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PLANT SCIENCES

## Abstracts

### An Automated, High-throughput Field Phenotyping System for Sorghum: Project Vision and Early Results

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<sup>1</sup>Purdue University, <sup>2</sup>IBM Research

A team from Purdue University, IBM, and the University of Queensland is developing a sorghum field phenotyping system focused on measuring, analyzing, visualizing, and improving biofuel-related sorghum plant traits. Data are being acquired by a suite of sensors on a mobile ground-based platform and unmanned aerial systems (UAS) to determine the geometric- and chemistry-based characteristics of sorghum plants in the field throughout the growing season via an automated, high-throughput approach. Advanced image and signal processing methods are being developed to extract information from sensor output to produce predictive models for plant growth, development, and, ultimately, biofuel productivity. Links between plant characteristics and their underlying genetics are also being identified, and predictive models are being developed via a combination of biophysically-based and machine learning approaches. The goal of this project is to produce a user-friendly phenotyping system that enables crop scientists to collect large quantities of data on plant characteristics, to analyze it rapidly via automated methods, and to link underlying genes with plant traits that are correlated with greater biofuel production. This presentation will highlight some of the first year results of this project including (i) a feature-based approach for registering push-broom imagery with frame camera-based orthophotos; (ii) methods for estimating sorghum traits (e.g., plant height, visible leaf count, canopy closure) based on RGB cameras onboard a UAS; (iii) spectral indices and spatial features derived from hyperspectral imagery; and (iv) machine learning-based models for predicting stem diameter and stalk volume.

### Genomes to Fields

Edward Buckler<sup>1</sup>, Natalia de Leon<sup>2</sup>, David Ertl<sup>3</sup>, Shawn Kaeppler<sup>2</sup>, Jonathan Lynch<sup>4</sup>, Patrick Schnable<sup>5</sup>, Nathan Springer<sup>6</sup>

<sup>1</sup>Cornell University, <sup>2</sup>University of Wisconsin-Madison, <sup>3</sup>Iowa Corn Promotion Board, <sup>4</sup>Pennsylvania State University, <sup>5</sup>Iowa State University, <sup>6</sup>University of Minnesota

There has been a revolution in our ability to profile and manipulate genomes. We can now easily document the information in a genome and are close to developing tools for large-scale genome engineering. In order to fully utilize these advances, it will be critical to develop a more detailed understanding of how the genome leads to phenotype in real world environments. The Genomes to Fields (G2F) initiative is working to develop a framework to apply robust phenotyping to plants with characterized genomes growing in different environments. G2F currently includes over 45 formal collaborators with field sites in 20 different states. We have developed the infrastructure for growing maize and collecting simple phenotypic measurements in these locations. G2F continues to develop opportunities for automated phenotyping and modeling of complex data arising from a large collaborative project. Our goal is to develop robust models to better understand maize phenotypes in a field setting and how genomic information contributes to these traits.

## Field-based Predictive Phenomics

*Patrick S. Schnable, Iowa State University, USA*

Our goal is to develop statistical models that will predict crop performance in diverse agronomic environments. Crop phenotypes such as yield and drought tolerance are controlled by genotype, environment (considered broadly) and their interaction (GxE). As a consequence of the next generation sequencing revolution genotyping data are now available for a wide diversity of accessions of each of the major crops. The necessary volumes of phenotypic data are not available and our understanding of the molecular basis of GxE is rudimentary. To address this limitation, we are constructing and deploying new sensors and robots that will facilitate the automated collection of large volumes of phenotypic data at multiple locations. For example, networked systems of hundreds of computer-controlled cameras that enable high-throughput, high-resolution, field-based time-lapse photography for studying maize growth/development and responses to environmental stresses have been deployed at four locations over two years.

## UASHub: Online Research Collaboration Portal for UAS Data

*Jinha Jung,<sup>1</sup> Angin Chang,<sup>1</sup> Juan Landivar,<sup>2</sup> and Murilo Maeda,<sup>2</sup>*

*<sup>1</sup>Texas A&M University, Corpus Christi, <sup>2</sup>Texas A&M AgriLife Research*

The long-term goal of this project is to develop, improve, and deploy Unmanned Aerial System (UAS) platforms, advanced computational algorithms, and a web-based tool to facilitate high throughput phenotyping (HTP) and precision management of cotton (*Gossypium hirsutum*) for breeding purposes. Specific objectives of this project are to: 1) Improve our established Unmanned Aerial System (UAS) platforms for high throughput phenotyping data collection, 2) Validate and improve an automated data processing workflow and feature extraction framework from UAS data to accurately estimate plant height, growth rate, canopy cover progression, earliness/maturity, and yield of cotton genotypes, and 3) Improve and further develop easy to use web-based tools to facilitate image and data sharing among scientists and end-users (also known as the UASHub, <http://uashub.tamucc.edu/>). The focus of this presentation is on objective 3 (above) to create a well-connected and facile environment to share UAS data and tools for agricultural scientists.

