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Genomic prediction in a multi-generation breeding population: maritime pine as a case study

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Context

Maritime pine breeding program

- Base population selected in the Southwest of France during the 60's(~700 G0 trees)
- From this base population, recurrent breeding scheme:
 - double-pair matings and forward selection to create the next breeding generation
- polycross matings and backward selection to select the best genotypes for seed orchards
- Currently reaches its 3rd generation (breeding population effective size ~ 135)
- Three main selection criteria
 - circumference (h² ~ 0.17)
 - height (h² ~ 0.32)
 - stem straightness (h² ~ 0.26)

> Breeding values evaluation

- Data base with > 400.000 trees over three generations (G0, G1, G2) connected with a pedigree matrix
- BLUP evaluation = multi-traits, multi-sites, multi-generations (Treeplan evaluation system)

Objectives

Genomic selection proof-of-concept for maritime pine

Low number of markers available (~3 markers / cM) → population of limited Ne

> Comparison of genomic predictions vs. pedigree predictions

Materials and Methods

Reference population: G2 trees + their ancestors (G0 and G1)



G2 selected for high growth and high stem straightness with a diversity constraint (maximum contribution of a single founder limited to 0.15)

Validation

→818 trees (Ne=24)

(Pedigree checked with parentage recovery analyses based on 80 SNPs)

Pseudo phenotypes: estimated breeding values (EBV) from BLUP evaluation for circumference, height and stem straightness

Model

Genotyping: 4,330 SNPs (only 0.05% of missing data)

Genomic predictions:

- 4 validation models
 - **G**0 **G2** Model_1 3 genomic prediction methods (GBLUP, Bayesian Ridge Model_2 **G2** Regression, Bayesian LASSO) Model_3 **G2** G0+G1 Model 4 G2 (80%) G2 (20%)

Training

Results

High accuracy for genomic prediction between and within generations



Genomic EBV vs. pseudo phenotype values (EBV) for circumference using the Bayesian LASSO method (G0, G1, G2, triangle= training set, dot=validation set)

Coefficient of numerator vs. realized relationship matrix in the reference population (n=818)



Conclusions

- High accuracy for genomic predictions
- > Inclusion of previous generations does not improve GS models
- Similar accuracy between pedigree and genomic predictions
 - Full pedigree relationships known through 3 generations
 - Poor estimates for G2 pseudo phenotypes (no clonal or progeny data)

Similar accuracy between pedigree and genomic predictions

EBV	r = 0.84 p < 0.001	r = 0.79 p < 0.001	EBV : estimated breeding value (pseudo phenotype)
		r = 0.93 p < 0.001	MPBV : mid-parent breeding value
		GBLUP	GBLUP: best linear unbiased prediction based on realized relationship matrix (Model_3 considered)







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