

Evolution of genomic selection

Jesse Poland

Wheat Genetics Resource Center
Kansas State University



60%

Increase in demand for wheat by 2050

- 20%

Potential yield decrease from climate change

2%

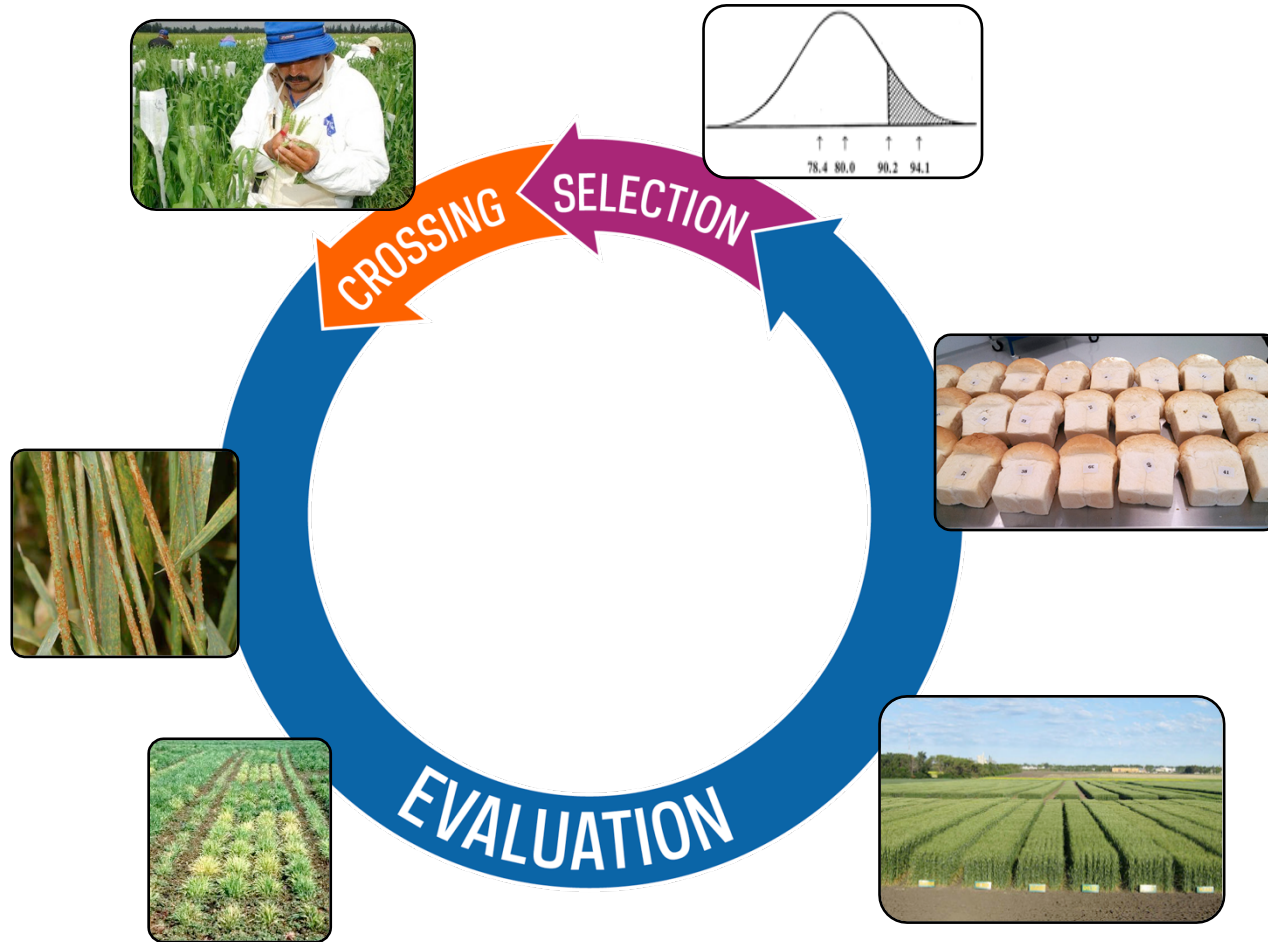
Rate of gain needed to meet projections

< 1%

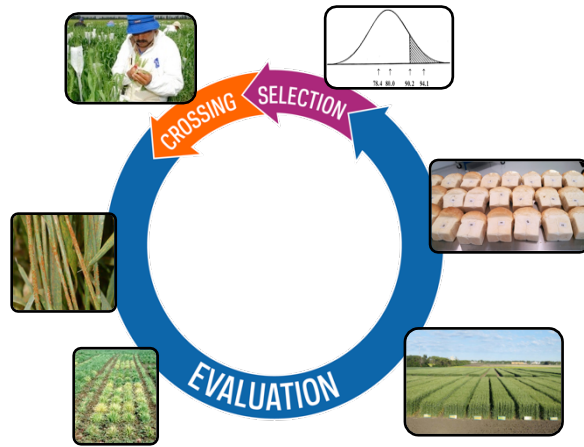
Current rate of gain



The Breeding Cycle



The breeder's (favorite) equation:



