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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 under contrasted soil water conditions**

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The vegetative development of plants results from the rate of leaf emergence (RLE), internode elongation and branching. Assuming that these processes are under genetic control and affected by environmental conditions such as temperature and soil water content, this study aimed at modelling them in the case of 1 year old apple tree. Previous studies have suggested that RLE modulates sylleptic branching since the number of sylleptic branches is often higher when the RLE is high during the season. We thus proposed to model the influence of RLE on sylleptic branching assuming that the plasticity of sylleptic branching results from that in RLE. These three processes, i.e. RLE, sylleptic branching and internode elongation are included in MAppleT, a functional-structural plant model (FPSM) for apple tree, to simulate its development.

Experimental data were collected on one year-old trees corresponding to a progeny issued from 'Starkrimson' × 'Granny Smith' cross (116 genotypes), with four replicates per genotype submitted to water stress or optimal irrigation. The number of newly emitted metamers was counted every week whereas the mean length of internodes and the number and position of sylleptic axes were assessed at the end of the growth season. Temperature and soil water potential (SWP) were measured over the experiment.

The RLE was modelled using a thermal-time based approach in degree days (dd). The probability of emergence of a sylleptic lateral (P<sub>syll</sub>) was estimated as a linear function of RLE<sub>dd</sub>, for each well-watered tree. Then, the markers effects on phenotypic values for RLE<sub>dd</sub>, and its interaction with SWP, P<sub>syll</sub> and the mean internode length, in either well-watered or water stress conditions, were estimated using a ridge regression (RR) for 106 out of the 116 genotypes. The accuracy of genomic predictions obtained by these RR was estimated using a 5-fold cross-validation and ranged from 0.24 to 0.37.

The last step of our approach will consist in considering the matrix of marker effects as an input of MAppleT to simulate the integrated phenotypes resulting from the three studied traits for the 10 genotypes not included in the RR, with or without water stress effect. Simulations will then be compared to the observed phenotypes to validate the overall approach.

This study is a first attempt to integrate genome-wide information in a functional-structural plant model for a perennial fruit tree taking into account environmental effects. It shows the potential of sustaining plant breeding by allowing in silico evaluation of the impact of genotypic polymorphisms on plant integrative phenotypes.