Mounted with sensor payloads, UAS enables the acquisition of crop data at spatial and temporal scales previously unobtainable via traditional remote sensing methods. In terms of data acquisition accuracy, cost-effectiveness, flexibility and high productivity, an integrated UAS-based remote sensing system provides an effective solution for precision agriculture applications. However, UAS data are inherently big since UAS platforms are usually operated at much lower altitude compared to traditional aerial platforms, and specialized software packages are needed to process the big data. The enormous data volume and lack of affordable software analysis packages make UAS technology underutilized by typical agricultural scientists. To address these issues, we developed UASHub that built using Free and Open Source Software (FOSS) packages. UAS data visualization tools (both in 2D and 3D) and advanced phenotypic measurement tools were developed so that end users can access UAS data and tools without download big UAS data or installing software packages.

## Remote Sensing Platform for Research, Phenotyping and Precision Management

Juan Landivar,<sup>1</sup> Jinha Jung,<sup>2</sup> Murilo Maeda,<sup>1</sup> and Angin Chang<sup>2</sup>

<sup>1</sup>Texas A&M AgrLife Research and <sup>2</sup>Texas A&M University, Corpus Christi

The long-term goal of this project is to develop, improve, and deploy Unmanned Aerial System (UAS) platforms, advanced computational algorithms, and a web-based tool to facilitate high throughput phenotyping (HTP) and precision management of cotton (*Gossypium hirsutum*) for breeding purposes. Specific objectives of this project are to: 1) Improve our established Unmanned Aerial System (UAS) platforms for high throughput phenotyping data collection, 2) Validate and improve an automated data processing workflow and feature extraction framework from UAS data to accurately estimate plant height, growth rate, canopy cover progression, earliness/maturity, and yield of cotton genotypes, and 3) Improve and further develop easy to use web-based tools to facilitate image and data sharing among scientists and end-users (also known as the UAShub, <http://uashub.tamucc.edu/>). The focus of this presentation is on objective 2 (above) and the interpretation of these data for the selection of elite genotypes. In the past, the acquisition of temporal and spatial crop data was performed by strenuous, destructive, expensive, slow, and labor-intensive hand sampling techniques. Such constraints often lead to under-representative crop information due to limited sampling area and the introduction of possible human errors. Although remote sensing technologies have been utilized in some precision agriculture studies, development of an UAS-based phenotyping system and full utilization of the system throughout the whole life-cycle of crops to monitor crop growth, overall health, and particularly yield has been very limited until now. The successful completion of this project has the potential to deliver tools and methodologies for UAS-based HTP to cotton breeders. Incorporation of these deliverables into their breeding programs will allow them to significantly increase genotype screening efficiency. Data gathered using the proposed framework will also provide breeders a high level of detail (both spatial and temporal) never before possible using manual sampling procedures.

## Precision Field-Based Wheat Phenotyping Platforms

Carolina Saint Pierre,<sup>1</sup> Amor Yahyaoui,<sup>1</sup> Pawan Singh,<sup>1</sup> Matthew Reynolds,<sup>1</sup>

Michael Baum,<sup>2</sup> and Hans Braun<sup>1</sup>

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This initiative, supported by the CGIAR (Consultative Group for International Agricultural Research) Research Program on Wheat, envisions a global network of Precision Field Based Wheat Phenotyping Platforms (PWPP) developed with co-investing National Agricultural Research Systems (NARS). Target traits and regions include: Septoria tritici blotch in durum wheat (Tunisia); Septoria tritici blotch in bread wheat (Ethiopia, Mexico); multiple diseases (Uruguay); wheat rusts (Ethiopia, Ecuador); wheat blast (Latin America); Helminthosporium leaf blight (Bangladesh/Nepal, Mexico); Fusarium head blight (China, Mexico); heat and drought tolerance in spring wheat (Sudan, Morocco, India, Pakistan, Bangladesh, Nepal); heat and drought tolerance in facultative/winter wheat (Turkey); yield potential (China, India, Pakistan, Egypt, Zimbabwe); strengthening collaborations with currently functional platforms for rusts (Kenya, Mexico) and heat/drought/yield potential (Mexico). The global network of PWPP will provide NARS partners with tools to participate in breeding applying more precise phenotyping approaches, using standardized protocols and novel tools to develop broad genetic based resistant, high yielding varieties. Additionally, the platforms provide NARS with earlier access to more diverse germplasm, enabling faster release of superior varieties. Training will also enhance the expertise necessary to mitigate different threats, providing capacities for adequate and reliable screening for biotic and abiotic stresses.

