“Phenomics”: another hype or something more?

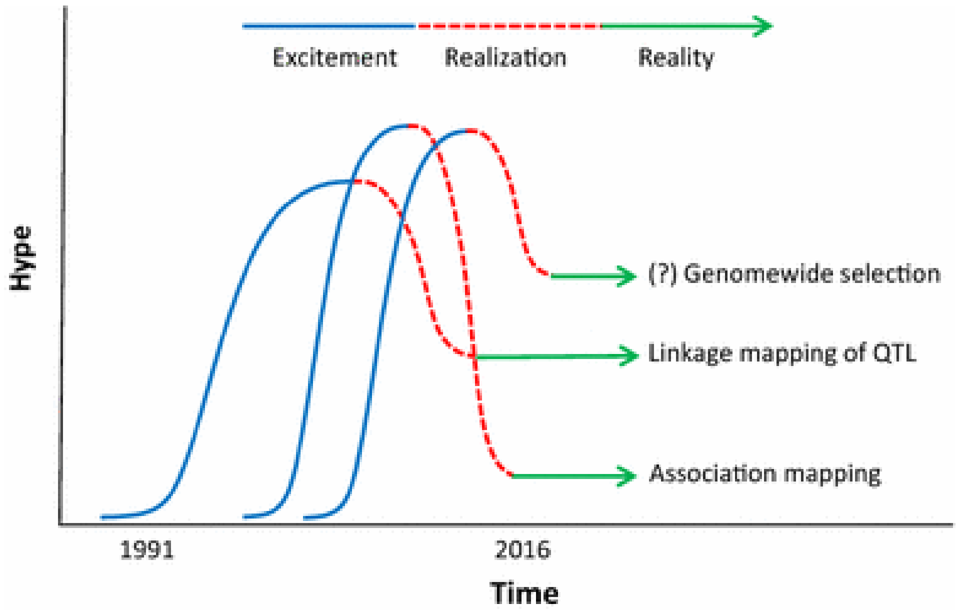
Soybean Breeder’s Workshop
Feb 14, 2017

Presentation outline

- Is Phenomics a bandwagon?
- “Phenomics”: past and present
- Examples of various tools and applications
- Thoughts…
- Acknowledgements

Is Phenomics a bandwagon?

- A bandwagon has **three phases**: excitement, realization, and reality
- **Excitement** phase: period of hype, attention, funding, and participation.
- **Realization** phase: extensive research and evidence on technology/tool.
- **Reality** phase: (1) is successful, becomes part of mainstream practice in the discipline OR (2) if unsuccessful, it is abandoned.



Source: Bernardo (2016). TAG, 129(12)

Phenomics, in early 2000’s…

- “The term ‘phenomics’ is coined to describe, **in anticipation**, the **new field** that is likely to form from the behavioral and other **phenotypic analyses** designed to **obtain a large amount of information** on the varying effects **of genetic mutations**.”
  - Gerlai (2002; Trends in Neurosciences, v25(10))
- Intent was to match the genomic revolution to phenotyping revolution (by removing the phenotyping bottleneck)

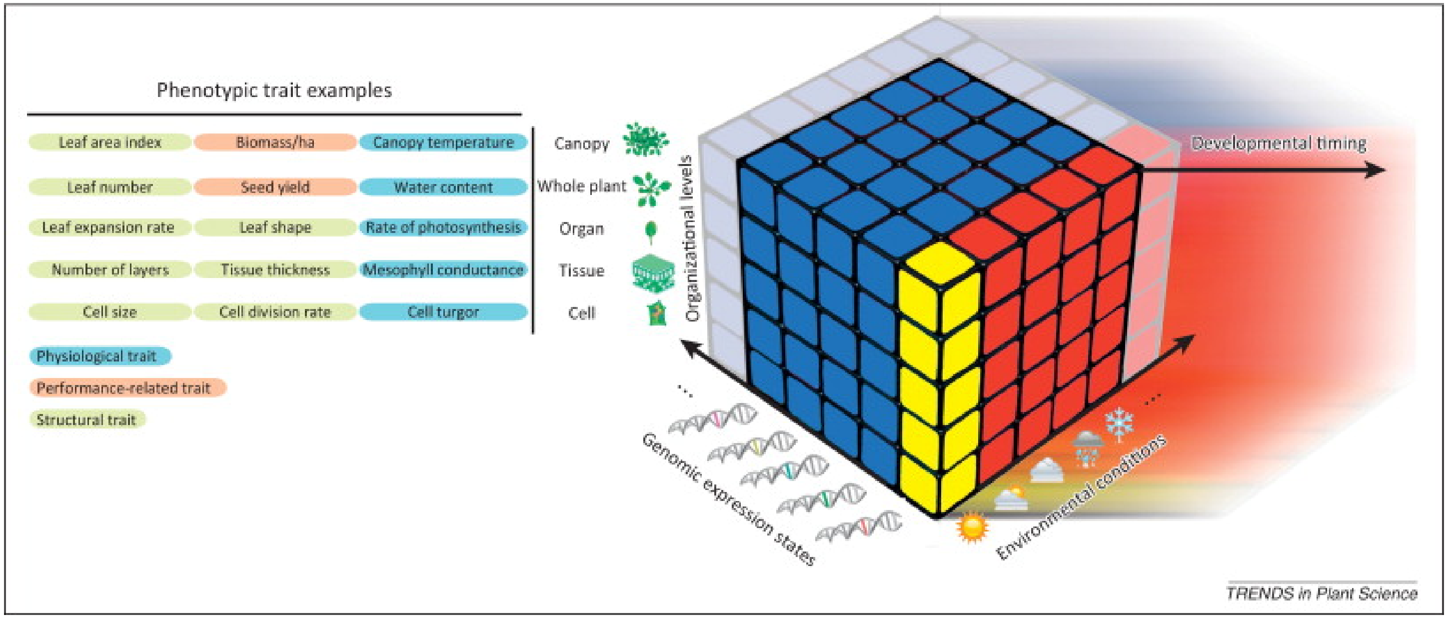
Post 2010, Phenomics definition has evolved….

