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

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Collaborative Research in forest genomics and tree breeding :

*Mutual benefits and future contribution
to adaptation of forests*

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ALIMENTATION
AGRICULTURE
ENVIRONNEMENT

INRA

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

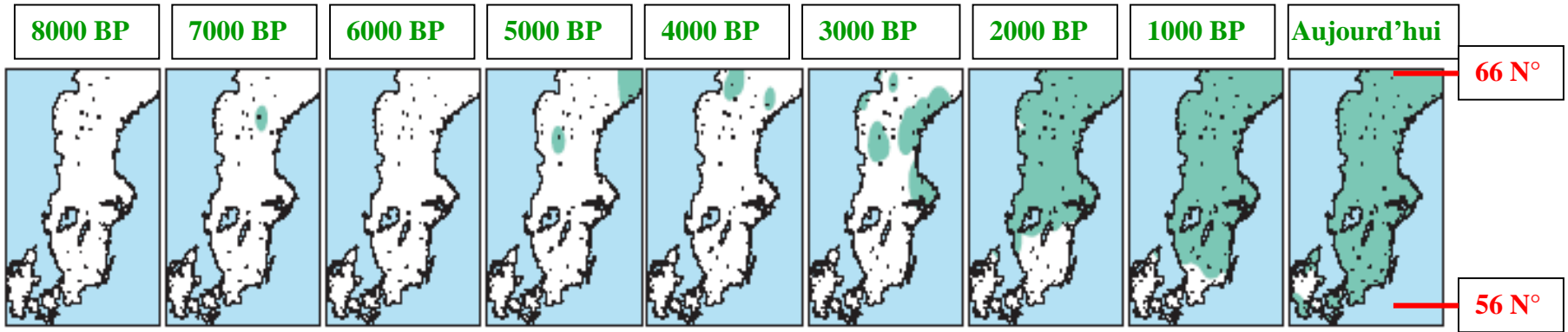


- Forests have already experienced climatic changes

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



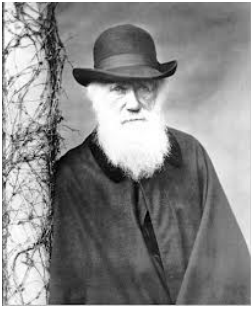
20 to 50 km per century !



Post quaternary glaciation migration of Spruce in Scandinavia

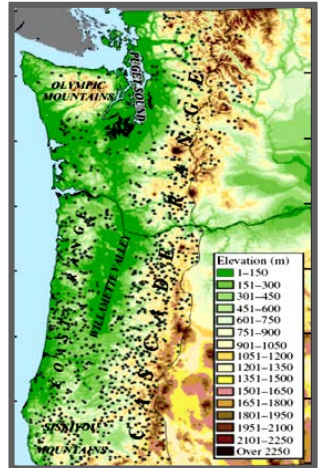
Hannerz et al 2000

• Forests have already experienced climatic changes



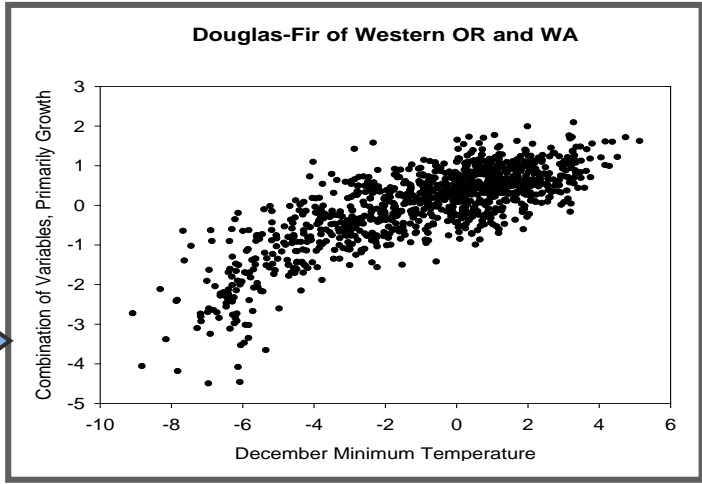
Selection = an evolutionary force at population level

