

Advanced Plant Breeding Symposium
Sept 13, 2:15 p.m. – 2:45 p.m.

Continuing the Journey of Excellence and Innovation in Plant Breeding

Jianming Yu

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Plant Sciences Institute Faculty Scholar
Raymond F. Baker Center for Plant Breeding

Design is a plan or specification for the construction of an object or system or for the implementation of an activity or process.

The New York Times

IBM's *Design*-Centered Strategy to Set
Free the Squares



THE EVOLUTION OF DESIGN THINKING

IT'S NO LONGER JUST FOR
PRODUCTS. EXECUTIVES ARE
USING THIS APPROACH
TO DEVISE STRATEGY
AND MANAGE
CHANGE.

PAGE 55



ABOUT DESIGN THINKING

Design Thinking is a human-centered mindset and problem-solving methodology that can be applied within and beyond the design function in any business, industry or profession to address complex problems and achieve remarkable results.



How to feed the 10 billion?

How to combine genome editing and genomic selection?



How to Feed the 10 billion?

REVIEW ARTICLE

<https://doi.org/10.1038/s41587-019-0152-9>

nature
biotechnology

37: 744–754 (2019)

Breeding crops to feed 10 billion

Lee T. Hickey^{1*}, Amber N. Hafeez², Hannah Robinson³, Scott A. Jackson⁴, Soraya C. M. Leal-Bertioli⁵, Mark Tester⁶, Caixia Gao⁷, Ian D. Godwin⁸, Ben J. Hayes⁹ and Brande B. H. Wulff^{2*}

Crop improvements can help us to meet the challenge of feeding a population of 10 billion, but can we breed better varieties fast enough? Technologies such as genotyping, marker-assisted selection, high-throughput phenotyping, genome editing, genomic selection and de novo domestication could be galvanized by using speed breeding to enable plant breeders to keep pace with a changing environment and ever-increasing human population.

Over the next 30 years, the global human population is expected to grow by 25% and reach 10 billion. Conventional breeding approaches have so far produced nutritious crops with high yields that can be harvested mechanically to meet the food needs of the growing population. But the current pace of yield increase for major crops, including wheat (*Triticum aestivum*), rice (*Oryza sativa*) and maize (*Zea mays*), is insufficient to meet future demand^{1,2}. Breeders and plant scientists are under pressure to improve existing crops and develop new crops that are higher yielding, more nutritious, pest- and disease-resistant and climate-smart.

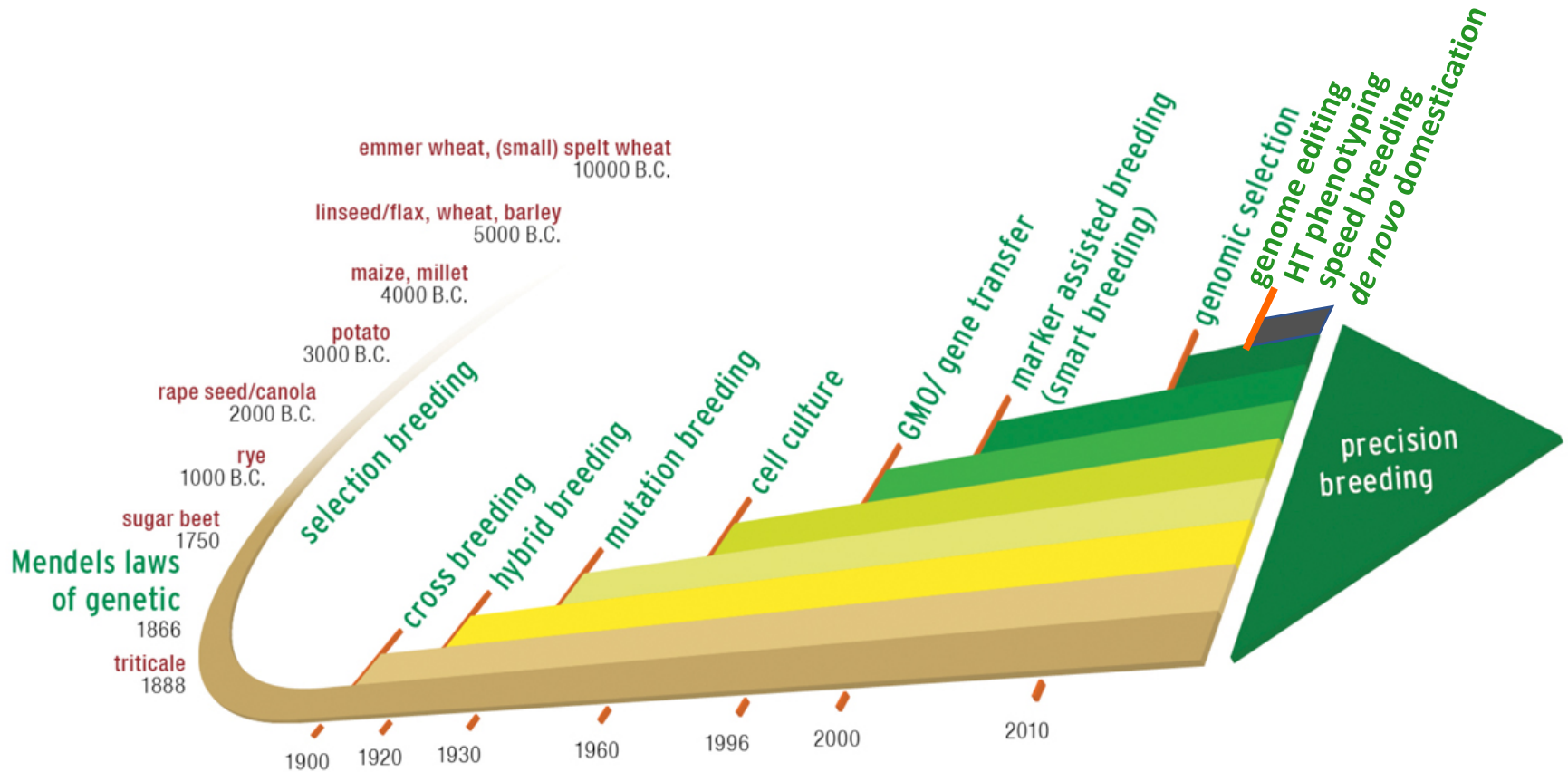
the possibility of growing rapid cycling wheat under constant light on space stations. This joint effort resulted in the development of 'USU-Apogee', a dwarf wheat line bred for rapid cycling¹⁰. Meanwhile, Russian scientists proposed testing 'space mirrors' in 1993 to turn night into day and theoretically improve agricultural productivity on Earth. In 1990, the effects of light-emitting diodes (LEDs) on plant growth were evaluated at the University of Wisconsin¹¹, and continuous improvements in LED technology¹² have substantially reduced the cost of indoor plant propagation systems that increase crop productivity¹³.

