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Accuracy of genomic prediction in a multi-generation population of maritime pine



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Maritime pine breeding program in France

- ▶ Initiated in the 60's with the selection of a base population (≈ 700 G0 trees) in Aquitaine natural forest.
- ▶ Followed a **recurrent selection** scheme that currently reached the **3rd generation of breeding** for an effective size $N_e \approx 135$.
- ▶ Breeding values estimation based on **BLUP evaluation** using a comprehensive database with more than 400,000 trees over three generations: G0 (base population), G1 (G0 progenies) and G2 (G1 progenies).
- ▶ **Three main selection criteria** characterized by medium heritabilities: circumference ($h^2 \approx 0.17$), height ($h^2 \approx 0.32$) and stem straightness ($h^2 \approx 0.26$).
- ▶ Improved generalist varieties from open pollinated seed orchards.



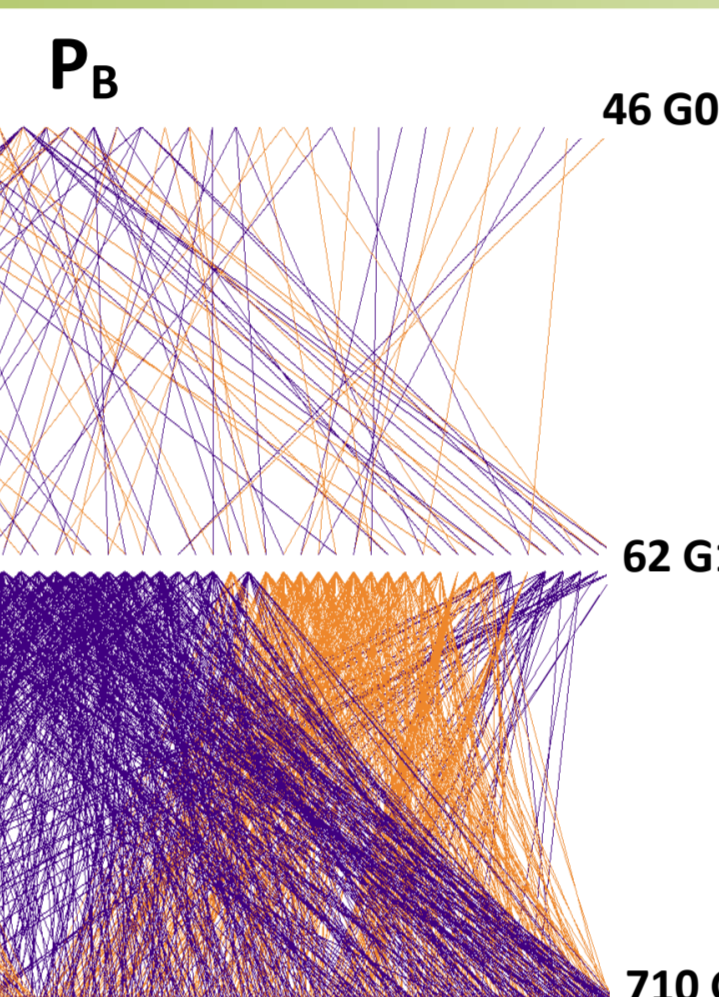
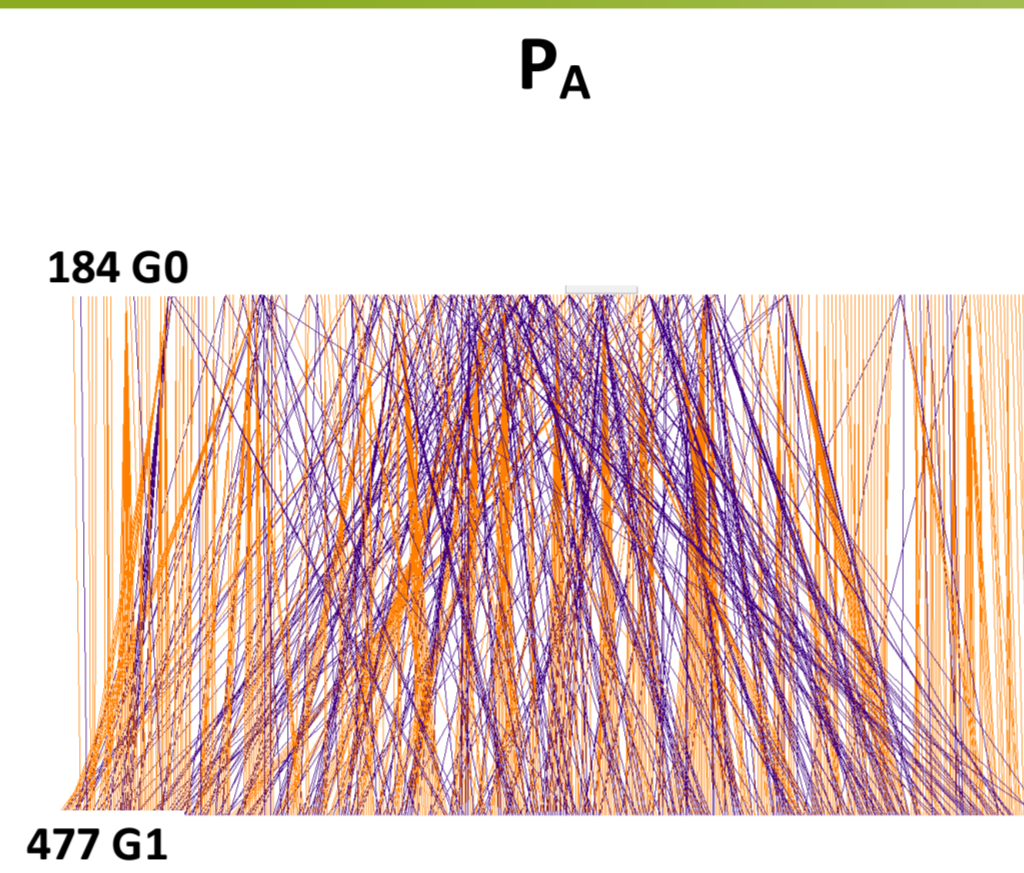
Objective