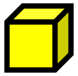
- Phenomics has been defined as the acquisition of high-dimensional phenotypic data on an organism-wide scale (Houle et al. 2010, Nature Review Genetics, 11)
- (Plant) Phenomics is the study of phenomes of multiple genotypes (Dhondt et al. 2013, TIPS 18(8))
  - Phenome: set of all possible phenotypes of a given genotype

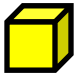
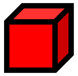
Connection with Plant breeding?

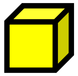
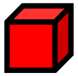
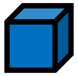
- # of plants or genotypes to phenotype is large; complex (morphological, maturity differences)
- We create new variation each year
- Measure several traits simultaneously (these traits vary in organizational scale – canopy, whole plant, tissue, cell level)
- Several environment of concurrent or non-concurrent testing
- Sometimes we are interested in time series measurements, for example diseases, physiology..

High-dimensional phenotypic data…



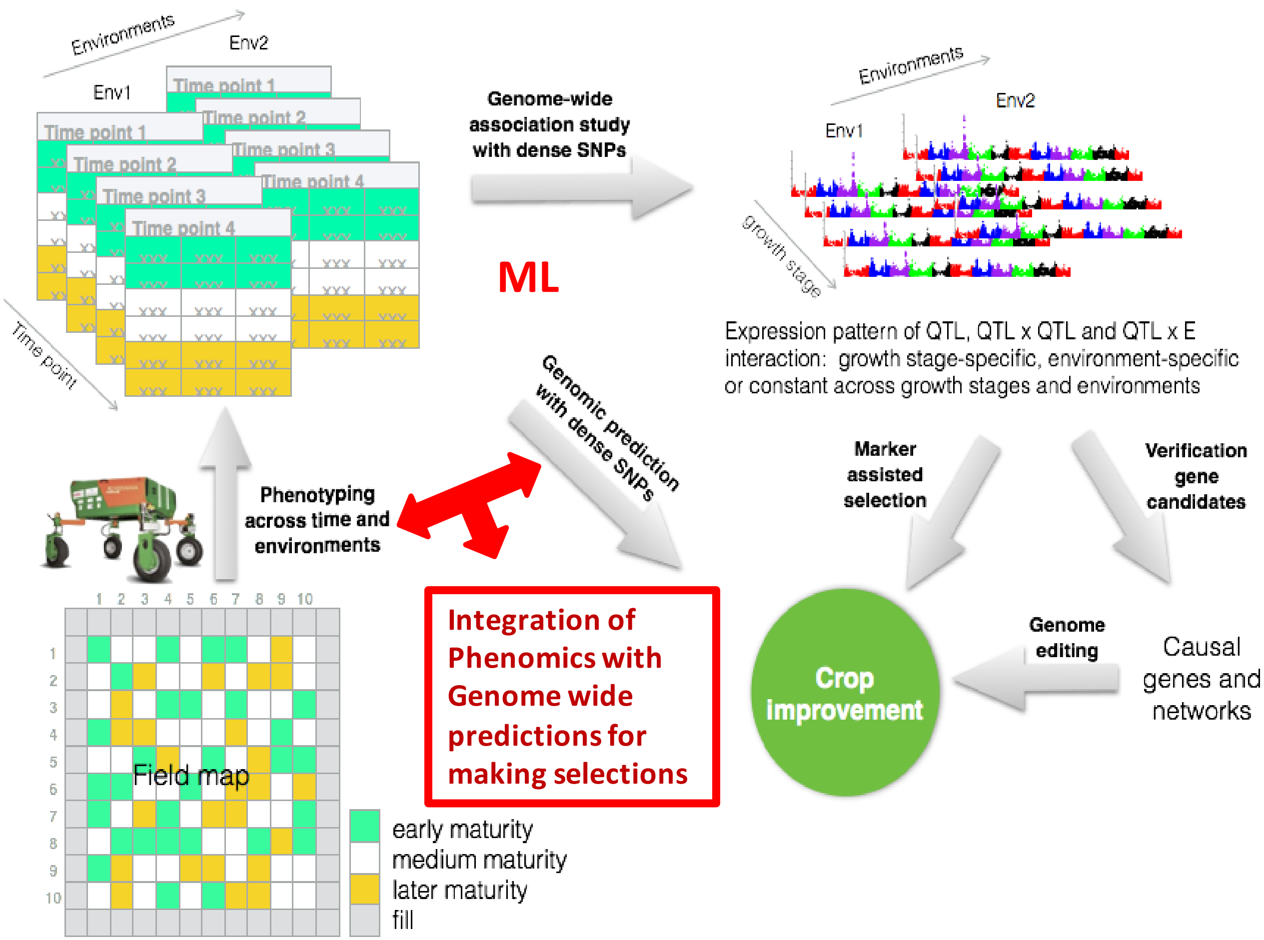
<u>Plant phenotyping</u> (shown as single column of  cubes) is the quantitative or qualitative investigation of traits (structural, performance based, physiological) at any organizational level, in a given genotype and a given environment.

