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To cite this version:
Vincent Migault, Benoit 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. International Conference on Functional-Structural Plant Growth Modeling, Simulation, Visualization and Applications (FSPMA 2016), Nov 2016, Qingdao, China. 2016. hal-02740169

HAL Id: hal-02740169
https://hal.inrae.fr/hal-02740169
Submitted on 2 Jun 2020

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

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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).

General objective: integrating genetic control in MAppleT

Material and methods

Modelling phylochron 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 (RLEGEO) was assumed to depend on the thermal time (Lescourret et al. 1998)

Table 1. New parameters of MAppleT

<table>
<thead>
<tr>
<th>Process</th>
<th>Parameter name</th>
<th>Parameter definition</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>leaf emergence</td>
<td>RLEGEO</td>
<td>Rate of leaf emergence depending on temperature</td>
<td>GDD</td>
</tr>
<tr>
<td>Sylleptic branching</td>
<td>a_syl</td>
<td>Probability of emergence of sylleptic branches</td>
<td>GDD²</td>
</tr>
<tr>
<td>Individual internode elongation</td>
<td>dI_length</td>
<td>Final internode length</td>
<td>cm</td>
</tr>
<tr>
<td>Individual leaf expansion</td>
<td>Leaf_area</td>
<td>Final leaf area</td>
<td>cm²</td>
</tr>
</tbody>
</table>

Sylleptic branching probability (P_syl) 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 (RLEGEO, a_syl, dI_length, Leaf_area) were estimated on 116 genotypes of the bi-parental (‘Starkrimson’ 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.

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 syllepts) in 2007 and under independent 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 independent genetics controls.

Table 2. Correlations between architectural traits for observations and simulations

<table>
<thead>
<tr>
<th>Trait</th>
<th>Nb_Leaves</th>
<th>Trunk length</th>
<th>Nb_Syll</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nb_Leaves</td>
<td>1.00</td>
<td>-0.95</td>
<td>-0.99</td>
</tr>
<tr>
<td>Trunk length</td>
<td></td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>Nb_Syll</td>
<td></td>
<td></td>
<td>1.00</td>
</tr>
</tbody>
</table>

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).

Model validation under independent 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 phylochron and sylleptic branching, are not sufficient to correctly simulate the GxE Interactions.

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 genetic polymorphisms on integrative phenotypes.

References


Funding

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