Large collection of natural populations



Douglas-fir
St Clair et al 2005

Studies in common gardens



Clinal variation along temperature gradients

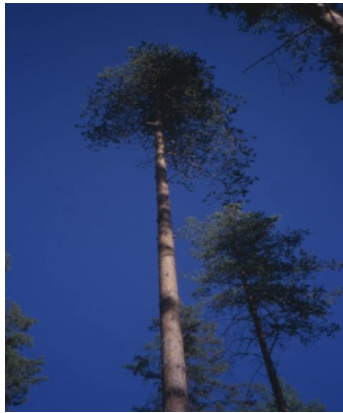
**Tree breeders could combine
assisted migration and
accelerated artificial selection
to assist adaptation of forests**



Genetic variation

intensively investigated in tree breeding and in genomics

Up to now mainly through Phenotype in tree breeding



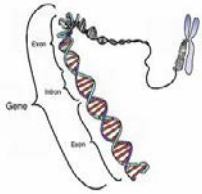
- Resemblance of phenotypes of related individuals is a proxy of **Breeding Value**
- Variation of phenotype of a given individual across environments describes **phenotypic plasticity**
- Breeding values allow prediction of **adaptive and economical gains** from selection



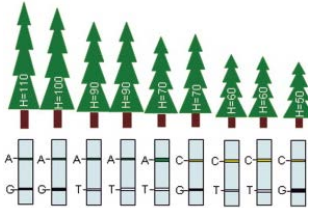
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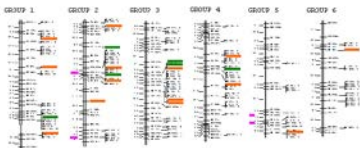


- DNA sequences of genes and individual genomes

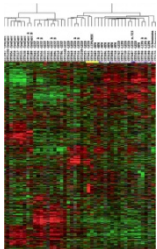


- Nucleotide variation and Structural variants

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

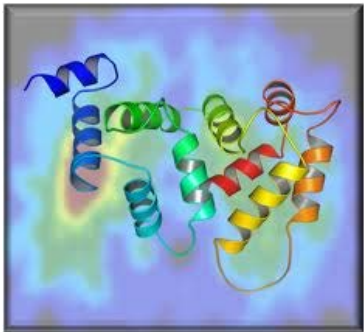


- Gene expression and gene function



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

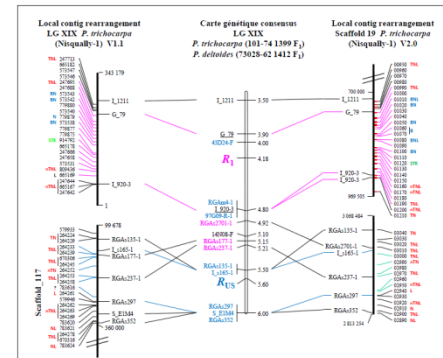
Breeders provided :

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

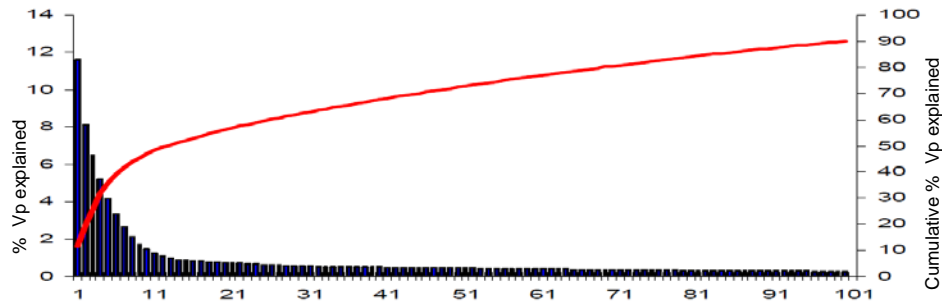


Molecular Geneticists provided :