Inspired by NASA's work, researchers at the University of

Sequencing & Genotyping
Genomic Selection
Genome Editing
HT Phenotyping
Speed Breeding
de novo Domestication

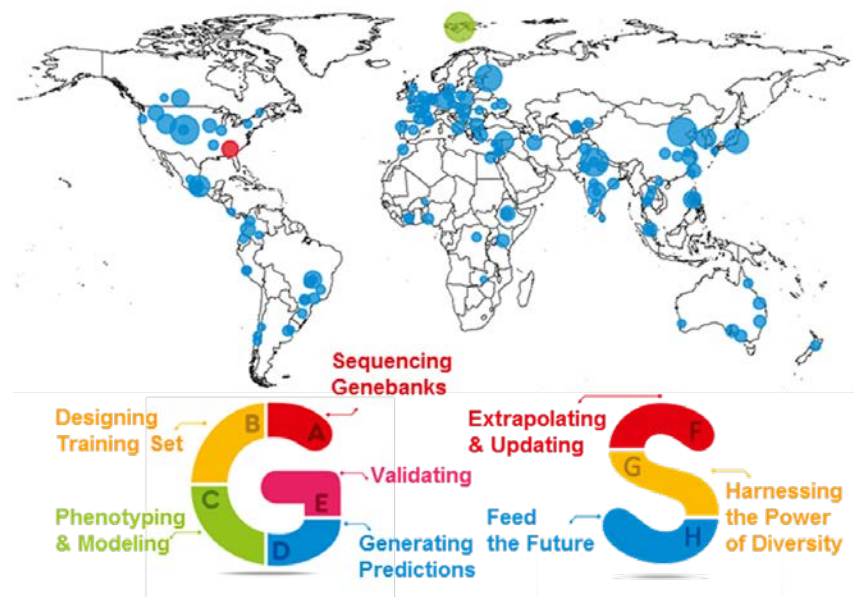
– NBT 37: 744–754 (2019)

Continuing the Journey of Excellence and Innovation in Plant Breeding



How to design a comprehensive strategy to mine the natural heritage stored in numerous gene banks?

7.4 million plant accessions are stored in about 1750 genebanks



nature
plants

ARTICLES

PUBLISHED: 3 OCTOBER 2016 | ARTICLE NUMBER: 16150 | DOI: 10.1038/NPLANTS.2016.150

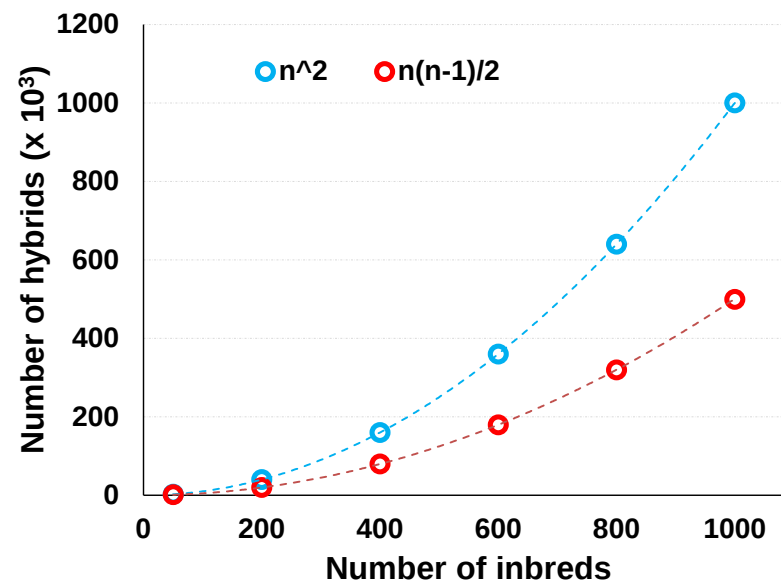
Genomic prediction contributing to a promising global strategy to turbocharge gene banks

Xiaoqing Yu¹, Xianran Li¹, Tingting Guo¹, Chengsong Zhu¹, Yuye Wu², Sharon E. Mitchell³,
Kraig L. Roozeboom², Donghai Wang², Ming Li Wang⁴, Gary A. Pederson⁴, Tesfaye T. Tesso²,
Patrick S. Schnable¹, Rex Bernardo⁵ and Jianming Yu^{1*}

The 7.4 million plant accessions in gene banks are largely underutilized due to various resource constraints, but current genomic and analytic technologies are enabling us to mine this natural heritage. Here we report a proof-of-concept study to integrate genomic prediction into a broad germplasm evaluation process. First, a set of 962 biomass sorghum accessions were chosen as a reference set by germplasm curators. With high throughput genotyping-by-sequencing (GBS), we genetically characterized this reference set with 340,496 single nucleotide polymorphisms (SNPs). A set of 299 accessions was selected as the training set to represent the overall diversity of the reference set, and we phenotypically characterized the training set for biomass yield and other related traits. Cross-validation with multiple analytical methods using the data of this training set indicated high prediction accuracy for biomass yield. Empirical experiments with a 200-accession validation set chosen from the reference set confirmed high prediction accuracy. The potential to apply the prediction model to broader genetic contexts was also examined with an independent population. Detailed analyses on prediction reliability provided new insights into strategy optimization. The success of this project illustrates that a global, cost-effective strategy may be designed to assess the vast amount of valuable germplasm archived in 1,750 gene banks.