**Utilizing Hyperspectral Information for Monitoring Plant Status**

*John J. Couture, Purdue University, USA*

The utilization of full-range hyperspectral data is emerging as an effective and efficient method for rapid, non-destructive plant monitoring. Based on the interaction of light with foliar structure, chemistry, and water, spectroscopy can reveal a great deal of information about plants, including phenotypes, disease infection status, and physiological responses to stress. Equally as important is that these responses can potentially be monitored in real time. Using model species I demonstrate the ability of hyperspectral information to 1) successfully phenotype multiple varieties of the same species, 2) pre-visually detect disease infection, 3) quantify physiological responses and examine phenotypic plasticity to stress and, 4) track real-time changes in plant chemistry in response to stress. By combining multiple approaches to understanding plant function, and linking them with hyperspectral data, the capability to manage plants can be rapidly advanced, with potential for real-time monitoring.

**The Critical Role of Phenotypic Data to Enhance Genetic Gains and Develop Climate-Smart Crops: Potato as a Case Study**

*M. Bonierbale, W. Amoros, A. Khan, R. Quiroz, D. Ramirez, E. Salas & H. Campos, International Potato Center, Lima, Peru*

Because of a wider than ever access to and dramatic cost reductions enabled by constant technology progress, molecular and -omic information has become a commodity. At the same time, there is an increasing societal demand for scientists to be more accountable and able to demonstrate meaningful impact at the farm level. One way to achieve that, and to mitigate the challenges brought about by climate change, is the development of climate-smart crops, i.e. resilient cultivars able to withstand an array of abiotic stress conditions yet delivering high yield and nutrients content under non- or mild stress conditions. The single most important factor to succeed with such endeavor is the quality, relevance and volume of the phenotype research efforts are based upon. CIP's approach to establish a large scale phenotypic platform is based on a multiple-prong approach: First, establishing Managed Stress Environments where genetic variation is consistently exposed to stringent selection pressures so high quality phenotypic data sets collected. Secondly, the development of targeted breeding populations carrying alleles providing drought and heat tolerance relevant to beneficiaries and end-users, using both conventional and molecular breeding approaches. Thirdly, developing proximal and remote sensing systems through reflectance, infrared thermography and passive and active fluorescence able to characterize experimental sites and rapidly identify stress tolerant genotypes based on measurable physiological traits. Finally, physiological research at the above and below ground level to understand the underpinnings of abiotic stress tolerance.

We share the main results and learnings achieved thus far and discuss further research themes to be addressed in order to deliver climate-smart crops.

## Graduate Training in Predictive Plant Phenomics (P3) at Iowa State University

Julie A. Dickerson, Theodore J. Heindel, Carolyn J. Lawrence-Dill, Patrick S. Schnable, Iowa State University

Modern sensors and data analysis techniques make it feasible to develop methods to predict plant growth and productivity based on information about their genome and environment. The ISU National Science Foundation Research Traineeship (NRT; [https://www.nsf.gov/funding/pgm\\_summ.jsp?pims\\_id=505015](https://www.nsf.gov/funding/pgm_summ.jsp?pims_id=505015)) Predictive Plant Phenomics (P3) Specialization brings together students with diverse backgrounds and provides them with data-enabled plant science and engineering training. The P3 NRT implements the T-training model proposed by the American Society of Plant Biology (ASPB) and described in “Unleashing a Decade of Innovation in Plant Science: A Vision for 2015-2025.” This traineeship will prepare M.S. and doctoral students with the understanding and tools to design and construct crops with desired traits that can thrive in a changing environment.

The first cohort of students begins their training in August 2016 with a two-week “boot camp” short course to introduce the students to the basic topics they will need to succeed. The four-credit P3 core course (Fundamentals of Predictive Plant Phenomics) taken the first year of the program has a hands-on laboratory component that all students will complete. The P3 core course has two key objectives: 1) bring all students’ knowledge up to the same level for issues that pertain to plant phenomics, sensor engineering, and data analysis, and 2) begin the process of teaching students the needed terminology to speak across disciplines. The collaborative spirit required for students to thrive will be strengthened through the establishment of a community of practice to support collective learning.

