



# Response to artificial selection in the maritime pine breeding program

Laurent Bouffier

## ► To cite this version:

Laurent Bouffier. Response to artificial selection in the maritime pine breeding program. Aurora Conference, Nov 2015, Bordeaux, France. hal-02792446

HAL Id: hal-02792446

<https://hal.inrae.fr/hal-02792446v1>

Submitted on 7 Oct 2024

**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.



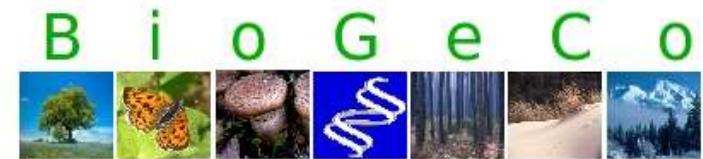
Distributed under a Creative Commons Attribution - NonCommercial 4.0 International License

Aurora meeting – November 4th, 2015



# Response to artificial selection in the maritime pine breeding program

Laurent Bouffier



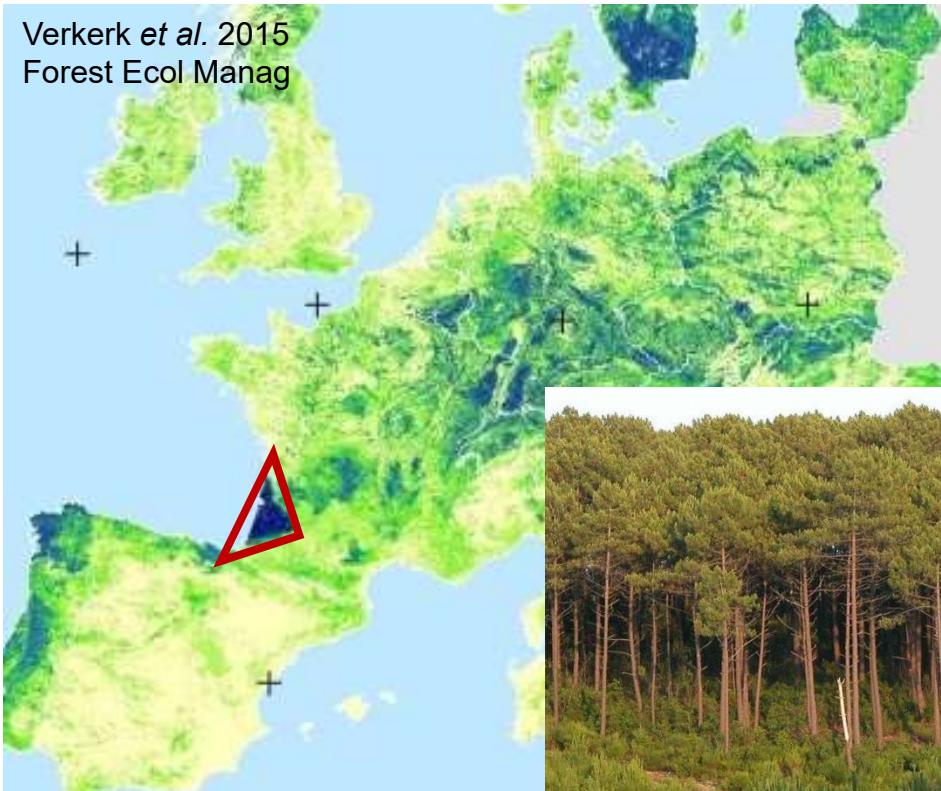
Biodiversité, gènes & communautés

- The maritime pine breeding program
- The current genetic evaluation system
- Genetic gains in improved varieties
- Evolution of genetic variation in successive breeding populations



**Maritime pine in France**

# Maritime pine in France

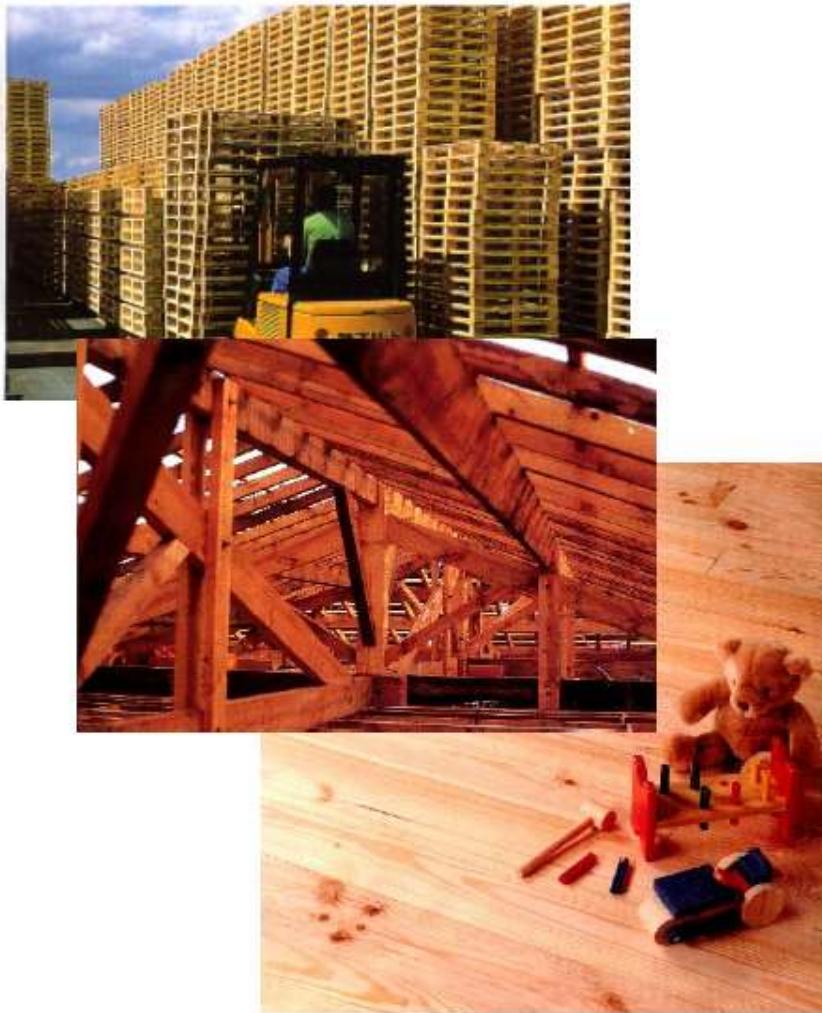


- Main plantation species
  - 10% of French forests
  - 24% of the harvest



- In Aquitaine
  - 0.8 million ha
  - 11 m<sup>3</sup>/ha/year
  - 8.5 M m<sup>3</sup> harvested /year

