FINAL REPORT

PROJECT TITLE: Phenomics tools for corn breeding and management decisions
PROJECT NUMBER: 4154-1SPX
PRINCIPAL INVESTIGATOR AND CO-INVESTIGATOR(S): Candice Hirsch, Nathan Springer, Cory Hirsch

ABSTRACT

Measuring phenotypes is at the core of corn breeding and management recommendation practices. Due to the time and labor intensive nature of manually phenotyping plants, the data used for these efforts has typically focused only on end of season traits such as plant height, ear height, and yield. Development of robust, rapid, and low cost methods to evaluate key morphological features will allow for measurements throughout the growing season. Recent technological advances in drones, sensors, and computational resources are allowing for this to become a reality. We developed methodology for collecting images from a drone mounted RGB camera that can be stitched together to create a 3D reconstruction of a field. From this reconstruction we are able to extract morphological information throughout the growing season and track plant growth rate and development. We further applied this method to determine lodging severity and recovery following the numerous wind events that occurred during the project period, and determine factors associated with more severe lodging and incorporated this information to better model end of season performance. We also developed methodology to use top-down high spectral resolution imaging to evaluate plants under a number of stress conditions and developed models that are able to accurately identify stress pixels in different genetic backgrounds. Detecting and understanding non-visible early symptoms will also provide valuable information for future physiological and genetic work to understand the specific mechanisms plants use to respond to their environment so that we can create more resilient plants for the future.

INTRODUCTION

The genome of an individual corn plant contains genetic elements that provide the blueprint for the phenotypic outcome of that individual. However, the ultimate phenotype (i.e. yield) that is observed is a product of how the genetic elements interact with the environment in which the plant is grown. Understanding how the genome interacts with the environment is important to maximize potential in good environments and minimize loss in poor environments. Indeed, through various simulation models based on current germplasm and expected weather conditions from climate change, it is estimated that corn yields could be impacted by at least 30% by 2050 (3).

We know different genotypes have varied responses to their growth environment throughout development, particularly in response to extreme weather and prolonged stress conditions. Furthermore, trait performance and trait plasticity are regulated by different parts of the genome (2). Despite the importance of having a plastic genome that is able to respond and be resilient to stresses, corn breeding has actually acted to reduce plasticity (1). This means there are opportunities to identify varieties with high performance and the ability to respond effectively to environmental challenges.

In an effort to connect our knowledge of the maize genome to in field performance and understand the genotype-by-environment interaction, members of the maize community formed the Genomes to Fields Initiative (https://www.genomes2fields.org). The overall objective of this project is to leverage genomic information with phenotypic and environmental data to enable working knowledge and prediction of plant performance under variable growing conditions. There are many dimensions to the goal of understanding genotype-by-environment interactions that are addressed by this initiative, such as which genes impact which traits, how genes interact among themselves, the relevance of specific genes under different growing conditions, and how these genes influence plant growth throughout development. Early on the G2F Project identified the need for high dimensional phenotypic data in understanding genome plasticity and the genotype-by-environment interaction.

High dimensional phenotyping data allows us to track how plants respond to environmental signals, identify hybrids that are most and least responsive, and determine management practices best suited to the combination of hybrid genotype and environmental conditions. High dimensional data can refer to spatial, temporal, and spectral dimensionality. This project focused on two of these aspects of high dimensional phenotypic data, temporal and spectral dimensionality. Only recently has technology advanced sufficiently to enable acquisition of either of these high dimensional data types. Advances in unmanned aerial systems (UAS), or drones, that carrying low payload sensors such as standard RGB cameras provide for high temporal resolution in field conditions. While these sensors are extremely valuable, they are only able to detect what can already be seen by the human eye. Other advanced sensors, such as hyperspectral sensors, are able to detect signals beyond those that can be seen by the human eye (Figure 1 - see attached file) and provide a spectral dimensionality that can be extremely useful to early detection of stress, allowing for management interventions before a non-recoverable yield penalty is realized.

The goal of this project was to develop tools that utilize advances in drone and sensor technologies to understand how corn plants interact with their environment (both climate and management practices). This will facilitate future efforts to breed for more plastic genomes that can favorably respond to their environment. It will also identify signals (morphological and spectral) that indicate different stress conditions to allow for more precise in season management decisions to protect from yield loss under different environmental conditions.

OBJECTIVE AND GOAL STATEMENTS

Objective 1: Develop crop models using UAS imagery in homogenous fields containing plots with variable genetic material and management practices.

Objective 2: Apply UAS imagery and crop models in heterogeneous production settings.

Objective 3: Identify spectral wavelengths and morphological features that differentiate stress response.

