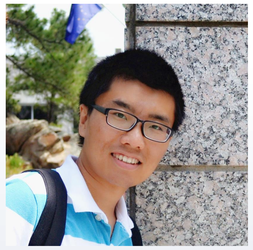

Computer Vision Based Phenotyping of Panicoid Crops

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Abstract

The rapid development of image-based plant phenotyping systems is creating a new bottleneck in data analysis, specifically the development and validation of computer vision based approaches to extract numeric phenotypic values from image data. Traditional phenotypic measurements have focused on what could be easily measured under field conditions (e.g. flowering time, plant height, angle between specific leaf and stem). Initial computer vision approaches have sought to measure the same phenotypes previously measured using manual means, however image based phenotyping also presents the opportunity to quantify thousands of new individual and derived phenotypes which previously could not be practically measured. Our current dataset (Panicoid Phenomap-1) consists of 40 panicoid genotypes measured by visible camera through 26 days at the NIC (Nebraska Innovation Campus) phenotyping greenhouse in University of Nebraska-Lincoln with a capacity of 672 plants and four imaging modalities (Thermal IR, fluorescence, RGB, and hyperspectral). We are testing broad-sense heritability as a way to screen and prioritize novel computer vision based on plant phenotypes, identifying those with significant genetic components. All the raw image data collected in the course of this research is being made available prior to publication to catalyze the development of further computer vision algorithms for extracting numeric phenotypic values from plant image data.

Panicoid Phenomap-1 Dataset

The Panicoid Phenomap-1 Dataset consists of 40 panicoid genotypes in vegetative growth stage including 32 maize genotypes (5 replicates each) and 8 other panicoid genotypes (3 replicates each) (Table 1) cultivated in NIC (Nebraska Innovation Campus) greenhouse for 26 days. Each plant was captured by four types of cameras (Thermal IR, fluorescence, RGB, and hyperspectral) once per day. Images from two side views (0º and 90º) combined with one top view were captured by visible camera for initial phenotype measurement and analysis. In parallel, daily measurements of water consumption and weight of pot with plant were accurately recorded.

Table 1. Plant Genotypes in Panicoid Phenomap-1 Dataset.

ID	Name	ID	Name	ID	Name	ID	Name
1	740	11	LH123HT	21	DHB47	31	W117HT
2	2369	12	LH145	22	PHG35	32	Wf9
3	A619	13	LH162	23	PHG39	33	Yugul
4	A632	14	LH195	24	PHG47	34	PI 614815
5	A634	15	LH198	25	PHG83	35	PI 583800
6	B14	16	LH74	26	PHJ40	36	Purple Majesty
7	B37	17	LH82	27	PHH82	37	BTx623
8	B73	18	Mo17	28	PHV63	38	PI 535796
9	C103	19	DKPB80	29	PHW52	39	PI 463255
10	CM105	20	PH207	30	PHZ51	40	PI 578074

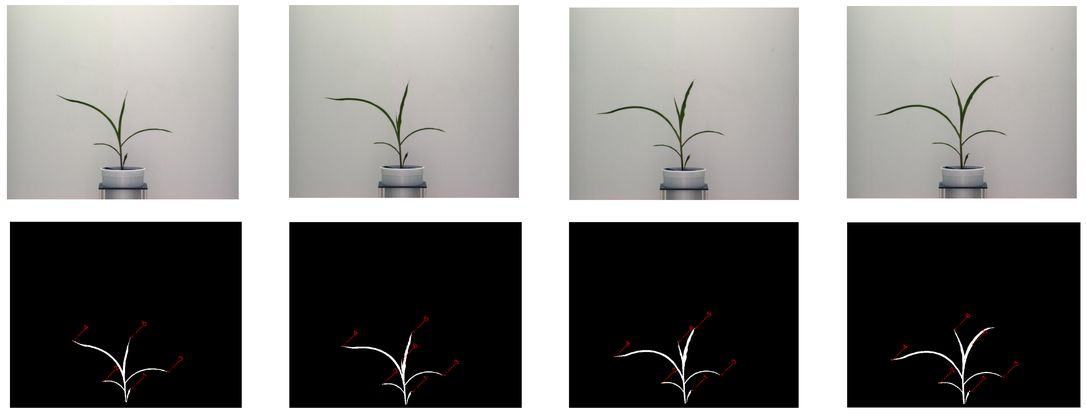
Data is publicly available at: http://plantvision.unl.edu/dataset