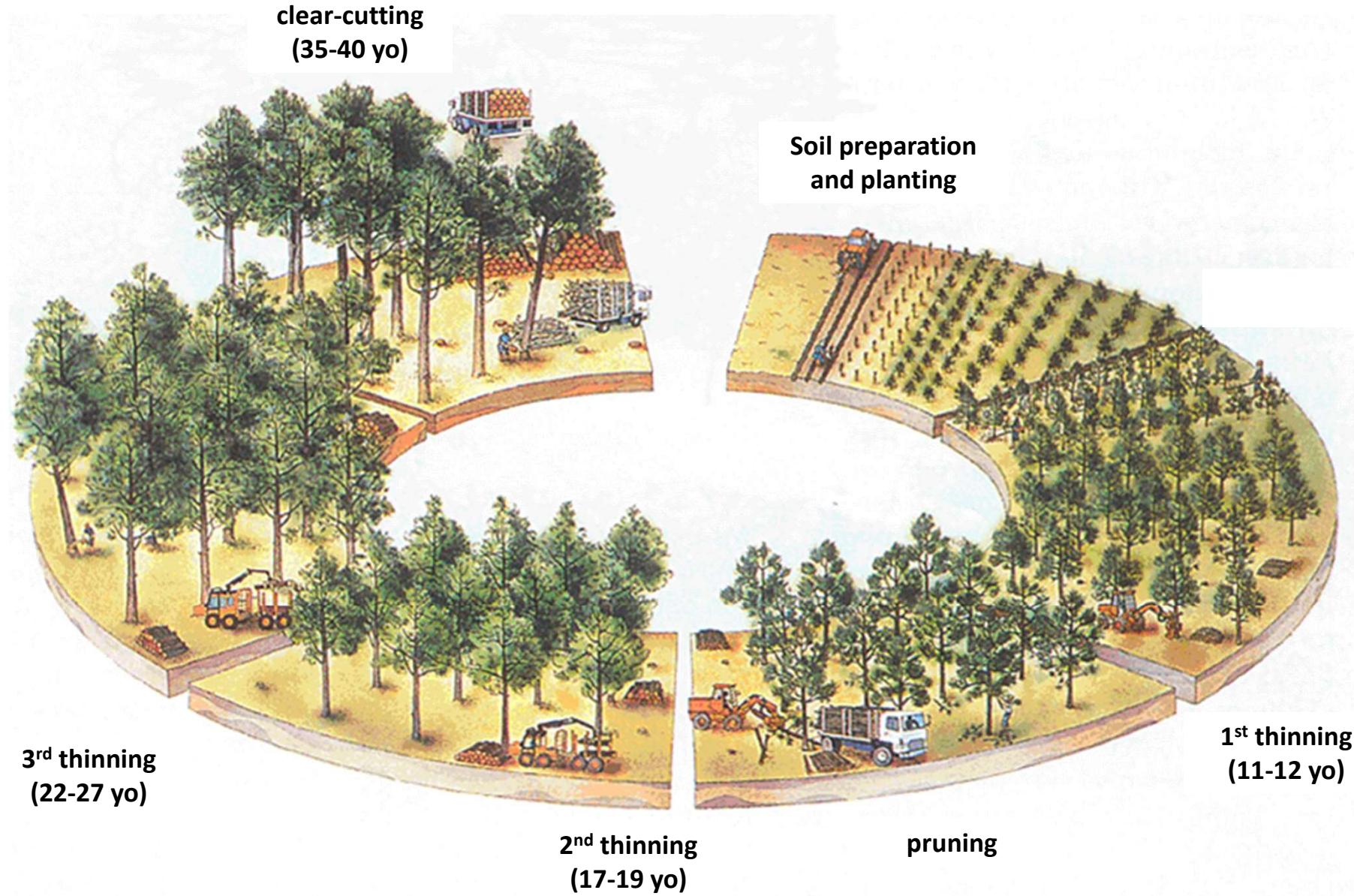
60% : Sawtimber



40% : Industrial wood

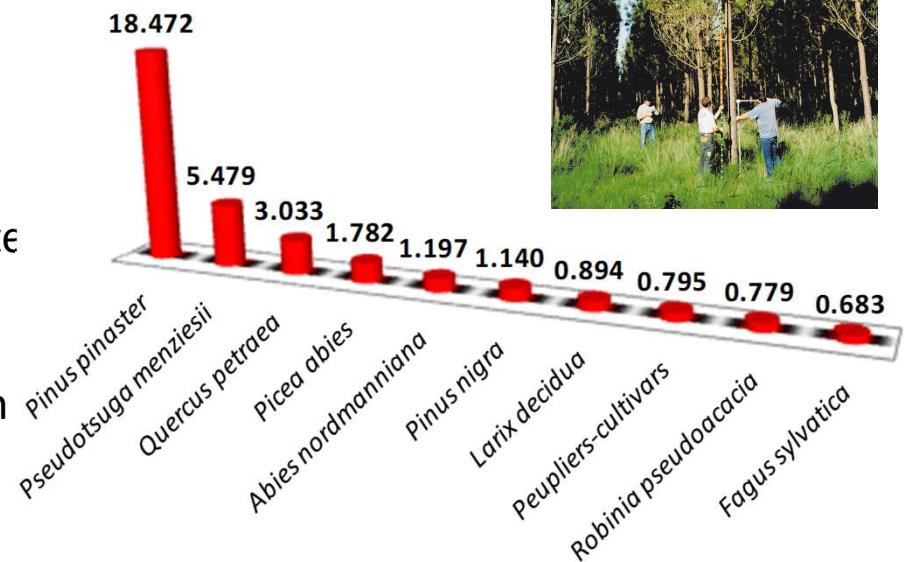


# Maritime pine plantations

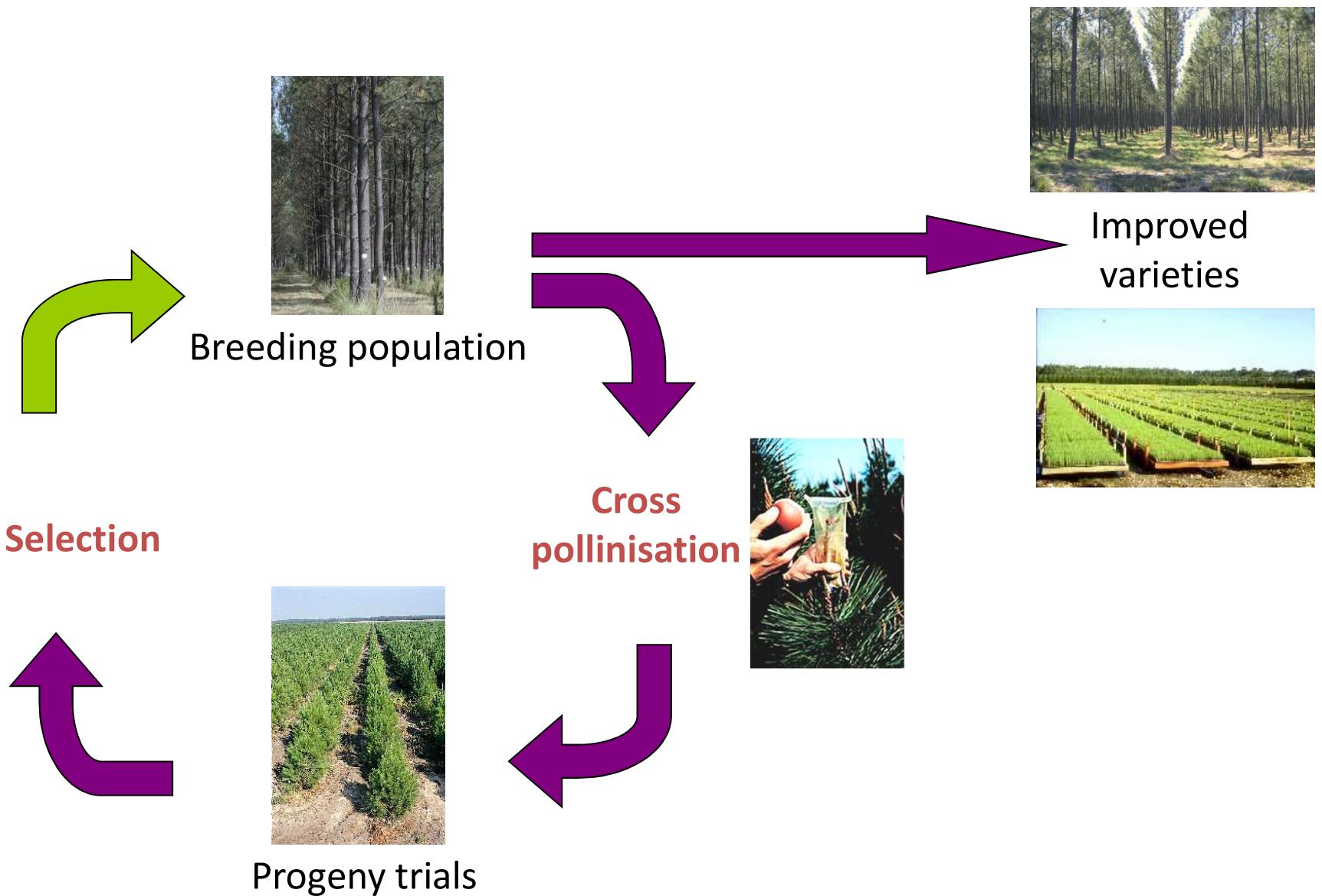


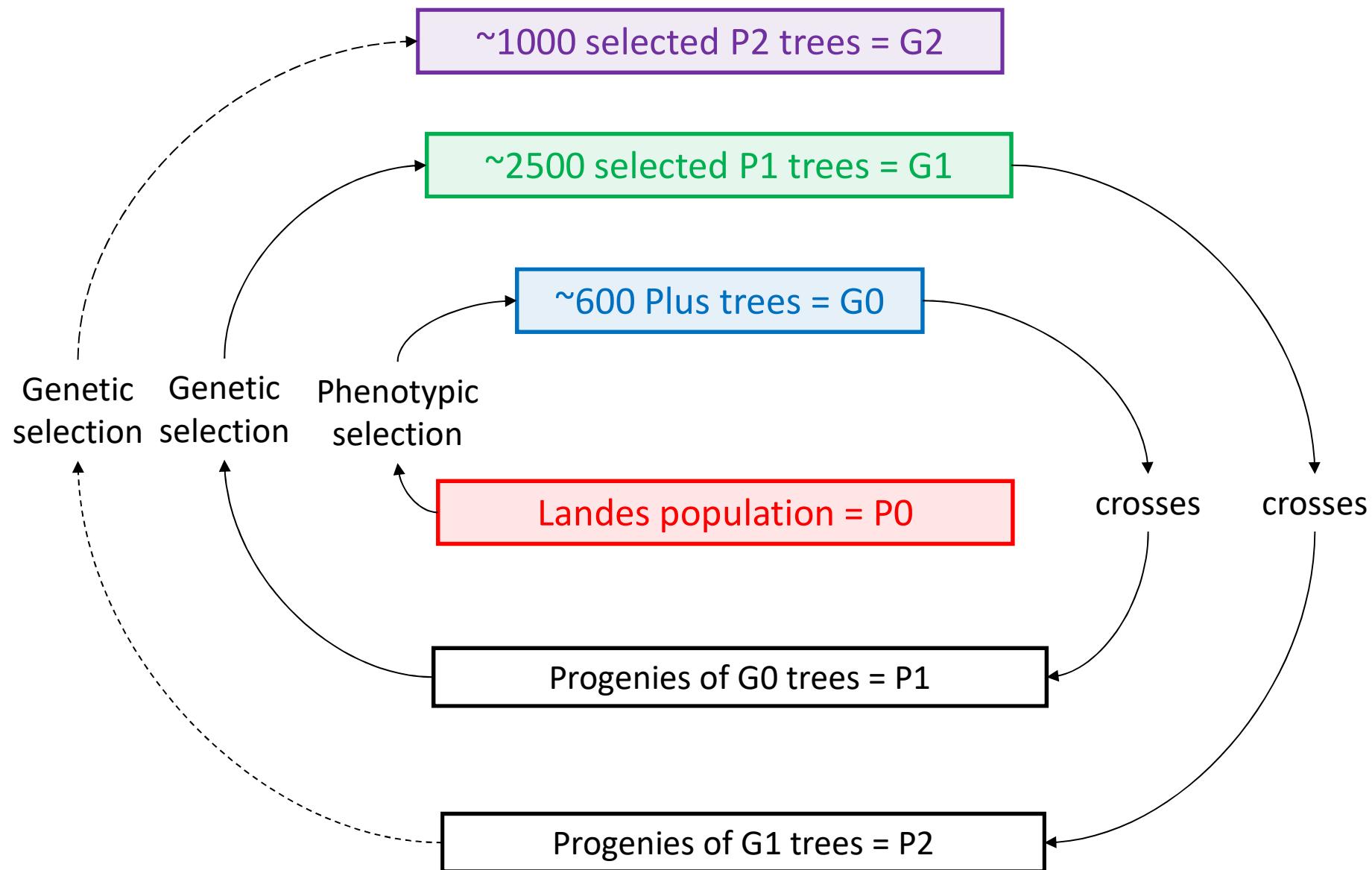
# Maritime pine breeding program

- Initiated in the 60's :
  - Base population ~600 plus trees selected in the Landes forest
  - Recurrent selection scheme
  - Managed by a public – private consortium (GIS « Pin Maritime du Futur ») since 1995
- Selection criteria
  - Evaluation at 10 – 12 years old
  - Volume (growth)
  - Wood quality (stem straightness)
- Seed orchards:
  - Generalist varieties from open pollinate seed orchards established with 40-50 genotypes
  - Improved varieties = 90% reforestation



# Recurrent selection scheme





# Large initial maritime pine breeding population...

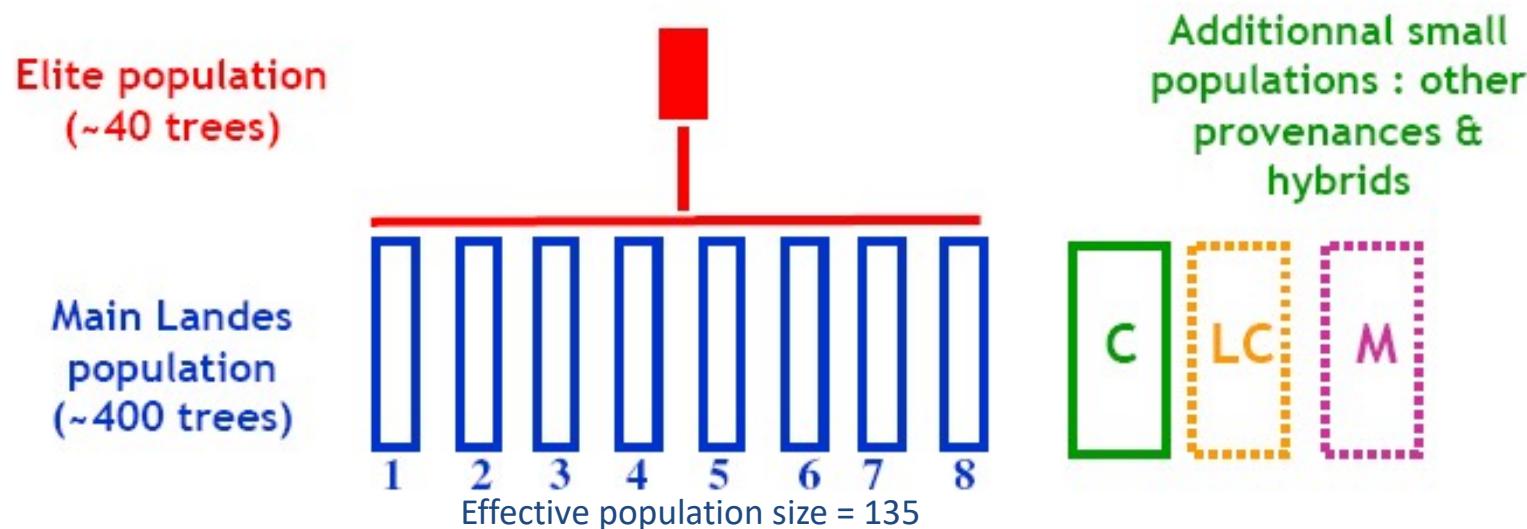
~ 600 G0 (« plus trees »)

~ 2600 G1

~ 1000 G2

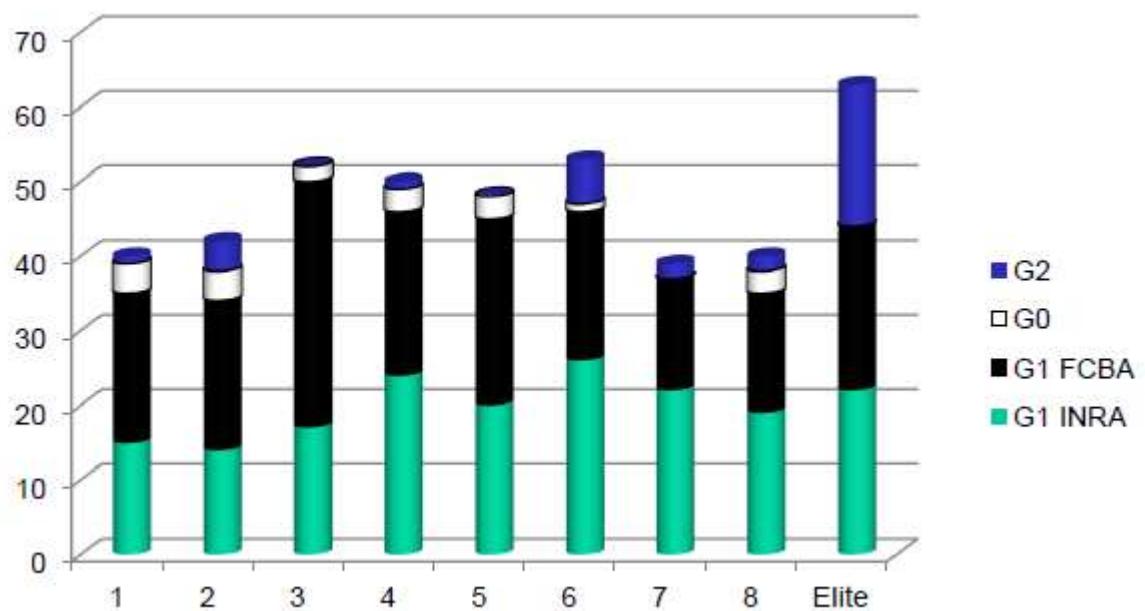
- phenotypic selection of plus trees in the 60's
- recurrent selection based on growth and straightness
- selection of G1 by INRA and FCBA (high level of relatedness between G1 trees)
- selection of G2 by INRA

## ... now structured into sublines



### ➤ sublining to control pedigrees:

- coancestry is controlled by subdivision of the breeding population into non-related sublines
- OP seed orchards will be constituted with selected trees from non-related sublines



Taille actuelle :  
364 individus dans  
8 lignées  
(en moyenne 45,5),  
et 63 dans la pop élite

# Schéma de sélection recurrente

## Population de conservation

Parc à clones

Sélection arbres plus = population G0

## Population d'amélioration

Croisements plein-frères

Croisements polycross

Selection des meilleurs descendants = G1

Selection des meilleurs parents

Parc à clones

Vergers à graines

Sélection « forward »

Sélection « backward »

Vergers à graines

## Population de multiplication

Croisements plein-frères

Croisements polycross

Selection des meilleurs descendants = G2

Selection des meilleurs parents

Parc à clones

Vergers à graines



**Genetic evaluation system**

# Previous methodology

- Phenotypic data adjusted for environmental effects
- Only simple pedigree relationships were taken into account (half-sib families for example)
- Analyses carried out trial by trial

# Limitations

- Breeding values from different trials are not comparable
- Informations from different trials were not combined

