HAL open science

Using agronomic models to predict cultivar performances under various environments and cropping systems

Marie-Helene Jeuffroy, Philippe Debaeke, Arnaud Gauffreteau, Christophe Lecomte, Chantal Loyce, Lorène Prost

To cite this version:

Marie-Helene Jeuffroy, Philippe Debaeke, Arnaud Gauffreteau, Christophe Lecomte, Chantal Loyce, et al.. Using agronomic models to predict cultivar performances under various environments and cropping systems. Farming Systems Design 2009 : an international symposium on Methodologies for Integrated Analysis of Farm Production Systems, Aug 2009, Monterey, Californie, United States. hal-01173230

HAL Id: hal-01173230

https://hal.science/hal-01173230v1

Submitted on 3 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.

Using agronomic models to predict cultivar performances under various environments and cropping systems

Marie-Hélène JEUFFROY[1], Philippe DEBAEKE[2], Arnaud GAUFFRETEAU[1], Christophe LECOMTE[3], Chantal LOYCE[4], Lorène PROST[5]
[1] INRA, UMR Agronomie INRA-AgroParisTech, 78850 Thiverval-Grignon, France (jeuffroy@grignon.inra.fr)
[2] INRA, UMR1248 AGIR, BP 52627, 31326 Castanet Tolosan Cedex, France
[3] INRA, URLEG, 17 rue Sully, BP 86510, 21065 DIJON Cedex, France
[4] AgroParisTech, UMR Agronomie INRA-AgroParisTech, 78850 Thiverval- Grignon, France
[5] INRA, UMR SAD-APT, 78850 Thiverval-Grignon

INTRODUCTION

The diversity of the environmental stakes among locations and the development of new outlets for agricultural products favour the diversity of crop management systems, including the choice of adapted cultivars (Loyce et al., 2008).

Multi Environment Trials (METs) are often conducted to compare the response of genotypes under a wide range of soil-weather conditions and, more rarely, of cropping systems (CS). In these METs, significant genotype (G) by environment (E) by Cropping systems (CS) interactions are often observed, representing 10-25% of the total yield variation. Various statistical methods have been proposed to analyze G by E interactions (Brancourt et al., 1997). Yet, they do not help to predict the performance of cultivars in various cropping systems or landscapes. Therefore it is difficult to use the results of METs to choose the suitable cultivars for a given cropping system or landscape or to design the crop management systems most suited to a given genotype. Finally, this experimental device has a poor predictive quality, particularly in the environments and cropping systems not included.

Dynamic crop models have been used to assess various performances of genotypes only since 10-15 years. More recently, spatially explicit models simulating gene flow or disease epidemics have been used to support breeding and cultivar evaluation. This paper reviews the potential and actual use of a diversity of agronomic models for predicting cultivar performance under various environments and cropping systems.

FOUR USES OF MODEL-BASED PREDICTIONS OF THE INTERACTION CULTIVAR*CROPPING SYSTEM

Four types of uses of model-based predictions of the Genotype x Environment x Cropping System Interactions (GECSI) can be identified in the literature:

(1) help defining breeding objectives, i.e. identifying the morphological and physiological traits to breed for a given aim. The criteria used by breeders as breeding targets are not always chosen taking into account of their impact on the complexity of the crop functioning. Agronomic models, making possible a rapid and multi-criteria evaluation of genotypic traits in interaction with various environmental conditions, can limit this problem (Fargue et al., 2005). The analyses of the model sensitivity to the studied trait allow to quantify the influence of the studied trait on the crop performances during the whole cycle, in various conditions of environment and cropping system. However, most studies use a weak representation of the environments and cropping systems, evaluate a low number of criteria, and assume that phenotypic traits are independent.

(2) help cultivar experiment management, i.e. characterizing the environments in order to optimize METs, and understand GECSI observed on a MET. Crop models are useful tools to characterize the limiting factors endured by the crops. Indeed, they can simulate the evolution of varying environmental states, which are difficult to measure continuously.

(3) Models can also be used to predict new cultivar behaviours in a larger range of conditions than those encountered in the experimental networks. They allow to identify the situations suited ot not to a varietal type.
(4) Models can help defining directions for use of new cultivars, that is to say choosing the best cultivar in a given cropping system, or the best crop management plan for a given cultivar.

HOW TAKING INTO ACCOUNT THE CULTIVAR IN CROP MODELS?

The first step is to choose/design a model allowing the best assessment of GECSI. To favour the link between model and breeding, models should be more efficient if involving relationships between parameters and genes or groups of genes. On the contrary, to define the conditions of use of cultivars, the model should include a simple method for phenotyping but should be robust in taking into account a large range of growth conditions and in giving account of various crop management strategies.

The second step is to identify and estimate the genotypic parameters. A sensitivity analysis to its parameters is a good way to identify those which have the highest influence on the outputs Yet, to choose the parameters it is also important to take into account the forecasted use of the model (and the future use of the genotypic parameters). For the estimation of the parameters, two methods are proposed. The first is based on optimizing model outputs. It aims at identifying the parameter values that minimize the gap between the simulated and observed values of outputs. The results show that, according to the number of parameters estimated simultaneously, the parameter values can be highly different, indicating compensations between the parameters. The biological meaning of the parameters estimated by fitting outputs is then questionable, as the values are directly dependent on the model structure and the values of the other parameters. The other way used in the literature is based on the direct measurement of parameters when possible, or on the fit of relationships in which they appear. Whatever the method of cultivar-parameter estimation, the choice of using specific cultivar parameters in crop models should be based on the comparison between the increase in predictive quality of the model and the increase of cost of measurement of the data required for the cultivar adaptation, which is rarely mentioned in the literature.

The third step is to assess the model for the forecasted uses. Besides the classical evaluation of the predictive quality of crop models, it appears essential to appreciate their ability to take a relevant decision, that is to say to reach the uses aimed by the potential users. Even if the model has a poor predictive quality, it can be a useful tool if it helps to take a better decision than with the available information and tools.

CONCLUSION

While studies on crop models with genotypic parameters are increasing in the literature, few of them are used by people in charge of cultivar evaluation. In this aim, it should be necessary to involve the end users in the design of the model.

REFERENCES

Loyce *et al.*, 2008. Interaction between cultivar and crop management effects on winter wheat diseases, lodging and yield. Crop protection, 27, 1131-1142.
Fargue et al., 2005. Introduction of genotypic effects into GeneSys-Rape : the example of height and male sterility. Agriculture, Ecosystems and Environment, 108, 318-328.
Brancourt-Hulmel et al., 1997. Repères dans l'analyse de la stabilité et de l'interaction génotype-milieu en amélioration des plantes. Agronomie, 17, 219-246.