Paternity recovery in a maritime pine polycross trial

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Maritime pine is the main plantation species in France with nearly one million hectares of cultivated forests in **South Western France**. A breeding program has been implemented since the early 1960s using **a recurrent selection scheme**. The breeding strategy combines two successive experimental designs: polymix crossing to evaluate parental breeding values and full-sib crossing from which selections are made for the next generation. This strategy is efficient both to increase genetic gains and to maintain genetic variability. The breeding program reaches its third generation: more than 300,000 trees have been phenotyped allowing accurate evaluation of genetic parameters and breeding values.

Future improved varieties must be adapted to ongoing environmental changes and to wood industry diversification. In this rapidly evolving context, forest tree breeding programs have to integrate an increasing number of selection criteria. They are also requested to propose different varieties adapted to various environments and diversified uses. **Thus, accelerating the breeding cycles to quickly renew variety composition is of main importance. Molecular tools can be of great help to cope with these challenges**.

Can pedigree recovery be implemented in forest tree breeding programs to shorten and simplify selection cycles?

Material and Methods

- **Sampling in a polycross trial**
  186 mothers x 2 father polymixes (PMX INRA and PMX FCBA)
  → 186 half-sibs families, 35trees/family, 6000 progenies

- **Sampling for paternity recovery**
  500 progenies from PMX FCBA
  → 50 half-sibs families x 10 trees
  Parental generation: 50 genotypes (mothers of HS families) +
  41 genotypes (composition of PMX FCBA)

- **SNP selection and genotyping**
  ➢ 2,480 polymorphic SNPs available
  ➢ SNP selection criteria for pedigree recovery: no LD and MAF>0.45
  ➢ 2 multiplexes of 32 and 35 SNPs
  ➢ Genotyping using Mass Array technology (Sequenom)

- **Phenotyping for numerous traits relative to:**
  ➢ Growth (height, circumference)
  ➢ Wood quality (straightness, wood density, spiral grain)
  ➢ Water use efficiency (WUE)


Polymix trial

Needles harvest with a saw

Pedigree recovery

- **Efficiency of paternity recovery**
  ➢ 56 validated SNP markers with manageable cost (10$/sample)
  ➢ Famoz software

- **17% of pollen contamination**

Variable contamination rates depending on families

P_E> 99,99% for 30 SNPs or more

- **354 realized matings in a single polycross**

Number of offspring per cross

50 ♀ x 42 ♂ = 2100 possible matings
→ 354 realized matings /399 studied progenies

42 ♂
50 ♀

- **Low Differential Reproductive Success between fathers**


Contribution of the 41 fathers of the FCBA PMX

Distribution expected (mean and confidence interval) if equal contribution

- **Further studies in progress with 1000 supplemental offspring**
  ➢ Comparison between 2 polymixes (contamination rate, male contribution)
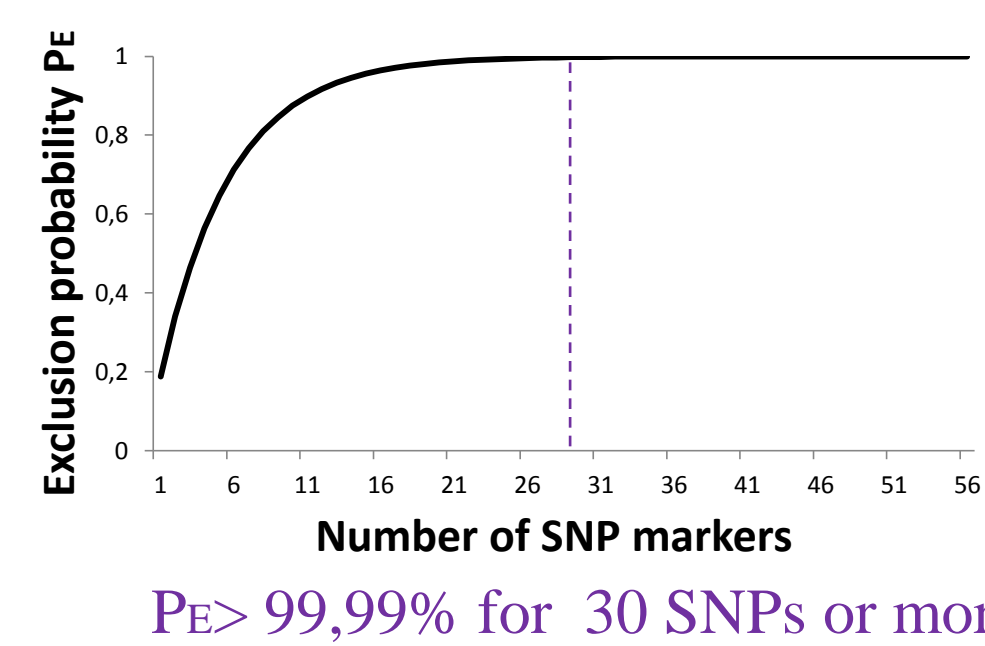
Consequences for genetic evaluation