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

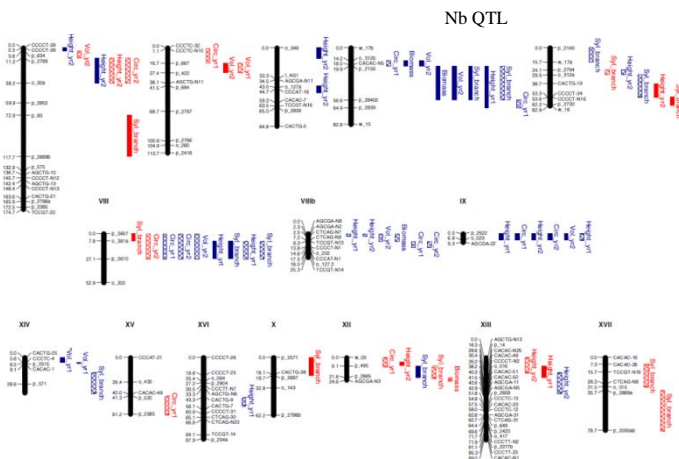


Results from 20 Years of QTL detection in forest trees



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

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



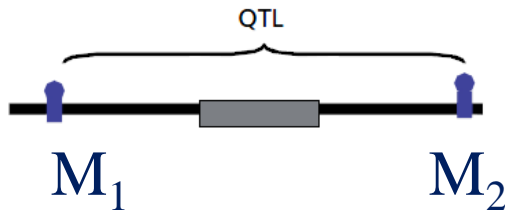
➤ Loci of interest are **widespread** on all chromosomes

➤ **epistatic** interactions exist

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

Potential of Marker Assisted Selection in forest trees

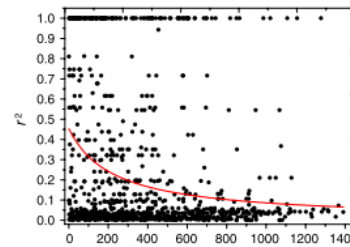
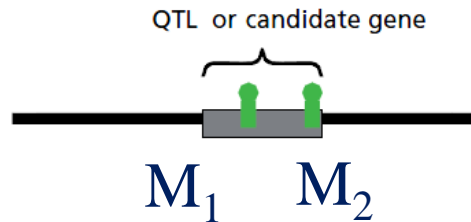
Flanking markers



- Request fine mapping & validation

- a small part of phenotypic variation explained

Markers in high LD with QTL or underlying gene

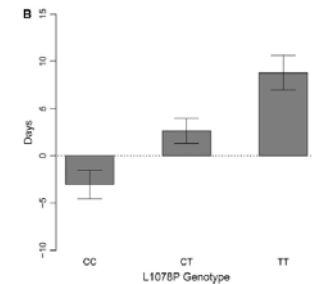
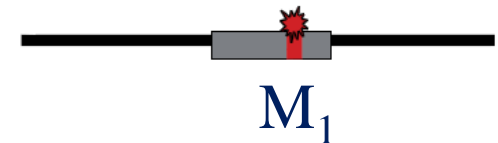


From Chu *et al. Genetica*, 2009

- Request high density of SNP markers

Causal mutation in underlying gene

Gene and exact polymorphism (QTN) identified



From Ingvarsson *et al., Genetics* 2008

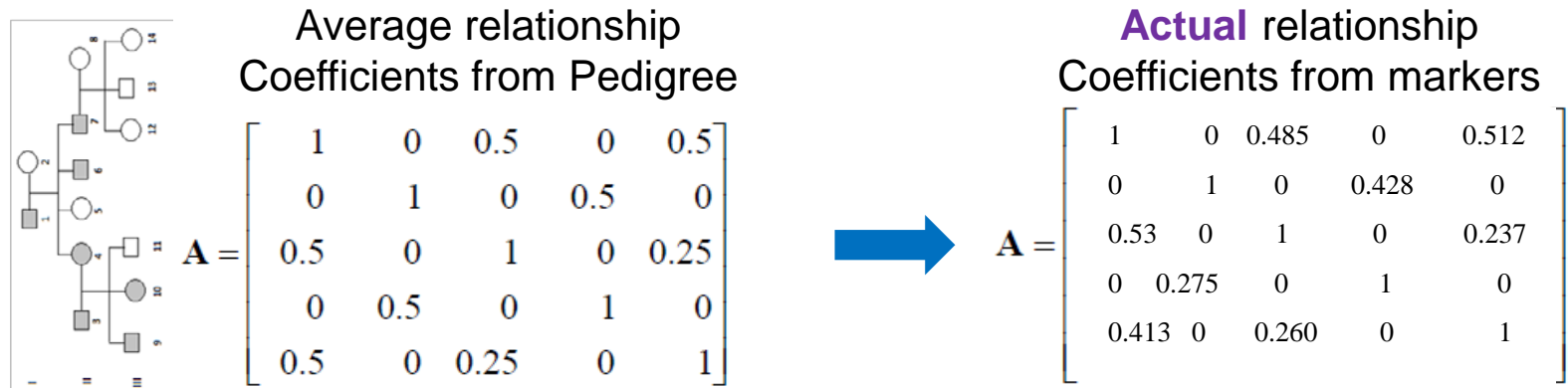
- Alleles with high additive effects are rare