MATERIALS AND METHODS

Objective 1: Develop crop models using UAS imagery in homogeneous fields containing plots with variable genetic material and management practices. A yield trial consisting of 30 maize hybrids was planted in four-row plots on three different dates (early May, mid May, and late May) under two planting densities (60k and 100k plants per hectare) with two replicates per treatment in St Paul, MN in the summer of 2019 and 2020. This experiment was grown on one hectare and 11 ground targets distributed around the field's border and internal alleys will be used as ground control points (GCPs) based on previously developed optimization algorithms. The field was imaged weekly after planting using a DJI Phantom 4 Advanced drone, and more frequently following lodging events. Manual measurements for stand count and plant height were obtained for plots from 15 of the 30 hybrids within the first planting, and five of the 30 hybrids in the remaining planting dates for a total of 180 hand-measured plots. Manual measurement of plant height were obtained weekly following imagery collection as the height from the ground to the topmost vegetative part of each plant within the middle two rows of the four row plots. Details regarding data analysis were conducted as described in:

Tirado, S., C. Hirsch, N. Springer. 2020. UAV Based Imaging Platform for Monitoring Maize Growth Throughout Development. Plant Direct. DOI: 10.1002/pld3.230

Tirado, S. C. Hirsch, N. Springer. 2021. Utilizing Temporal Measurements from UAVs to Assess Root Lodging in Maize and its Impact on Productivity. Field Crops Research. 262:108014.

Objective 2: Apply UAS imagery and crop models in heterogeneous production settings. We flew three production fields on a bi-weekly basis and trait data was extracted using the methods we developed as part of this project (please see below). From each of the five fields, 10 regions were identified that ranged from low expected performance to high expected performance. Grain from 20 plants in the region were hand harvested prior to mechanical harvesting of the remaining plants in the field. Extrapolated grain yield from the 20 plants harvested in each of these regions were compared to the predicted values.

Objective 3: Identify spectral wavelengths and morphological features that differentiate stress response. For this Objective two experiments were conducted. For both experiments, seeds were planted approximately 5 cm (2 inches) below the surface in 655.5 cm^3 (40 $inch^3$) D-40 DeePots (Stuewe and Sons, Inc.) containing a 1:1 mix of SunGro horticulture professional growing mix and autoclaved field soil. All plants were grown in Conviron growth chambers with a 16 h 30℃ and 8 h 20℃ day/night cycle and watered every other day. In experiment E1, five maize genotypes (B73, Mo17, PH207, Ki11, and MS71) were subjected to four treatment conditions (control, cold, heat, salt). Plants for all treatments were grown in standard (non-stress) conditions until 11 days after sowing (DAS) when the stresses were applied for the cold, heat, and salt treatments. The cold-stress treatments were implemented using a Thermo Scientific refrigerated incubator programmed with a 16 h 6℃ and 8 h 2℃ day/night cycle and applied for 48 h. The heat-stress treatments were implemented using a Thermo Scientific refrigerated incuba- tor programmed with a 16 h 39℃ and 8 h 29℃ day/night cycle and applied for 48 h. The salt stress was a single 50 ml 0.75 M NaCl treatment at Zeitgeber Time 2 (ZT2) at 11 DAS. Plants were imaged with our hyperspectral and RGB imaging systems at the end of the stress treatment at ZT2 at 13 DAS. Three experimental replicates were grown each consisting of three plants per genotype per treatment condition, for a total of nine plants per genotype per treatment. Experiment E2 consisted of two maize genotypes (Mo17 and PH207) subjected to four treatment conditions (control, low salt, medium salt, and high salt stress). The low, medium, and high salt stress treatments were implemented by a single 50 ml 0.5 M NaCl, 0.75 M NaCl, or 1 M NaCl treatment, respectively, at ZT2 at 11 DAS. Plants were imaged with our hyperspectral and RGB imaging systems before undergoing stress at ZT2 at 11 DAS, at the end of the stress treatment at ZT2 at 13 DAS and 2 d after the stress treatment at 15 DAS. The experiment consisted of 15 plants per genotype per treatment.

We used two existing phenotyping platforms for this Objective. The first phenotyping platform is a high throughput imaging system that was developed by Co-PIs CD Hirsch and Springer. In this platform, plants are imaged using a standard RGB camera, and images are processed using MATLAB software while parallelizing the analysis by utilizing the high performance compute cluster resources available through CyVerse (https://www.cyverse.org). This process is highly automated through sample tracking using QR codes that are contained within the image and extracted during the image processing step. This platform measures the longest path through the plant, plant height, plant width, stem diameter, leaf curvature, leaf number, digital biomass, center of mass, and distribution of mass. Additionally, obtaining images of plants over consecutive days allows for rate of change to be derived for each trait in addition to the point values obtained on a daily basis. The second phenotyping platform we used was the University of Minnesota Plant

Spec 10 hyperspectral phenotyping platform. The Plant Spec 10 systems are equipped with a VNIR high dynamic range camera that acquires 580 wavebands ranging from 362 to 1038 nm. We developed a robust set of tools to automate data handling, manipulation, and analysis of images acquired by this system. Details regarding statistical analysis were conducted as described in:

Tirado, S., S. St. Dennis, T. Enders, N. Springer. 2021. Utilizing spatial variability from hyperspectral imaging to assess variation in maize seedlings. The Plant Phenome Journal. 4:e20013.

