

Merging Crop Modeling and Genetics Workshop Agenda*

Date	Time	Site	Topic	Presenter	
Jul 20	Mon	8:15 am	MBI	Welcome and Introductions	
		8:30 am	MBI	Overview of NSF Project	C. E. Vallejos
		9:30 am	MBI	Phenotyping	C. E. Vallejos
		10:00 am	MBI	Coffee Break	
		10:15 am	MBI	CM1-Dynamic Crop Models	J. W. Jones
		11:10 am	MBI	CM2-CROPGRO-Bean Model	K. J. Boote
		12:00 pm	MBI	Lunch (Provided) Discussion	Led by Vallejos et al.
		1:00 pm	MBI	CM3-Installing/Using DSSAT	C. H. Porter
		1:55 pm	MBI	(Continued)	C. H. Porter
		2:50 pm	MBI	Move to ICBR	
			ICBR	Coffee Break	
		3:00 pm	ICBR	Genetic Analysis - DNA XT	Vallejos Lecture & Lab
		4:00 pm	ICBR	Genetic Analysis - DNA XT	Vallejos Lecture and Lab
		5:00 pm	End		
Jul 21	Tue	8:15 am	ICBR	Genetic Analysis – GBS/Lab/Lect	C. E. Vallejos
		9:05 am	ICBR	Genetic Analysis – GBS/Lab/Lect	C. E. Vallejos
		10:00 am	ICBR	Coffee Break	
		10:15 am	ICBR	Genetic Analysis – GBS Data Proc	M. Bhakta
		11:10 am	ICBR	Genetic Analysis – MapMaker	C. E. Vallejos
		12:00 pm		Lunch (On your own)	
		1:30 pm	MBI	CM4-Applications of models	K. J. Boote
		2:25 pm	MBI	CM5-New Genotypes and GSP Sensitivity	K. J. Boote/C. H. Porter
		3:20 pm	MBI	Coffee Break	
		3:35 pm	MBI	CM5-New Genotypes (continued)	K. J. Boote/C. H. Porter
		4:30 pm	MBI	CM7-Crop Model Discussion	K. J. Boote/J. Jones
		5:00 pm	End		
Jul 22	Wed	8:15 am	MBI	CM6-Simulating Parents	M. Correll/T. Bongiovanni
		9:10 am	MBI	CM8-GSP Estimation	P. Alderman/K. Boote
		10:00 am	MBI	Coffee Break	
		10:15 am	MBI	CM9-Estimating GSPs	P. Alderman/M. Correll/T. Bongiovanni
		11:10 am	MBI	CM9-Estimating (continued)	P. Alderman/M. Correll/T. Bongiovanni
		12:00 pm		Lunch (On your own)	
		1:00 pm	MBI	Experimental Design	S. A. Gezan
		1:55 pm	MBI	Linear Mixed Models	S. A. Gezan
		2:50 pm	MBI	Coffee Break	
		3:00 pm	MBI	Genetic Analysis – QTLs	M. Bhakta
		4:00 pm	MBI	Overall Discussion	
		5:00 pm	End		

*See pages 3-7 for Session Descriptions.

Merging Crop Modeling and Genetics Workshop Agenda (cont'd)*

Jul 23	Thu	8:15 am	MBI	Genetic Analysis – Q Genetics	S. A. Gezan
		9:10 am	MBI	Genetic Analysis – QTLGenstat	S. A. Gezan
		10:00 am	MBI	Coffee Break	
		10:15 am	MBI	CM10-Incorporating QTLs	M. Correll
		11:10 am	MBI	Discussion	M. Correll
		12:00 pm		Lunch (On your own)	
		1:00 pm	MBI	Discussion	
		1:55 pm	MBI	CM11-Discussion-gene-based models	K. Boote/J. Jones/M. Correll
		2:50 pm	MBI	Coffee Break	
		3:00 pm	MBI	Advanced Topics in Analysis of Genetic Data	S. Gezan
		4:00 pm	MBI	Discussion	M. Correll
		5:00 pm	End		
Jul 24	Fri	8:15 am	ICBR	Genetic Analysis	
		9:10 am	ICBR	Genetic Analysis	
		10:00 am	ICBR	Coffee Break	
		10:15 am	ICBR	Genetic Analysis	
		11:10 am	ICBR	Genetic Analysis	
		12:00 pm	MBI	Lunch (Provided)	Discussion
		1:30 pm	MBI	Discussion	
		2:25 pm	MBI	CM12-Developing Modules	J. Jones/C. Hwang
		3:20 pm	MBI	Coffee Break	
		3:35 pm	MBI	CM13-R modules – hands on	C. Hwang/J. Jones
		4:30 pm	MBI	CM14-Discussion-modules for NextGen Models	J. Jones/E. Vallejos/K.Boote/ all
		5:00 pm	End		
		7:00 pm		Dinner at Leonardo's 706	
Jul 25	Sat	8:15 am	MBI	Discussion	
		9:10 am	MBI	Discussion	
		10:00 am	MBI	Coffee Break	
		10:15 am	MBI	Discussion	
		11:10 am	MBI	Discussion	
		12:00 pm	End	END	

Topics	Sessions (~50 min)	Subtopics
Phenotyping	1	
Experimental Design	1-2	
Genetic Analysis	8-10 (lectures and wet lab)	
QTL analysis	2-4	
Mixed-effects Models	6	
Computer Simulation Models	17	
	43 sessions	

*See pages 3-7 for Session Descriptions.

