molecular markers (h^2=1) tightly linked to genes involved in control of target traits can help them !

QTL Research

20 Years of QTL detection in forest trees
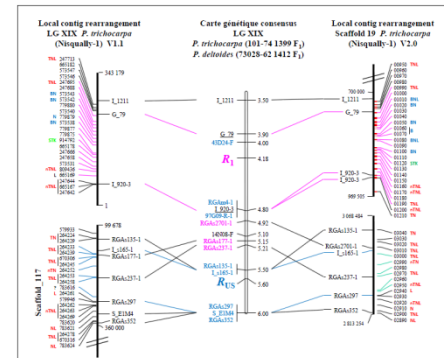
Quantitative Trait Loci

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)
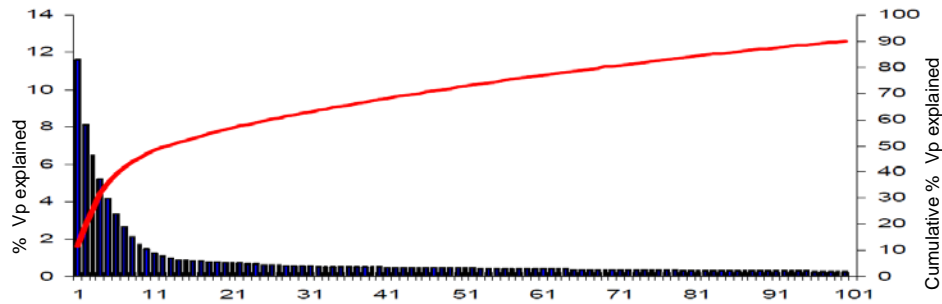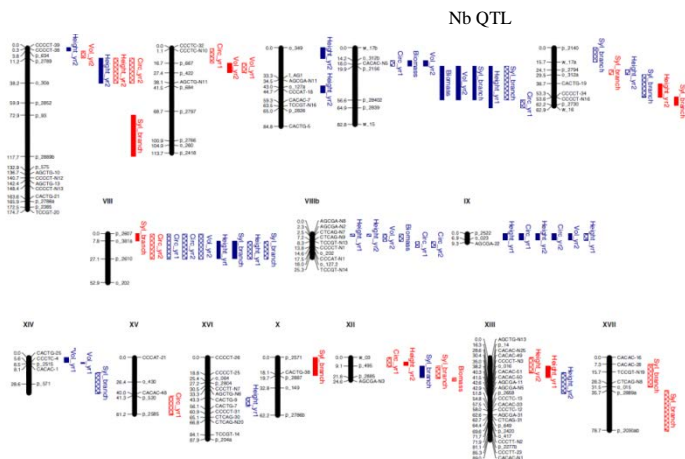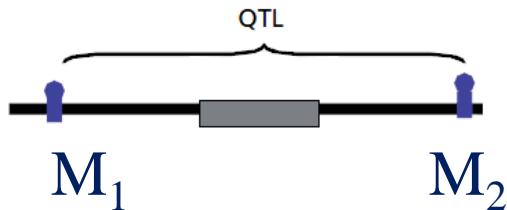
➤ Loci of interest are widespread on all chromosomes

➤ epistatic interactions exist

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

Potential of Marker Assisted Selection
in forest trees

Flanking markers

Markers in high LD
with QTL or underlying gene

Causal mutation
in underlying gene

QTL

M_1 M_2

QTL or candidate gene

M_1 M_2
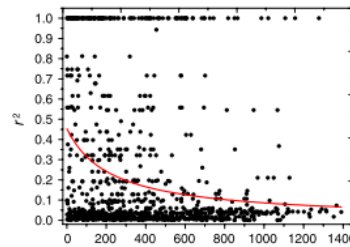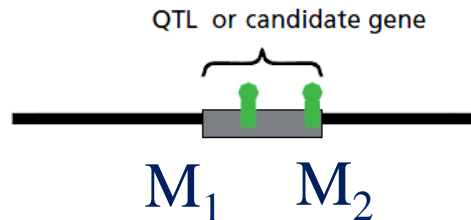
From Chu *et al. Genetica*, 2009