## The Plant Imaging Consortium (PIC): Collaborative Approaches for Imaging Plant Stress Responses

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The Plant Imaging Consortium (PIC) is an NSF-funded research consortium that links investigators at eight academic institutions in Arkansas and Missouri. It brings together teams of scientists in four major areas of expertise (Plant Biology, Phenomics, Radiochemistry and Imaging, and Computing and Bioformatics) to apply molecular imaging (MI) and high-throughput phenotyping (HTP) to the study of plant stress biology. Members of these four core groups are working collaboratively on four model projects focused on nutrient uptake, accumulation of reactive oxygen species, antioxidant synthesis, and resource partitioning in plants under stress. These projects are not only designed to shed light on fundamental aspects of plant stress adaptation, but also to drive methodological advances in plant MI and HTP. The consortium has expanded access to infrastructure for MI and HTP through a seed grant program, and is promoting training in these technologies through hands-on workshops, funded industry internships, and seminar series. We are also communicating the importance of plant phenotyping research to the public through a hands-on classroom module for high school students, and through numerous outreach events for K12 students and the general public.

**PlantCV: Analysis Tools for High-throughput Phenotyping**

*Malia Gehan, Noah Fahlgren, Monica Tessman, Andy Lin, Michael Miller, Donald Danforth Plant Science Center*

The geographical distribution of food and bioenergy crops is limited by several factors including temperature, soil salinity, and water availability. To tackle the challenge of producing more food and fuel with fewer inputs a variety of strategies to improve and sustain crop yields are necessary. Plans for crop improvement may include: mining natural variation of wild crop relatives to breed crops that require less water; increasing crop tolerance to temperature extremes to expand the geographical range in which they grow; and altering the architecture of crops so they can maintain productivity while being of grown more densely. These strategies can be advanced with a variety of methodologies, but they will require both high-throughput sequencing and phenotyping technologies. However, a major bottleneck in plant science is the ability to efficiently and non-destructively quantify plant traits (phenotypes) through time. This research develops high-throughput phenotyping technologies and open-source platform-independent analysis tools (PlantCV; <http://plantcv.danforthcenter.org/>) for both model and crop plants, and demonstrates the utility of high-throughput phenotyping data in identifying critical points in abiotic stress progression.

**NSF Big Data Hub: Digital Agriculture Spoke**

*Aaron Bergstrom<sup>1</sup>, Joe Colletti<sup>2</sup>, Greg Monaco<sup>3</sup>, Jennifer Clarke<sup>4</sup>*

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The purpose of the Hubs is to facilitate collaborative research and education in Big Data relevant to scientific areas of national importance. The Spoke in Digital Agriculture has two initial foci, namely, unmanned aerial systems and plant phenotyping. We have engaged partners from both academia and industry, and would like to encourage additional partners to join and participate. We anticipate annual in-person meetings, online educational opportunities, and funding for seed projects relevant to the objectives of the Spoke.

## **X-ray Tuber Analysis for 3D Biomass Determination**

*Stefan Gerth, Norbert Wörlein, Joelle Claußen, Norman Uhlmann*

*Development Center X-Ray Technology EZRT, Fraunhofer Institute for Integrated Systems IIS, Germany*

During the last years, X-ray computed tomography (CT) has been applied to study below ground growth of potato tubers. The reconstructed volume data set consists of grey levels which represent information about the X-ray attenuation depending on the mass attenuation coefficient, the density distribution of the material and the spectral distribution of the X-ray source. The calculation of tuber and root volumes of potted plants embedded in soil requires the segmentation from other materials in the X-ray CT volume data. Increasing the dimensionality from 2D to real 3D enhances the complexity of image segmentation algorithms. At the same time volume information are accessible for direct correlation with volumetric traits, as e.g. tuber volumes or form factors. The method itself is non-destructive. Thus, time resolved growth parameters can be extracted from one individual plant. Additionally, differences between genotypes are detectable.

We will present the tuber growth of the varieties Saturna, Tomensa, Diamant, Ramses and Agria in a combined heat and drought stress scenario. For all these varieties non-destructive X-ray CT measurements were conducted and automatically segmented and analyzed. Using this method for 3D biomass prediction, it is possible to monitor the growth of each individual tuber and to detect already small differences in the growth behavior as a function of external stress parameters.