Merging Crop Modeling and Genetics Workshop Session Descriptions

- CM1. Working with dynamic crop models – an introduction (50 minutes).** J. Jones
Refer to Wallach et al. text book, introduce dynamic model forms, simple crop model, parameters, and example uses of crop models (including and beyond breeding tools).
- CM2. The CROPGRO-Bean model in DSSAT. (50 minutes)** K. Boote
Briefly introduce the DSSAT Cropping System Model (CSM) and all of its components (including soil, weather, management, and crop). Then focus on the CROPGRO-Bean model for development (vegetative and reproductive), biomass growth and partitioning, with summaries of environmental and genetic effects.
- CM3. Installing and using DSSAT and the bean model. (100 minutes)** C. Porter & K. Boote
This will be hands-on. Installing the model and running a bean experiment already in the experiment list varying some GSPs. Use the GBUILD graphics. Review the DSSAT data standards. Use the XBUILD to modify an existing experiment by adding a cultivar.
- CM4. Applications of Crop Models – Examples from DSSAT. (50 minutes)** K. Boote
In a second 50-minute talk, present examples of different uses of the DSSAT models, first on sensitivity analysis to understand model performance (e.g., planting date, cultivar choice among the DSSAT list of 23 cultivars, GSPs, irrigation, weather). Then discuss varying GSPs to hypothesize yield improvement, highlighting the creation of virtual crop cultivars in the IFPRI work with some results. Finally, present the concept of design of cultivars to fit particular environments, from crop modeler perspective.
- CM5. Creating and Analyzing New Genotypes of Common Bean (50 minutes)** K. Boote & C. Porter)
This is a second hands-on exercise using the DSSAT bean model. In this exercise, participants will use the SENSITIVITY Tool to analyze different GSPs in the bean model and learn how predicted performance varies with weather and management. Participants will create virtual cultivars to determine the cultivar “design” that produces the best yield in a particular environment. They will evaluate separately the effects of SIZELF on early LAI, effects of SLAVR on LAI, effects of LFMAX on biomass and yield, effects of EM-FL on LAI, biomass, and yield, and effects of SD-PM on biomass and yield. Then they will evaluate combinations of these traits to improve yield. Ranges of traits will be restricted to those in present model and listed in Boote lecture notes. This exercise will be put into perspective with work on our NSF project and approaches for including genetic and environmental effects.
- CM6. Simulate parent cultivar bean performance across 5 locations. (50 minutes)** M. Correll & C. Porter/T. Bongiovanni
Data from parents with the estimated GSPs, weather data, management data, soil data, and observation data will be placed in a DSSAT directory. Demonstrate the simulation of the one Parent and have them run the other Parent across sites. Reference the future method for parameter estimation that was used to get these values for the GSPs.

- CM7. **Crop model Status, Limitations Discussion (50 minutes)** K. J. Boote/J. W. Jones
 General discussion about existing crop models and their use in simulating genotype, environment, and management effects on crop production. This discussion will precede methods being used to develop gene-based models.
- CM8. **GSP estimation for RILs – Concepts & implementation. (50 Minutes)** P. Alderman/K. Boote
 Introduce concepts of selecting parameters, running sensitivity analyses, equifinality and the sequential approach developed to minimize those issues and reliably estimate GSPs. Discuss reasons for using sequential approach to minimize equifinality effects where possible. General outline of the MH algorithm and its implementation (program page).
- CM9. **Estimation of GSPs by participants. (100 Minutes)** P. Alderman/M. Correll/T. Bongiovanni
 Hands-on. Demonstrate process using PC and HPC, have participants estimate GSPs for one (or two parents). Compare results with what we obtained from previous exercise #6.
- CM10. **Incorporating molecular marker effects in the current bean crop model. (50 Minutes)** M. Correll
 Lecture, presenting example results from our work with example outputs/histograms of GSPs and QTLs found with GSPs comparing with field data QTLs (a few examples, PPSEN, EMLF, TRIFL and FLVS). Present limitations of using the QTLs to re-estimate GSPs due to loss of G X E effect and only selecting highly significant QTLs (dropping small contributing QTLs). Also compare QTL profiles from field data with “model” outputs (e.g., ADAP field vs. ADAP using estimated GSP) which relatively good recapture of QTLs.
- CM11. **Discussion of Concepts for Incorporating Genetic Effects in Existing Models. (50 minutes)** K. Boote/J. Jones/ M. Correll
 This discussion will focus on the approaches that most crop modeling groups have been using to incorporate genetic effects into crop models, their advantages and limitations.
- CM12. **Example Gene-Based Modules for Leaf Area Development (50 minutes)** J. Jones C. Hwang/
 Lecture on concepts for using linear and nonlinear mixed effects models for specific processes for developing modules, with examples on node appearance and leaf area dynamics. Also implications of this approach on GSPs and future directions will be discussed.
- CM13. **Presentation of example gene-based component models based on NSF data (50 minutes)** C. Hwang/J. Jones
 Present 2 examples, including “modules” developed in R for implementation of these models. Demonstrate effects of implementation of node addition rate and main stem leaf area expansion. Discuss these relative to a suggested roadmap toward a next generation gene-based common bean model.

CM14. **Discussion of Concepts for Developing Modules for Gene-Based Crop Models. (50 minutes)** J. Jones/E. Vallejos/K. Boote/S. Gezan/M. Correll

CM15. **Overall Summary Lectures/Discussion (100 minutes).** E. Vallejos/K. Boote /S. Gezan/M. Correll/J. Jones.

Compare the direct approach of QTLs linked to present GSPs, to the mixed model effect (with new modules) also linked to the crop model. This is a summarization of what has been accomplished. Provide participants the opportunity to discuss other methods and discuss new methods GENOME WIDE SEQUENCING ETC. (Functional Structural Models, L-systems, Statistical/ Empirical methods).

We may want to have a set of questions designed to solicit discussion/debate amongst the participants.