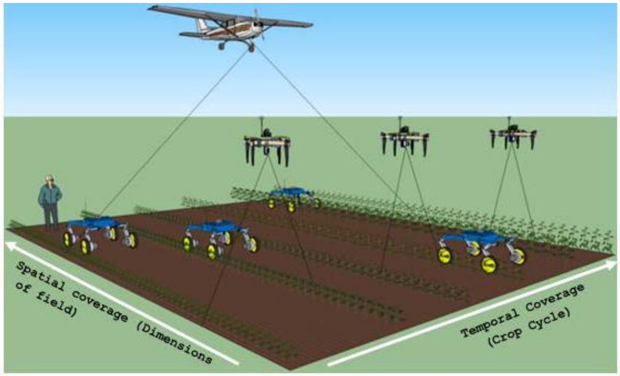
A **<u>phenome</u>** (shown by combination of  and  cubes) corresponds to all possible phenotypes under different environmental conditions of a given genotype.

<u>Plant phenomics</u> (shown by combination of  ,  ,  cubes) could be considered as the study of phenomes of multiple genotypes.

Dhondt et al. 2013, TIPS 18(8)

+ Spatio-temporal phenotyping





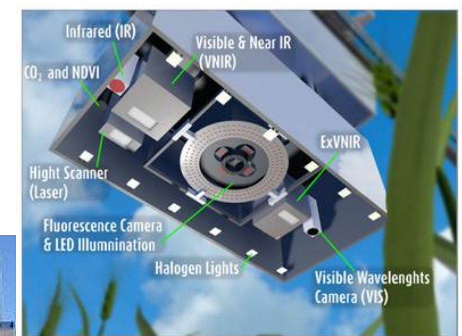
- Large scale phenotyping
- Multiple scales of phenotyping
- Limited timeframe
- Multi-dimensional
- Inter- and Intra-rater variability

Funding:

Monsanto Chair in Soybean Breeding; ISU PIIR

USDA NIFA – NSF

Examples of ground systems and their capabilities....



BoniRob: http://www.fieldrobot.com/event/wp-content/uploads/2016/06/Bonirob-16.jpg; In-between rows phenotyping: http://vigir.missouri.edu/FieldPhenotyping.htm; Apple orchard: http://www.freshfruitportal.com/news/2013/09/02/australian-researchers-branch-out-with-robot-farming/; Field phenomics (high clearance sprayer converted unit): http://www.fieldphenomics.org/research/vehicles; Lemnatec: http://www.lemnatec.com/products/hardware-solutions/scanalyzer-field/;

Automated vs manual phenotyping

nature COMMUNICATIONS

ARTICLE

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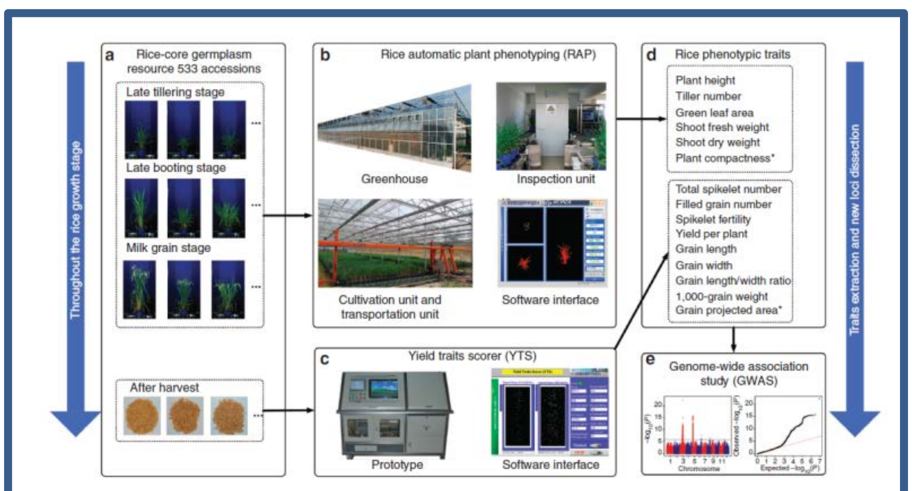
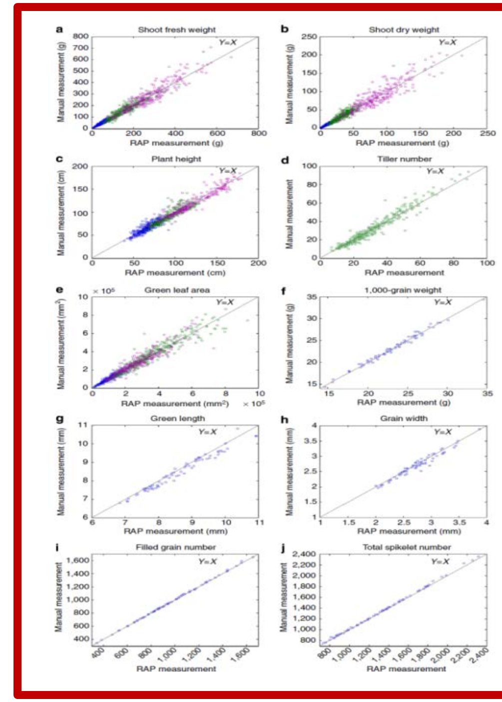
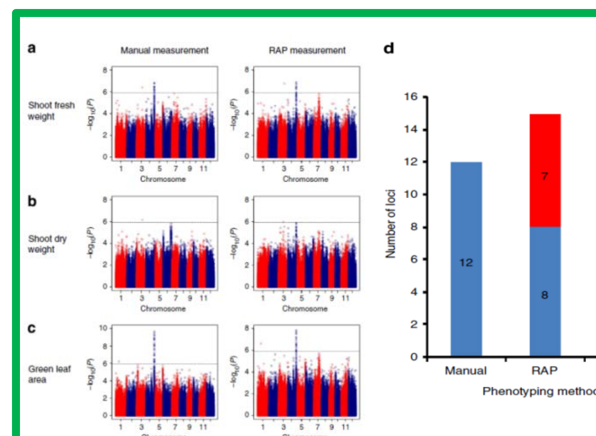
OPEN