# Individual model

- Mixed model: fixed effects (environmental components) and random effects (genetic components)
- Phenotypes are linked by a genetic relationship matrix computed from the pedigree
- Effects estimated simultaneously by maximum likelihood (ASReml software)
- All the pedigree information is taken into account to accurately estimate both the genetic parameters and the breeding values
  - ➔ Best Linear Unbiased Predictor (BLUP)

$$y = \underline{Xb} + \underline{Za} + e$$

Fixed effect      Random effects

Environment      Genetics

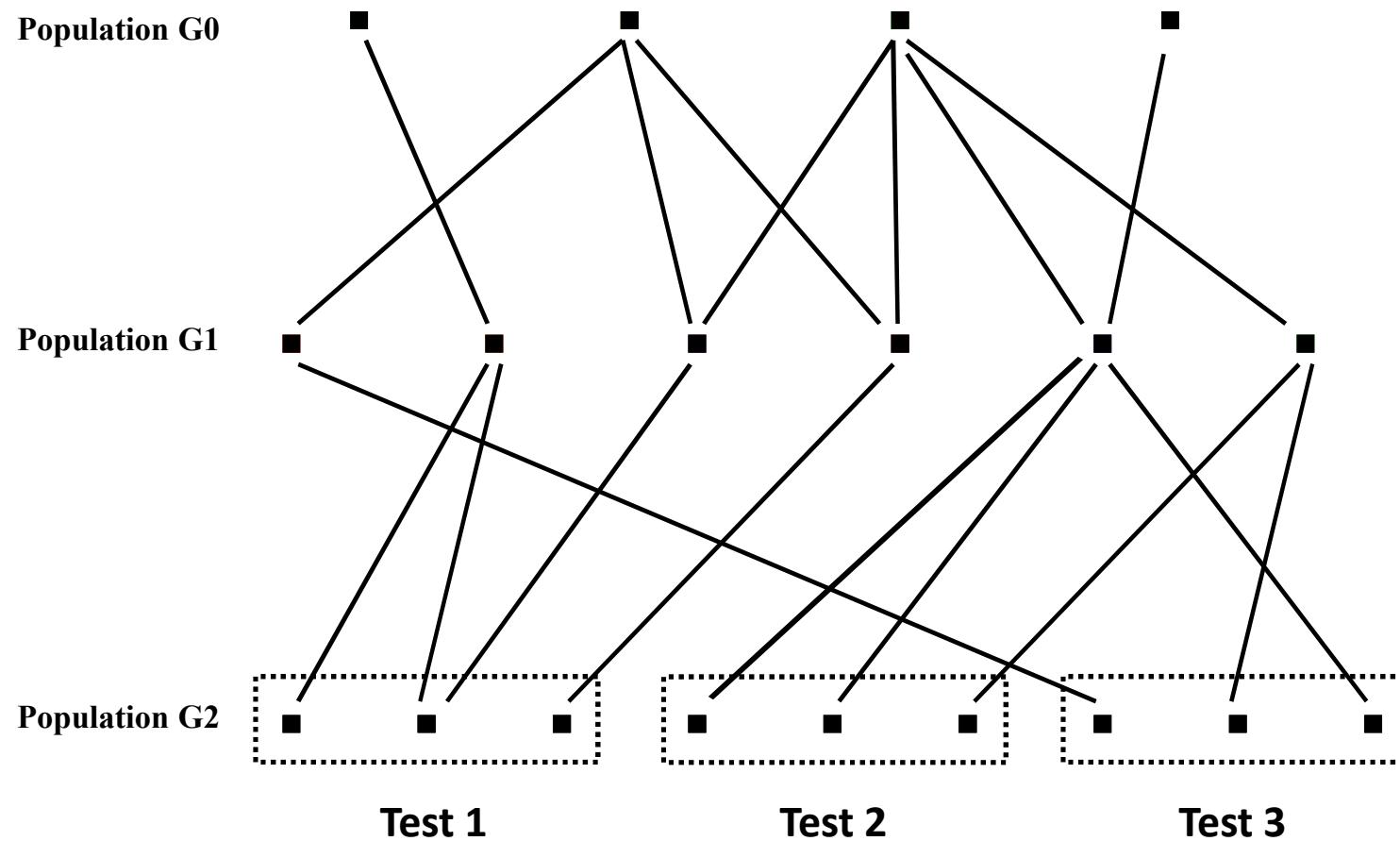
$\text{Var}(a) = \mathbf{A} \cdot \sigma^2_A$   
 $\sigma^2_A$  = additive variance  
**A = genetic relationship matrix**

$$\mathbf{A} = \begin{pmatrix} & & 2 \times \Phi_{ij} \\ & \ddots & \\ & & 1 + F_i \\ 2 \times \Phi_{ij} & & \ddots & \\ & & & \ddots \end{pmatrix}$$

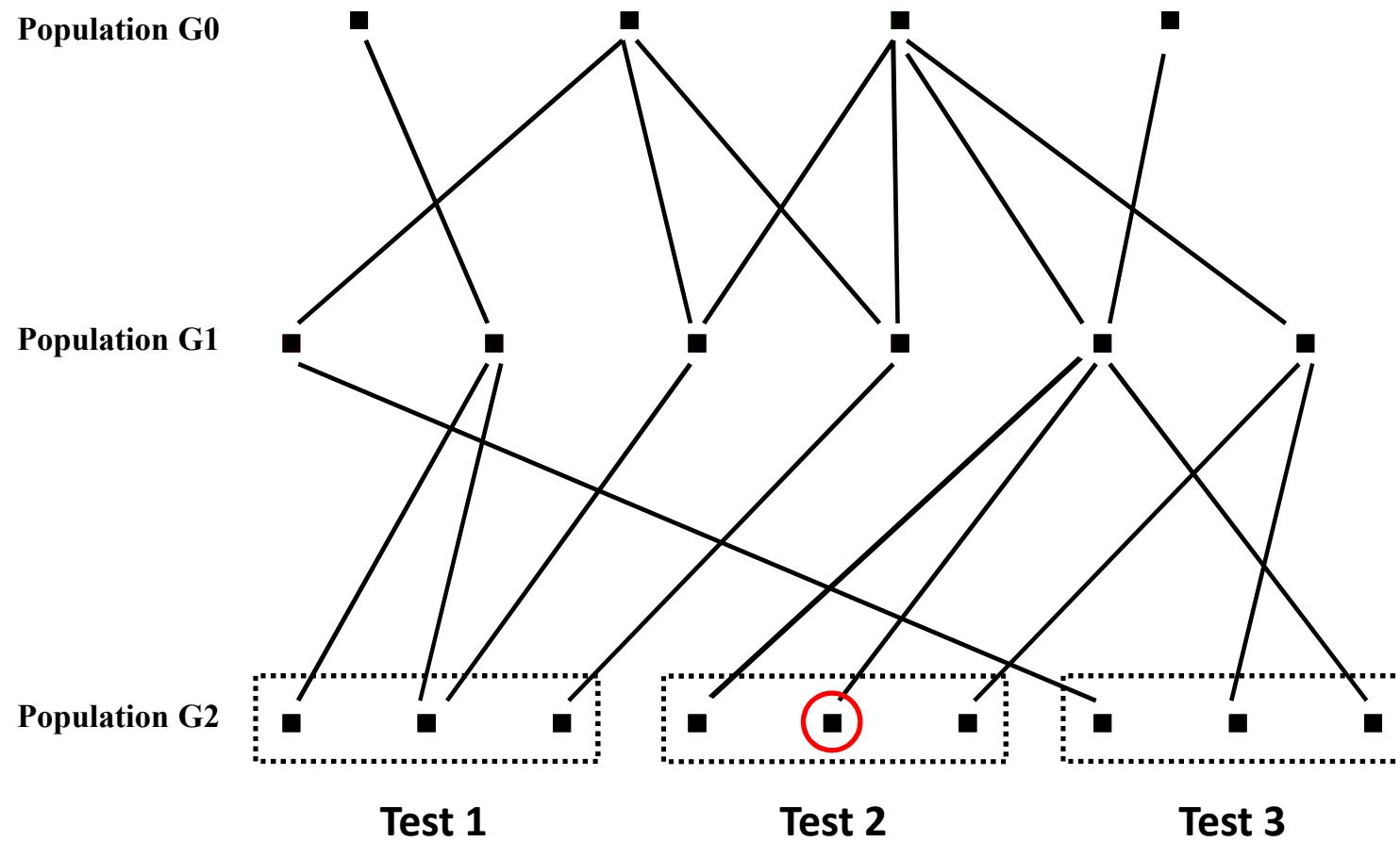
$\Phi_{ij}$  = coancestry or coefficient of kinship