Nature Plants 2016, 2:16150

*How to
efficiently
explore the
enormous
inference space
of genetic
combinations?*



CellPress
PARTNER JOURNAL

Molecular Plant
Research Article

Optimal Designs for Genomic Selection in Hybrid Crops

Tingting Guo¹, Xiaoqing Yu¹, Xianran Li¹, Haozhe Zhang², Chengsong Zhu¹, Sherry Flint-Garcia³, Michael D. McMullen³, James B. Holland⁴, Stephen J. Szalma⁴, Randall J. Wisser⁵ and Jianming Yu^{1,*}

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⁴USDA-ARS and Department of Crop and Soil Sciences, North Carolina State University, Raleigh, NC 27695, USA

⁵Department of Plant and Soil Sciences, University of Delaware, Newark, DE 19716, USA

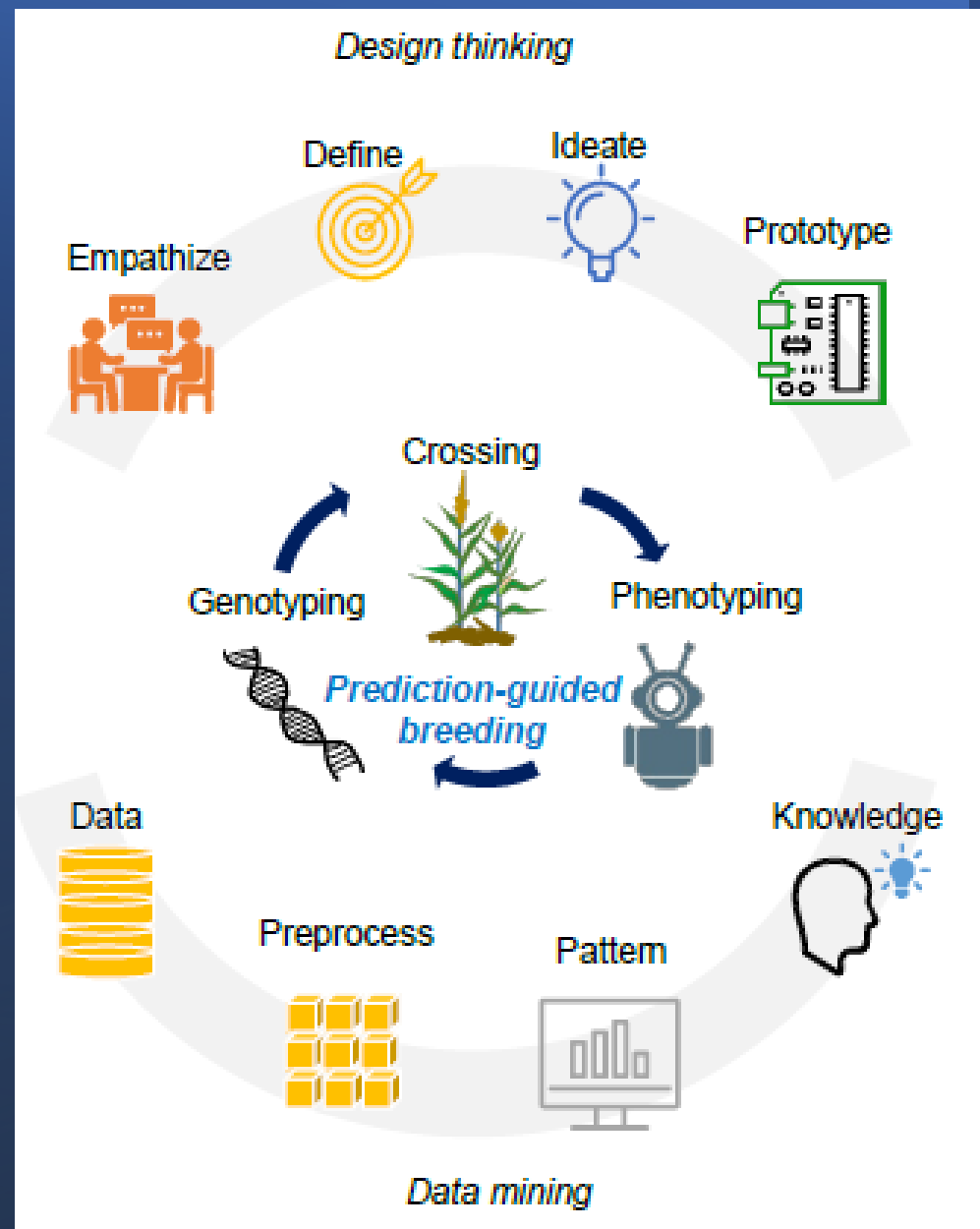
*Correspondence: Jianming Yu (jmyu@iastate.edu)

<https://doi.org/10.1016/j.molp.2018.12.022>

ABSTRACT

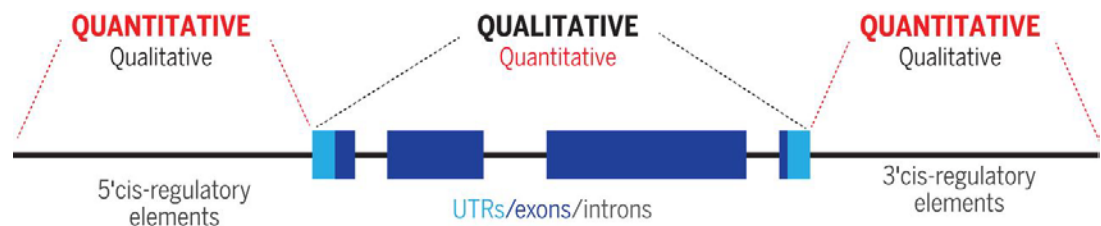
Improved capacity of genomics and biotechnology has greatly enhanced genetic studies in different areas. Genomic selection exploits the genotype-to-phenotype relationship at the whole-genome level and is being implemented in many crops. Here we show that design-thinking and data-mining techniques can be leveraged to optimize genomic prediction of hybrid performance. We phenotyped a set of 276 maize hybrids

Molecular Plant 2019, 12:390-401



What does Genome Editing Offer?

- “Generating a wide range of novel alleles and associated quantitative variation that can be selected to fit specific genotypic background or environmental needs.”
 - Generations of regular backcrossing
 - Linkage drag
- Multiple edits in a single genotypic background may be possible.



Qualitative Changes

New loss-of-function alleles into old and new crops
Generating identical alleles in elite backgrounds
Introduction of species-specific gene modifications
e.g., Male sterility for hybrid seed production, disease resistance, allergen or toxin removal, etc.