Combining high-throughput phenotyping and genome-wide association studies to reveal natural genetic variation in rice

Wanneng Yang[1,2,3,4,*], Zilong Guo[2,*], Chenglong Huang[1,3,*], Lingfeng Duan[1,3,4,*], Guoxing Chen[5,*], Ni Jiang[1,3], Wei Fang[1,3], Hui Feng[1,3], Weibo Xie[2], Xingming Lian[2], Gongwei Wang[2], Qingming Luo[1,3], Qifa Zhang[2], Qian Liu[1,3] & Lizhong Xiong[2]



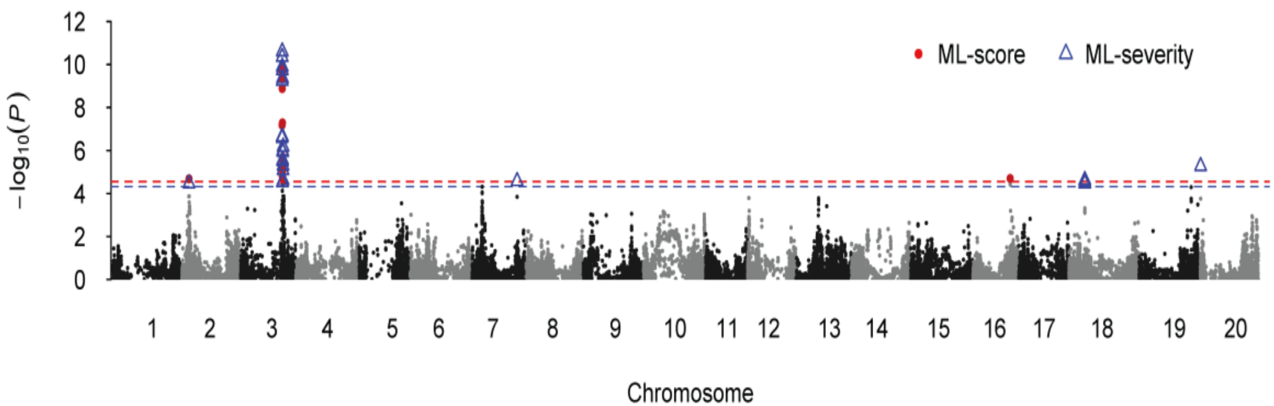


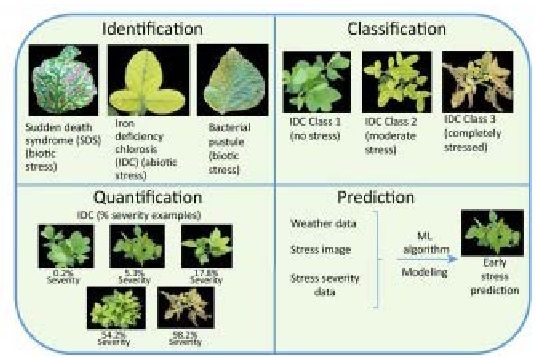


Source: Yang et al. 2014, Nature Comm, 5:5087

Phenomics: new insights, better predictions…

- >450 unique soybean PI accessions phenotyped (**IDC**) using tri-band channels to extract pixel information
- Deployed machine learning algorithms to generate ML-score (1-5 scale) and ML-severity (0-100 scale) for genome wide association
- ML identified useful candidate gene, not picked up by visual ratings