$F_i$  = coefficient of inbreeding

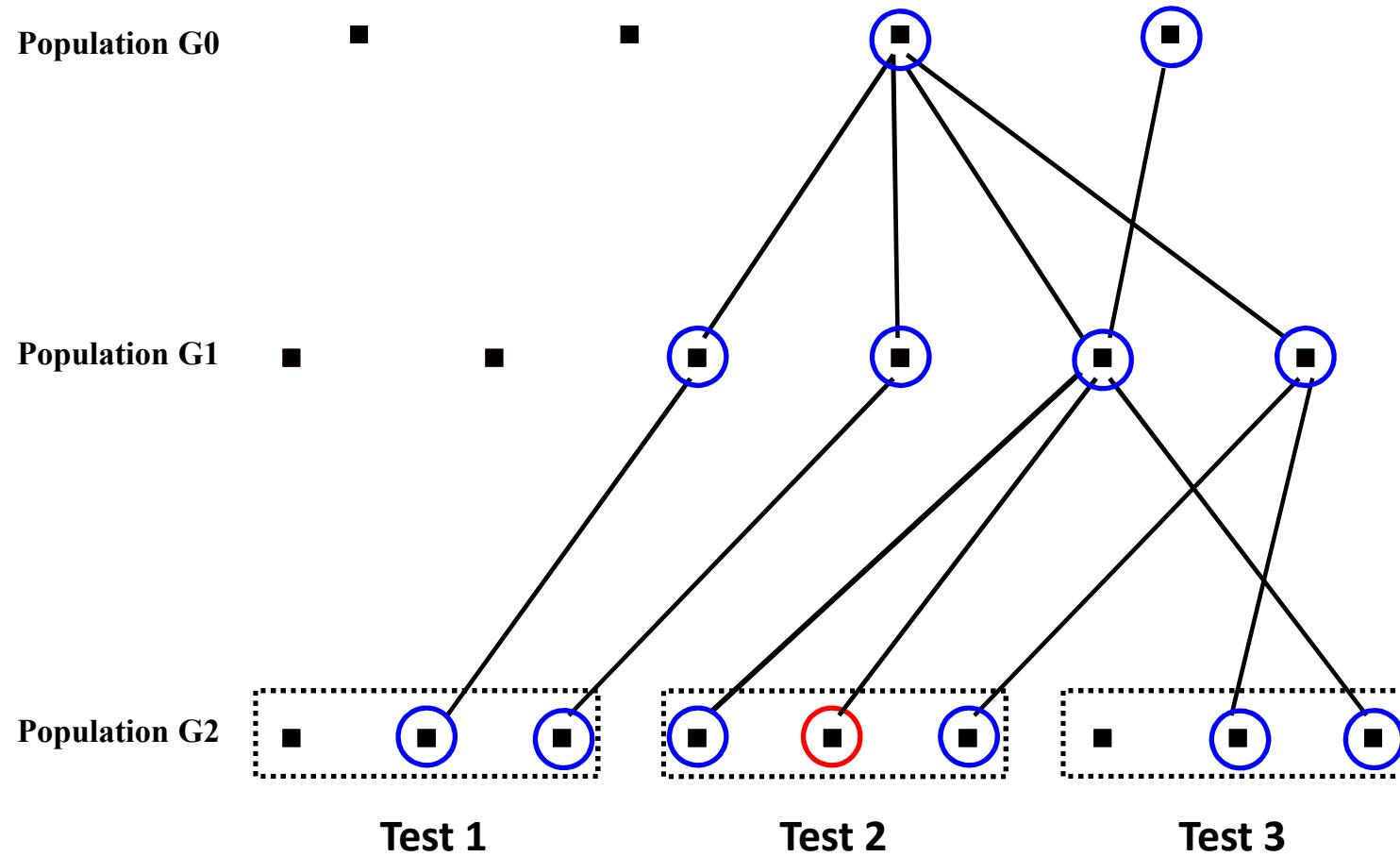
# BLUP evaluation

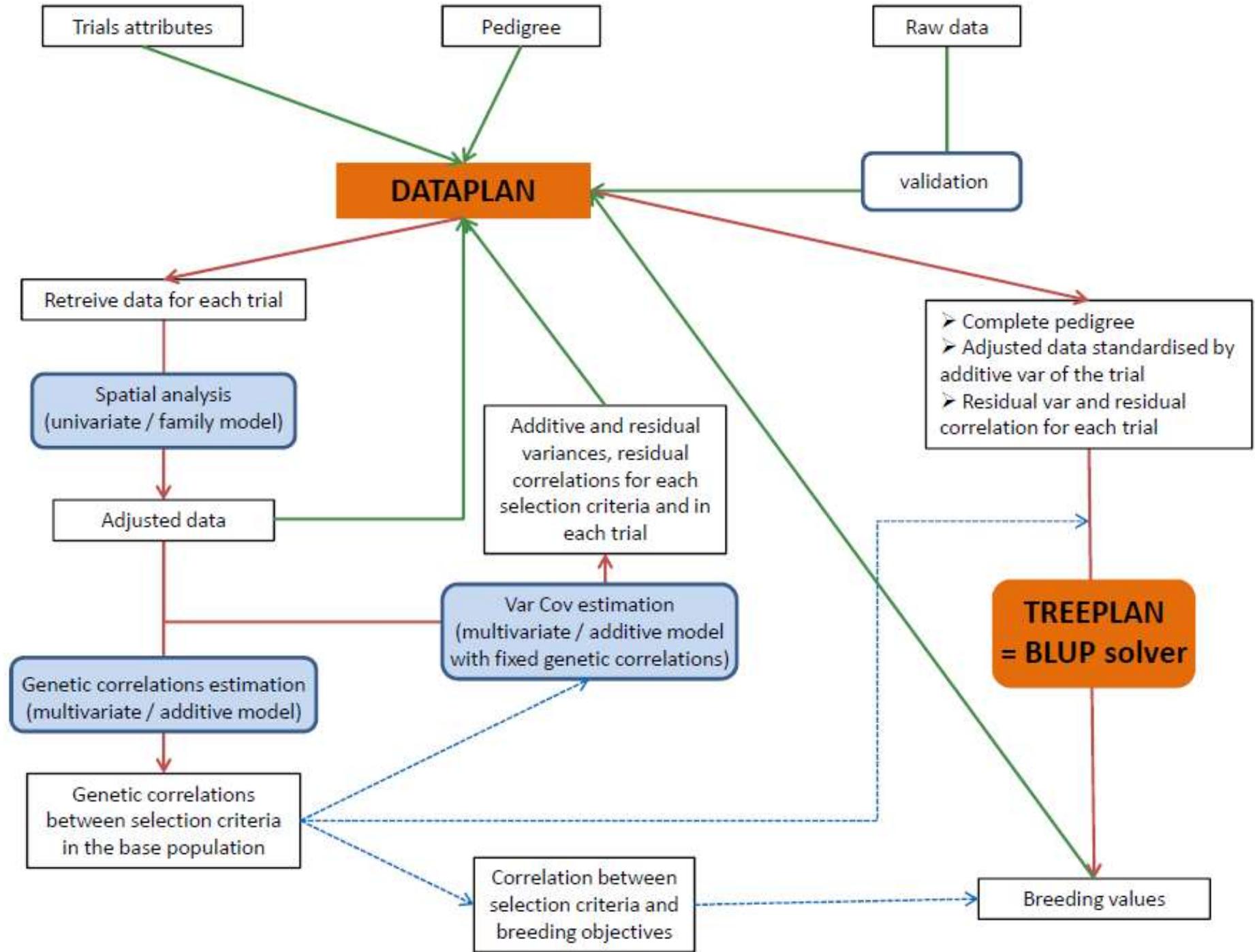


# BLUP evaluation



# BLUP evaluation





# Maritime pine breeding values

More than 500,000 trees in the database

## Pinus pinaster

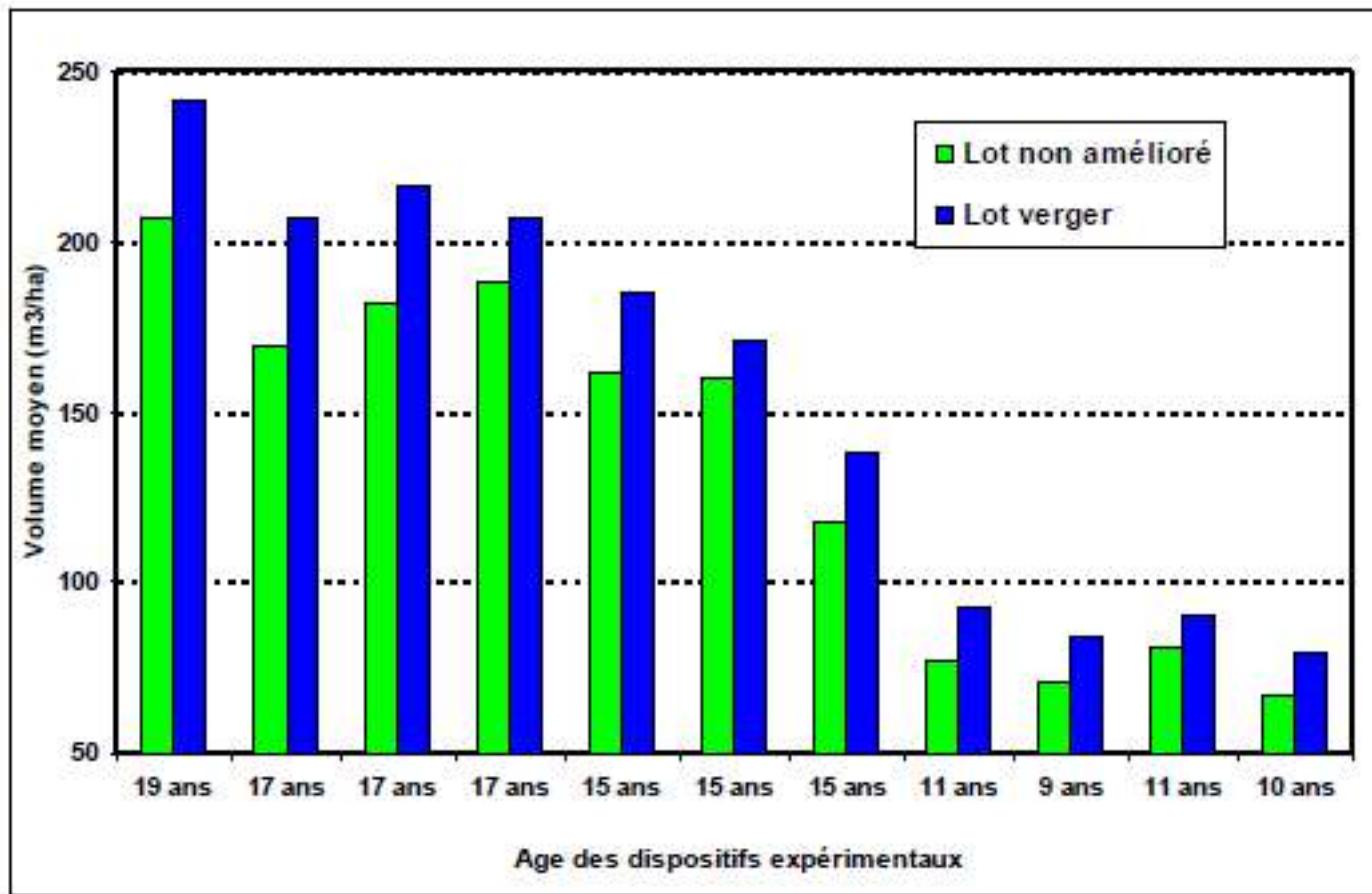
Home		Pedigree		Trials		Documents		TREEPLAN		Inventory											
Home : Pedigree : Genotypes : Show																					
<a href="#">Retrieve</a>   <a href="#">Download</a>   <a href="#">Bookmark</a>   <a href="#">Add genotype</a>   <a href="#">Import genotypes</a>   <a href="#">Import attributes</a>																					
GENOTYPE ID <input checked="" type="checkbox"/>	GENOTYPE NAME <input type="checkbox"/>	FAMILY ID <input checked="" type="checkbox"/>	FAMILY NAME <input checked="" type="checkbox"/>	MUM ID <input checked="" type="checkbox"/>	MUM NAME <input checked="" type="checkbox"/>	DAD ID <input checked="" type="checkbox"/>	DAD NAME <input checked="" type="checkbox"/>	CIR 12 EBV	CIR 12 EBV	EV 08 EBV	EV 08 EBV										
3786068	F1.2324	67949	1317x0003	3710004	1317 (Genotype)	3709890	0003 (Genotype)	1.0446	0.9537	0.3006	-0.5973										
3786053	F1.1733	68101	0024x0152	3709906	0024 (Genotype)	3752274	0152 (Genotype)	1.1644	0.9477	0.3192	-1.9987										
3786034	F1.1714	68347	1321x3814	3710007	1321 (Genotype)	3710070	3814 (Genotype)	0.7364	0.9470	0.3213	-0.9296										
3786001	F1.1681	68345	1901x3814	3710039	1901 (Genotype)	3710070	3814 (Genotype)	2.0242	0.9472	0.3208	-0.6769										
3785998	F1.1678	68348	3110x3814	3710048	3110 (Genotype)	3710070	3814 (Genotype)	2.4634	0.9242	0.3819	-1.6435										
3785989	F1.1669	68294	0056x3111	3709919	0056 (Genotype)	3710049	3111 (Genotype)	2.0742	0.9473	0.3203	-0.1338										
3785913	F1.1587	68039	0161x0108	3709969	0161 (Genotype)	3709942	0108 (Genotype)	2.1362	0.9463	0.3234	0.0752										