Quantitative Changes

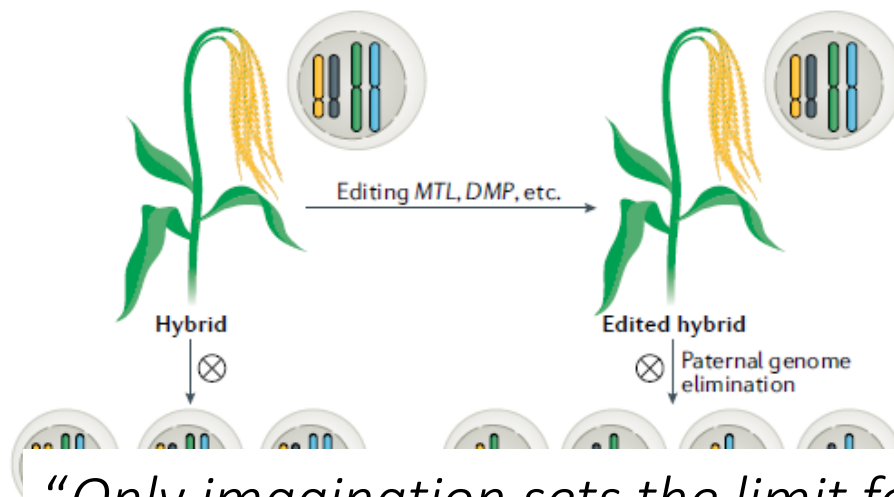
Generating allelic series for phenotypic selection
Base edits or in-frame deletions in coding regions
Interfering with RNA or protein stability
Modifying cis-regulatory elements (activators/repressors)

Applications of CRISPR–Cas in agriculture and plant biotechnology

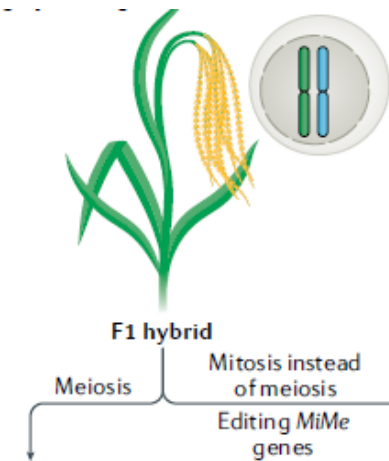
Haocheng Zhu^{1,2,3}, Chao Li^{1,2,3} and Caixia Gao^{1,2} 

Nature Review
Mol Cell Biology 2020
21:661-677

Haploid Induction

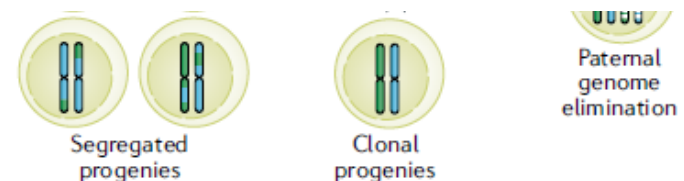
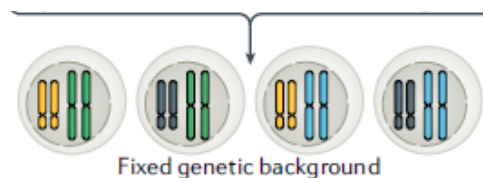


Fixing Hybrid Vigor



“Only imagination sets the limit for what this chemical tool that is too small to be visible with our eyes can be used for future.”

- Introduction given by Pernilla Stafshede during the announcement of the 2020 Nobel Prize in Chemistry



High-Throughput CRISPR/Cas9 Mutagenesis Streamlines Trait Gene Identification in Maize

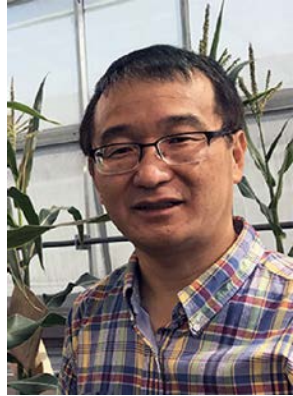
Plant Cell 2020,
32:1397–1413

Multiplexed CRISPR/Cas9-based high-throughput targeted mutagenesis with genetic mapping and genomic approaches to target 743 candidate genes

412 edited sequences covering 118 genes were precisely identified from individuals showing clear phenotypic changes.

The integration of forward and reverse genetics via a targeted mutagenesis library promises rapid validation of important agronomic genes for crops with complex genomes.

Grand Challenges in Genome Editing in Plants



Overcoming Species- and Genotype-Dependent Transformation

Broadening Targets for Crop Improvement through Genome Editing

Achieving High-Efficiency Base Replacement

Toward Better Public Perception and Regulatory Oversight of Genome Editing in Agriculture

Grand Challenges in Genome Selection in Plants

Generating whole-organism performance predictions across a plant's life span

Building systems prediction beyond the target population of environments

Integrating new technologies to boost the accuracy and efficiency of genomic selection