Additionally, applying destructive sampling of a subset of all measured pots allows to correlate the dry weight with absorption parameters from the X-ray measurement. Thus, it is possible to discriminate whether volume growth is due to water or starch accumulation in the recovery phase.

## **The Delta is that Fertile Ground Between Phenotyping, Modeling and Forecasting**

*Keith Koutsky, Measurements Discovery Lead, The Climate Corporation*

With the advent of precision Ag, phenotyping, modeling and forecasting have made the leap to the farm. When phenotyping crop fields, variation is going to be evident. Due to differences in soil types, planting densities and so forth, it's expected. Also expected are differences between forecasted weather at the beginning of the season, which drove many agronomic decisions and actual weather. Phenotyping allows the farmer to accurately quantify the delta between expected productivity and what's currently going on in his fields. That delta is where opportunity lies.

## Latin-American Plant Phenomic Network (LatPPN)

**Gustavo A. Lobos<sup>1</sup>** and **Anyela Camargo<sup>2</sup>**

<sup>1</sup>*Plant Breeding and Phenomic Center, Facultad de Ciencias Agrarias, Universidad de Talca, Chile.*

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The success of breeding programs is reflected in the number of individuals released at the end of the selection process. In order to be successful, breeders must generate thousands of hybrids annually and evaluate them for a number of years. To effectively develop cultivars well adapted to fluctuations in environmental stresses, breeders will have to evaluate a number of morpho-physiological and physico-chemical traits that they are not used to considering. The only reasonable way to fulfill all these needs is through acquisition of high-dimensional phenotypic data (high-throughput field phenotyping) or “Phenomics”. While phenomics in Europe, Oceania and North America have begun to be used in the breeding of grain crops in the last 10 years, Latin-America have not experience an equivalent level of development. Because of this, during 2015 the Plant Breeding and Phenomic Center (Universidad de Talca, Talca, Chile) and the National Plant Phenomics Centre (IBERS, Aberystwyth University, UK) organized the First Latin-American Conference on Plant Phenotyping and Phenomics for Plant Breeding. In order to strengthen Latin-America’s research capabilities in the field of plant phenotyping and phenomics, another main goal of the conference was to setup the Latin-American Plant Phenomic Network (LatPPN). This network was conceived to facilitate training breeders and developing scientists on several aspects of phenotyping and pre-breeding methodologies, scientific exchange of young/senior researchers and students, and international access to resources and research facilities. Among the more immediate issues identified for LATPPN in this first meeting, one of the highlights was the importance of developing an identity. There is urgency to progress with phenomics on important species in Latin-America. Many of these species include fruit and vegetables that currently support or may potentially support significant export markets. Additional important topics of discussion were fund search, human resource training, challenges due to climate change, obtaining support from entities with experience in network development, needs of an interdisciplinary work, creation of common protocols among institutions, data support, development of low cost phenotyping tools, and organizational visibility.

## Abstracts

### **Plant Growth Chamber Design Factors for Achieving Homogeneous Plant Growth**

*Jens Beator and Carsten Richter, Conviron, Canada*

Plant growth chambers and rooms offer precision controlled environments with uniform, repeatable environmental conditions. Scientists can manipulate variables and observe outcomes with confidence that all plants in an experiment experienced the same environment. Plants in growth chambers require specific conditions e.g. light for photosynthesis, ventilation for evaporation of water, heat dissipation of irradiant energy, and gas exchange for normal physiological performance. Meeting requirements for precision control, uniformity, repeatability and plant physiological requirements necessitates a design approach very different from, for example, cold rooms.

### **Using High-Throughput Phenotyping in Cotton Germplasm Trials in the Southeast US**

*Philip J. Bauer, Kari Hugie, B. Todd Campbell, Kenneth C. Stone, USDA-ARS, Florence, SC*

Early season growth of cotton (*Gossypium hirsutum* L.) is important in determining final yield potential. Larger plants just before flowering allows for more fruiting sites and leaf area to support developing bolls. A high-throughput phenotyping platform that contained NDVI sensors was used to evaluate the potential of using NDVI at early bloom as a selection tool for yield. Data were collected from a germplasm evaluation trial in 2014. The trial had 288 genotypes with two replicates. An alpha lattice experimental design was used in this trial. The trial had a common genotype as check rows planted next to each germplasm line. At early bloom, NDVI data were collected. Yield data were collected at the end of the season. The data were analyzed with and without using the check plot data as covariates. A significant linear relationship occurred between NDVI at early bloom and yield. The R<sup>2</sup> increased slightly when the check plot data were used in the analysis. These preliminary data suggest that comparing NDVI at early bloom may be a method to identify and eliminate low yielding lines from germplasm trials.