Selection Intensity

- ✓ Increase (to a limit)
- ✓ Need bigger populations

Selection Accuracy

- ✓ Increase
- ✓ More precise measurements
- ✓ Reduce Errors
- ✓ Correct for environment

selection intensity

selection accuracy

genetic variance

genetic gain over time

$$R_t = \frac{ir\sigma_A}{y}$$

← years per cycle

Genetic Variance (Diversity)

- ✓ Increase
- ✓ Mixed bag (not all good)
- ✓ A must have

Years per Cycle

- ✓ Decrease!
- ✓ Constant 'rate' of return



Where it all began....

“Recent advances in molecular genetic techniques will make **dense marker maps available** and **genotyping many individuals for these markers feasible.**”

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Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps

T. H. E. Meuwissen,* B. J. Hayes[†] and M. E. Goddard^{†,‡}

**Research Institute of Animal Science and Health, 8200 AB Lelystad, The Netherlands, [†]Victorian Institute of Animal Science, Attwood 3049, Victoria, Australia and [‡]Institute of Land and Food Resources, University of Melbourne, Parkville 3052, Victoria, Australia*

Manuscript received August 17, 2000
Accepted for publication January 17, 2001

“It was concluded that **selection on genetic values predicted from markers** could substantially **increase the rate of genetic gain** in animals and plants...”



Where it got going...

“The **economy of scale** associated with these improvements is rapidly pushing genotyping **below \$20** per sample. Projected gains in the near future could result in a further four to five fold **reduction to \$5 or less per sample.**”

OPEN  ACCESS Freely available online

A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species

Robert J. Elshire¹, Jeffrey C. Glaubitz¹, Qi Sun², Jesse A. Poland³, Ken Kawamoto¹, Edward S. Buckler^{1,4}, Sharon E. Mitchell^{1*}

¹ Institute for Genomic Diversity, Cornell University, Ithaca, New York, United States of America, ² Computational Biology Service Unit, Cornell University, Ithaca, New York, United States of America, ³ Hard Winter Wheat Genetics Research Unit, United States Department of Agriculture/Agricultural Research Service, Manhattan, Kansas, United States of America, ⁴ Plant, Soil and Nutrition Research Unit, United States Department of Agriculture/Agricultural Research Service, Ithaca, New York, United States of America



Where it came together...

“...genotyping-by-sequencing (GBS) can be used for de novo **genotyping of breeding panels** and to **develop accurate GS models**, even for the large, complex, and polyploid wheat genome.”

Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing

Jesse Poland,* Jeffrey Endelman, Julie Dawson, Jessica Rutkoski, Shuangye Wu, Yann Manes, Susanne Dreisigacker, José Crossa, Héctor Sánchez-Villeda, Mark Sorrells, and Jean-Luc Jannink



Genomic Selection

Prediction of *total genetic value* using dense *genome-wide markers*

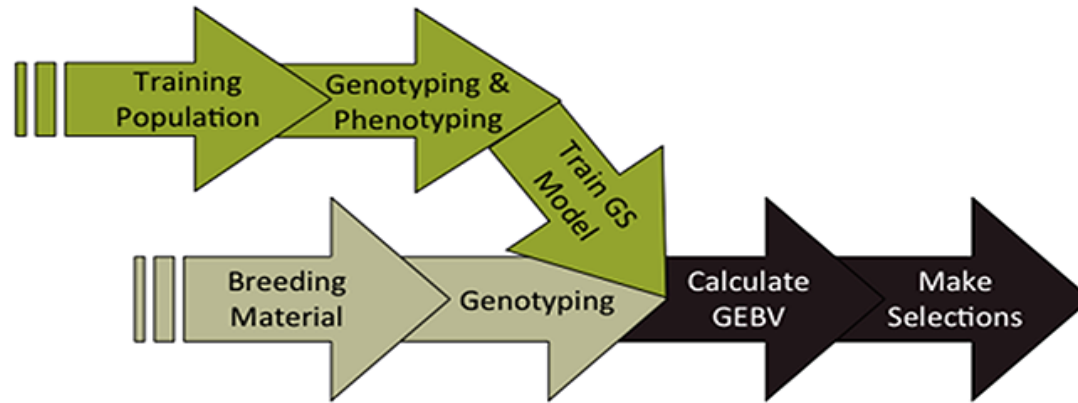
✓ Estimate Kinship (realized relationship) with markers