RESULTS AND DISCUSSION

UAV Based Imaging Platform for Monitoring Maize Growth Throughout Development. Plant height (PH) data collected at high temporal resolutions can give insight into how genotype and environmental variation influence plant growth. However, in order to increase the temporal resolution of PH data collection, more robust, rapid, and low-cost methods are needed to evaluate field plots than those currently available at the start of this project. Due to their low cost and high functionality, unmanned aerial vehicles (UAVs) provide an efficient means for collecting height at various stages throughout development. We developed a procedure for utilizing structure from motion algorithms to collect PH from RGB drone imagery (Figure 1,2) and have used this platform to characterize a yield trial consisting of 24 maize hybrids planted in replicate under two dates and three planting densities. PH data was collected using both weekly UAV flights and manual measurements. The comparisons of UAV-based and manually acquired PH measurements revealed sources of error in measuring PH and were used to develop a robust pipeline for generating UAV-based PH estimates with high accuracy (Figure 3). This pipeline was utilized to document differences in the rate of growth between genotypes and planting dates (Figure 4). Our results also demonstrate that growth rates generated by PH measurements collected at multiple timepoints early in development can be useful in improving predictions of PH at the end of the season (Figure 5). This method provides a low cost, high throughput method for evaluating plant growth in response to environmental stimuli on a plot basis that can be implemented at the scale of a breeding program. Additional information about this method can be found in the following publication:

Tirado, S., C. Hirsch, N. Springer. 2020. UAV Based Imaging Platform for Monitoring Maize Growth Throughout Development. Plant Direct. DOI: 10.1002/pld3.230

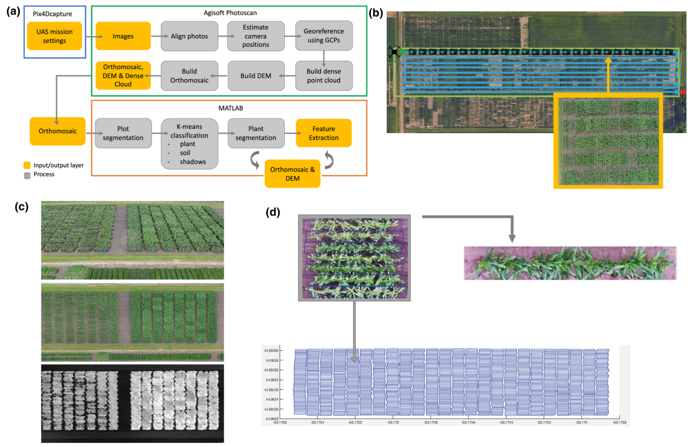

Figure 1. Procedure for feature extraction from UAV images. (a) Image generation and processing pipeline. (b) UAV flight mission structure for gathering images. (c) Dense cloud (top), orthomosaic (middle) and DEM (bottom) output from Agisoft Photoscan Professional Edition. (d) Plot boundary extraction from grid shapefile for plot segmentation.

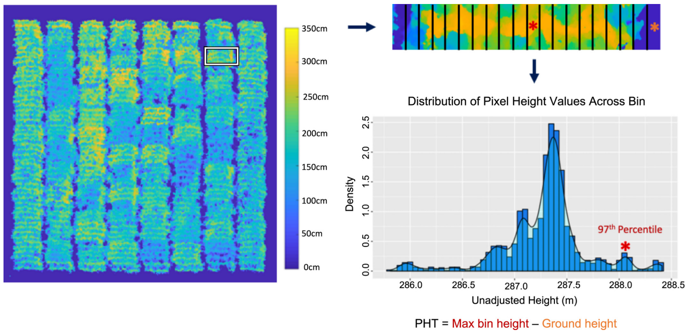

Figure 2. Method for extracting mean PH_{UAV} values for a given plot. The plot is segmented and broken down into 20 bins. The 3rd and 97th percentiles for each bin are extracted and used to calculate the average plot height by subtracting the minimum 3rd percentile of all bins from the 97th percentile of each bin

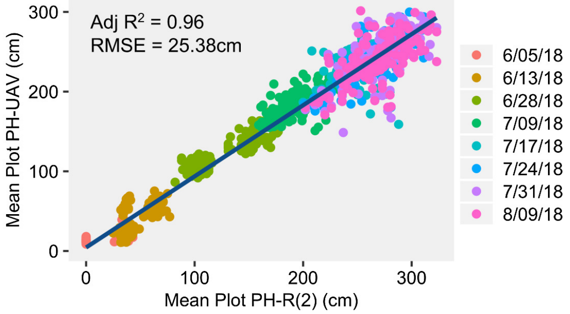

Figure 3. Pearson correlation of mean plot PH_{UAV} and mean plot PH_R across all dates

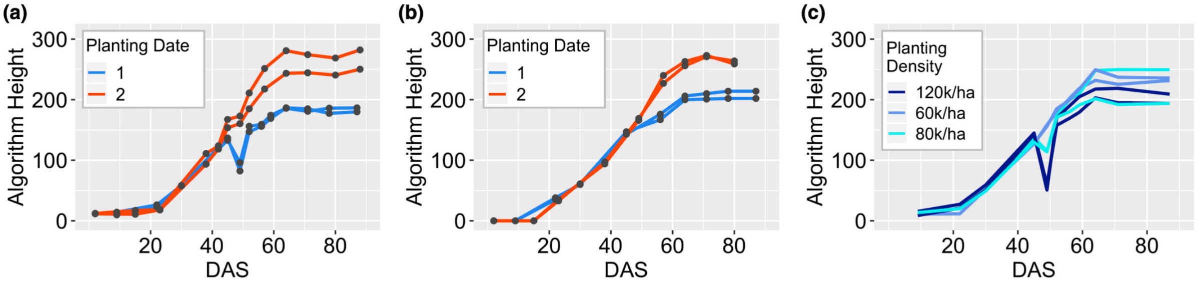

Figure 4. Height through time for various genotypes and treatments. (a and b) Height through time as measured by the UAV (a) and hand measurements (b) for two replicate plots of a single genotype (LH82 × DK3IIH6) planted under high density across two planting dates. Dots indicate timepoints of measurement. (c) Height through time as measured by the UAV for two replicate plots of a single genotype (LH82 × PHK76) in the early planting date treatment and the three planting densities. UAV, unmanned aerial vehicle

