

Workshop:

**Phenotypic Plasticity and Genotype by Environment Interaction:
Dissection and Prediction**

Monday, Feb. 22, 1:00 PM – 4:00 PM (CST)

One of the major challenges in plant breeding is the differential response of genotypes from one environment to another, or phenotypic plasticity. Different phenotypic plasticity across a set of genotypes gives rise to the varied phenotypic values, the variation of which is typically partitioned into genotype, environment, genotype by environment interaction, and residual. Although various methods have been developed, many of these methods lack forecasting capacity and our understanding of genomic and environmental determinants is still limited. We have recently established an integrated analytical framework to answer long-standing questions in phenotypic plasticity and genotype by environment interaction. The essence of this framework is to combine knowledge from physiology, genetics, and statistics to identify the determinants rather than only model fitting. It is about identifying hidden patterns and biological insights to enable the forecasting capacity and profile the gene effect continuum. We hope to significantly enrich our understanding of genes and environmental factors underlying phenotypic plasticity and translate this understanding to application by enabling the in-season, on-target crop performance prediction.

In this workshop, we plan to 1) explain the interdependence of genotype and environment and two different origins of this genotype by environment interaction concept to help understand the complexity of phenotypic observation; 2) test an open-source package to facilitate the research community to dissect and model phenotypic variation in flowering time and plant height, two most studied quantitative traits; 3) showcase the analytical method to identify environmental determinants underlying phenotypic plasticity of a set of agronomically important traits from different types of populations in different crops. Detailed workshop modules have been prepared.

Instructors:

- Jianming Yu, Professor and Pioneer Distinguished Chair in Maize Breeding, Department of Agronomy, Iowa State University
- Xianran Li, Adjunct Associate Professor, Genomics and Bioinformatics, Department of Agronomy, Iowa State University
- Tingting Guo, Research Associate, Quantitative Genetics, Department of Agronomy, Iowa State University

Module 1: Lecture on Basic Concepts: Phenotypic Plasticity, Reaction Norm, Genotype by Environment Interaction
(20 - 30 minutes)

Triple Helix: Gene, Organism and Environment, by Richard Lewontin
Crop Growth Model

CKH's Evolution in Changing Environments

Fisher's Biometric origin and Lancelot Hogben's Developmental origin of G x E

Joint Regression Analysis: Finlay & Wilkinson, Eberhart & Russel

Genomic Prediction, Resource Allocation in Plant Breeding
What is missing? What can we do?

Module 2a: Lecture: Pattern Finding and Model Fitting to Identify the Environmental Index and What It Empowers

(20 minutes)

Phenotypic Plasticity from a Multi-environment Trial
Joint Regression Analysis (JGR)
CERIS - Critical Environmental Regressor through Informed Search
CERIS-JGRA Prediction: Site-Specific, In-Season, On-Target, Whole-Genome, Simple-Straightforward

Module 2b: Computer Demo: Pattern Finding and Model Fitting to Identify the Environmental Index and What It Empowers

(40 minutes)

Traditional Variance Component Analysis
Partitioning $G \times E$ into Heterogeneity of Genotypic Variance and Lack of Genetic Correlation
Data Visualization and Analysis: Reaction Norm, Environmental Factors, PCA and Clustering
Genomic Prediction and Environment Prediction: Tested and Untested
JGRA - Joint Genomic Regression Analysis
JGRA through Reaction-Norm Parameter Estimation
JGRA through Genome-Wide Marker Effect Continuum

Module 3: Hands-on Practice and Discussion: Searching for the Hidden Patterns that are the Explanation and that Enable the Prediction

(60 minutes)

Practice demo: Code, Input and output files for CERIS-JGRA with a sorghum flowering time
Practice with other crop-trait combinations to identify the environmental index (a combination of environmental parameter and growing period)
Short discussion

| Crop | Trait | envPara | Start | End |
|-------|-------|---------|-------|-----|
| Maize | DTA | | | |
| | PH | | | |
| | YLD | | | |
| Rice | FTdap | | | |

Module 4: Summary and Wrap-up: Clarifying the Concepts and Enriching the Understanding
(20 - 30 minutes)

The Science of Learning New Concepts

From a Regular QTL Mapping Study to CERIS-JGRA

Reflection on Findings: Genetics (genomic prediction, QTL, gene, network), Environment (location, year, environmental factors, environmental index), G x E (gene by environment, genotype by environment, physiology, biometric and developmental origins), Phenotypic Plasticity, Reaction Norm(s)

Final Questions

Required Reading

- [Genomic and environmental determinants and their interplay underlying phenotypic plasticity](#). *PNAS* (2018) 115:6679-6684.
Information contained in [Supporting Information](#)
- [Dynamic effects of interacting genes underlying rice flowering-time phenotypic plasticity and global adaptation](#). *Genome Research* (2020) 30:673-683.
Information contained in [Supporting Information](#)

Recommended Reading:

[An expanded view of complex traits: From polygenic to omnigenic](#). *Cell* (2017) 169:1177-1186.
[R. A. Fisher, Lancelot Hogben, and the origin\(s\) of genotype-environment interaction](#). *Journal of the History of Biology* (2008) 41:717-61.
[Evolution in changing environments: the "synthetic" work of Clausen, Keck, and Hiesey](#). *The Quarterly Review of Biology* (2001) 76:433-57.
[Genotype-by-environment interaction and plasticity: Exploring genomic responses of plants to the abiotic environment](#). *Annual Review of Ecology, Evolution, and Systematics* (2013) 44:5-29.

Notice to Workshop Attendees

1. Complete the required reading before the workshop. Have a computer with R and R Studio installed.
2. Specific instruction on installing different R-packages and CERIS-JGRA will be provided.
3. All types of attendees are welcome: only interested in phenotypic data (Variance Partitioning, JRA, CERIS-JRA); both genotype and phenotype data (CERIS-JGRA, genomic prediction, mapping, and QTL-gene-marker-effect reaction norms); with or without own data for practice; beginners or experts in certain but not all areas.
4. For graduate students and postdocs who are leading research projects and have demonstrated their ability during the workshop, after-workshop consultation will be provided. No collaboration requirement.
5. For advanced attendees, specific instruction on how to prepare attendee's own MET (and genotyping) data will be provided

