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GENETIC PARAMETERS ESTIMATION AND BREEDING VALUES PREDICTION FOR GROWTH AND WOOD QUALITY TRAITS IN THE FRENCH MARITIME PINE BREEDING PROGRAMME.

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Maritime pine (*Pinus pinaster Ait*.) represents one million hectares of cultivated forest in southwestern France. A breeding programme has been implemented since the early 1960s following a recurrent scheme from a base population selected in unimproved plantations. Today, it has reached its third generation with genetics gains of 30% for the improved growth and stem straightness varieties. The aim of this study was to carry out a joint-analysis of 44 main progeny trials (i.e. more than 450,000 trees) with advanced statistical methods in order to accurately estimate genetic parameters and predict breeding values. Twelve traits related to growth, stem straightness, branching, wind damage and wood density in up to four age classes were considered, making a total of 33 selection criteria for the breeding value prediction.

Genetic parameters were first calculated within each trial after adjustment for spatial heterogeneity (spatial autocorrelation models) and tabulated into a database. This genetic parameter database allowed estimation of inter-traits and age - age genetic correlations at the population level. Then, multivariate analyses with derived fixed population genetic correlations were carried out on adjusted data in order to estimate additive variances, residual variances and residual correlations for each trait in each trial. Finally, these parameters were used to run the BLUP solver TREEPLAN, and predict breeding values and their associated accuracies.

This study represents the first wide scale use of spatial analyses in Maritime pine trials and first joint multivariate analysis of all trials. The large data set analysed here allows the estimation of accurate genetic parameters for various traits related to wood production. The genetic evaluation with the TREEPLAN system demonstrates the possibility if integration of all available information from the successive breeding generations to increase the accuracy of breeding values and maximise gain from selection.

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

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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 progam 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**

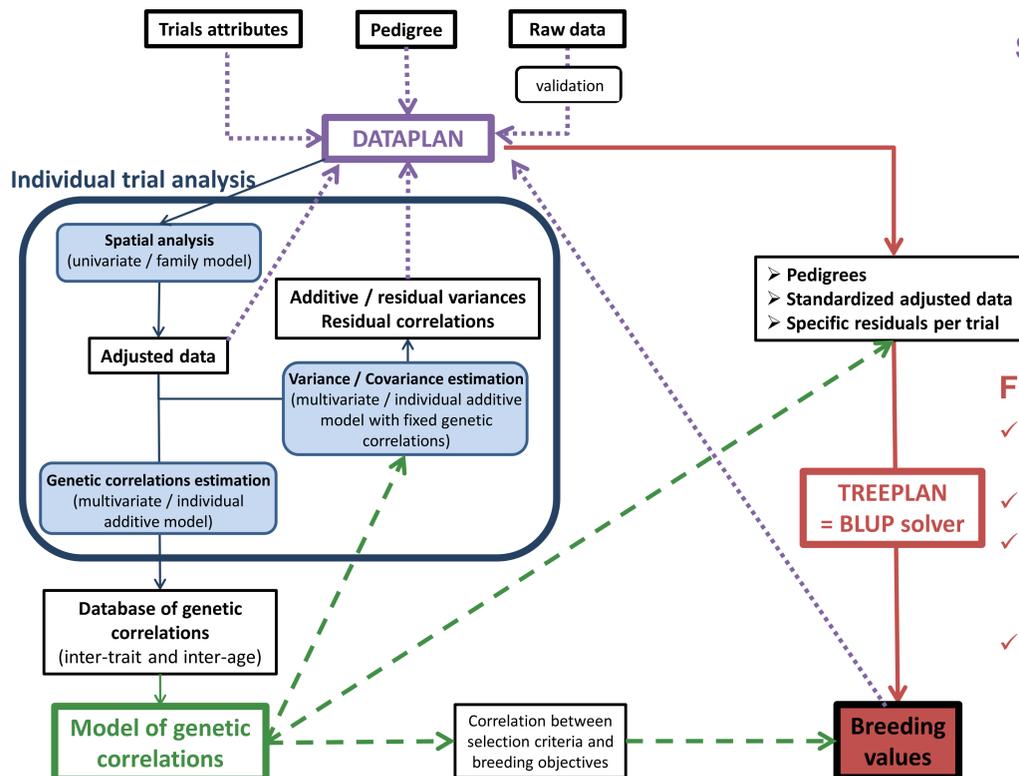|	Growth		Sweep	Wood quality		Branching			
	Height	Circumference	Deviation from verticality	Wood density	Spiral grain	Branch diameter	Branch angle	Fork nber	Ramicorn nber
Nber of trials evaluated	70	71	42	9	7	7	7	15	20
Evaluation mean age	9,4	11,0	8,8	16,7	14,1	11,4	11,4	8,5	8,4