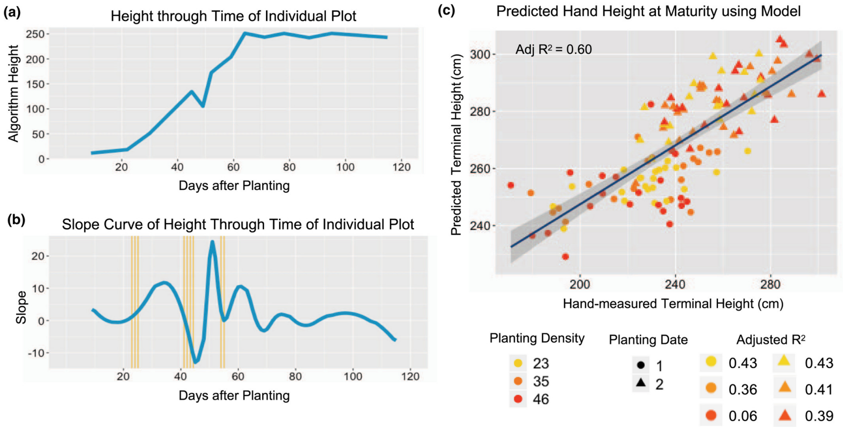

Figure 5. Predicting terminal height using rate of change in height at certain intervals. (a) Height through time for an individual plot as recorded by the UAV. (b) First derivative of the height through time spline curve in blue and the selected timepoints were the slope contributed most to the prediction of terminal height in yellow. (c) Correlation of predicted terminal height on the test dataset utilizing a linear regression model derived from the training dataset based on slope values of selected timepoints and the hand-measured height values at maturity.

Utilizing temporal measurements from UAVs to assess root lodging in maize and its impact on productivity. Both stalk and root lodging can cause significant yield losses in maize; however, maize plants are often able to recover from root lodging. There is potential among breeding programs for developing lines that are more tolerant and can more rapidly recover from root lodging. We assessed the incidence of root lodging utilizing end-of-season lodging scores collected among the Genomes 2 Fields (G2F) initiative trials and found a large yet variable incidence of lodging across states, years, and genotypes (Figure 6). Lodging in this dataset was scored manually at the end of the season, and little is known about the drivers of lodging and lodging recovery. We therefore developed an approach for utilizing temporal plant height measurements collected from unmanned aerial vehicles to capture in-season lodging and recovery in a yield trial consisting of 24 maize hybrids planted in replicate under two dates and three planting densities in St Paul, MN in the summers of 2018 and 2019 (Figure 7). We found that growth rates during vegetative development as well as the developmental timing of plants when exposed to a storm are predictive of the amount of lodging maize plots will experience. We also found that utilizing temporal height measurements can help in not just estimating lodging and early vegetative growth rates, but that utilizing these estimates can also aid in assessing end of season yield (Figure 8). Additional information from this study can be found in the following publication:

Tirado, S. C. Hirsch, N. Springer. 2021. Utilizing Temporal Measurements from UAVs to Assess Root Lodging in Maize and its Impact on Productivity. Field Crops Research. 262:108014.

Information about the G2F datasets used in this study is described in the following publication:
McFarland, B., et al. 2020. Maize Genomes to Fields (G2F): 2014-2017 field season's genotype, phenotype, climatic, soil, and inbred ear images datasets. BMC Research Notes. 13:71.