Develop genomic prediction proof-of-concept studies for maritime pine in order to explore key factors for the implementation of genomic selection.

Materials and Methods

Population P_A (Isik *et al.* 2015)

- 661 individuals: 184 G0 + 477 G1
- Large effective population size ($N_s \approx 100$)
- **Incomplete pedigree**: 62% of the G1 had at least one parents not sampled
- G1: 191 maternal HS families (≈ 2.5 trees / family)
- 2,600 SNPs



Population P_B (Bartholomé *et al.* submitted)

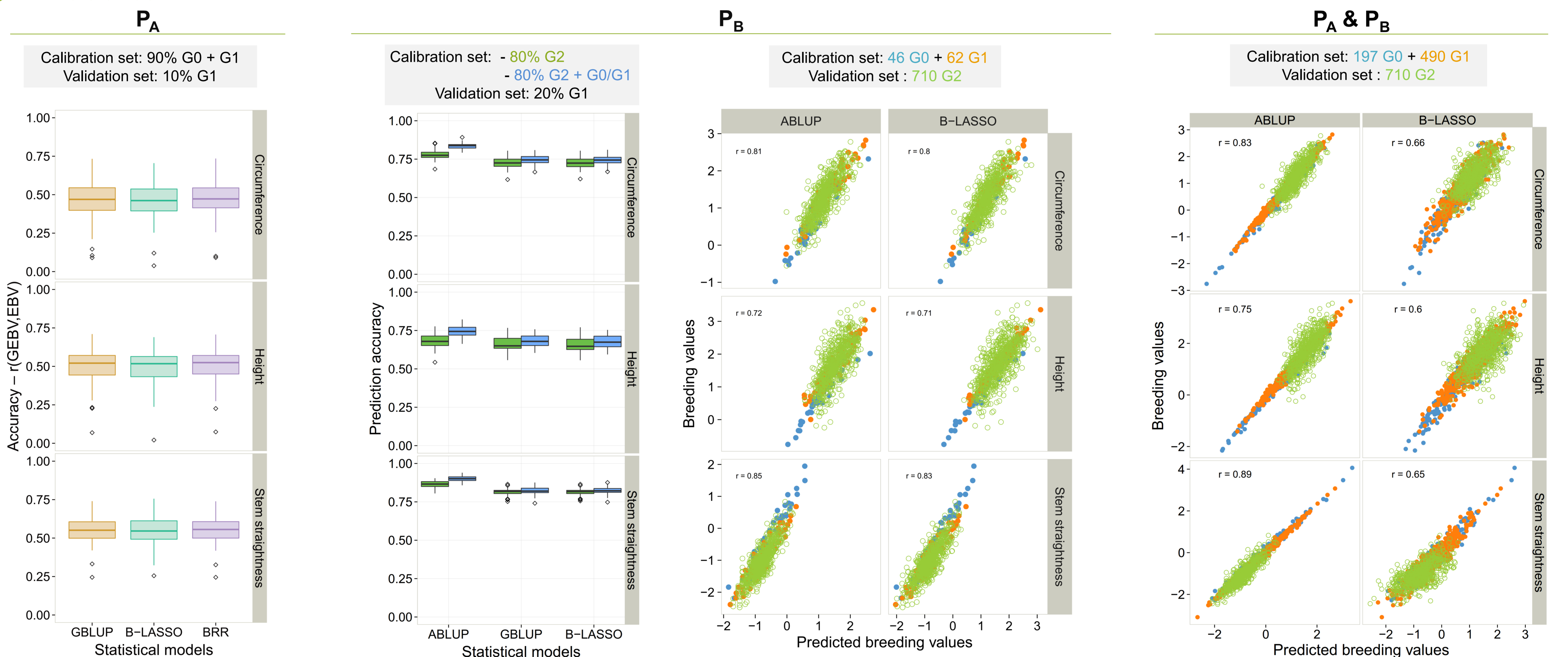
- 818 individuals: 46 G0 + 62 G1 + 710 G2
- Limited effective size ($N_s = 25$)
- **Completed pedigree**: all ancestors (G1 and G0) of the 710 G2 were sampled
- G2: 32 maternal HS families (≈ 22 trees / family) representing 355 FS families
- 4,400 SNPs

P_A and P_B combined : 2,200 SNPs in common, 1,397 individuals (197 G0, 490 G1 and 710 G2).

Pseudo-phenotypes: EBV for circumference, height (12years old), and stem straightness (8years old), based on BLUP evaluation

Genomic prediction based on different statistical methods: GBLUP, Bayesian LASSO, Bayesian ridge regression

Results



- ▶ Accuracy of genomic predictions ranging from 0.3 to 0.85 depending on the trait and the validation methods
- ▶ Higher accuracies in average for stem straightness compared to circumference and height.
- ▶ Similar accuracy between PBLUP and other GS models (GBLUP, Bayesian LASSO, Bayesian ridge regression).
- ▶ High accuracy for genomic prediction between generations when all the ancestor are sampled (P_B).

Conclusion and Prospects

- ▶ We showed that a model trained on parental generations (G0 and G1) can be used to predict progeny performances with high accuracies. However, the pedigree-based model (ABLUP) had prediction accuracies similar to or greater than that of marker-based models. The use of EBV as pseudo-phenotypes in combination with families of small size may have reduced the additional gain of information provided by molecular markers relative to the pedigree.
- ▶ The optimization of the current breeding strategy based on polymix breeding will therefore be required to enhance the potential of the GS in the maritime pine breeding program. A first step toward the implementation of GS will be the Single Step that combined pedigree and marker data (Legarra *et al.* 2014).

References - Bartholomé *et al.* Submitted. Performance of genomic prediction within and across generations in maritime pine - Isik *et al.* 2016. Genomic selection in maritime pine. Plant Science 242: 108-119. - Legarra *et al.* 2014. Single Step, a general approach for genomic selection. Livestock Science, 166:54-65.

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