Comparison of genetic parameters (h²) and breeding values (BLUPs) from 2 individual mixed models:
- •**"mother" Model**: relationship matrix based on mother ID (pedigree before paternity recovery)
- •**"mother+father" Model** : relationship matrix based on mother ID +father ID (pedigree after paternity recovery).
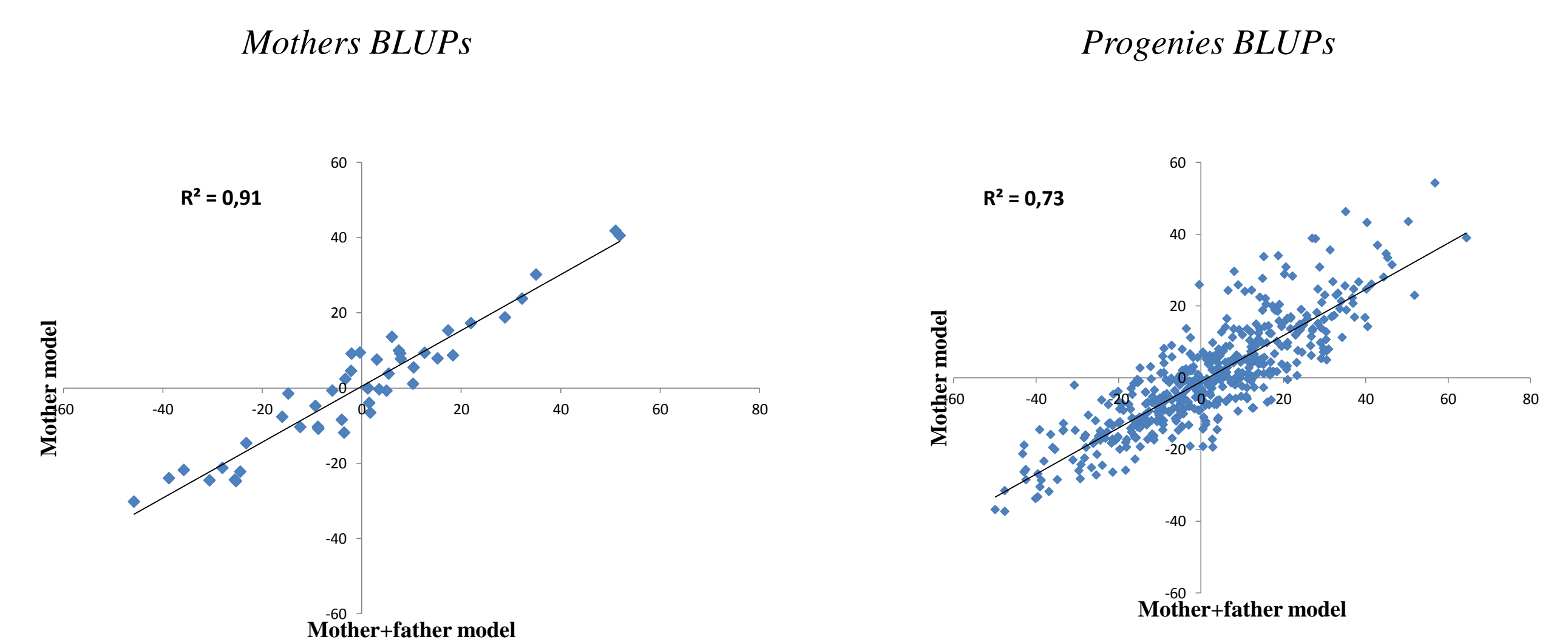
- **Higher accuracy for genetic parameter estimation**