## **A Comparative Study of Genetic Mapping of Sorghum Height Using Directly Measured and Remote-Sensed Phenotypic Data**

Addie M. Thompson,<sup>1</sup> Karthikeyan Ramamurthy,<sup>2</sup> Zhou Zhang,<sup>1</sup> Fangning He,<sup>1</sup> Melba M. Crawford,<sup>1</sup> Ayman F. Habib,<sup>1</sup> Clifford F. Weil,<sup>1</sup> Mitchell R. Tuinstra<sup>1</sup>  
<sup>1</sup>Purdue University, <sup>2</sup>IBM Research

Traditional plant breeding and trait mapping involve surveying hundreds (if not thousands) of different varieties for the phenotypes of interest, using time-consuming ground measurements taken by hand. The shift to automated, high-throughput, remotely sensed phenotypes is beginning to enable data collection on a larger scale: more data points per plot, more genotypes, and more time points. The accuracy and predictive power of these sensor-based estimates can be assessed using hand measurements as ground-truth data, but what is less clear is how well any can predict the underlying genetic variation. Hand measurements often target one to three “representative” plants from each plot, whereas sensors have the potential to more accurately capture the variation present among plants. The sensors could possibly provide a more complete description of the genetics contributing to the phenotypic diversity by capturing a lot more variability than just representative-looking plants. However, they could also possibly add technical or environmental noise to the dataset, for example, by including non-plant parts in the image. When predicting traits, the ability of the model to uncover latent features that capture the phenotype of interest is a key issue, as is the degree of relatedness necessary between training and test populations in order to attain an adequate level of accuracy for mapping. Using a large population of diverse sorghum segregating for several dwarfing genes, we attempted to leverage Genome-Wide Association Mapping (GWAS) to map plant height measured or estimated using four approaches: 1) direct ground measurements, 2) point clouds from RGB imagery as a multivariate model of histogram features, 3) model predictions from an unrelated calibration panel, and 4) model predictions trained from a subset of 60 genotypes from the diversity panel itself. Based on previous work, the calibration models used Support Vector Regression (SVR) to predict height based on RGB point clouds and hyperspectral data (selected band ratios and Extended Multi-Attribute Profiles, or EMAPs). These four approaches were then combined into a GWAS meta-analysis to assess whether increased power, noise reduction, or more refined intervals could be attained by leveraging the multiple data types. All significant GWAS results were compared with locations of known dwarfing and height-related genes to determine their approximate power to detect “true” associations. This research will enable an informed approach to experimental planning for high-throughput phenotyping projects whose end-goals involve mapping quantitative traits.

## Application of Optical Sensing Techniques for Predicting Simultaneously Nutritional and Processing Quality Properties of Dried Beans

Fernando A. Mendoza,<sup>1</sup> Jason Wiesinger,<sup>1</sup> Dennis Katuuramu,<sup>1</sup> Renfu Lu,<sup>2</sup> James D. Kelly,<sup>1</sup> and Karen A. Cichy,<sup>1,2</sup>

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Fast, accurate and noninvasive sensing techniques are needed by dry bean breeders and processors to predict various quality parameters simultaneously. A prior knowledge of some key physicochemical and sensory quality traits before processing would substantially help in the rapid and objective quality characterization and inspection of dry beans. The present study evaluated the suitability of visible and near-infrared spectroscopy (Vis/NIRS) over the wavelength range of 400–2,498 nm and an hyperspectral imaging system (HIS) over the range of 400–1,000 nm for predicting minerals (Ca, Cu, Fe, K, Mg, Mn, P, S and Zn), texture and cooking time quality traits simultaneously. Different sets of bean samples harvested and tested in 2014 and 2015 were used for analysis. For analysis, several preprocessing techniques for reflectance spectra including: smoothing, first and second derivatives, continuous wavelet transform decomposition and two-band ratio methods were evaluated and compared. More than 600 parameters were extracted by these methods for each bean sample. The best parameters were then selected for predicting the quality traits based on partial least squares regression (PLSR) analysis. The prediction models using both systems were compared in terms of their correlation coefficients (R) and standard error of prediction (SEP). Overall, prediction results were significantly improved using the two-band ratio preprocessing method for both techniques and all measured traits (reducing the SEP in more than 15% as compared with the traditional methods). Overall, Vis/NIRS technique showed better prediction results for minerals than those using HIS with accuracies higher than 86.0% and 77.8%, respectively, which should be explained by the wider range of wavelength points used in the Vis/NIRS analysis. However, comparable prediction results were found for cooking time using either Vis/NIRS or HIS giving accuracies higher than 85.0%. These results indicate that optical sensing techniques (i.e., Vis/NIR and HYP) combined with a suitable preprocessing technique have great potential for predicting mineral and processing quality properties of dried seeds with a single measurement. Currently, spectral data is being processed for predicting the bioavailability of nutrients in a similar set of beans.