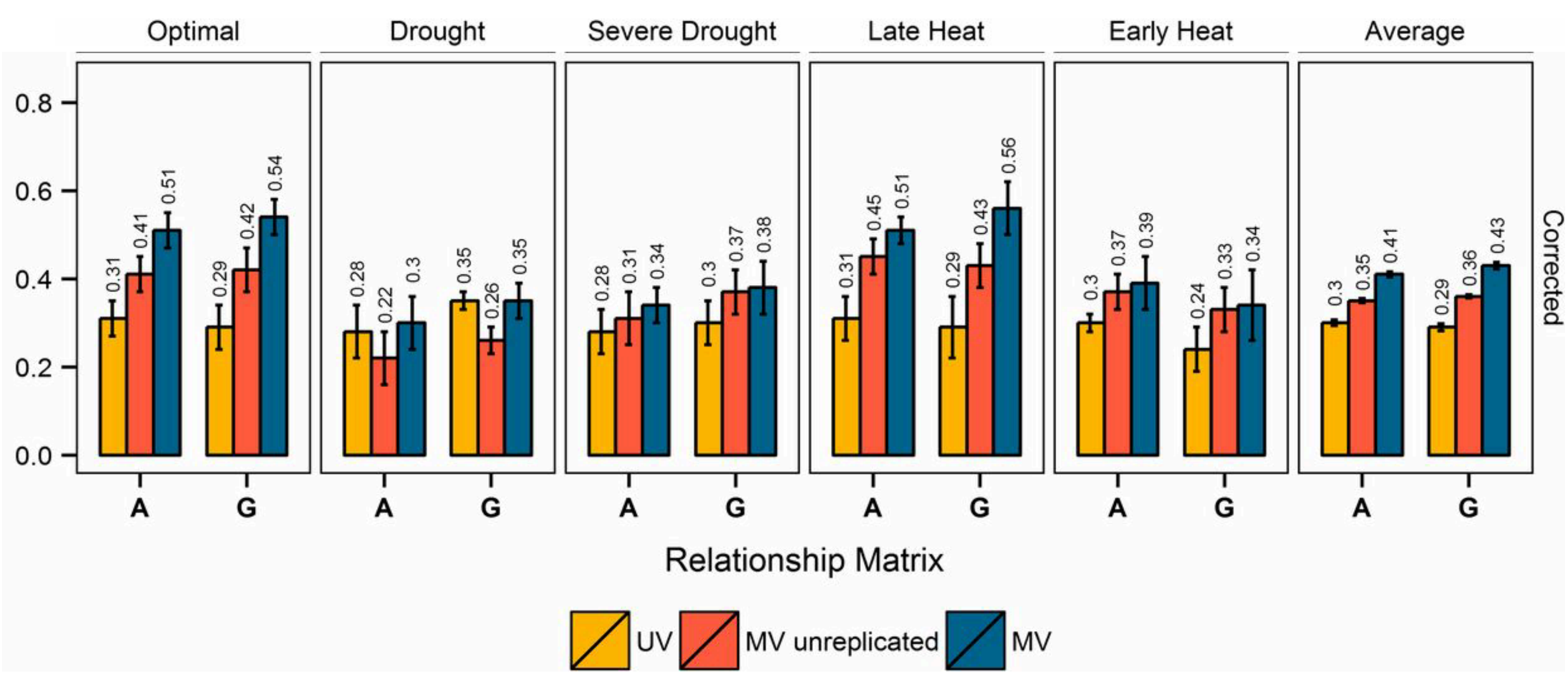
- Developed an ability to automated rating (to more traits..
- Improvements in prediction accuracy by integrating phenotyping information in prediction models

Source: Zhang et al. (2017) (Submitted), Singh et al. (2016) TIPS

Canopy Temperature and Vegetation Indices from High-Throughput Phenotyping Improve Accuracy of Pedigree and Genomic Selection for Grain Yield in Wheat

Jessica Rutkoski,*,†,‡,1 Jesse Poland,§ Suchismita Mondal,‡ Enrique Autrique,‡ Lorena González Pérez,‡ José Crossa,‡ Matthew Reynolds,‡ and Ravi Singh‡

*International Programs, College of Agriculture and Life Sciences, and †Plant Breeding and Genetics Section, School of Integrated Plant Sciences, Cornell University, Ithaca, New York 14853, ‡Global Wheat Program, International Maize and Wheat Improvement Center (CIMMYT), Ciudad de Mexico, 06600, Mexico, and §Department of Plant Pathology, Kansas State University, Manhattan, Kansas 66506



Source: Rutoski et al. 2016. G3, 6, 2799-2808

More easily capturing traits previously not possible..

jove Journal of Visualized Experiments www.jove.com

Video Article

Tomato Analyzer: A Useful Software Application to Collect Accurate and Detailed Morphological and Colorimetric Data from Two-dimensional Objects

Gustavo R. Rodríguez[1], Jennifer B. Moyseenko[1], Matthew D. Robbins[1], Nancy Huarachi Morejón[1], David M. Francis[1], Esther van der Knaap[1]

[1]Department of Horticulture and Crop Science, The Ohio State University

Correspondence to: Esther van der Knaap at vanderknaap.1@osu.edu

URL: http://www.jove.com/video/1856
DOI: doi:10.3791/1856

Keywords: Plant Biology, Issue 37, morphology, color, image processing, quantitative trait loci, software

Date Published: 3/16/2010

Citation: Rodríguez, G.R., Moyseenko, J.B., Robbins, M.D., Huarachi Morejón, N., Francis, D.M., van der Knaap, E. Tomato Analyzer: A Useful Software Application to Collect Accurate and Detailed Morphological and Colorimetric Data from Two-dimensional Objects. *J. Vis. Exp.* (37), e1856, doi:10.3791/1856 (2010).

- measures 37 attributes
- Can this be done by human raters?