3785907	F1.1580	68292	4301x3110	3710104	4301 (Genotype)	3710048	3110 (Genotype)	2.5012	0.9430	0.3327	-0.1998										
3785880	F1.1548	68026	0041x0022	3752236	0041 (Genotype)	3709904	0022 (Genotype)	1.4977	0.9544	0.2985	-1.1036										
3785866	F1.1533	68274	3113x1902	3710051	3113 (Genotype)	3710040	1902 (Genotype)	1.1818	0.9486	0.3165	-1.3258										
3785839	F1.1505	68260	3823x1317	3710077	3823 (Genotype)	3710004	1317 (Genotype)	0.9123	0.9422	0.3351	-0.0923										
3785833	F1.1498	68027	1307x0022	3709995	1307 (Genotype)	3709904	0022 (Genotype)	1.4056	0.9488	0.3160	-1.0792										
3785817	F1.1482	68027	1307x0022	3709995	1307 (Genotype)	3709904	0022 (Genotype)	1.0735	0.9236	0.3835	-1.4722										
3785789	F1.1453	68261	3112x1317	3710050	3112 (Genotype)	3710004	1317 (Genotype)	1.1250	0.9486	0.3164	-0.8143										
3785783	F1.1447	68026	0041x0022	3752236	0041 (Genotype)	3709904	0022 (Genotype)	1.6430	0.9382	0.3460	-1.5745										
3785782	F1.1446	68026	0041x0022	3752236	0041 (Genotype)	3709904	0022 (Genotype)	1.1764	0.9444	0.3289	-1.8604										
3785764	F1.1428	68026	0041x0022	3752236	0041 (Genotype)	3709904	0022 (Genotype)	0.8769	0.9203	0.3913	-2.0129										
3785702	F1.1359	67842	1329x0105	3710015	1329 (Genotype)	3709940	0105 (Genotype)	0.9335	0.9489	0.3156	-1.1484										
3785560	F1.0790	68240	3110x1309	3710048	3110 (Genotype)	3709997	1309 (Genotype)	1.4834	0.9672	0.2542	-0.4687										
3785547	F1.0777	68168	1319x0243	3710005	1319 (Genotype)	3709979	0243 (Genotype)	1.6486	0.9749	0.2228	0.1237										

[First](#) <<[Prev](#) [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) ... [Next>](#)> [Last](#) | All 818 rows



**Genetic gains in improved varieties**

# Traits under selection

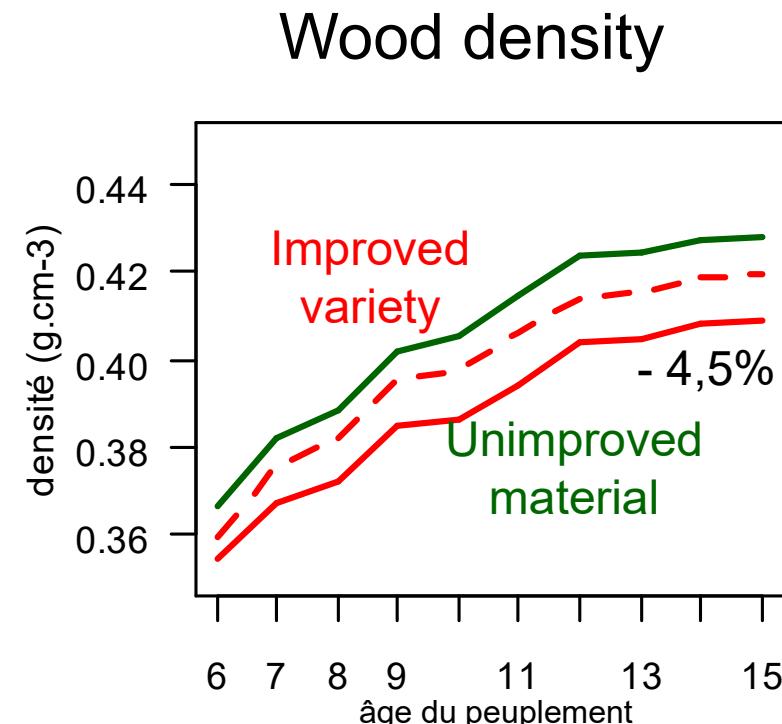
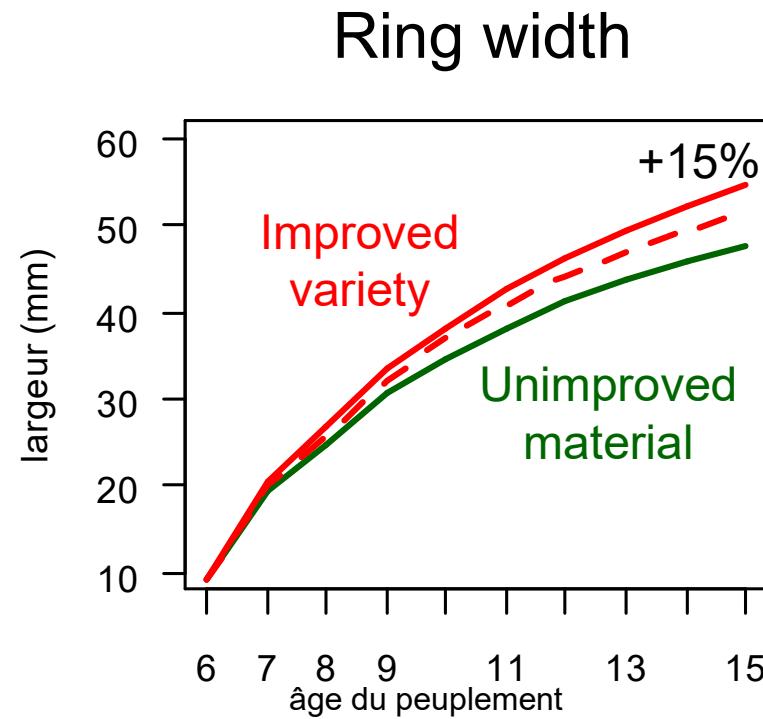


