

Using genome-wide predictions in a functional-structural plant model to simulate the genetic variation of 1-year-old apple tree development under contrasted soil water conditions

Vincent Migault, Benoît Pallas, Jean-Michel Legave, Yann Guédon, Evelyne Costes

► To cite this version:

Vincent Migault, Benoît Pallas, Jean-Michel Legave, Yann Guédon, Evelyne Costes. Using genome-wide predictions in a functional-structural plant model to simulate the genetic variation of 1-year-old apple tree development under contrasted soil water conditions. IEEE International Conference on Functional-Structural Plant Growth Modeling, Simulation, Visualization and Applications (FSPMA 2016), Nov 2016, Qingdao, China. poster abstracts (96), 2016 IEEE International Conference on Functional-Structural Plant Growth Modeling, Simulation, Visualization and Applications (FSPMA 2016). hal-01400054

HAL Id: hal-01400054

<https://hal.inria.fr/hal-01400054>

Submitted on 23 Nov 2016

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Using genome-wide predictions in a functional-structural plant model to simulate the genetic variation of 1-year-old apple tree development



Vincent Migault¹, Benoît Pallas¹, Jean Michel Legave¹, Yann Guédon², Evelyne Costes¹

¹INRA, UMR AGAP, ²Cirad UMR AGAP & Virtual Plants Team. Avenue d'Agropolis, 34000 Montpellier.

contact: pallas@supagro.inra.fr



Context

A large genetic variability in tree architecture has been observed in bi-parental apple tree populations (Segura et al., 2006)

QTLs related to architectural traits have been identified (Segura et al., 2008).

These genotypic effects have not been integrated in the apple tree FSPM, MAppleT (Costes et al. 2008).



Fig 1. Architecture variability in the Starkinson x Granny F1 progeny

General objective: integrating genetic control in MAppleT

Material and methods

Modelling phyllochron and probabilities of sylleptic branching

Four new parameters (Table 1) with major impact on the first year of growth were included in MAppleT.

The rate of leaf emergence (RLE_{GDD}) was assumed to depend on the thermal time (Lescourret et al. 1998)

Table 1. New parameters of MAppleT

Process	Parameter name	Parameter definition	Units
Leaf emergence	RLE_{GDD}	Rate of leaf emergence depending on temperature	GDD
Sylleptic branching	a_{syll}	Probability of emergence of sylleptic branches	GDD ⁻¹
Individual internode elongation	IN_length	Final internode length	cm
Individual leaf expansion	Leaf_area	Final leaf area	cm ²

Main equations used to simulate genotypic effects

$$RLE(t) = RLE_{GDD} \times T_{eff}(t)$$

$$P_{syll}(t) = a_{syll} \left(\frac{1}{n_{days}} \sum_{i=t-n_{days}}^t RLE_i \right) \times RLE(t)$$

Sylleptic branching probability (P_{syll}) was assumed to depend on the rate of leaf emergence during the season (Peyrhardi et al. 2013)

Model calibration and genome wide prediction

Parameter values (RLE_{GDD} , a_{syll} , IN_length, Leaf_area) were estimated on 116 genotypes of the bi-parental ('Starkinson' x 'Granny Smith') population, observed in 2007.

Genotyping allowed detecting 3123 SNPs polymorphisms that were used for genome wide predictions.

Genome wide prediction was performed using Ridge Regression Blups (Endelman, 2011; Fodor et al. 2013).

Marker effects were evaluated using a mixed effect model assuming infinitesimal effects.

$$Y = \mu + Xg + e \quad \text{with} \quad g \sim N(0, I_n \sigma_g^2)$$

Vector of model parameter s

$$\begin{pmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{pmatrix}$$

$$\begin{pmatrix} -1 & 1 & -1 & 1 & \dots & -1 & 1 \\ -1 & 1 & 1 & -1 & \dots & 1 & 1 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 1 & -1 & 1 & 1 & \dots & -1 & 1 \end{pmatrix}$$

Matrix of genotypes at each marker

$$\begin{pmatrix} g_1 \\ g_2 \\ \vdots \\ g_n \end{pmatrix}$$

Vector of markers effects

Model simulation and validation

When running simulations, values of MAppleT parameters were estimated using the genetic information provided by the genome wide prediction model.