Collecting high throughput phenotypic data for field phenotype prediction

High throughput imaging data was collected from the same inbreds grown by in the Genomes to Fields project (http://www.genomes2fields.org/). As part of G2F, traditional phenotypes (e.g. morphological traits, agronomic traits and traits of productivity) were measured in 19 unique locations across 13 states in 2014 and 24 unique locations across 16 states in 2015. Thousands of potential phenotypes (e.g. curvature of leaves, extension rate of leaves, hyperspectral components) can be derived and evaluated from the image-based datasets. Our goal is to test whether with appropriated modeling and testing it may be possible to predict some of these phenotypes in the field based on combinations of different phenotypes measured in the greenhouse.

Developing algorithms for measuring novel phenotypes from computer vision

Using the Panicoid Phenomap-1 dataset, a wide range of phenotypes can feasibly be measured using computer vision tools. For example, a wide range of traits related to leaf emergence order, and changes in leaf-stem angle, and curvature over time (Fig 1). In order to achieve this, the very first step is to trace the same leaf across time from a batch of images.



(A) (B) (C) (D)

Fig 1. Leaf tracking from Day 13 to Day 16 of Inbred PHV63. Upper figures show original captured images by visible camera and lower images are segmented by computer collaborator Srinidhi with leaf tracking. (A) Day 13; (B) Day 14; (C) Day15; (D) Day 16.

Variation in water use efficiency in maize inbreds

By integrating image-based data and actual dry weight of above-ground plants, a model was constructed and applied to predict dry weight of plants based on detecting pixels. Water evaporation in empty pots were used to calibrate whole accumulated evaporation of each genotype for its life cycle in greenhouse. The estimated dry weight in the end of day would be considered as its harvest dry weight. The water use efficiency of maize inbred will be determined by the ratio of accumulated consumed water to amount of estimated dry tissue. In order to estimate genetic component affecting this phenotypic variation, the broad-sense heritability was estimated as 30.9%. This moderate number means that around 1/3 phenotypic variations can be explained by genetics. In this way, we evaluate the variation of water use efficiency through the whole plant imaging cycle among inbreds grown in the NIC greenhouse (Fig 2).

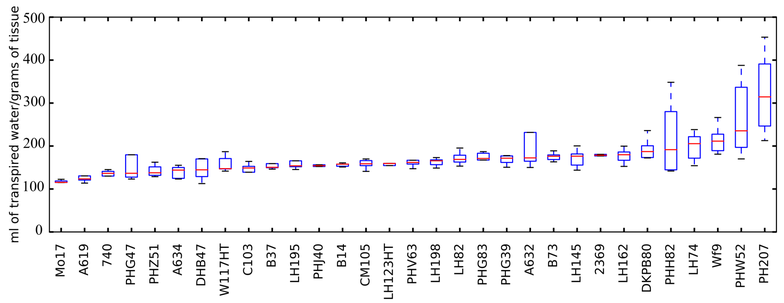


Fig 2. Variations of the amount of transpired water per amount of estimated dry tissue among inbreds.

Fig 3. Ground truth phenotype measurements for hybrids grown in NIC greenhouse.

Phenotyping exPVP hybrids on field and greenhouse conditions

140 off-patent maize F1 ex-PVP hybrids (expired Plant Variety Protection) generated from same inbreds were planted both in the NIC greenhouse and in the field (Mead, NE). Ground truth phenotypes, including, but not limited to, height, tiller number, leaf angle and stem width, were recorded 63 days after planting (Fig 3) with the Android app “Field book” (http://wheatgenetics.org/field-book). We are also collecting the same hyperspectral and RGB data from the hybrid plants and that at 63 days most hybrids had already flowered in greenhouse system, allowing us to develop algorithms to measure ear and tassel phenotypes. Meanwhile, early stage phenotypes from the same hybrids were measured in the field using phenotyping platform developed by the Ge lab (Fig 4).

Fig 4. Image-based phenotypes collection for hybrids in early stage using phenotyping platform developed by the Ge lab.

Future work

1. The abundance of 20 different minerals will be quantified using leaf tissue from the same plants phenotyped above using inductively coupled plasma-mass spectrometry.
2. Root and soil samples have been collected from the same plants phenotyped above and will be used to quantify the root associated microbiomes of individual plants using metagenomic sequencing.
3. Building appropriate models to predict mature stage phenotypes based on and early stage phenotypes.

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