mother Model
mother+father Model
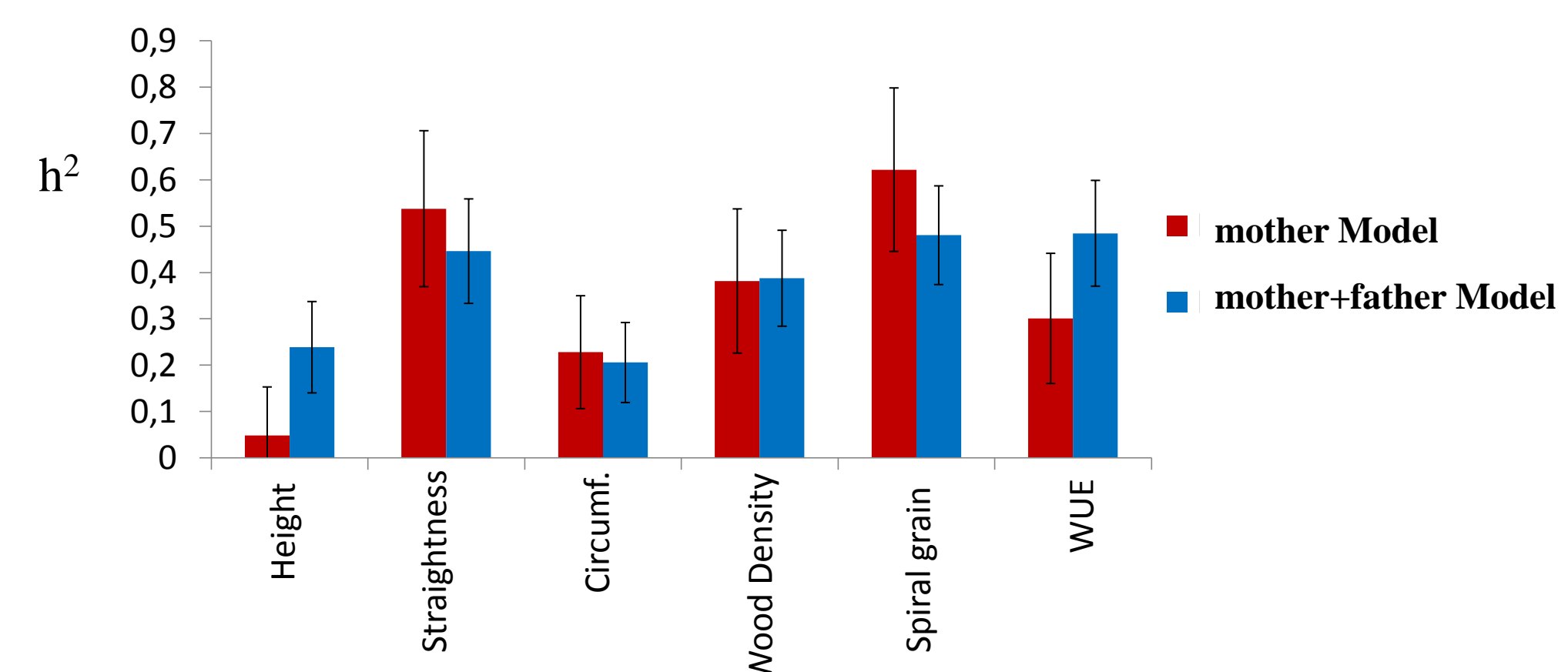
➢ Lower Standard Errors for "mother+father" model.

- **BLUP evaluation can be highly modified after paternity recovery**

Correlation between BLUPs estimated with "mother "and "mother +father" Models

Mothers BLUPs

R² = 0,91

Progenies BLUPs

R² = 0,73

➢Strong correlation between mother BLUP estimated by the two models.
→ Low impact for backward selection

➢ **Integration of father identity can modify significantly progeny BLUP evaluation**
→ High impact for forward selection

- **BLUP accuracy is improved when the full-pedigree is known**

Towards new breeding strategies based on pedigree recovery

✳ **More accurate BLUP estimates thanks to pedigree recovery in progeny trials (knowledge of the pedigree + identification of mislabeled trees)**

✳ **Polymix breeding with parental analysis** (Lambeth *et al.*, 2001)
  1. Maximizing the number of crossings with polymix strategies
  2. Pedigree recovery
     → Simplification of breeding and testing and shortening selection cycles.

  Simulations are required to define optimal breeding strategy:
  - number of polymix(es),
  - polymix composition (number of pollens, genetic merit, relatedness)
  - number of crossings/ polymix
  - defining a pre-screening step to limit the number of genotyped trees

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