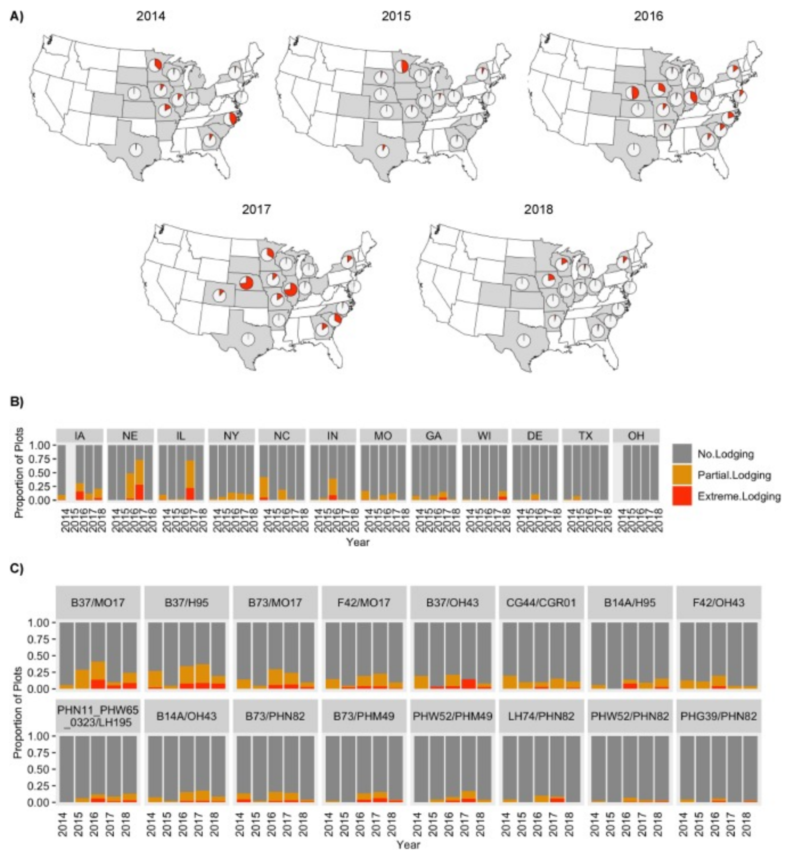

Figure 6. A) Percent of plots in G2F locations across years with lodging data where more than 5% of plots lodged. B) Percent of plots per state across all years where less than 5% of plants lodged (grey), between 5 and 50 % of plants lodged (yellow) and more than 50 % of plants lodged (red). C) Percent of plots across all locations and years for the 16 genotypes with lodging data in at least 6 locations all five years where less than 5% of plants lodged (grey), between 5 and 50 % of plants lodged (yellow) and more than 50 % of plants lodged (red). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

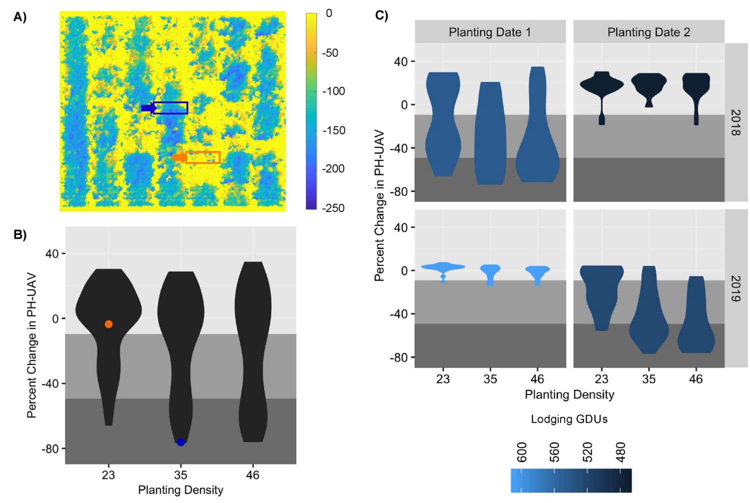

Figure 7. A) Height difference (in cm) for the 2019 late planting date treatment at 7/16/2019 compared to 7/15/2019 following the wind storm that occurred the night of 7/15/2019. Boxes represent plots with low (orange) and high (blue) degrees of lodging. B) Density plot of lodging percent height change for all plots across all treatments in the 2018 and 2019 seasons. The background shading represents the areas where plots where depicted as having no height change (light grey), moderate height change (medium grey), and severe height change (dark grey). Points represent plots marked in panel A with low (orange) and high (blue) degrees of lodging. C) Density plot of lodging percent height change for all plots across individual planting date treatments and years. The color represents the growing degree units (GDUs) of the specific treatment-year