Potential of Marker Assisted Selection in forest trees

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

BUT

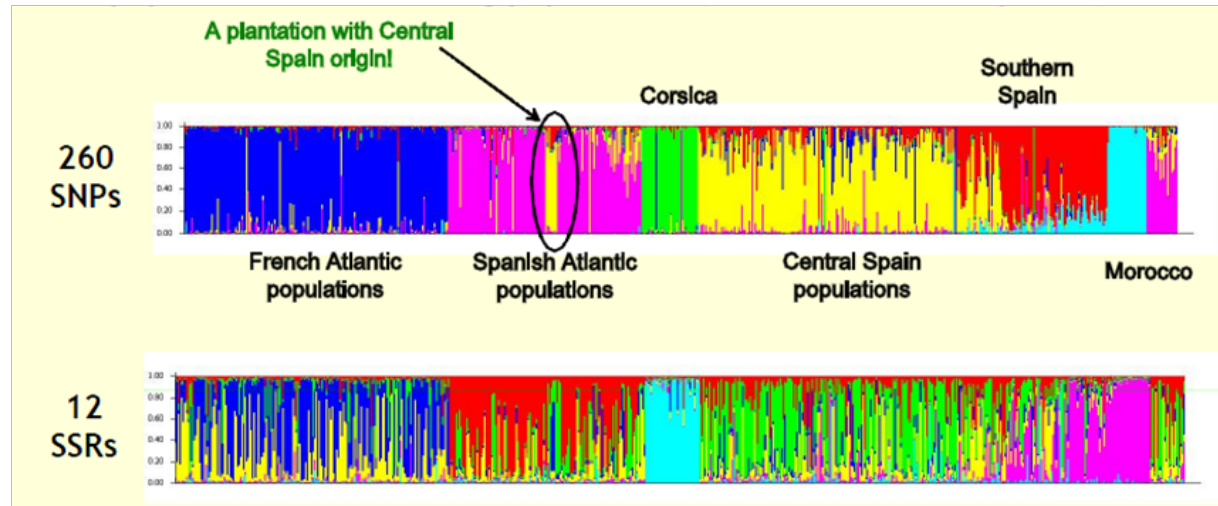
other perspectives are offered by molecular markers



- **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

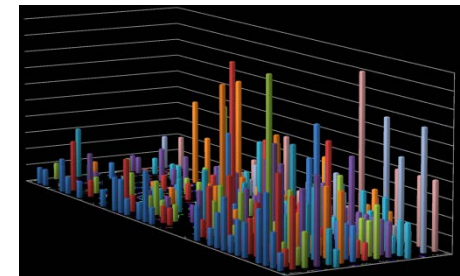
(Wheeler et al 2006)