Balancing short-term genetic gains and long-term sustainability

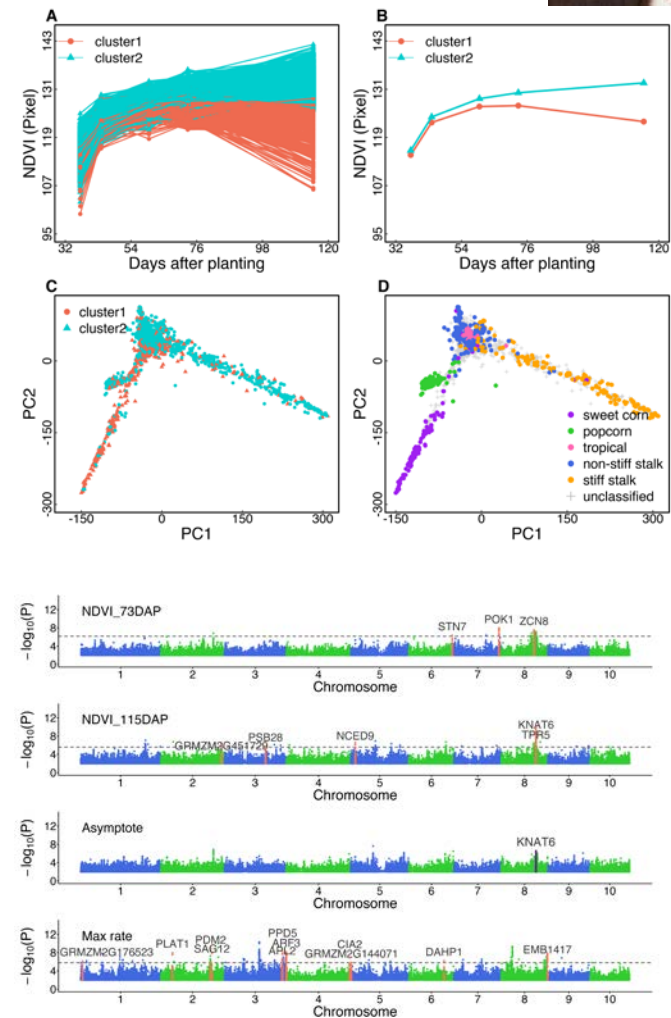
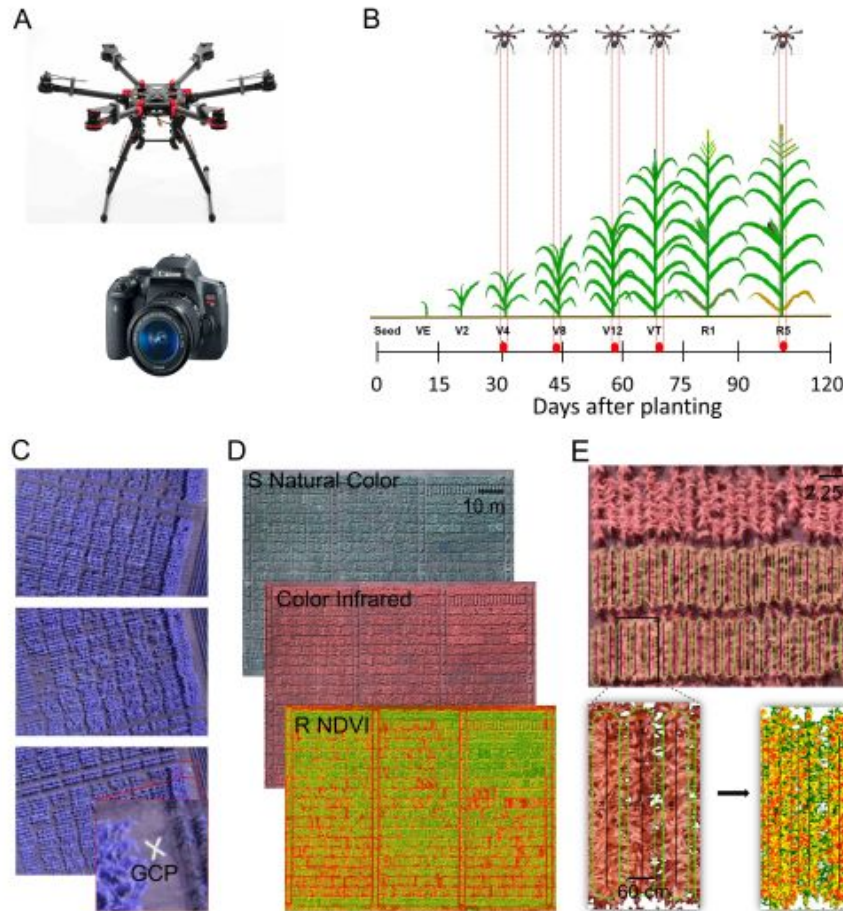
Synergy Between Genome Editing & Genomic Selection

- “Engineered alleles” generated by Genome Editing leverage the knowledge of gene and pathway information.
 - Can the processes of discovery and engineering be combined to be self-sustainable?
- General genotypic backgrounds, from which specific sets of genotypes are to be selected and edited, can be improved through genomic selection.
 - Could the intensive application of genomic selection and resulted narrower genetic diversity be a problem to fully realize the potential of “engineered alleles”?

Synergy Between Genome Editing & Genomic Selection

- Once engineered alleles are incorporated into the breeding pool, genomic selection continues to work on both types of genetic variants: natural and engineered.
 - Is there a right balance between the two? How much can design play a role beforehand?
- Genomic prediction to quantify which genotypes are likely to be readily edited, and to predict what might result from genome editing.
 - How is editability controlled and how much modification can be done?