Gene and exact polymorphism (QTN) identifi

M_1
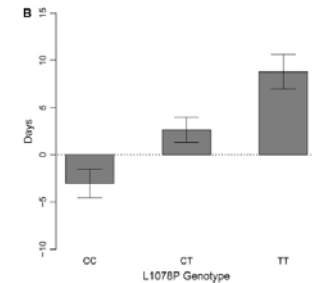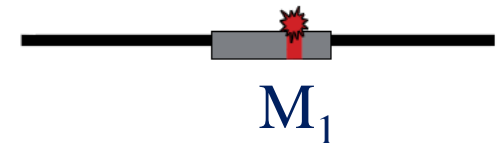
From Ingvarsson *et al.*, Genetics 2008

- Request fine mapping & validation

- a small part of phenotypic variation explained

- Request high density of SNP markers

- 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

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

Actual relationship
Coefficients from markers

$$A = \begin{bmatrix} 1 & 0 & 0.485 & 0 & 0.512 \\ 0 & 1 & 0 & 0.428 & 0 \\ 0.53 & 0 & 1 & 0 & 0.237 \\ 0 & 0.275 & 0 & 1 & 0 \\ 0.413 & 0 & 0.260 & 0 & 1 \end{bmatrix}$$
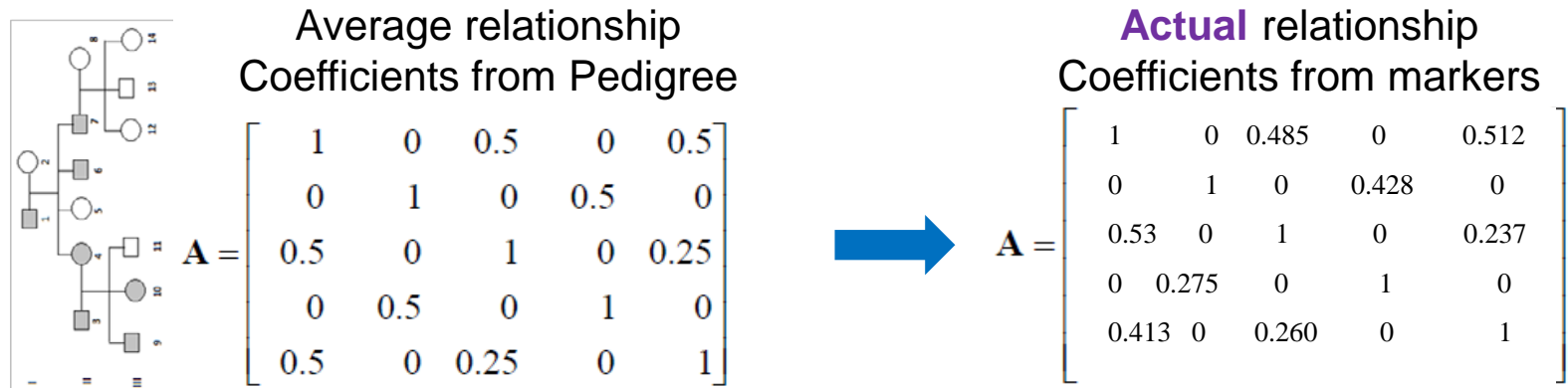
- **Predict more precisely breeding values**