- First generation improved varieties: +15% for volume and stem straightness (but very variable depending on site characteristics)
- +30% is expected for second generation improved varieties

# What are the consequences of growth selection on wood density in the French maritime pine breeding programme?

Laurent Bouffier · Annie Raffin · Philippe Rozenberg ·  
Céline Meredieu · Antoine Kremer

Tree Genetics & Genomes (2009) 5:11–25  
DOI 10.1007/s11295-008-0165-x



Improved varieties: genetic gain for growth associated with a slight decrease of wood density

# Correlations between wood density and selection criteria in the breeding population

	Corrélation phénotypique	Corrélation génétique
<b>circonférence - densité</b>	-0,09 (0,04)	-0,21 (0,19)
<b>hauteur - densité</b>	0,00 (0,04)	-0,08 (0,16)
<b>écart à la verticalité - densité</b>	0,00 (0,04)	0,08 (0,17)

*Estimation à partir des tests Hermitage et Pisos (1150 arbres)*



# Evolution of genetic variation in successive breeding populations

Heredity (2008) 101, 156–165  
© 2008 Nature Publishing Group All rights reserved 0018-067X/08 \$30.00

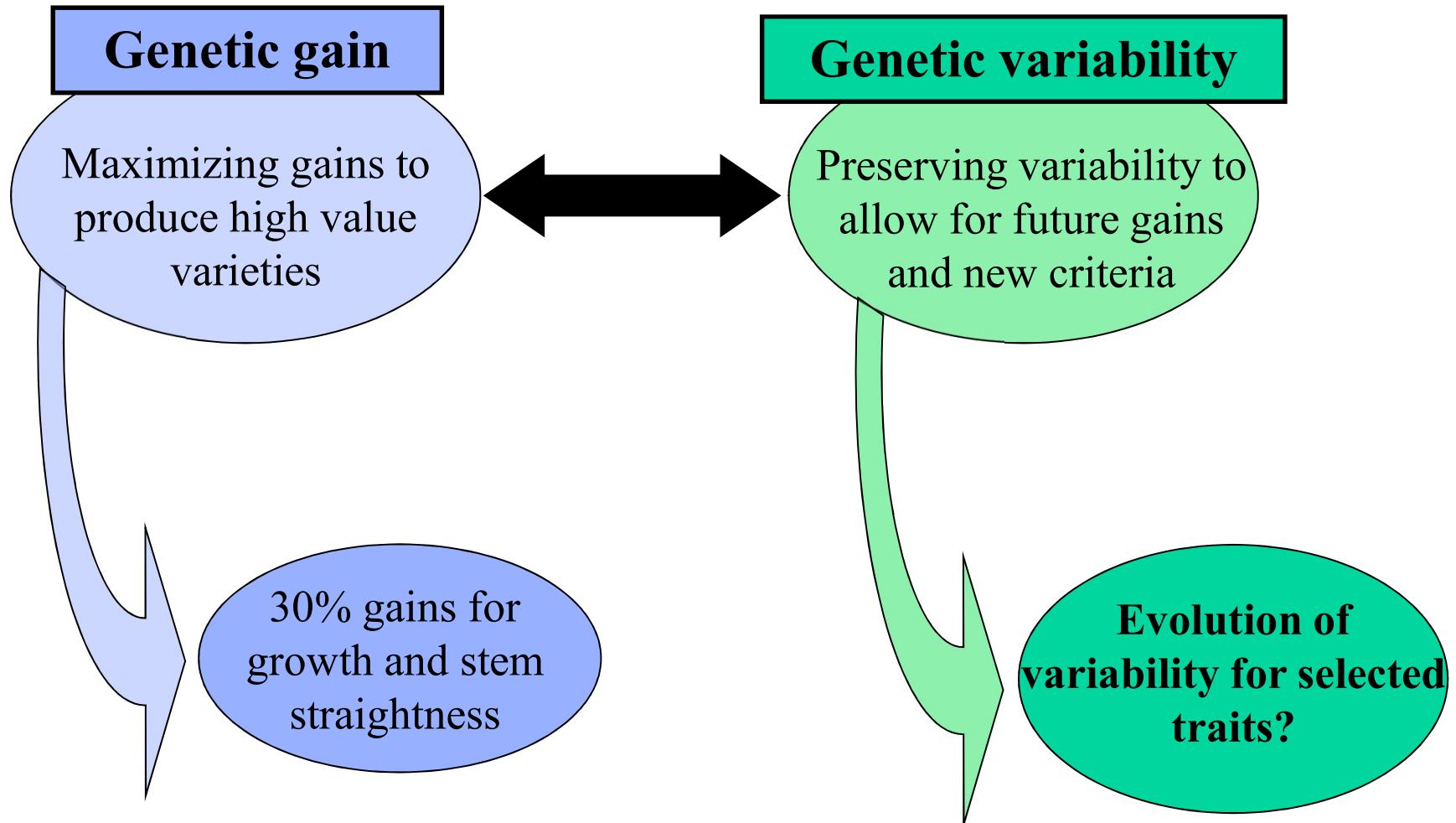
[www.nature.com/her](http://www.nature.com/her)

## ORIGINAL ARTICLE

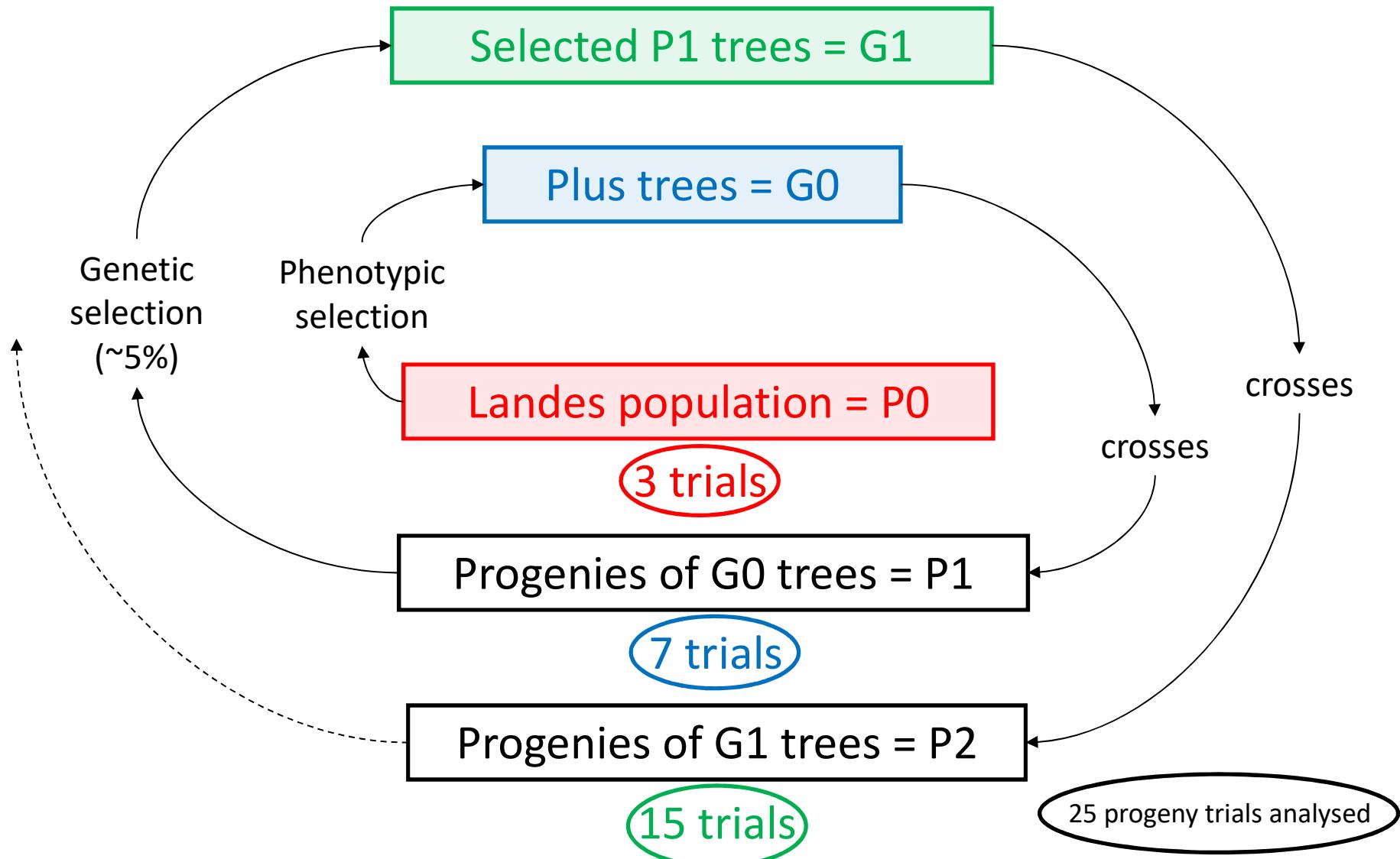
Evolution of genetic variation for selected traits in  
successive breeding populations of maritime pine

