

Whole plant modeling within the context of a maize breeding program where drought tolerance is a primary objective: Technology development and application and status of GCP-WPM activities

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Background

Many plant breeding strategies have been advocated for the genetic improvement of complex traits. In the evaluation of the merits of such recommendations it is useful to distinguish between two general classes of problem that the plant breeder has to tackle: (1) Breeding objectives where a genetic answer to the problem is known; *e.g.*, a target genotype, haplotype or gene has been identified and the objective is to close the genetic gap between the current germplasm and the defined target to test the hypothesis, (2) Breeding objectives where plausible genetic answers to the problem are currently unknown; *e.g.*, to increase grain yield or drought tolerance beyond the current levels of the elite commercial products. Clearly we can consider that scenario 2 is a more complex breeding objective than the first. For scenario 2 the feasibility of achieving the breeding objectives has to be assessed, genetic and breeding targets have to be defined and appropriate technologies have to be identified to enable the breeding strategy to be implemented. It is in this second area that the whole plant modeling technologies that were the focus of the Generation Challenge Program project review have the greatest potential to add new capabilities to enhance the likelihood of success of the desired plant breeding outcomes. At Pioneer we have gained some experience in developing and working with such technologies. The objective of this paper is to define some of the key lessons we have learnt that could provide some guidance for future efforts by the Generation Challenge project participants.

Breeding Applications

A central concept that motivates our research investments to evaluate potential applications of crop modeling principles within a maize breeding program is that by creating an enhanced understanding of the physiological-genetic basis of the standing genetic variation for key traits in the reference population of a breeding program we can identify testable genetic hypotheses that open up new opportunities for further genetic improvement. These testable hypotheses can then be included as components of the breeding program and evaluated for their merits in comparison to other breeding targets under evaluation. This principle can be applied at the inbred and hybrid creation levels, and with appropriate research extended to the QTL and gene levels. Here we summarize the development and application of whole plant modeling (WPM) concepts that parallel the focus areas of the WPM Generation Challenge Project and focus the summary from the perspective of genetic improvement of drought tolerance in temperate maize for the US corn-belt. From the outset it is important to view the WPM research efforts that we have invested in at Pioneer as a focused discovery effort designed to determine how these technologies can increase the likelihood of successful outcomes from an active maize breeding program. In this manner as ideas develop they can be rapidly evaluated for their potential within the operation of the targeted breeding program. When positive results are demonstrated the methods can be rapidly and efficiently integrated within the breeding program cycle and appropriately resourced as a component of the breeding program. Further the methods can be deployed to other breeding programs as appropriate.

Technology Development

Three relevant breeding technologies that include a crop modeling component and were investigated within the GCP-WPM project are listed below. For each area a summary of motivations and key issues for their application to maize breeding in Pioneer is provided.

Environmental Characterization: Initial research efforts in the area of environmental characterization were undertaken to help understand the potential sources of genotype-by-environment interactions (GEI) for different traits, stages of breeding and target regions. These efforts have enabled new opportunities for describing important features of the environments at two levels: (1) the Target Population of Environments (TPE) level, representing a broad high-level geographical view across multiple years (>50 years for the northern US), (2) the Multi-Environment Trial (MET) experiment level, targeted at specific experiments conducted at specific locations in particular years under the relevant management conditions (Fig. 1). Within these applications the crop growth model has been applied as an integrator of multiple environmental data sources (soils, weather, hybrid and management conditions) to assist in the definition of key environmental events that impact crop growth and development and trait genetic variation. One technology development from these efforts was the creation of the ENCLASS® system that is routinely used for many applications within Pioneer (Loeffler et al. 2005).

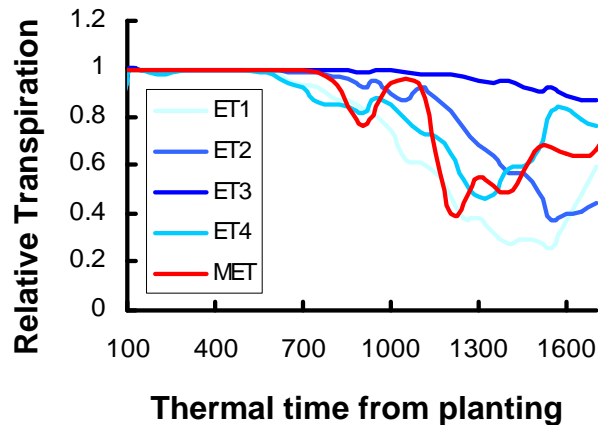


Fig. 1. Drought stress pattern for a location in a MET experiment positioned relative to environment types (ET) that define the Target Population of Environments for drought stress. Relative transpiration simulated for a check hybrid.

Precision Phenotyping: We can view the crop growth model as an advanced multi-trait phenotyping framework. As such the quantitative relationships defined within the crop growth model provide a dynamic time-dependent framework for integrating the observations of traits at specific developmental stages within specific environments to understand their importance in determining genetic variation for other measured traits (e.g. grain yield) as an outcome of the relationships encoded within the model. As such genetic concepts such as epistasis (gene-by-gene and trait-by-trait interactions), pleiotropy (genes influencing multiple traits), and GEI (genes and traits having different levels of influence and expression in different environments) can be studied as features of a crop growth model parameterized for components of the standing genetic variation in the reference population of the breeding program. Further this methodology can be used to define the value of collecting additional types of phenotypic data.