The quality of simulations was assessed by comparing model simulations and observations of integrative plant variables (trunk length, number of sylleptics) in 2007 and under independant climatic conditions in 2004.

Results

Simulations of phenotypic variability

The MAppleT model simulated large range of 1-year-old apple tree phenotypes (Fig. 2).

Correlations between simulated traits (trunk length, number of branches, number of leaves) were consistent with the correlations for the observed traits (Table 2), suggesting independant genetics controls.

Table 2. Correlations between architectural traits for observations and simulations

	Nb_Leaves	Trunk length	Nb_Syll
Nb_Leaves		0.34	0.26
Trunk length	0.41		-0.09
Nb_Syll	0.25	-0.03	

Correlations from observed data (blue)
Correlations from simulated data (red)

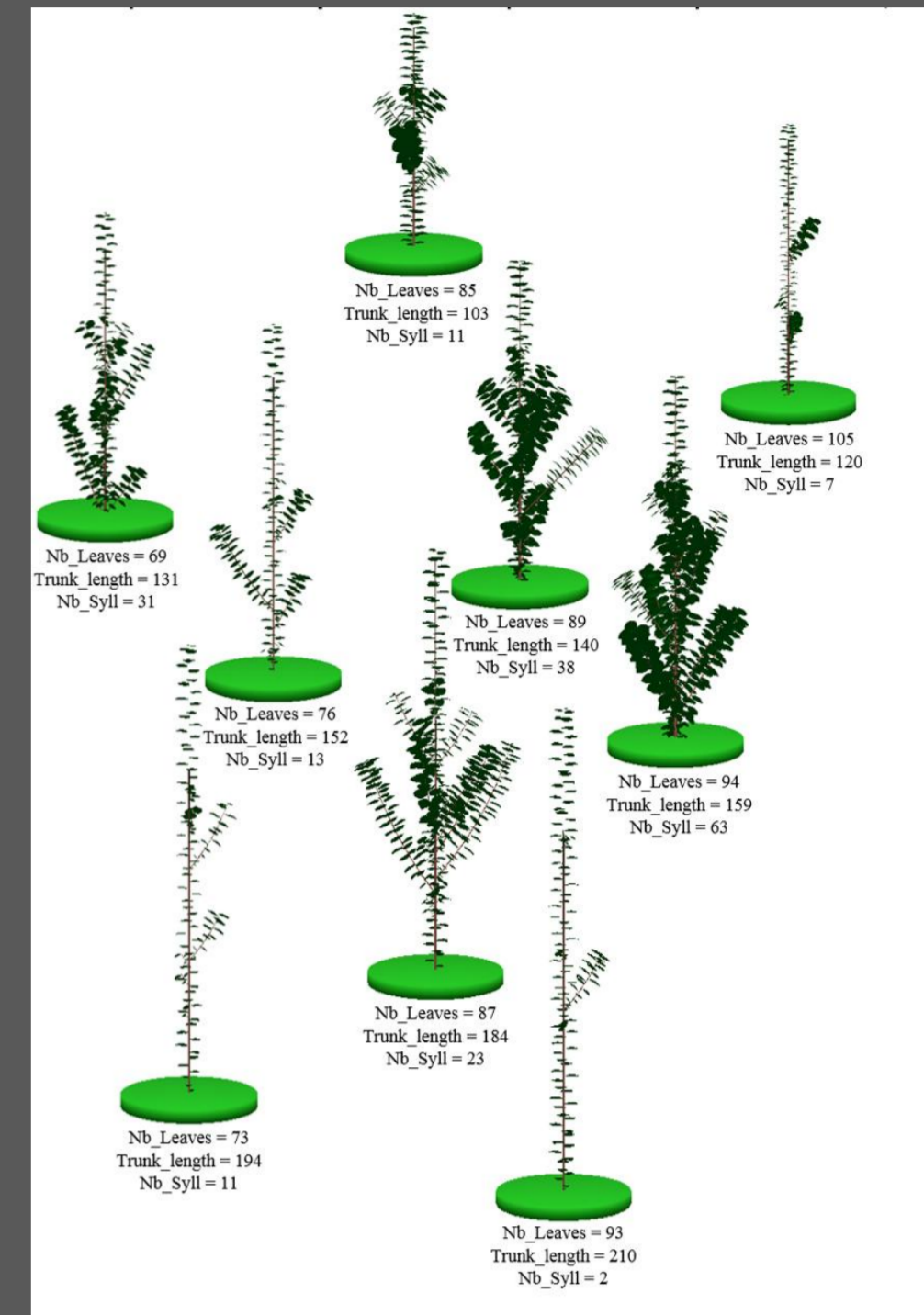


Fig 2. Graphical outputs of MAppleT simulations for nine apple tree genotypes with contrasted architecture

Model validation on integrative traits

High correlations and low RMSE between observations and simulations were found for the simulations of integrative traits in 2007 (Fig. 3).

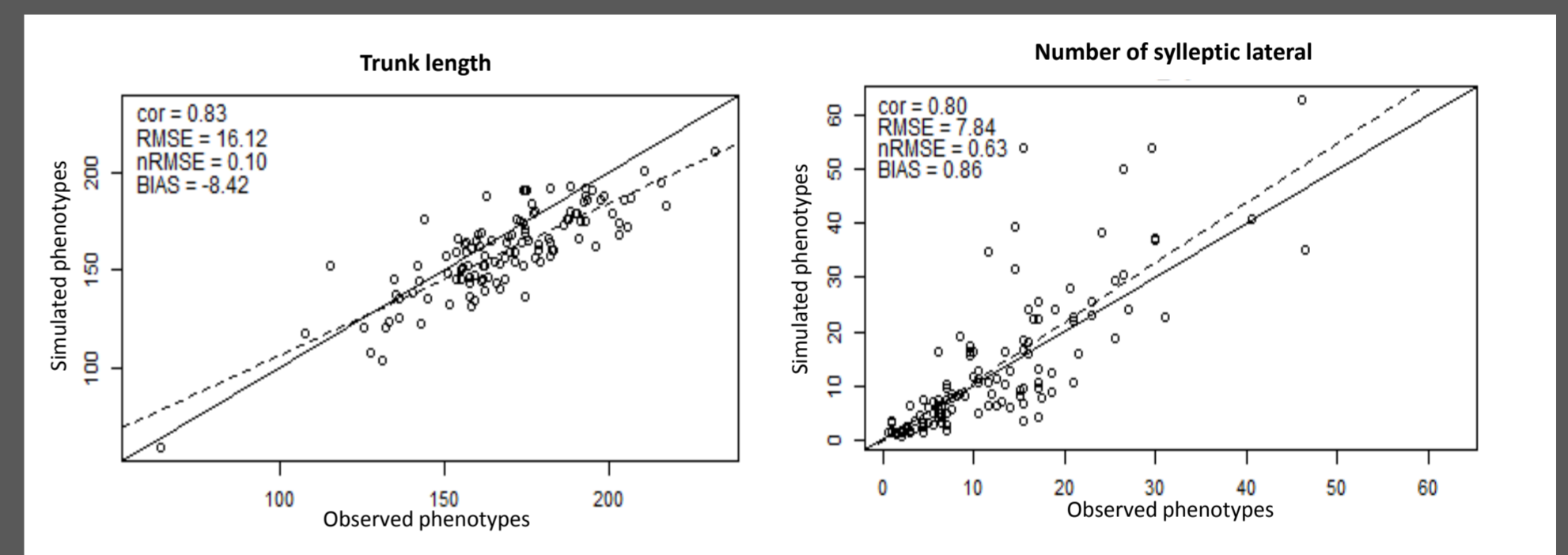


Fig 3. Comparison of observed and simulated phenotypes in 2004.