Source: Rodriquez et al. 2010. *J. Vis. Exp.* 37: e1856

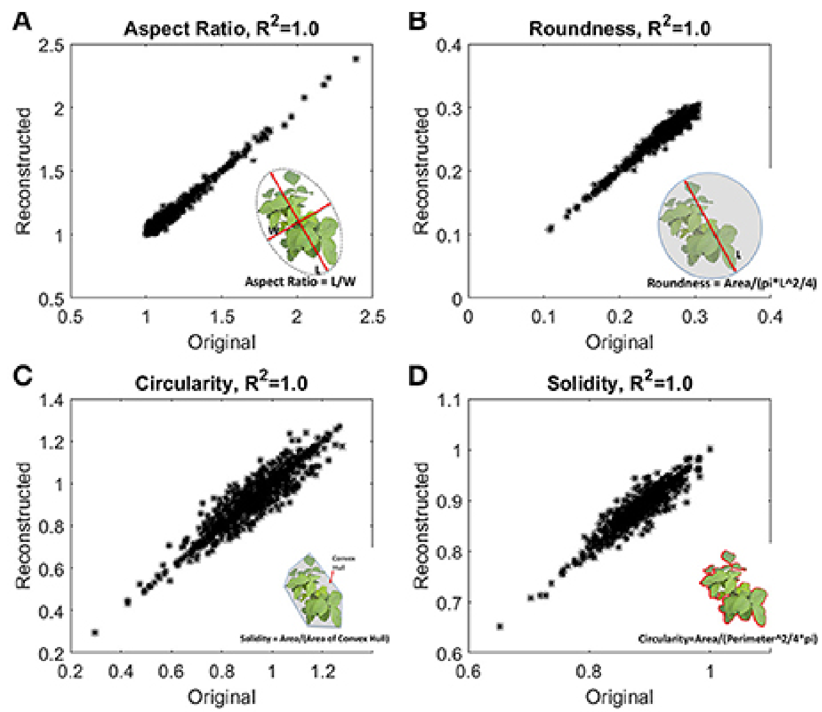
More easily capturing traits previously not possible… (shape descriptors, lifecycle)

frontiers in Plant Science

Deploying Fourier Coefficients to Unravel Soybean Canopy Diversity

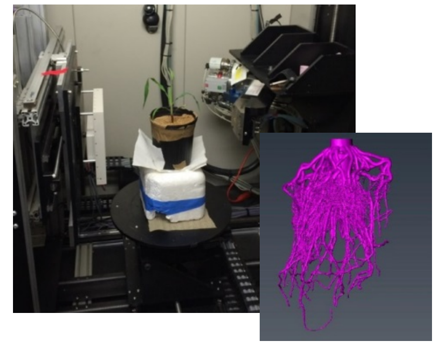
Talukder Z. Jubery[1], Johnathon Shook[2], Kyle Parmley[2], Jiaoping Zhang[2], Hsiang S. Naik[1], Race Higgins[2], Soumik Sarkar[1], Arti Singh[2], Asheesh K. Singh[2] and Baskar Ganapathysubramanian[1,3,4]**

[1] Department of Mechanical Engineering, Iowa State University, Ames, IA, USA, [2] Department of Agronomy, Iowa State University, Ames, IA, USA, [3] Department of Electrical and Computer Engineering, Iowa State University, Ames, IA, USA, [4] Plant Sciences Institute, Iowa State University, Ames, IA, USA



Source: Jubery et al. 2017. FIPS, 7:2066

Going where we dared not go before - Root Exploration



Computed Tomography (CT); Magnetic Resonance Imaging (MRI)

ground penetrating radar

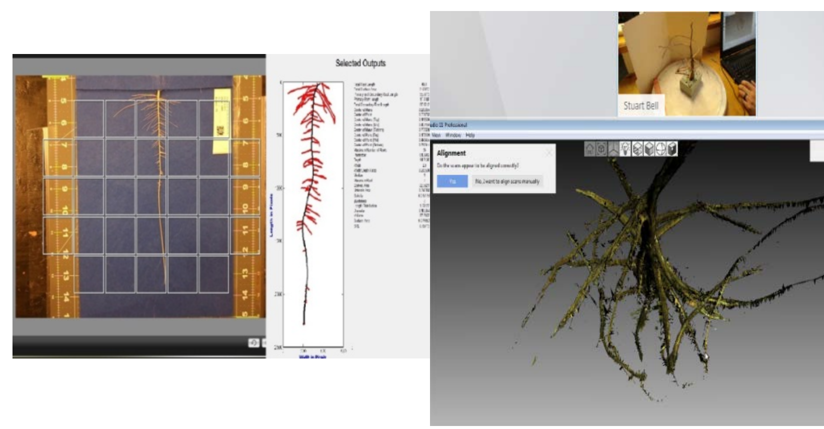
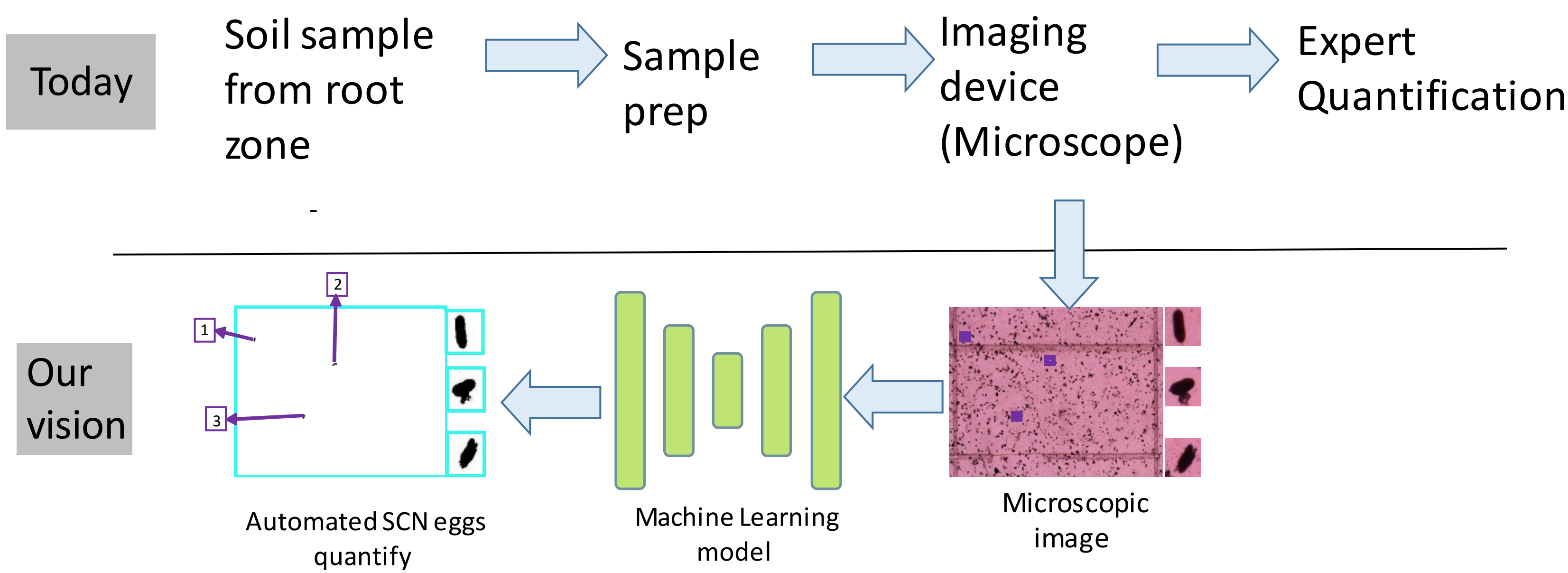