Implementation of Genomic Selection

- Remove focus from line *per se* and focus on individual allele
- Rapidly select prior to phenotyping

1. Training population (genotypes + phenotypes)
2. Selection candidates (genotypes)



CIMMYT Bread Wheat Breeding

Training set: elite breeding lines (n=5,520)

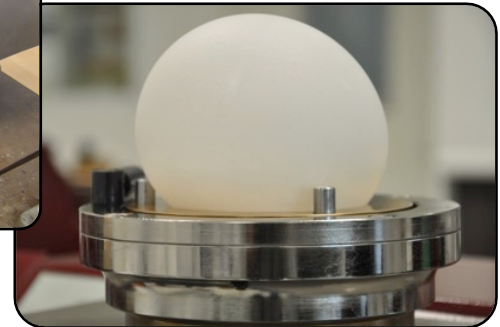
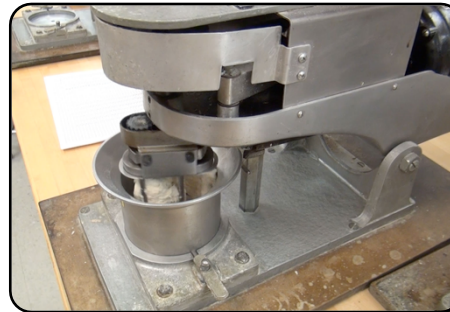
- Cycle 45 - 50 International Bread Wheat Screening Nursery
- Preliminary yield trials (6 environments: 1 for quality)
 - Ciudad Obregon, Mexico
- Milling and baking phenotypes: (1 rep/year for quality)

Year	Total in Yield Trial	Quality Tested & Genotyped
2010	4,956	250
2011	6,685	995
2012	10,196	850
2013	9,436	886
2014	7,672	1,114
2015	8,872	1,425
Total	47,817	5,520



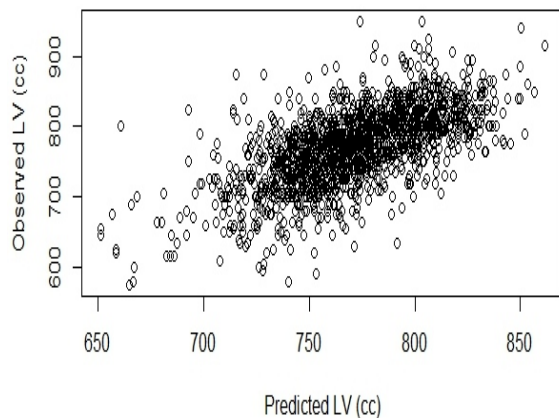
Wheat Quality Phenotypes

- Grain
 - thousand kernel weight
 - protein content
 - hardness
- Milling
 - flour protein
 - flour yield
- Dough
 - mixograph
 - alveograph
- Baking
 - loaf volume





GS: Prediction of wheat quality



TRAIT	PREDICTION ACCURACY (r)
Test Weight	0.725***
Grain Hardness	0.513***
Grain Protein	0.630***
Flour Protein	0.604***
Flour SDS	0.666***
Mixograph Mix Time	0.718***
Alveograph W	0.697***
Alveograph P/L	0.476***
Loaf Volume	0.638***

Sarah Battenfield, KSU



Accelerating Gain: “Indirect” Selection

$$\frac{CR}{R} = \frac{i_Y h_Y r_A}{i_X h_X} \quad \xrightarrow{r_P = h_X h_Y r_A} \quad \frac{CR}{R} = \frac{i_{GS} r_{P:GS}}{i_X h_X^2}$$

Diagram illustrating the transition from direct selection to indirect selection using Genomic Selection (GS).

The left equation represents direct selection: $\frac{CR}{R} = \frac{i_Y h_Y r_A}{i_X h_X}$.

The right equation represents indirect selection using GS: $\frac{CR}{R} = \frac{i_{GS} r_{P:GS}}{i_X h_X^2}$.

The transition is indicated by a large arrow labeled $r_P = h_X h_Y r_A$.