- **Allow better control of inbreeding**

Potential of Marker Assisted Selection in forest trees
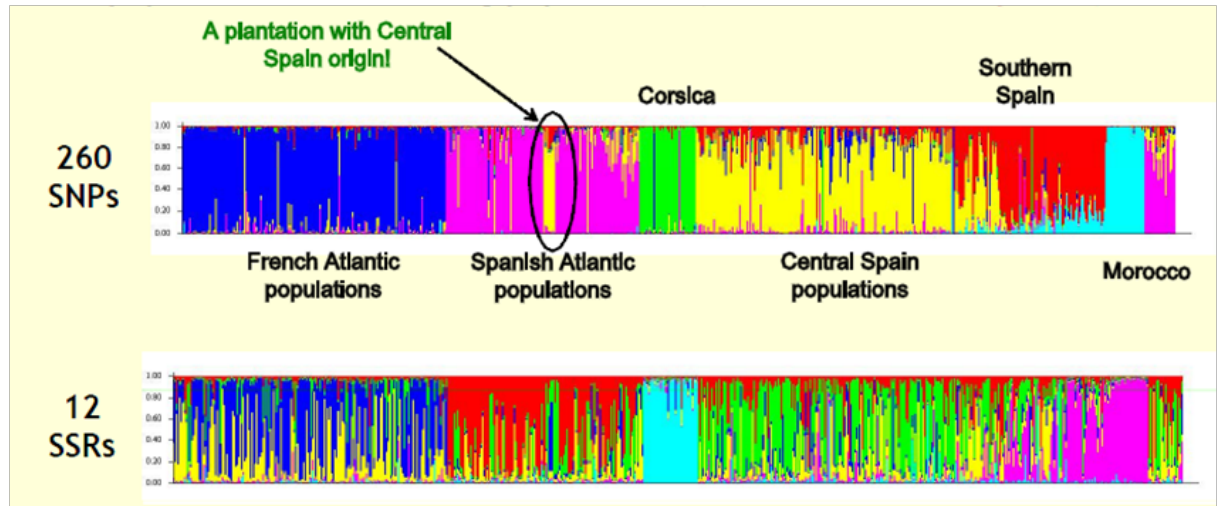
Other perspectives offered by molecular markers

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
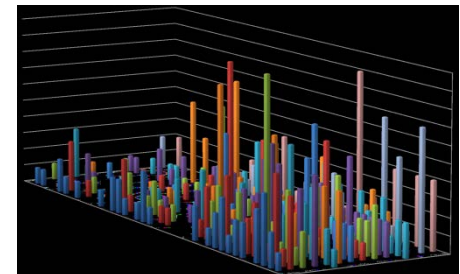
- **Reduce crossing costs thanks to pedigree reconstruction in polymix families**

INRA

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
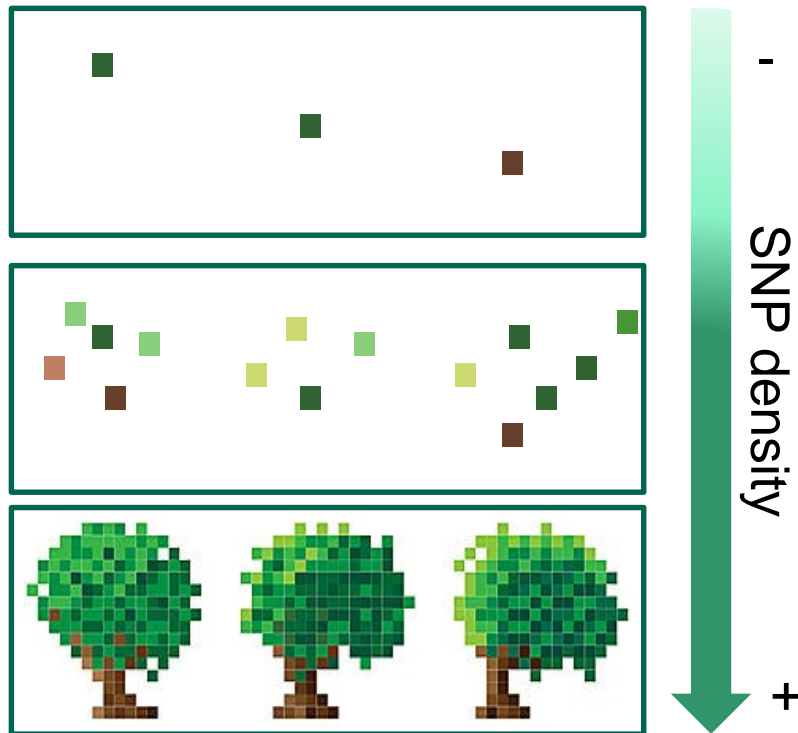
A Reference or training population

