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

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**Laurent BOUFFIER[1], Annie RAFFIN[1], Greg DUTKOWSKI[2]**

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 ñVF3ò): +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 |

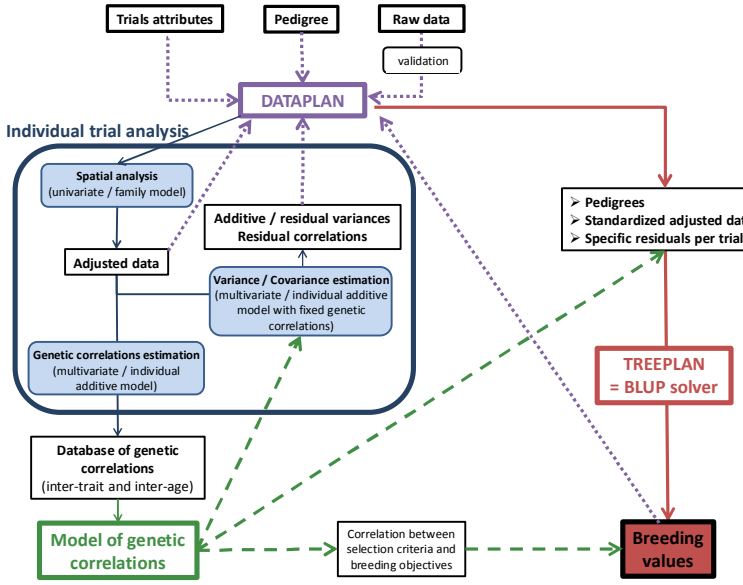
## Multivariate BLUP predicts breeding values in three generation breeding program

### 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




### 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 |

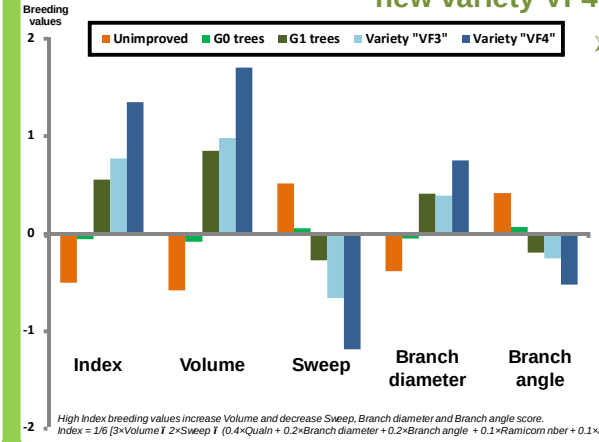
* = correlation not estimated due to limited number of measurements (correlation fixed to 0)

- ✓ Moderately unfavorable correlations growth ï sweep
- ✓ No or slightly unfavorable correlation growth ï 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




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

### ➢ 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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