L Bouffier, A Raffin and A Kremer  
*INRA, UMR1202 Biodiversity Genes and Communities, Cestas, France*

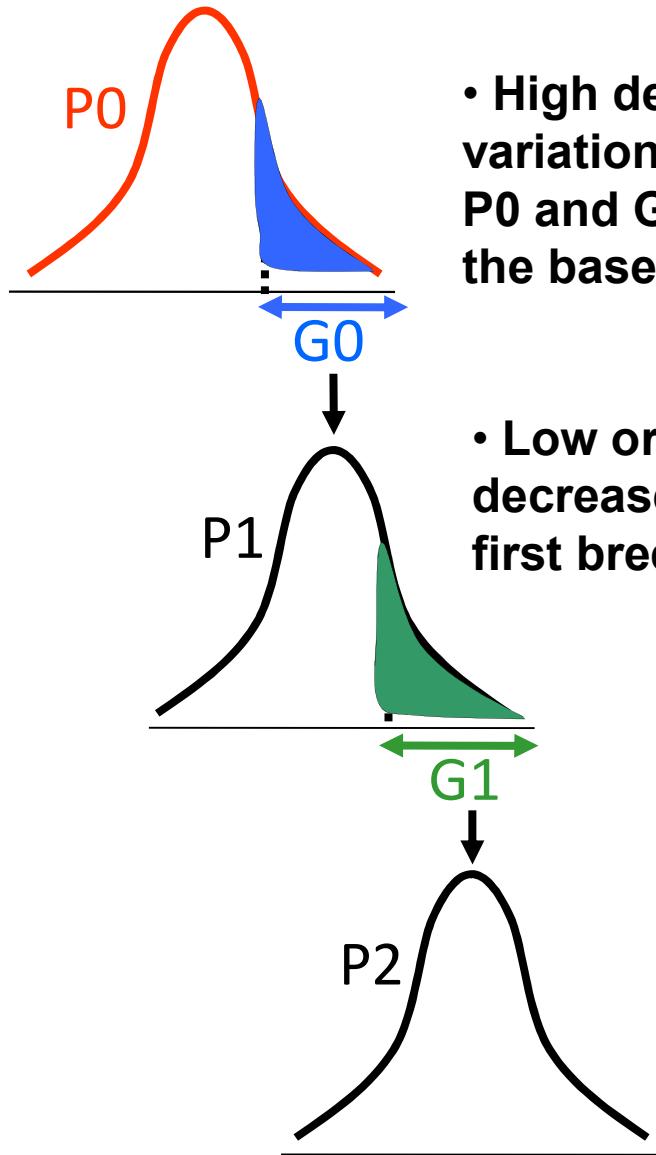
# Trade-off between gain and variability



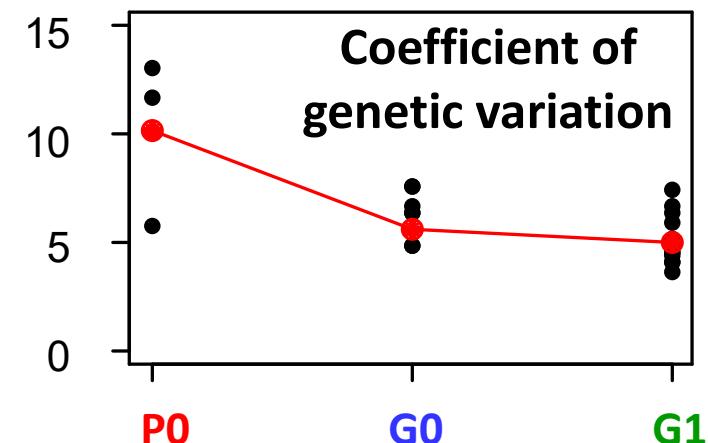
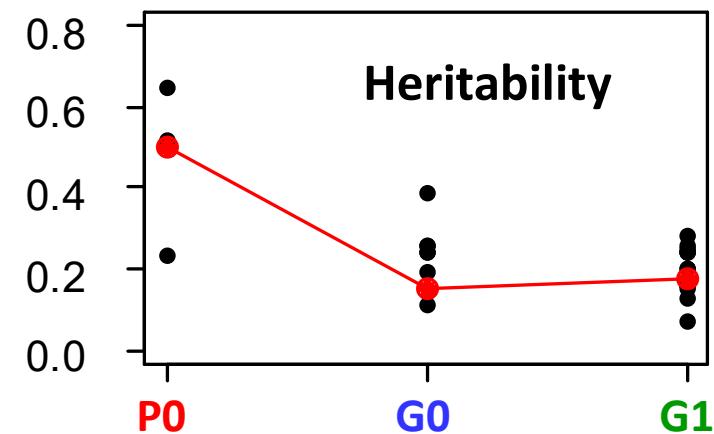
# Breeding populations and progeny trials studied



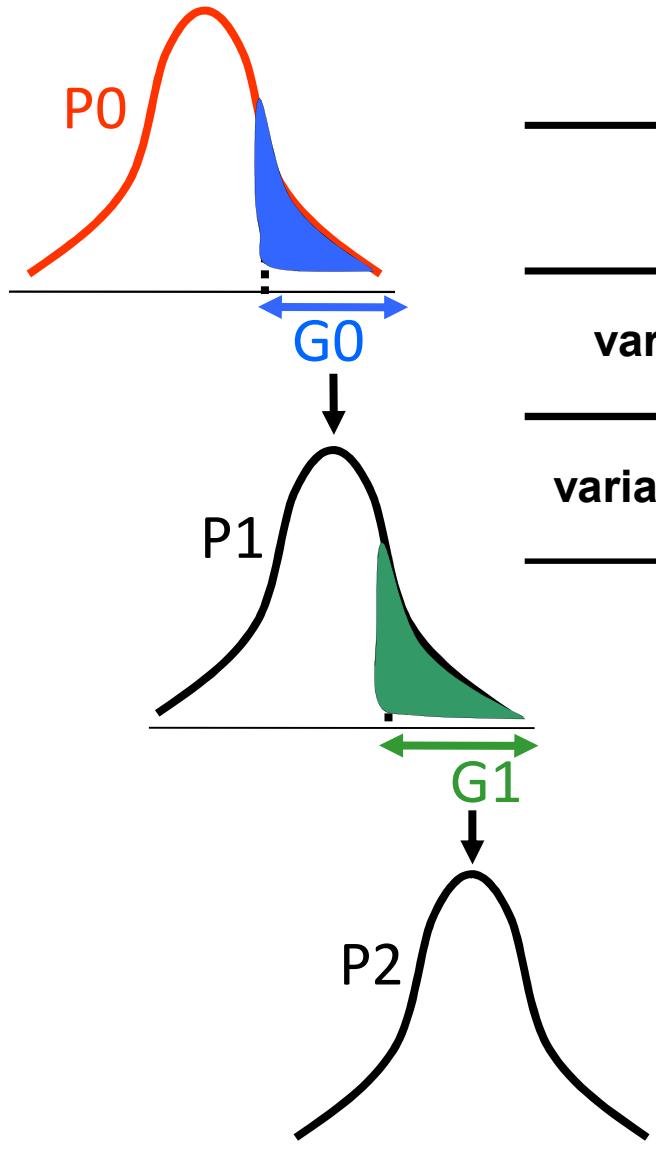
# Evolution of genetic variation for selection criteria



- High decrease of genetic variation (~30%) between P0 and G0 (selection of the base population)
- Low or non significant decrease between the two first breeding populations



# Evolution of genetic variation for wood density



	Densité du bois	
héritabilité	population P0	0,53 (0,18)
	population G0	0,45 (0,09)
variabilité génétique	population P0	5,5% (1,0)
	population G0	5,1% (0,6)
variabilité phénotypique	population P0	7,5% (0,3)
	population G0	7,5% (0,2)

- Non significant decrease of genetic variation for wood density between P0 and G0

Evolution of mean  
(varieties)

Growth

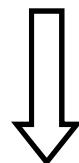
Wood density



Evolution of genetic variation  
(breeding population)

from P0 to G0  
Stable or low decrease  
between G0 and G1

Stable



Future genetic gains

New selection criteria