Model validation under independant climatic conditions

Under environmental conditions not used for model calibration (year 2004), correlations between simulated and observed values were lower (Fig. 4).

The environmental effects presently included in MAppleT, i.e. temperature effect on the phyllochrone and sylleptic branching, are not sufficient to correctly simulate the GxE interactions.

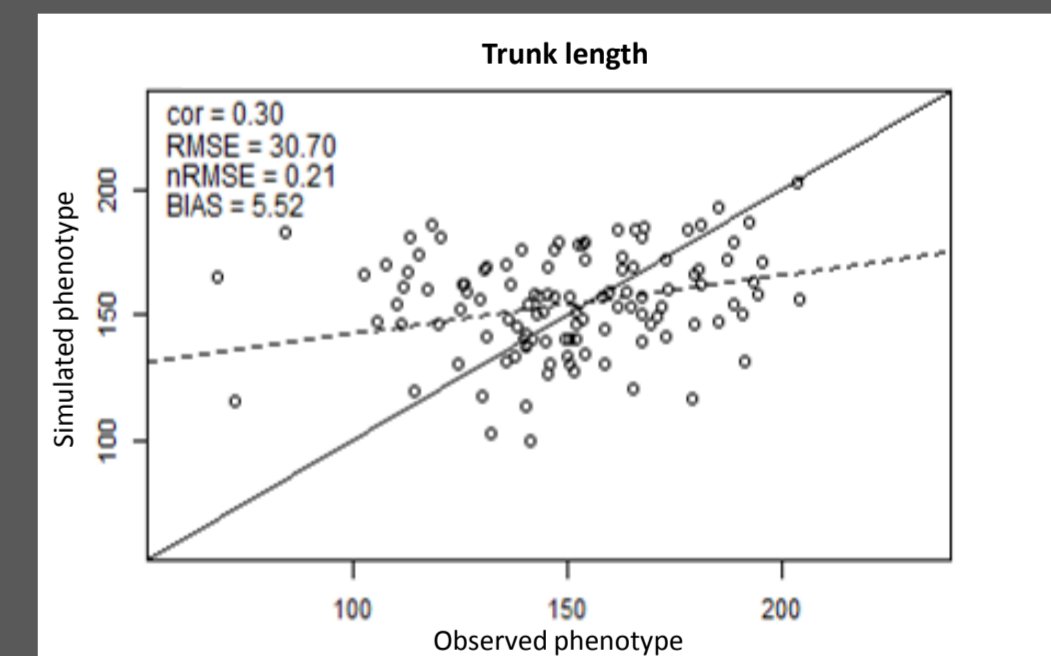


Fig 4. Comparison of observed and simulated phenotypes in 2004

Conclusions

This study corresponds to a first attempt to introduce genome-wide information in a FSPM for a fruit tree.

Even though further improvements are required to better model genotype x environment interactions, it opens new possibilities for supporting plant breeding by *in-silico* evaluations of the impact of genotypic polymorphisms on integrative phenotypes.

References

Costes et al. 2008, *Funct. Plant Biol.*, 35: 936-950. Endelman, 2011, *Plant Genome*, 4: 250-255. Fodor et al. 2014, *PLOS ONE*, 9: e110436. Lescourret et al. 1998, *Eur. J. Agron.*, 9: 173-188. Peyrhardi et al. 2013, *FSPM 2013*. Segura et al. 2006, *Tree Genet. Genomes*, 2: 140-151. Segura et al. 2008, *New Phytol.*, 178: 302-314

Fundings

This project is funded by the Agence Nationale de la Recherche (ANR) and by the Deutsche Forschungs-gemeinschaft (DFG).