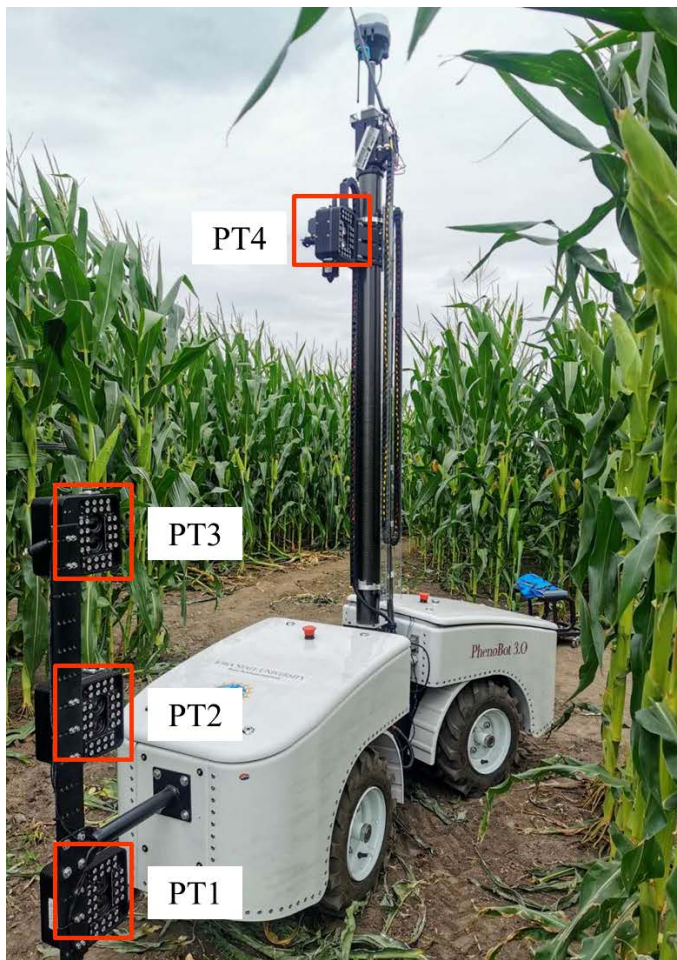
High Throughput Phenotyping



High Throughput Phenotyping



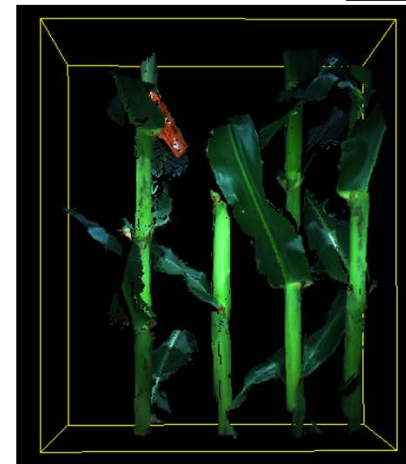
PhenoBot 3.0



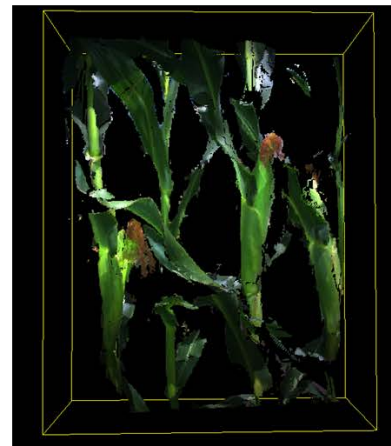
(a)



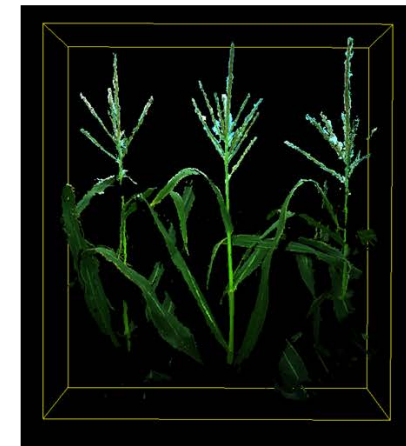
(b)



(c)



(d)



(e)

What does HTP Offer?

Accuracy and efficiency in phenotyping

Potential for phenomic selection

Understand the developmental process

Generate input data to feed into crop growth models

Ask questions that we have not asked in the past:

- Transient QTL versus stable QTL
- Developmental trajectory
- Environmental effect and developmental window

AIIRA: AI Institute for Resilient Agriculture



Baskar
Ganapathysubramanian

Aiira.iastate.edu



AI-driven digital twin – virtual representation
integrating knowledge & data

Explore foundational questions in AI

USDA Science Blueprint drives applications in
breeding and production agriculture

Social science focus to ensure adoption and long-
term payoffs

Creating a diverse, AI-aware workforce

Building a resilient US agricultural system

IOWA STATE
UNIVERSITY

Carnegie
Mellon
University

THE UNIVERSITY
OF ARIZONA

Mizzou
University of Missouri

GEORGE
MASON
UNIVERSITY

UNIVERSITY OF
Nebraska
Lincoln

NYU

IOWA SOYBEAN
Association

USDA

United States
Department of
Agriculture



National Institute
of Food and
Agriculture

De Novo Domestication: An Alternative Route toward New Crops for the Future

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²National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan 430070, China

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<https://doi.org/10.1016/j.molp.2019.03.016>

ABSTRACT

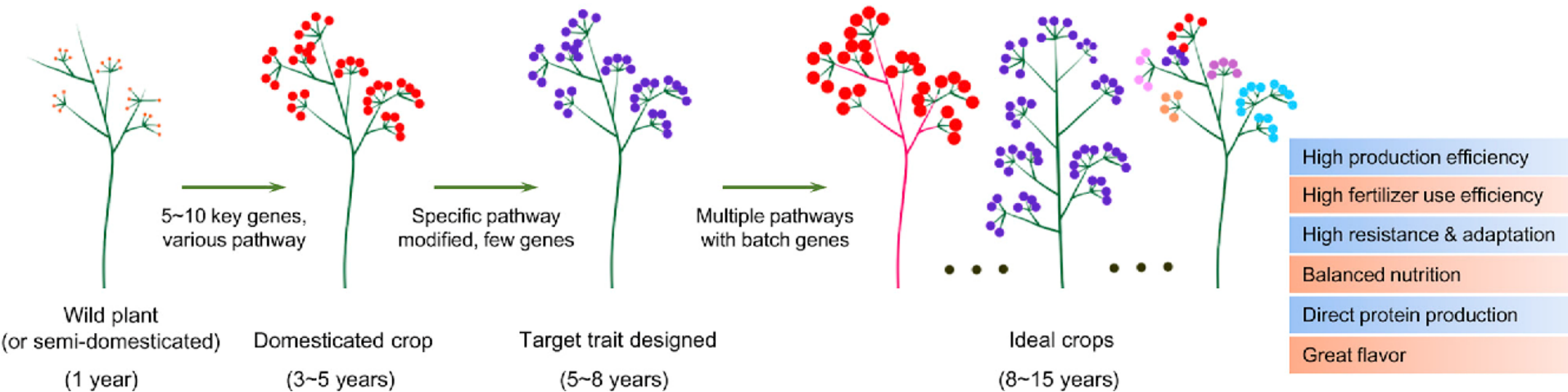
Current global agricultural production must feed over 7 billion people. However, productivity varies greatly across the globe and is under threat from both increased competitions for land and climate change and associated environmental deterioration. Moreover, the increase in human population size and dietary changes are putting an ever greater burden on agriculture. The majority of this burden is met by the cultivation of a very small number of species, largely in locations that differ from their origin of domestication. Recent technological advances have raised the possibility of *de novo* domestication of wild plants as a viable solution for designing ideal crops while maintaining food security and a more sustainable low-input agriculture. Here we discuss how the discovery of multiple key domestication genes alongside the development of technologies for accurate manipulation of several target genes simultaneously renders *de novo* domestication a route toward crops for the future.

Key words: *De Novo* Domestication, Redomestication, New Crops, Genome Editing, Food Security, Sustainable Agriculture

Fernie A.R. and Yan J. (2019). *De Novo* Domestication: An Alternative Route toward New Crops for the Future. Mol. Plant. 12, 615–631.