**Keywords:** Dry beans, bean quality traits, Vis/NIR spectroscopy, hyperspectral imaging.

**Practical Application:** Bean is a nutritionally rich legume. Hence, improved consumer acceptance of its processed products will contribute to the health and nutrition and further increase bean production opportunities for farmers and processors. The present study tests the feasibility of Vis/NIR spectroscopy and hyperspectral imaging techniques for predicting from 'intact dry beans' nutritional, textural and cooking time traits which are essential for phenotyping. A prior knowledge of these quality traits before canning would allow better decisions by bean breeders and processors.

## Drone-based High-throughput Phenotyping for the Selection of High-yielding Soybean Lines

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The annual rate of genetic gains for soybean grain yield is decreasing. A more efficient selection pipeline in the early stages is the proposed way of increasing the rate of genetic gains. The Soybean Breeding program at Purdue University has previously indicated that early-season canopy development in soybean has a strong genetic association to yield and high-throughput drone-based phenotyping of canopy development can predict the yield potential of soybean lines. Usually the selection in early stages of soybean breeding is performed virtually at random, (i.e. without data-driven criteria) due to the extensive number of field plots. This phenotyping bottleneck could be alleviated using drones. However, data collected in a large number of unreplicated entries creates the need to account for spatial heterogeneity in the data. This study aims to select high yield potential soybean lines using yield performance supplemented with drone-based data of canopy development to demonstrate whether new sources of data and analytical approaches can improve selection efficiency in the early generation stages of soybean breeding pipelines. Weekly measurements of canopy coverage from early vegetative to mid reproductive growth and yield were acquired for 4640 progenies rows and 13 checks during the 2015 season. Variance components and breeding values were estimated using Henderson model fitted with a Bayesian Gibbs sampling algorithm. Kinship matrix was generated using pedigree information and residual correlation matrix using field distance among plots, thus accounting for the heteroscedasticity associated to the field variation. Phenotypic correlation between yield and average canopy coverage (AC) was estimated to be 0.64. Spearman correlation between the breeding values was 0.47. Effectiveness of selection using yield and AC jointly in comparison to yield alone will be evaluated in 2016. Current result indicate that stringent selection based on AC in early generations may be a cost-effective way of selection high yielding lines.

## FieldScan - A Novel Semi-field Platform to Phenotype Traits Controlling Plant Water Budget

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We describe the concept and realisation of a high-throughput phenotyping platform (FieldScan) combined with lysimetric capacity, to assess canopy traits affecting water use. The platform is based on a novel 3D scanning technique to capture canopy development, a scanner-to-plant concept to increase throughput (2500 plants/h), and analytical scales to combine gravimetric transpiration measurements. We present how the technology functions, how data are visualised via a web-based interface, and how data extraction and analysis is interfaced through 'R' libraries. Close agreement between scanned and observed leaf area data of individual plants in different crops was found (R<sup>2</sup> between 0.86 and 0.94). Similar agreement was found when comparing scanned and observed area of plants cultivated at densities reflecting the field conditions. Example of the monitoring, the plant transpiration by the analytical scales is presented. Moreover we present some on-going applications of the platform to target key phenotypes: (i) the comparison of the leaf area development pattern of fine mapping recombinants of pearl millet; (ii) the leaf area development pattern of pearl millet breeding material targeted to different agro-ecological zones; (iii) the assessment of the transpiration response to high VPD in sorghum and pearl millet.

## Collaborative Phenotyping: Make Every Field a Research Field

*Greg Austic, DOE Plant Research Laboratory, Michigan State University, USA*

Phenotyping crops in a growth chamber, a research plot, and a farmer's field can produce completely different results. Transitioning trials from one to the next costs millions of dollars and wastes years of development time. And yet there are orders of magnitude more farmers fields than there are growth chambers in the world. This imbalance of cost and opportunity begs the question: how can we make every field a research field, while respecting the rights, desires, and most importantly time of the farmer who owns it?

