



HAL
open science

Using pedigree and trait relationships to increase gain in the French maritime pine breeding program

Laurent Bouffier, Annie A. Raffin, Greg Dutkowski

► To cite this version:

Laurent Bouffier, Annie A. Raffin, Greg Dutkowski. Using pedigree and trait relationships to increase gain in the French maritime pine breeding program. IUFRO Conference "Forest Genetics for Productivity", Mar 2016, Rotorua, New Zealand. 2016. hal-02801580

HAL Id: hal-02801580

<https://hal.inrae.fr/hal-02801580v1>

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.

Using pedigree and trait relationships to increase grain gain in the French maritime pine breeding program.



Laurent BOUFFIER¹, Annie RAFFIN¹, Greg DUTKOWSKI²

1/ INRA, UMR1202, BIOGECO, Cestas 33610, France
2/ PlantPlan Genetics, Hobart, Australia



More than 20 million improved seedlings produced per year

> 1 million hectares forest in southwestern France

- Maritime pine (*Pinus pinaster* Ait.): fast growing species (rotation = 35 years) adapted to the constrained environment of the Landes region forest (poor sandy soils, hydromorphic soils in winter, dry summers)
- 24% of French wood harvest (60% for saw timber, 40% for industrial wood)

> A three generation breeding population

- Breeding program since the early 1960s with a base population selected in the Landes forest (~600 G0 trees) and an additional population selected in Corsica
- Recurrent breeding scheme:
 - double-pair mating and forward selection to create the next breeding generation
 - polycross mating and backward selection to select the best genotypes for seed orchards

> Improved varieties for growth and sweep

- Open-pollinated seed orchards with ~50 genotypes (one breeding zone)
- Genetic gains estimated (variety %VF3): +30% for growth and +30% for stem straightness

OBJECTIVES:

Take advantage of pedigree connections between progeny trials and traits to best predict breeding values in the breeding program

- Data are connected through pedigree and trait correlations
- BLUP used to produce comparable breeding values over trials and generations

505,875 genotypes in pedigree and 8.3M data points stored in DATAPLAN

> DATAPLAN: database designed for breeding program pedigree and phenotypic data

> Stores all data from the main trials established since the 1960s

- 44 progeny trials with tree data + 19 trials with family mean data (6,231 families)
- Data from a variety of cross types (open and control pollinated, polymix)

> 9 major traits evaluated

	Growth		Sweep	Wood quality		Branching			
	Height	Circumference	Deviation from verticality	Wood density	Spiral grain	Branch diameter	Branch angle	Fork nber	Ramicorn nber
Nber of trials evaluated	70	71	42	9	7	7	7	15	20
Evaluation mean age	9,4	11,0	8,8	16,7	14,1	11,4	11,4	8,5	8,4

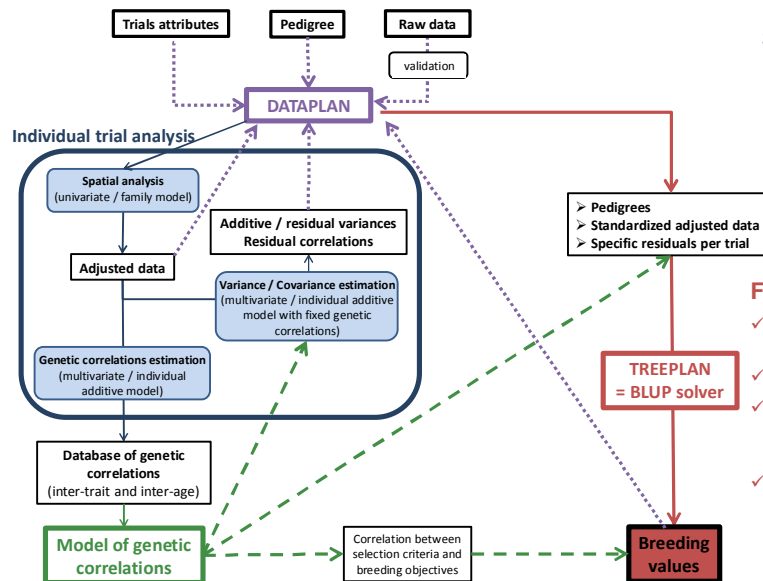
Multivariate BLUP predicts breeding values in three generation breeding program

Individual trial analyses (ASReml)

- Identify the best environmental model for each trait (spatial analysis)
- Multi-variate analysis contributes to the database of correlations
- Estimate additive variance for data standardisation

Genetic correlation model

- Minimises the weighted error sum of squares between the model estimates and the database of correlations.
- Used to:
 - Carry out multivariate analysis within each trial with fixed correlations
 - Predict harvest age traits from the measured traits



Stored in DATAPLAN

- Trial attributes
- Pedigree over three generations
- Design information and tree data
- Analysis outputs (adjusted data, variances / covariances, breeding values)

Final BLUP analysis (TREEPLAN)

- Full pedigree information up to the base population
 - Correlations between traits and ages
 - Data standardised by the additive variance of the trial to make them comparable across trials
 - Error variances and correlations different for every trial
- more weight given to higher heritability data

No strong adverse genetic correlations

Circumference	0.69								
Sweep	0.17	0.31							
Wood density	0*	-0.11	0.13						
Spiral grain	0.03	-0.19	-0.09	0.18					
Branch diameter	0.53	0.70	0.28	0*	0*				
Branch angle	-0.16	-0.27	0.01	0*	0*	-0.14			
Fork nber	0.16	0.30	0.12	0*	0*	0.41	0.21		
Ramicorn nber	0.11	0.27	0.15	0*	0*	0.41	0.22	0.63	

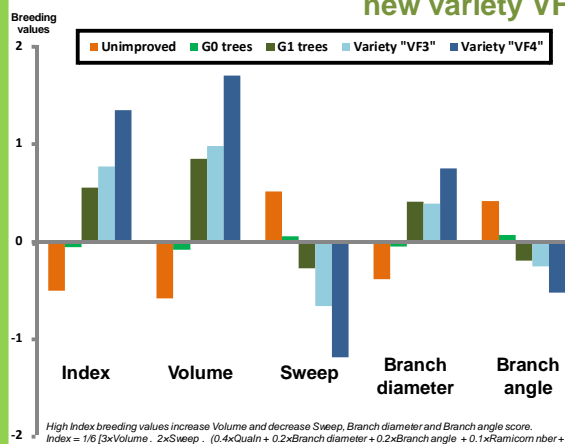
* = correlation not estimated due to limited number of measurements (correlation fixed to 0)

- Moderately unfavorable correlations growth . sweep
- No or slightly unfavorable correlation growth . wood quality
- Moderately unfavorable correlation growth - branching

> High heritability for height and wood quality

Heritability	0.34	0.18	0.24	0.42	0.46	0.15	0.17	0.06	0.08
Coefficient of additive variation	4.8%	7.0%	19.6%	7.4%	51.0%	10.3%	11.0%	61.7%	37.9%

Index breeding values increase volume and branching quality for new variety VF4



> Breeding values show progress over time

- In the breeding population: G1 trees (2nd gen parents) better than G0 trees (founder parents)
- Selection of ~50 genotypes for seed orchards establishment allows high genetic gains (VF3 = current variety; VF4 = next variety)

> All trees measured for at least one trait get breeding values for all traits

- Accuracy depends on correlated traits and related trees evaluated
- Harvest age traits breeding values integrate information from all traits and all ages