
Session 2.5 Crop Model Improvement and Genetics Applications

Oral Presentation

Title: Toward Next Generation Gene-based Crop Models: Implications on Experiments, Data, Modeling, and Modularity

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Abstract: Studies have shown that some dynamic plant processes can be modeled to depend on genes (G), the environment (E), and GxE interactions. Most notably, phenological development of plants has been modeled by taking into account gene networks, RNA synthesis, and expression of first flower. However, prior research has been based primarily on empirical approaches to simulate the consequences of G, E, and GxE for processes such as first flower appearance, node addition rate, etc. Whereas one might argue that it is more desirable to model E responses as a function of G, we suggest that the two should coevolve. Characterization of dynamic plant functional E responses by specific G, including GxE, can lead to the discovery of underlying mechanisms using increasingly large genetic and phenotypic datasets. Furthermore, models developed from large datasets show promise for improving assumptions used in existing crop models. We use a bean dataset with 180 recombinant inbred lines grown over 5 environments to demonstrate that assumptions used in existing models about variations among genotypes may be wrong. We also show that development of process-oriented modules can improve previously used functional relationships, and that these modules can replace components in existing models. We focus on models for two different dynamic processes: Leaf Appearance Rate and Progress toward Flowering. Extending this effort to other crops and processes will contribute to next generation crop models. Implications of this approach on experiments, data collection, modeling processes, and modularity in crop models are discussed.

Oral Presentation

Title: High-throughput phenotyping platform reveals genetic variability and quantitative trait loci of light-related parameters in maize models

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Abstract: Radiation interception efficiency (RIE) and radiation use efficiency (RUE) are the main driving forces of dry mass accumulation in many crop models, so parameters related to RIE and RUE, e.g. light extinction coefficient (k) and photosynthetic parameters, have strong influences on the results of simulations. In this work, we propose a new method to estimate the RIE- and RUE-related parameters in maize models by a high-throughput phenotyping platform, PHENOARCH (<https://goo.gl/x3C6oN>), where images of 330 maize lines were taken and used to reconstruct the 3D-structure of the plants. The 3D plants were used to construct a virtual canopy to calculate RIE based on the RATP light model. Leaf area index (LAI) was estimated by the reconstructed 3D-structure and k was calculated from RIE and LAI. Relationship between RIE and plant developmental stage was fitted to a sigmoidal function with three parameters: maximum RIE (RIEmax), maximum change of RIE (smax) and time taken to reach smax (ts). Between genotypes, significant differences in k, RIEmax, smax and ts were found and genome wide association analysis revealed 16 QTL for k, 77 for RIEmax, 1 for smax and 7 for ts. Further parameters including RUE and relative canopy photosynthetic capacity can be also estimated by our method. We conclude that 3D-structure of plants reconstructed in a phenotyping platform can be used to discover the genetic variability of light-related parameters for crop models.