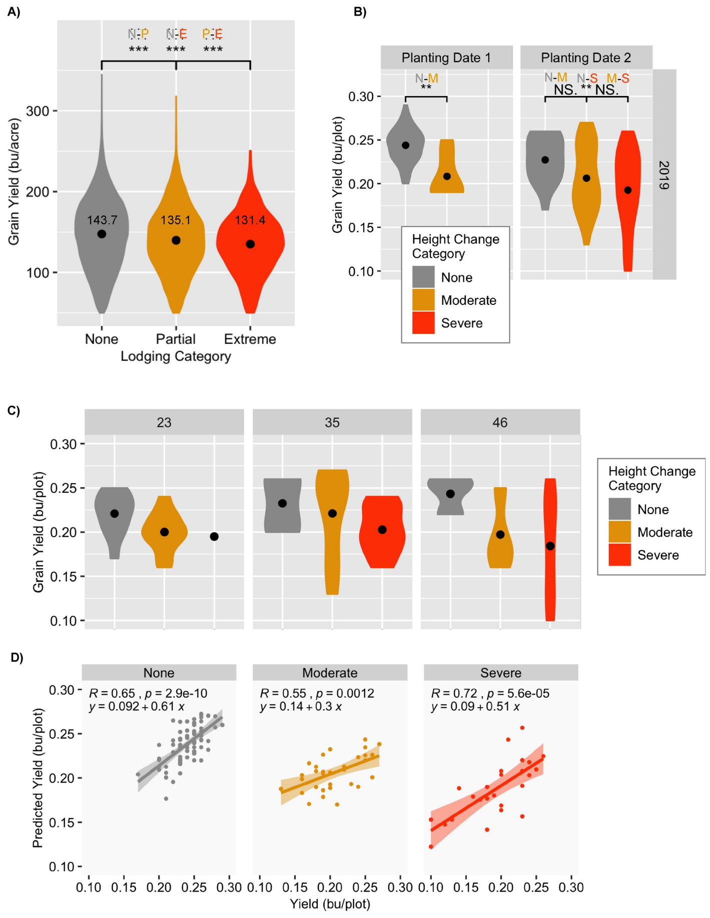

Figure 8. A) Density plot of grain yield (in bushels/acre) for all the Genomes 2 Fields Initiative hybrid plots with lodging data grown across all states and years grouped by lodging score category (none, partial and extreme). Significance values based on *t*-test comparing different groups are plotted (* significant at p = 0.05; ** significant at p = 0.01; *** significant at p = 0.001; N.S., not significant). **B)** Density plot of grain yield (in bushels/plot) for all the 2019 experimental plots grouped by height change category (none, moderate and severe) and by planting date. Significance values based on *t*-test comparing different the groups are plotted (* significant at p = 0.05; ** significant at p = 0.01; *** significant at p = 0.001; NS., not significant). **C)** Density plot of grain yield (in bushels/plot) for all the 2019 experimental plots in the second planting date treatment grouped by height change category (none, moderate and severe) and by planting density (23, 35, and 46 seeds/row). **D)** Grain yield predictions split by height change category on 1/2th of all 2019 plots using a model generated with the other 1/2th of the dataset compared to the measured yield values. The model contained genotype, early-season growth rate, lodging height change, and terminal PH as the predictor variables.

<u>*Utilizing spatial variability from hyperspectral imaging to assess variation in maize seedlings.*</u> There is significant enthusiasm about the potential for hyperspectral imaging to document variation among plant species, genotypes, or growing conditions. However, in many cases the application of hyperspectral imaging is performed in highly controlled situations that focus on a flat portion of a leaf or side-views of plants that would be difficult to obtain in field settings. We were interested in assessing the potential for applying hyperspectral imaging from a top-down view to document variation in genotypes and abiotic stresses for maize (*Zea mays* L.) seedlings grown in controlled environments. A top-down image of a maize seedling includes a view into the funnel-like whorl at the center of the plant with several leaves radiating outward. There is substantial variability in the reflectance profile of different portions of this plant. To deal with the variability in reflectance profiles that arises from this morphology we implemented a method that divides the longest leaf into 10 segments of equal length from the center to the leaf tip (Figure 9). We showed there is large variability in the hyperspectral profiles across leaf segments, which are masked when performing whole-plant averages as tend to be done when analyzing hyperspectral data. We found that using these segments provides improved ability to discriminate different genotypes (B73, Mo17, Ki11, MS71, PH207) (Figure 10) and abiotic stress conditions (heat, cold, or salinity stress) for maize seedlings (Figure 11). This provides an approach that can be implemented to help classify genotype and environmental variation for maize seedlings from a top-down view such as that which would be collected in field settings. Additional information from this study can be found in the following publication:

Tirado, S., S. St. Dennis, T. Enders, N. Springer. 2021. Utilizing spatial variability from hyperspectral imaging to assess variation in maize seedlings. The Plant Phenome Journal. 4:e20013.

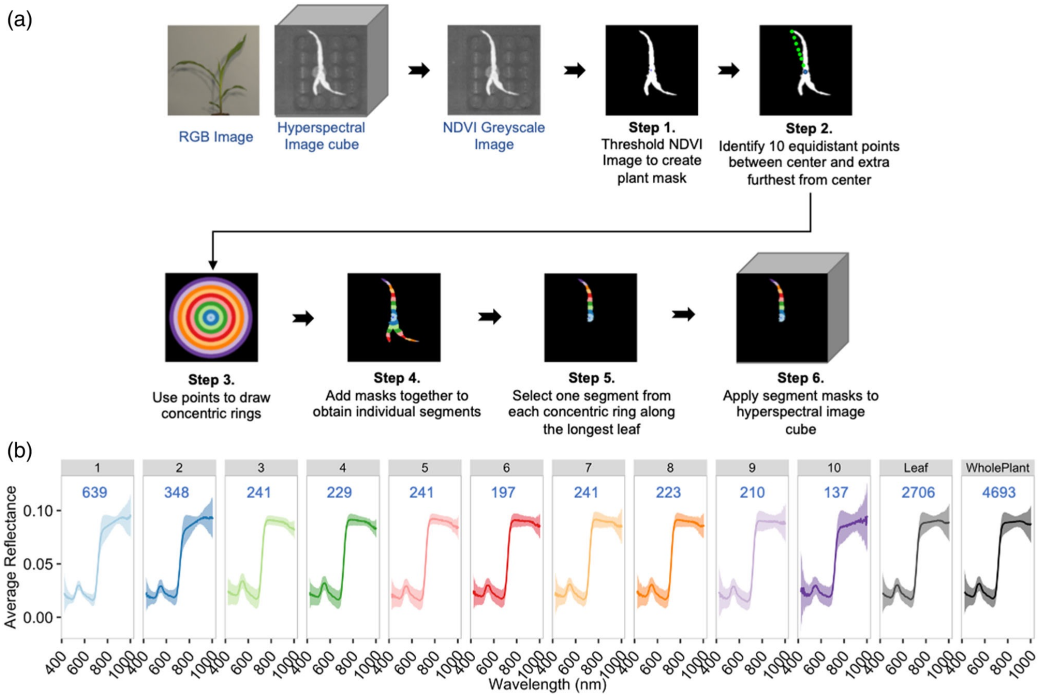

Figure 9. Evaluating individual leaf segments. (a) Procedure for extracting hyperspectral data from10 segments across the longest leaf of each plant. (b) Mean (dark line) and variance in reflectance of individual leaf segments, the entire longest leaf (all leaf segments combined) and the entire plant of a Mo17 control plant at 13 d after sowing. Pixel counts represented in each panel are indicated by the blue text. Leaf segment is indicated at the top of each panel in black text