A	A'

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

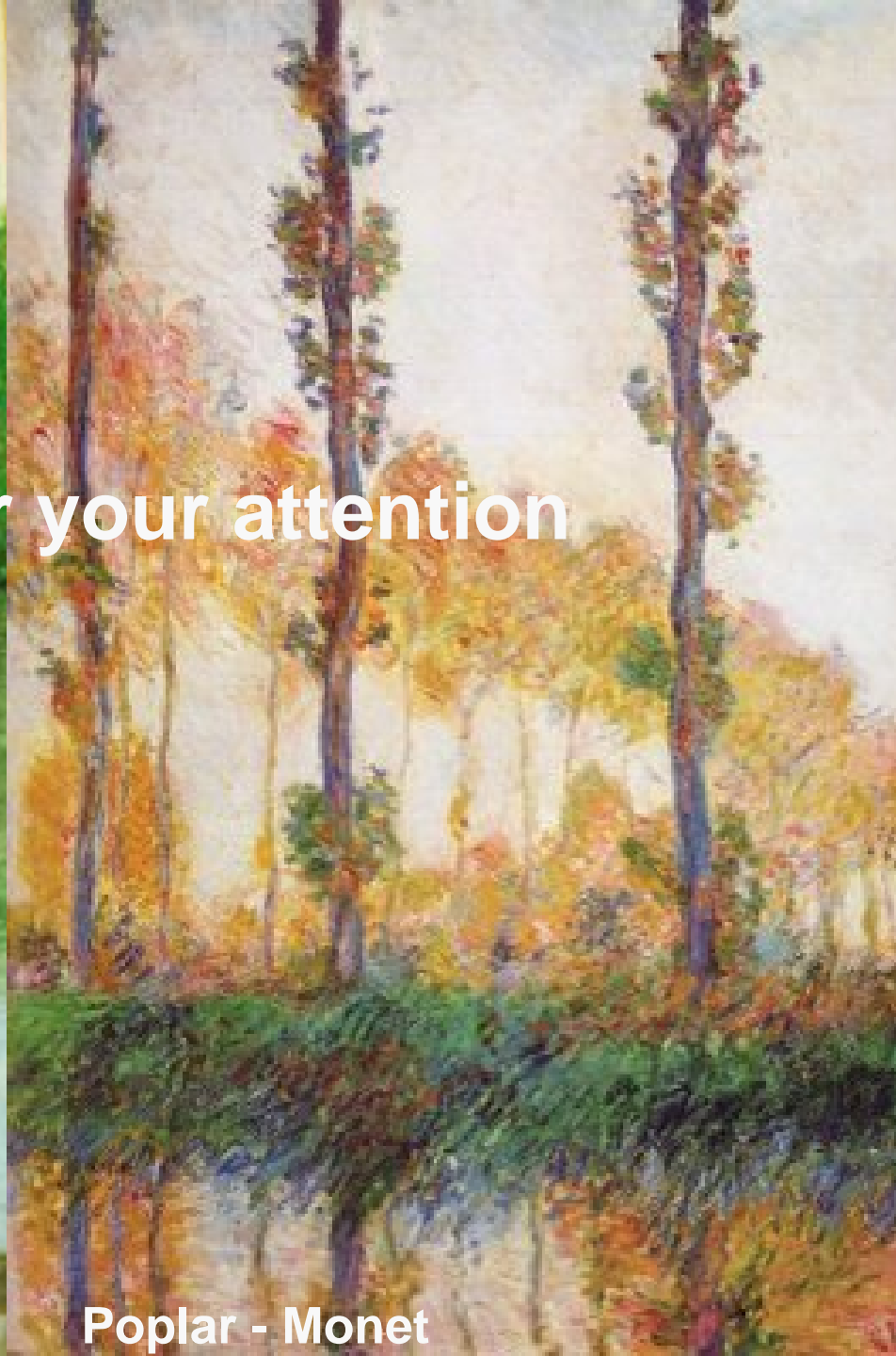SNP density

\-

\+

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