Gene-to-Phenotype modeling: Perhaps one of the more challenging areas where crop growth models have been considered to have a potential role is in examining and quantifying the influence of specific genes and multi-gene models on complex trait variation. In this role the crop growth model represents a complementary integrative framework that can both guide trait mapping and dissection investigations that seek to identify Quantitative Trait Loci (QTL) and the underlying sequence variation and evaluate the impact that the revealed variation is predicted to have at the whole plant level. Examples of this application of crop models were reviewed by Hammer et al. (2006) and were a major focus of the GCP-WPM project. One example that illustrates the capacity developed in Pioneer to apply the crop growth modeling framework to breeding for drought stress in temperate maize is presented in Fig 2. The simulated breeding trajectories enable us to understand observed breeding trajectories for traits contributing to yield improvement, to identify emergent, in some cases counterintuitive, behavior of the breeding system, and to quantify trait and environmental context dependencies. This understanding along with quantitative knowledge on QTL function enables us to make predictions to be evaluated in the target breeding program.

Synopsis: State of the Science and the GCP-WPM project

As with any proposed breeding technology Pioneer undertakes proprietary research to examine the suitability of the technology for its role in enhancing the likelihood of success of targeted breeding outcomes. Potential applications of WPM concepts have been examined. Three areas that have progressed beyond initial discovery efforts and are undergoing further investigation are listed: (1) Environmental characterization, (2) Precision phenotyping, and (3) Gene-to-Phenotype modeling. All three of these areas were investigated by the GCP-WPM project participants within the scope of the project for a range of crop-environment scenarios. Different levels of success were reported for the crops and regions targeted. In a number of cases the preliminary research conducted as a component of the GCP-WPM project was not of an adequate scale to assess the potential benefits of the technology. For example for the Environmental Characterization component in Brazil the project participants noted difficulties with access to suitable data sets and definition of appropriate measurements and resources to obtain measurements in plant breeding experiments. Our experience at Pioneer is that the GCP-WPM are going through similar preliminary issues that need to be resolved to scale the areas of research to realize the benefits and to support their application for plant breeding. In some of the focus areas the project participants demonstrate international scientific leadership in developing these

technologies. Specific examples that were presented at the meeting include the use of biophysical models to assist with definition of appropriate phenotyping strategies for QTL detection and validation. The project team collectively possesses an advanced scientific and technical skill in this area that could further support phenotyping efforts relevant to the priorities of the GCP. Examples of how these methods could be used to assist breeding were discussed. Some preliminary applications to grain sorghum in Australia were reviewed. Major assessments that can be provided from Pioneer in the advisory role on this project are:

1. The environmental characterization work would need to be scaled up significantly to achieve the expected outcomes to enhance understanding of GEI and impact plant breeding methods. This effort if continued should be separated from the other crop modeling activities and more directly linked to the phenotyping needs of targeted breeding programs.
2. Promising results in the definition of specific trait phenotypes based on application of WPM concepts were demonstrated and provide opportunities for further research. While there is a need for coordination across these efforts currently there is limited justification for these all to be included as one project. At present the resources available for each example are limited and progress would be enhanced by greater levels of funding.
3. The gene-to-phenotype modeling efforts should be resourced and coordinated to complement the Precision Phenotyping and QTL discovery work. At present there are multiple heterogeneous targets included in the single project and there would be advantages to considering the different crop-trait targets as different projects.

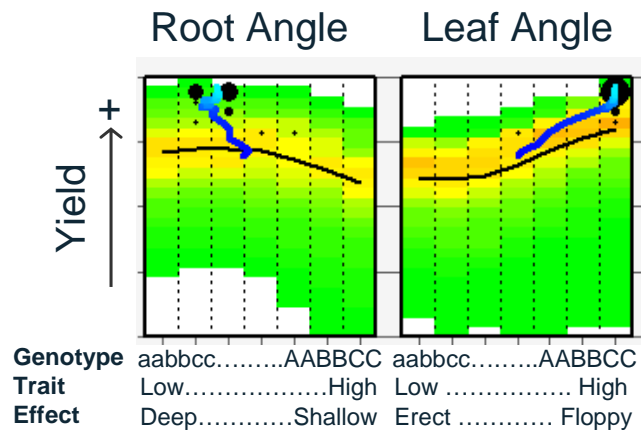


Fig 2. Breeding trajectories (blue lines) in a gene-to-phenotype adaptation landscape (genotype frequency: green=low, red=high; black dots=individuals in the breeding population). The adaptation landscape was generated by using a Pioneer proprietary model developed to simulate maize growth and development. The landscape is represented by a number (7 in this case) of genotypic bins describing the yield distribution for all combinations of traits (e.g. leaf angle) conditioned to a given expression state (more than one genotype could give rise to the same state) for the varying trait (e.g. low root angle). Breeding strategies were simulated using QU-GENE (Podlich and Cooper, 1998).

References

- Hammer, G., Cooper, M., Tardieu F., Welch, S., Walsh, B., van Eeuwijk F., Chapman, S., Podlich, D. (2006). Models for navigating biological complexity in breeding improved crop plants. *Trends in Plant Science* 11: 1360-1385.
- Löffler, C.M., Wei, J., Fast, T., Gogerty, J., Langton, S., Bergman, M., Merrill, R.E., Cooper, M. (2005). Classification of Maize Environments using Crop Simulation and Geographic Information Systems. *Crop Science* 45: 1708-1716.
- Podlich, D and Cooper. M. (1998). QU-GENE: a simulation platform for quantitative analysis of genetic models. *Bioinformatics* 14: 632-653