This talk presents one vision for how we might answer that question. Using our project, PhotosynQ ([www.photosynq.org](http://www.photosynq.org)) as a test case, I propose to talk about our experiences in field phenotyping using global networks of sensors and human input. We have spent the last 4 years developing scientific-quality tools to measure photosynthesis-related phenotypes in field conditions, while also building global social networks among 100s of individuals. In total, we have collected 275,000+ field measurements from farmers to professors across 4 continents. The success, failures, and lessons from our experience highlight the challenges and opportunities in the future of collaborative, global plant phenotyping.

## Building Plant HTP Devices while Training the Next Generation of Users

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High-throughput plant phenotyping is an emerging and fast-moving field that requires active collaboration across disciplines, including plants sciences, engineering and computer sciences. Currently, there are commercial instruments that can be acquired to pursue large scale high-throughput phenotyping (HTP) experiments. However, there are also small labs interested in pursuing HTP screens using diversity panels available for some plant species or mutant collections that can be screen in specific conditions. Moreover, some labs need specific requirements in terms of design that may not be commercially available. So who is going to build these devices and how can we ensure that our students are well trained to take advantage of HTP technologies?

At the University of Missouri, we have started an interdisciplinary program where teams of students from engineering and plant sciences work together to design, build and test automatic platforms for high-throughput phenotyping of plants. Furthermore, during the entire academic year (2015-2016) an MU journalist followed the team and conducted interviews at regular intervals to document how members from distant fields exchange ideas to solve the different problems that appeared at different stages of the project.

Our first cohort of interdisciplinary students graduated in Spring 2016 after successfully assembling S.P.I.P. v1.0 [Small Plant Imaging Platform v1.0].

Learn more about the project @ NSF Broader Impacts: <https://goo.gl/cf580t>

## **Data Management and Analysis Solutions for Maize Predictive Phenomics: A Partnership with the GxE Subgroup of the Genomes to Fields (G2F) Initiative**

*GxE Data Management Team, Iowa State University, and University of Wisconsin, Madison, Genomes to Fields Initiative, North America*

Breeding decisions to develop improved cultivars for industrial and agricultural uses are greatly facilitated by simultaneously leveraging phenotypic, genotypic, weather, and image data. Development of standardized data collection and analysis practices by working directly with the data generators in the initial stages of the data collection process, is an important first step to support a multi-institutional, multi-year breeding projects. The Genotype by Environment (GXE) subproject within the maize Genomes to Fields (G2F) is a multi-institutional project spanning 25 North American locations. The GXE group is collectively addressing environmental effects on the performance of a large collection of maize inbreds and hybrids grown in 25 diverse locations. Each location is collecting data on 14 core phenotypic traits, as well as weather measurements with image data for a subset of locations. To assist in the management of these diverse data types, we are developing and deploying a robust, yet flexible, data management and analysis platform that meets their immediate needs but is also extendable to the broader plant breeding community. In this poster, we present progress made over the past year working with partners at the CyVerse and the Breeding Management System software development team at CIMMYT, as well as project status and an overview of emerging initiatives.

## **Phenome 2017: Inaugural Conference to Connect the Plant Phenomics Research and Development Community**

*Crispin Taylor, American Society of Plant Biologists*

The Phenome 2017 conference (February 10-14, 2017) will bring together a multidisciplinary audience comprising plant biologists, engineers, agronomists, and computer scientists interested in plant phenomics. There is substantial excitement about the potential for plant phenomics but real advances will require the development of an active, multidisciplinary community of researchers. The goals of Phenome 2017 are to share discoveries, ideas, and connections in order to foster collaboration, innovation, and the initiation of multi-investigator and multi-institution projects. The four day conference will include presentations in plenary sessions entitled “Phenomic insights into quantitative traits,” “Environmental stress biology,” “Metabolomics,” and “Plasticity in plant traits.” Each day, attendees will engage around poster presentations to discuss cutting edge developments in plant phenomics. Concurrent afternoon sessions will allow attendees hear about exciting topics such as “Emerging technologies for use in the field and controlled environments,” “Data tools and standards,” and “Modeling: from multivariate data to climate and crop models to predict plant traits based on environment.” Phenome 2017 will be an excellent meeting for students from diverse academic backgrounds to meet and mingle with leaders in their fields. Those interested in identifying future collaborations will find opportunities to discuss research projects and commercialization potential. The National Plant Science Council established the Phenome 2017 Conference as one of the outcomes of Unleashing a Decade of Innovation in Plant Science: A Vision for 2015-2025. Visit [www.phenome2017.org](http://www.phenome2017.org) to register for the Phenome 2017 conference.