Image source: Topp et al, 2016; Kochian, 2016, Falk (2017, ISU)

Funding:
Monsanto Chair in Soybean Breeding; Baker Center (ISU)
NSF (EAGER)
IA Soybean Research Center

Finding new applications (microscope level); No need to re-invent the wheel..



Source: Akintayo et al. (ISU)

Soybean breeders moving to technology adoption

Computers and Electronics in Agriculture 128 (2016) 181–192

Contents lists available at ScienceDirect

Computers and Electronics in Agriculture

journal homepage: www.elsevier.com/locate/compag

Original papers

A multi-sensor system for high throughput field phenotyping in soybean and wheat breeding

Geng Bai [a], Yufeng Ge [a,*], Waseem Hussain [b], P. Stephen Baenziger [b], George Graef [b]

[a] Department of Biological Systems Engineering, University of Nebraska-Lincoln, Lincoln, NE 68583, USA
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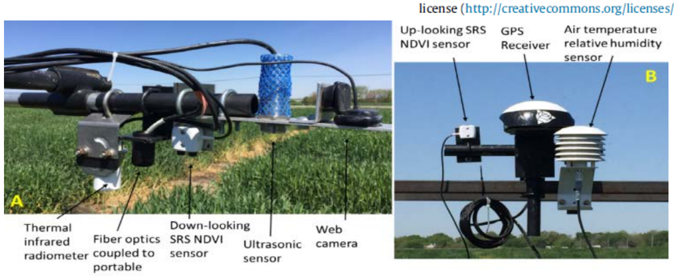
Keywords:
High throughput field phenotyping
Canopy reflectance
Canopy temperature
LabVIEW
RGB image

ABSTRACT

Collecting plant phenotypic data with sufficient resolution (in both space and time) and accuracy represents a long standing challenge in plant science research, and has been a major limiting factor for the effective use of genomic data for crop improvement. This is particularly true in plant breeding where collecting large-scale field-based plant phenotypes can be very labor intensive and costly. In this paper we reported a multi-sensor system for high throughput phenotyping in plant breeding. The system comprised five sensor modules (ultrasonic distance sensors, thermal infrared radiometers, NDVI sensors, portable spectrometers, and RGB web cameras) to measure crop canopy traits from field plots. A GPS was used to geo-reference the sensor measurements. Two environmental sensors (a solar radiation sensor and air temperature/relative humidity sensor) were also integrated into the system to collect simultaneous environmental data. A LabVIEW program was developed to control and synchronize measurements from all sensor modules and stored sensor readings in the host computer. Canopy reflectance spectra (by portable spectrometers) were post processed to extract NDVI and red-edge NDVI spectral indices; and RGB images were post processed to extract canopy green pixel fraction (as a proxy for biomass). The sensor system was tested in a soybean and wheat field trial. The results showed strong correlations among the sensor-based plant traits at both early and late growing season. Significant correlations were also found between the sensor-based traits and final grain yield at the early season (Pearson's correlation coefficient r ranged from 0.41 to 0.55) and late season (r from 0.55 to 0.70), suggesting the potential use of the sensor system to assist in phenotypic selection for plant breeding. The sensor system performed satisfactorily and robustly in the field tests. It was concluded that the sensor system could be a powerful tool for plant breeders to collect field-based, high throughput plant phenotyping data.