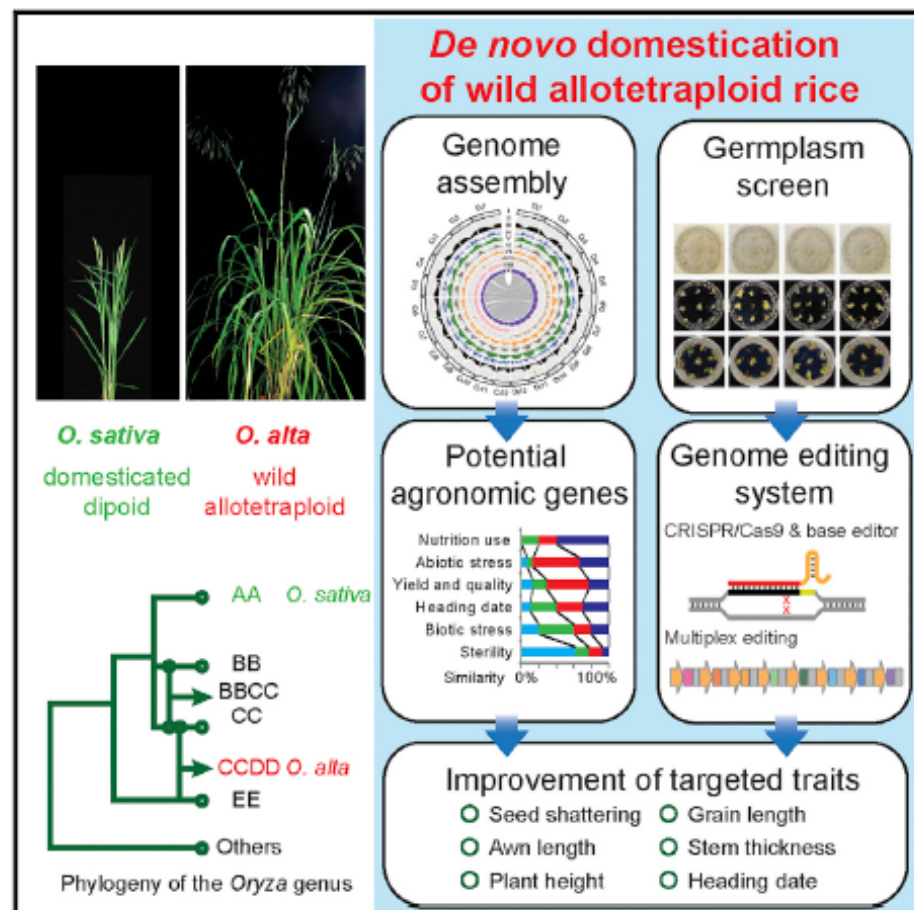
A Roadmap and Timeline for Ideal Crop Breeding