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

Trials attributes — Pedigree — Raw data
validation
DATAPLAN

Individual trial analysis

Spatial analysis (univariate / family model)

Adjusted data

Additive / residual variances
Residual correlations

Variance / Covariance estimation (multivariate / individual additive model with fixed genetic correlations)

Genetic correlations estimation (multivariate / individual additive model)

Database of genetic correlations (inter-trait and inter-age)

Model of genetic correlations

Correlation between selection criteria and breeding objectives

➢ Pedigrees
➢ Standardized adjusted data
➢ Specific residuals per trial

TREEPLAN = BLUP solver

Breeding values

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

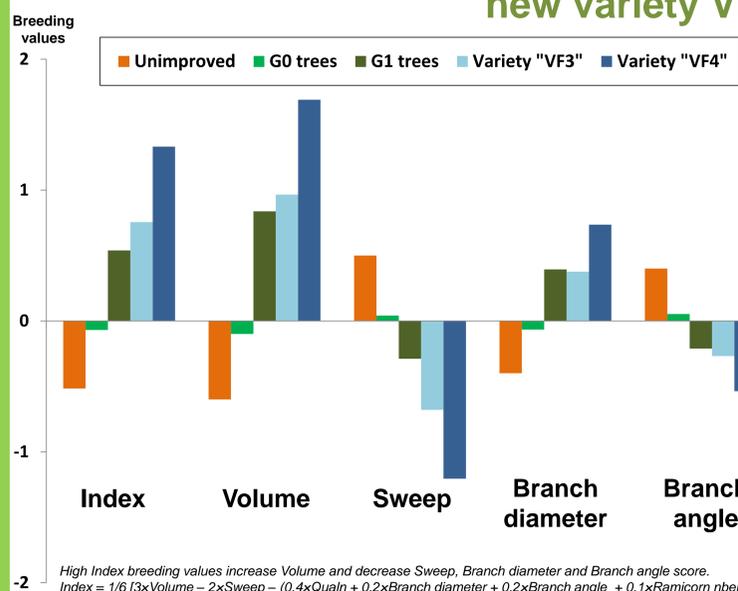|	Height	Circumference	Sweep	Wood density	Spiral grain	Branch diameter	Branch angle	Fork nber
Circumference	0.69							
Sweep	0.17	0.31						
Wood density	0*	-0.11	0.13					
Spiral grain	0.03	-0.19	-0.09	0.18				
Branch diameter	0.53	0.70	0.28	0*	0*			
Branch angle	-0.16	-0.27	0,01	0*	0*	-0.14		
Fork 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**

	Height	Circumference	Sweep	Wood density	Spiral grain	Branch diameter	Branch angle	Fork nber	Ramicorn nber
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

Legend: Unimproved — G0 trees — G1 trees — Variety "VF3" — Variety "VF4"

Categories: Index, Volume, Sweep, Branch diameter, Branch angle

➢ **Breeding values show progress over time**

- In the breeding population: G1 trees (2nd gen parents) better than G0 trees (founder parents)
- Selection of ~50 gentotypes 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

High Index breeding values increase Volume and decrease Sweep, Branch diameter and Branch angle score.
Index = 1/6 [3×Volume – 2×Sweep – (0.4×Qualn + 0.2×Branch diameter + 0.2×Branch angle + 0.1×Ramicorn nber + 0.1×Fork nber)]