Remote Sensing of Environment 187 (2016) 91–101

Contents lists available at ScienceDirect

Remote Sensing of Environment

journal homepage: www.elsevier.com/locate/rse

Development of methods to improve soybean yield estimation and predict plant maturity with an unmanned aerial vehicle based platform

Neil Yu [a], Liujun Li [b], Nathan Schmitz [a], Lei F. Tian [b], Jonathan A. Greenberg [c], Brian W. Diers [a,*]

[a] Department of Crop Sciences, University of Illinois at Urbana-Champaign, 1101 W. Peabody Drive, Urbana, IL 61801, USA
[b] Department of Agricultural and Biological Engineering, University of Illinois at Urbana-Champaign, 1304 W. Pennsylvania Avenue, Urbana, IL 61801, USA
[c] Department of Geography and Geographic Information Science, University of Illinois at Urbana-Champaign, 605 East Springfield Avenue, Champaign, IL, USA

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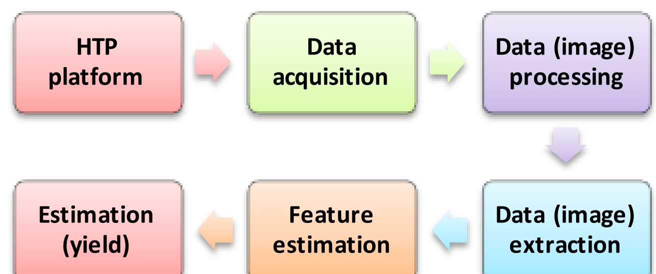
Keywords:
Soybean
Breeding efficiency
UAV
Multispectral image
Object classification

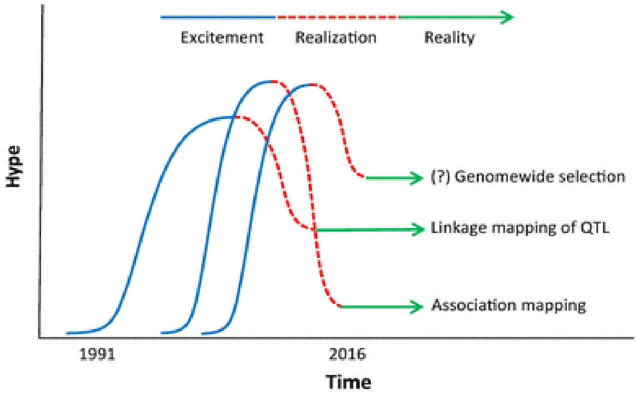
ABSTRACT

Advances in phenotyping technology are critical to ensure the genetic improvement of crops meet future global demands for food and fuel. Field-based phenotyping platforms are being evaluated for their ability to deliver the necessary throughput for large scale experiments and to provide an accurate depiction of trait performance in real-world environments. We developed a dual-camera high throughput phenotyping (HTP) platform on an unmanned aerial vehicle (UAV) and collected time course multispectral images for large scale soybean [*Glycine max* (L.) Merr.] breeding trials. We used a supervised machine learning model (Random Forest) to measure crop geometric features and obtained high correlations with final yield in breeding populations ($r = 0.82$). The traditional yield estimation model was significantly improved by incorporating plot row length as covariate ($p < 0.01$). We developed a binary prediction model from time-course multispectral HTP image data and achieved over 93% accuracy in classifying soybean maturity. This prediction model was validated in an independent breeding trial with a different plot type. These results show that multispectral data collected from the UAV-based HTP platform could improve yield estimation accuracy and maturity recording efficiency in a modern soybean breeding program.



Numerous other examples of breeder engagement in similar activities: Indiana, Iowa, Kansas, Missouri, …….

Is Phenomics a bandwagon or a discipline?



- A bandwagon has **three phases**: excitement, realization, and reality
- **Excitement** phase: period of hype, attention, funding, and participation. (**YES**)
- **Realization** phase: extensive research and evidence on technology/tool. (**YES**)
- **Reality** phase: (1) is successful, becomes part of mainstream practice in the discipline OR (2) if unsuccessful, it is abandoned. (**TBD**)

While the Linkage, Association mapping, GWP are tools/techniques, "Phenomics" is not a tool… (**is it a field of study or perhaps a discipline similar to genomics?**)

New definition?: Phenomics is the discipline that studies phenomes of multiple genotypes through acquisition of high-dimensional phenotypic data on an organism-wide scale?

"**The culture of the discipline, for example, consists of a "knowledge tradition" that includes categories of thought, a common vocabulary, and related codes of conduct.**"

It will require continued participation of (and partnerships between) breeders, scientists, engineers, statisticians; and linkages with funding agencies!!!

(Big Data and ML/DL are here to stay; new tools applicable in phenomics are being built) **Producer, Private, Public partnership to shape this emerging discipline**

Source: Bernardo (2016). TAG, 129(12); Frost and Jean, 2003. The Journal of Higher Education, 74(2): 119-149

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- Iowa Soybean Association
- Iowa State University (including, PIIR DDS: D3AI)
- Monsanto Chair in Soybean Breeding
- R.F. Baker Center for Plant breeding
- USDA NIFA
- NSF EAGER

People

- Staff, research fellows, graduate and undergraduate students
- Colleagues (A. Singh, B Ganapathysubramanian, S Sarkar, S Bhattacharya, G Tylka, L Cademartiri, G Beattie, …+++..)

THANK YOU!!