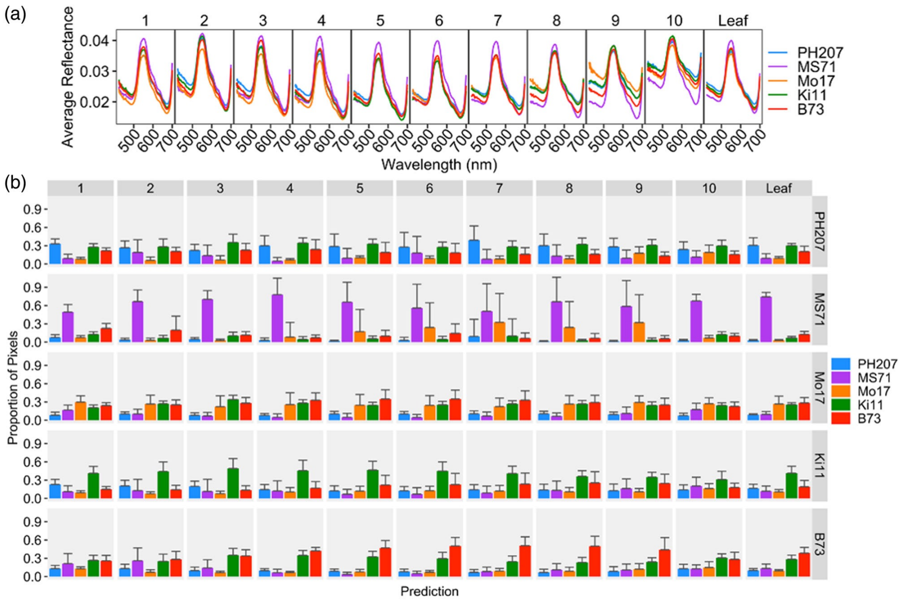

Figure 10. Genotypic differences in hyperspectral profiles for all control plants of each genotype. (a) Average reflectance values across all control plants of each genotype. (b) Average proportion of pixels per plant from all plants of a certain genotype (rows) for each leaf segment (columns) predicted to belong to a certain genotypic class. Error bars indicate the standard deviation in pixel values from the mean

Figure 11. Differences in hyperspectral profiles across treatments for Ki11 and Mo17 plants. (a) Average reflectance values for all plants in the cold, control, heat, and salt stress treatments of Ki11 and Mo17. (b) Average proportion of pixels from all Ki11 plants of a certain treatment (rows) for each leaf segment (columns) predicted to belong to a certain treatment class. Bars represent the mean proportion of all plants per category and error bars represent the standard deviation around the mean. (c) Average proportion of pixels from all plants of a certain treatment (rows) for genotypes across selected leaf segments predicted to belong to a certain treatment class. Bars represent the mean proportion of all plants per genotype and treatment class predicted to belong to a certain treatment

CONCLUSIONS

Developing the resilient crops of the future will require access to a broad set of tools. While advances in sequencing and marker technologies have facilitated marker-trait associations and the ability to predict the phenotype of an individual from its genotypic information, other tools such as high-throughput phenotyping are still in their infancy. Advances in sensors, aeronautics, and computing have enabled progress. In this project we developed new analysis methods to extract information on plant morphology from aerial drone imagery, and use this information to monitor growth rates throughout development, assess lodging severity and recovery, and better model end of season yield performance by incorporating all of this information. We also developed important methodology for transitioning from using hyperspectral imagery on flat leaves to methods that can be translated into aerial data collection applications in field settings, and demonstrated these methods can fingerprint different stress conditions that plants are experiencing. These methods and the biological findings from these studies will have profound impacts on the ability to breed for the next generation of climate resilient varieties.

EDUCATION, OUTREACH, AND PUBLICATIONS

Peer Reviewed Publications:

