



Using numerical plant models and phenotypic correlation space to design achievable ideotypes

Pierre Casadebaig, Victor Picheny, Ronan Trépos, Robert Faivre, David da Silva, Patrick Vincourt, Evelyne Costes

► To cite this version:

Pierre Casadebaig, Victor Picheny, Ronan Trépos, Robert Faivre, David da Silva, et al.. Using numerical plant models and phenotypic correlation space to design achievable ideotypes. Society of Experimental Biology Annual Main Meeting (SEB 2017), Jul 2017, Gothenburg, Sweden. , 344 p., 2017, Abstract book: Society of Experimental Biology. hal-01603216

HAL Id: hal-01603216

<https://hal.science/hal-01603216>

Submitted on 2 Jun 2020

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.



Distributed under a Creative Commons Attribution - ShareAlike 4.0 International License

PC8.24 USING NUMERICAL PLANT MODELS AND PHENOTYPIC CORRELATION SPACE TO DESIGN ACHIEVABLE IDEOTYPES

WEDNESDAY 5 JULY, 2017 15:00

PIERRE CASADEBAIG (INRA, FRANCE), VICTOR PICHENY (INRA, FRANCE), RONAN TRÉPOS (INRA, FRANCE), ROBERT FAIVRE (INRA, FRANCE), DAVID DA SILVA (INRA, FRANCE), PATRICK VINCOURT (INRA, FRANCE), EVELYNE COSTES (INRA, FRANCE)

@ PIERRE.CASADEBAIG@INRA.FR

Numerical plant models can predict the outcome of plant traits modifications resulting from genetic variations, on plant performance, by simulating physiological processes and their interaction with the environment. Optimization methods complement those models to design ideotypes, i.e. ideal values of a set of plant traits resulting in optimal adaptation for given combinations of environment and management, mainly through the maximization of a performance criteria (e.g. yield, light interception). As use of simulation models gains momentum in plant breeding, numerical experiments must be carefully engineered to provide accurate and attainable results, rooting them in biological reality.

Here, we propose a multi-objective optimization formulation that includes a metric of performance, returned by the numerical model, and a metric of feasibility, accounting for correlations between traits based on field observations. We applied this approach to two contrasting models: a process-based crop model of sunflower and a functional-structural plant model of apple trees. In both cases, the method successfully characterized key plant traits and identified a continuum of optimal solutions, ranging from the most feasible to the most efficient. The present study thus provides successful proof of concept for this enhanced modeling approach, which identified paths for desirable trait modification, including direction and intensity.

PC8.25 APPLYING THE ARABIDOPSIS FRAMEWORK MODEL TO LINK SNPS TO CLINES

WEDNESDAY 5 JULY, 2017 15:45

ANDREW J MILLAR (SYNTHSYS AND SCHOOL OF BIOLOGICAL SCIENCES UNIVERSITY OF EDINBURGH, UNITED KINGDOM), YIN HOON CHEW (UNIVERSITY OF EDINBURGH, UNITED KINGDOM), DANIEL D SEATON (UNIVERSITY OF EDINBURGH, UNITED KINGDOM), URIEL URQUIZA (UNIVERSITY OF EDINBURGH, UNITED KINGDOM), ALASTAIR HUME (EPCC UNIVERSITY OF EDINBURGH, UNITED KINGDOM), EILIDH TROUP (EPCC UNIVERSITY OF EDINBURGH, UNITED KINGDOM), TOMASZ ZIELINSKI (UNIVERSITY OF EDINBURGH, UNITED KINGDOM), ARGYRIS ZARDILIS (UNIVERSITY OF EDINBURGH, UNITED KINGDOM), ROBERT MUETZELFELDT (SIMULISTICS LTD., UNITED KINGDOM)

@ ANDREW.MILLAR@ED.AC.UK

The 24-hour circadian clock controls the sleep-wake cycle, the cell cycle and seasonal reproduction through photoperiodism. Breeders have selected alleles of clock-associated genes in multiple crops. We seek to understand how the clock gene circuit controls plant growth, biomass and life history in *Arabidopsis thaliana*. This work links genotype to phenotype, quantitatively and mechanistically. However, the proof of concept for a 'crops *in silico*' approach should ideally start from increasingly available crop genome sequences and reach up to field traits, in a transparent and accessible fashion.

We previously built mechanistic, mathematical models of the clock gene circuit, and of each clock-regulated process between germination and flowering, including the nightly utilisation of starch carbon stores. Linking specific aspects of the clock model to genome sequence (SNPs) is one current challenge. We also combined three further models to form the Arabidopsis Framework Model (FMv1; www.plasmo.ed.ac.uk/plasmo/models/model.shtml?accession=PLM_76), which predicts rosette biomass quantitatively in simple reference conditions (Chew et al. PNAS 2014). In the FMv2 (Chew et al. *bioRxiv* 2017, <https://doi.org/10.1101/105437>), we modelled the clock-regulated processes in the whole-plant context, to understand quantitatively the pleiotropic phenotypes of a 'slow' clock mutant, from the gene circuit dynamics to biomass. Testing the FMv2 under multiple environments now suggests the potential to link from SNPs to clinal variation.

To address the challenge of making such models accessible, I will contrast a very simple, online simulator (<http://turnip.bio.ed.ac.uk/fm/>) with previous approaches. The FAIRDOM data management system (www.fair-dom.org) promises to organise relevant data and models, and seems easily applicable to crop models.