	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



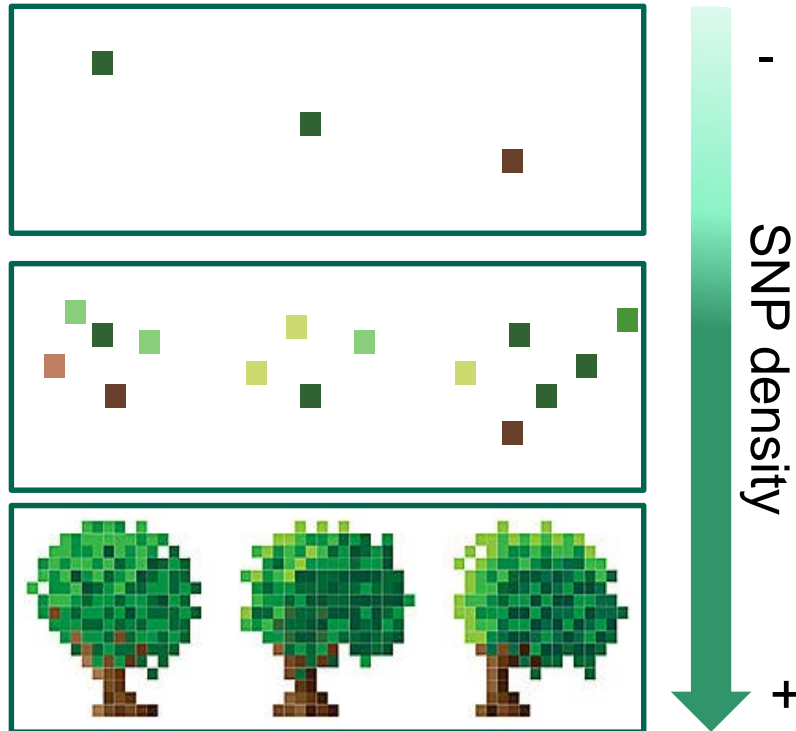
Under work in Sweden

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

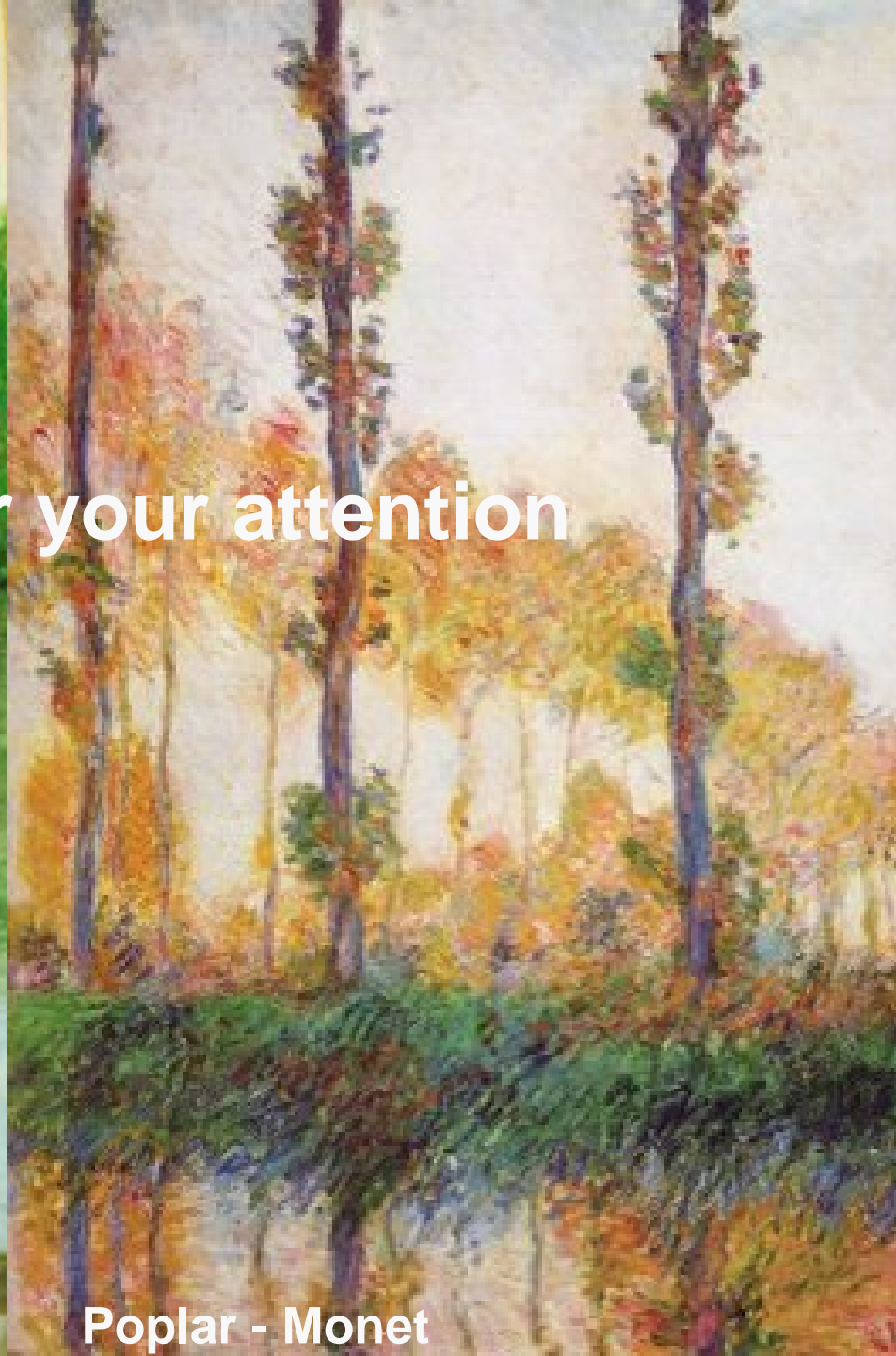


- Don't forget **high quality phenotyping !!!**
 - ✓ for good **association genetics**
 - ✓ for good **prediction** in MAS or GWS
 - ✓ for an optimized multi-trait **selection strategy**
- Genome sequences arise from **collaborative efforts**. But high quality **phenotyping** will also benefit of collaborative 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