1. Sweet, D., S. Tirado, N. Springer, C.N. Hirsch, C.D. Hirsch. 2022. Opportunities and challenges in phenotyping row crops using drone-based RGB imaging. The Plant Phenome Journal (*in press*).
2. Jarquin, D. N. de Leon, C. Romay, M. Bohn, E. Buckler, I. Ciampitti, J. Edwards, D. Ertl, S. Flint-Garcia, M. Gore, C. Graham, C. Hirsch, J. Holland, D. Hooker, S. Kaeppler, J. Knoll, E. Lee, C. Lawrence-Dill, J. Lynch, S. Moose, S. Murray, R. Nelson, T. Rocheford, J. Schnable, P. Schnable, M. Smith, N. Springer, P. Thomison, M. Tuinstra, R. Wisser, W. Xu, J. Yu, A. Lorenz. 2021. Utility of Climate Information via Combining Ability Models to Improve Genomic Prediction for Yield within the Genomes to Fields Maize Project. Frontiers in Genetics. 11:592769.
3. Tirado, S. C. Hirsch, N. Springer. 2021. Utilizing Temporal Measurements from UAVs to Assess Root Lodging in Maize and its Impact on Productivity. Field Crops Research. 262:108014.
4. Tirado, S., S. St. Dennis, T. Enders, N. Springer. 2021. Utilizing spatial variability from hyperspectral imaging to assess variation in maize seedlings. The Plant Phenome Journal. 4:e20013.
5. Falcon, C., S. Kaeppler, E. Spalding, N. Miller, N. AlKalifah, M. Bohn, E. Buckler, D. Campbill, I. Ciampitti, A. Ignacio, L. Coffey, J. Edwards, D. Ertl, S. Flint-Garcia, M. Gore, C. Graham, C. Hirsch, J. Holland, D. Jarquin, J. Knoll, N. Lauter, C. Lawrence-Dill, E. Lee, A. Lorenz, J. Lynch, S. Murray, R. Nelson, C. Romay, T. Rocheford, P. Schnable, B. Scully, M. Smith, N. Springer, M. Tuinstra, R. Walton, T. Weldekidan, R. Wisser, W. Xu, N. de Leon. 2020. Relative Utility of Agronomic, Phenological, and Morphological Traits for Assessing Genotype-by-Environment Interaction in Maize Inbreds. Crop Science. 60:62-81.
6. Kusmec, A., C. Yeh, N. AlKhalifah. M. Bohn, E. Buckler, D. Campbell, I. Ciampitti, D. Ertl, S. Flint-Garcia, J. Gardiner, M. Gore, C. Hirsch, S. Kaeppler, J. Knoll, J. Kolkman, G. Kruger, N. Lauter, C. Lawrence-Dill, E. Lee, N. de Leon, S. Liu, A. Lorence, B. McFarland, C. Poudyal, M. Romay, J. Schnable, R. Sekhon, K. Silverstein, M. Smith, N. Springer, K. Thelen, J. Wallace, R. Walls, R. Walton, T. Weldekidan, D. Willis, R. Wisser, P. Schnable. 2020. Data-driven identification of environmental variables influencing phenotypic plasticity to facilitate breeding for future climates: a case study involving grain yield and hybrid maize. SSRN. 3684755
7. Li, Z., S. Tirado, D. Kadam, L. Coffey, N. Miller, E. Spalding, A. Lorenz, N. de Leon, S. Kaeppler, P. Schnable, N. Springer, C. Hirsch. 2020. Characterizing allele-by-environment interactions using maize introgression lines. Theoretical and Applied Genetics. 133(10): 2761-2773.
8. McFarland, B., N. AlKhalifah, M. Bohn, J. Bubert, E. S. Buckler, I. Ciampitti, J. Edwards, D. Ertl, J. Gage, C. Falcon, S. Flint-Garcia, M. Gore, C. Graham, C. Hirsch, J. Holland, E. Hood, D. Hooker, D. Jarquin, S. M. Kaeppler, J. Knoll, G. Kruger, N. Lauter, E. Lee, A. Lorenz, J. Lynch, J. McKay, N. Miller, S. Moose, S. Murray, R. Nelson, C. Poudyal, T. Rocheford, O. Rodriguez, M. Romay, J.

Schnable, P. Schnable, B. Scully, R. Sekhon, K. Silverstein, M. Singh, M. Smith, E. Spalding, N. Springer, K. Thelen, P. Thomison, M. Tuinstra, J. Wallace, R. Walls, R. Wisser, W. Xu, C. Yeh, N. de Leon. 2020. Maize Genomes to Fields (G2F): 2014-2017 field season's genotype, phenotype, climatic, soil, and inbred ear images datasets. BMC Research Notes. 13:71.

9. Rogers, A., J. Dunne, C. Romay, M. Bohn, E. Buckler, I. Ciampitti, J. Edwards, D. Ertl, S. Flint-Garcia, M. Gore, C. Graham, C. Hirsch, E. Hood, D. Hooker, J. Knoll, E. Lee, A. Lorenz, J. Lynch, J. McKay, S. Moose, S. Murray, R. Nelson, T. Rocheford, J. Schnable, P. Schnable, R. Sekhon, M. Singh, M. Smith, N. Springer, K. Thelen, P. Thomison, A. Thompson, M. Tuinstra, J. Wallace, R. Wisser, W. Xu, S. Kaeppler, N. de Leon, J. Holland. 2020. The Importance of Dominance and Genotype-by-Environment Interactions on Grain Yield Variation in a Large-Scale Public Cooperative Maize Experiment. Genes Genomes and Genetics | G3. 11(2):jkaa050
10. Tirado, S., C. Hirsch, N. Springer. 2020. UAV Based Imaging Platform for Monitoring Maize Growth Throughout Development. Plant Direct. DOI: 10.1002/pld3.230.

Oral and Poster Presentations:

1. Sweet, D., S. Tirado, N. Springer, C.D. Hirsch, C.N. Hirsch. Variability in maize growth rates and utility in predicting end of season performance. 63rd Annual Maize Genetics Meeting. Virtual poster presentation. March 8-12, 2021.
2. Sweet, D., S. Tirado, N. Springer, C.D. Hirsch, C.N. Hirsch. Variability in maize growth rates and utility in predicting end of season performance. North American Plant Phenotyping Network Annual Conference. Virtual presentation. February 16-19, 2021.
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4. Hirsch, C. Utilizing Phenomics to Better Understand Corn Growth and Development Under Variable Environmental Conditions. Corteva Virtual Plant Science Symposium. April 24, 2020.
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