Molecular Plant 12:615-631



A route to *de novo* domestication of wild allotetraploid rice

Graphical Abstract



Authors

Hong Yu, Tao Lin, Xiangbing Meng, ..., Caixia Gao, Chengzhi Liang, Jiayang Li

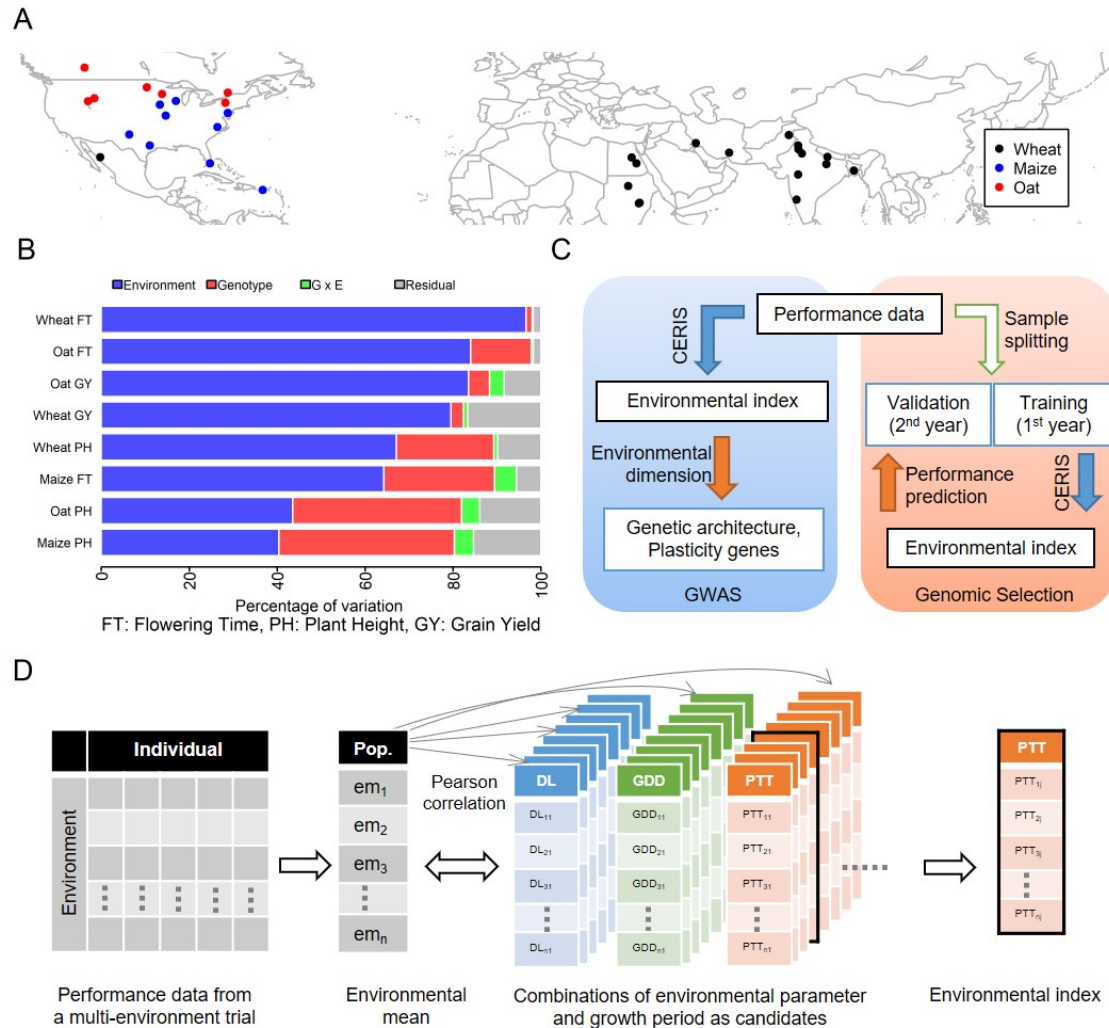
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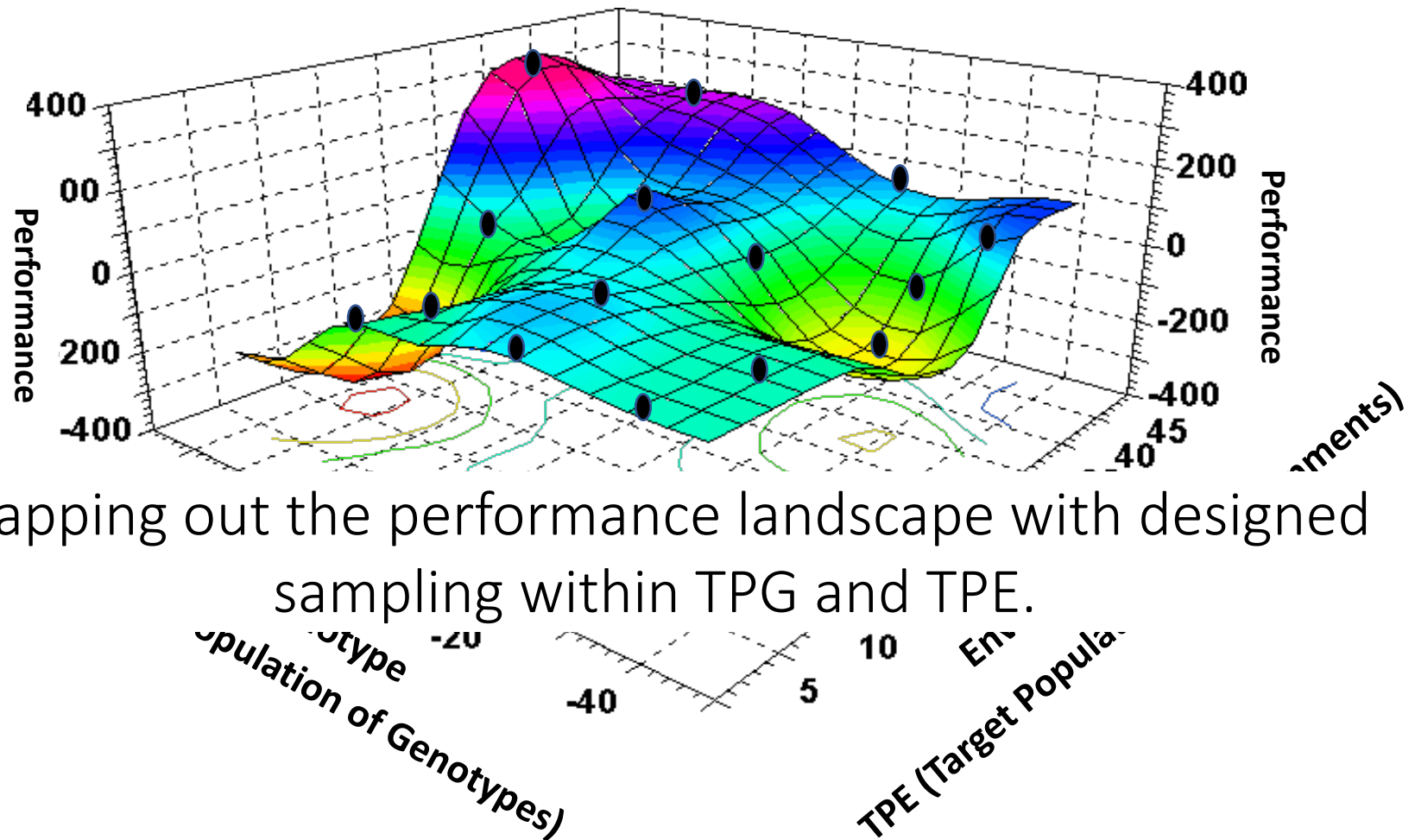
In Brief

Li and colleagues developed a breeding route to *de novo* domestication of wild allotetraploid rice that provides a rational strategy for creating novel crops and generated a series of allotetraploid rice lines edited in domestication-related and agronomically important genes.

An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops



Reflection





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Tabare Abadie (Corteva)

Geoff Graham (Corteva)



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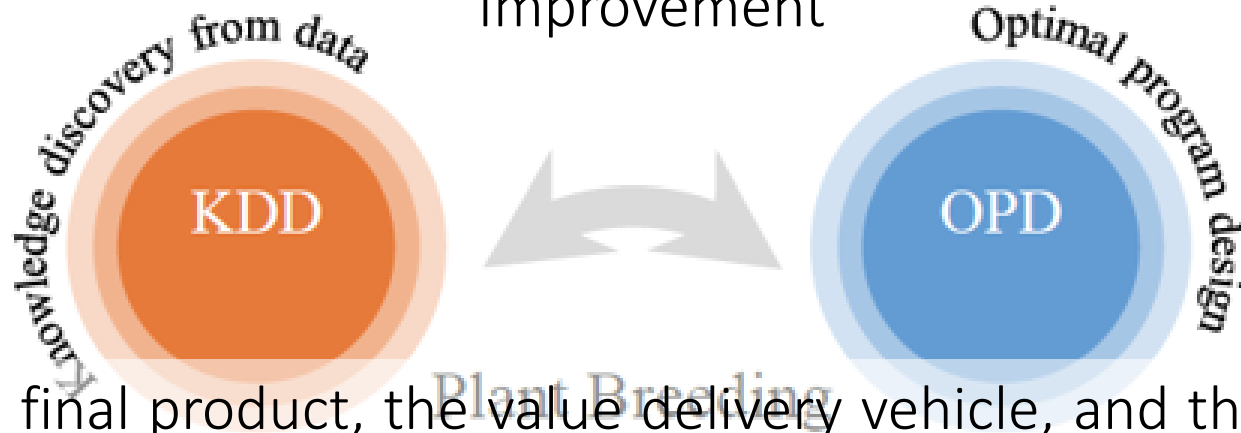
Department of Agronomy



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Plant Sciences Institute

Integrating Design, Analytics, Genomics, Phenomics, ..., into Crop Improvement



BPC: the final product, the value delivery vehicle, and the ultimate integration;

KDD: the scientific understanding, the underlying principles, the pattern finding, and the power of large-scale data collection and mining;

OPD: the evolving nature of the system, the need to change and adapt, the expectation of innovation, and the hope to stay relevant and successful.