Annotations for the right equation:

- i_{GS} : selection intensity genomic
- $r_{P:GS}$: prediction accuracy
- i_X : selection intensity phenotypic
- h_X^2 : trait heritability

Notes:

- 1) select 1,000
 - > from phenotype of 2,000 (50% selection intensity)
 - > from genotype 10,000 (10% selection intensity)
- 2) h^2 estimated for each trait
- 3) observed correlation between phenotype and GS prediction



Increased gain from genomic selection

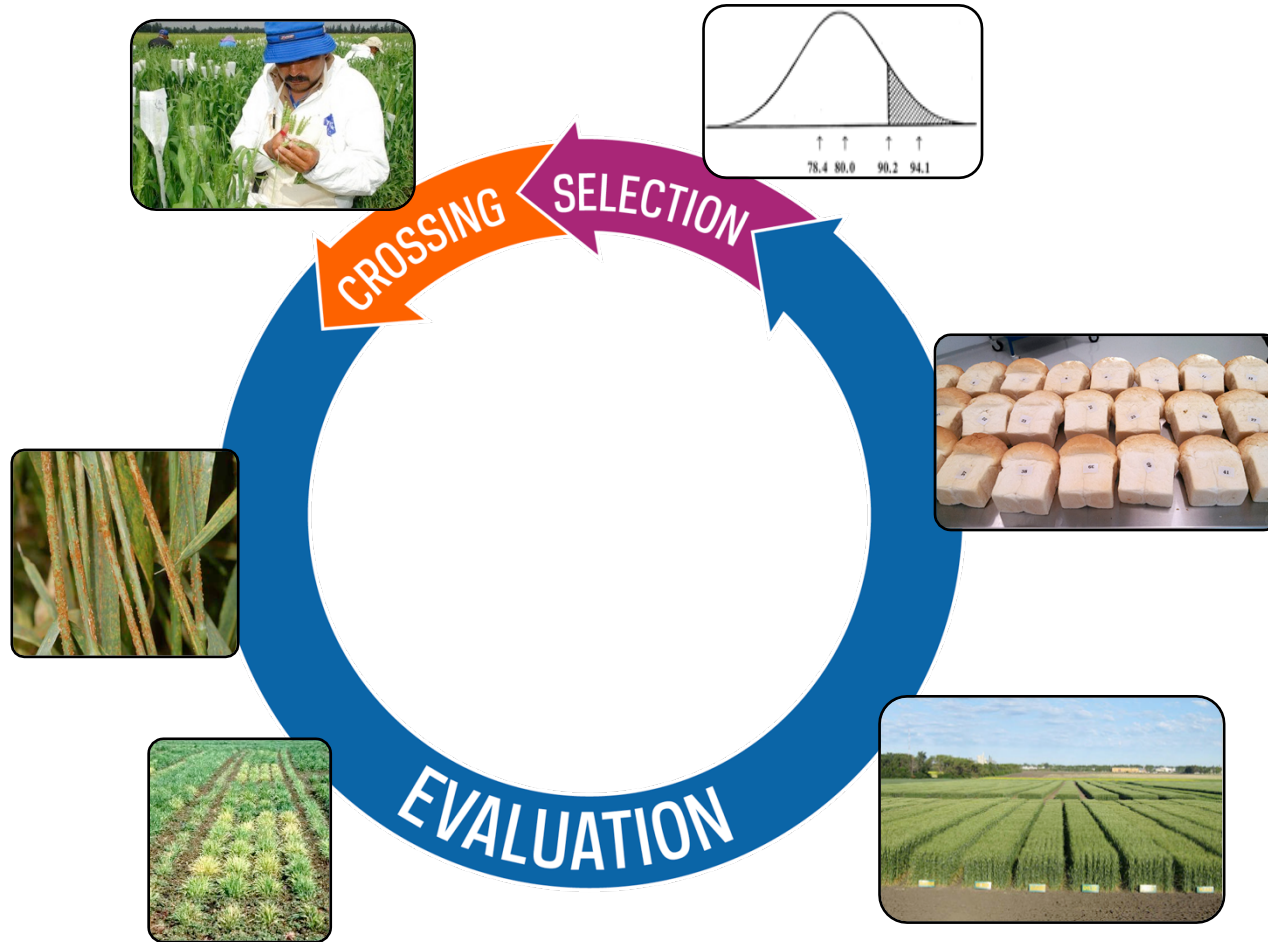
Wheat Quality

- *increased selection intensity from ability to **genotype more entries than can be phenotyped***
- *expected gain of **1.3x to 2.5x** over phenotypic selection*

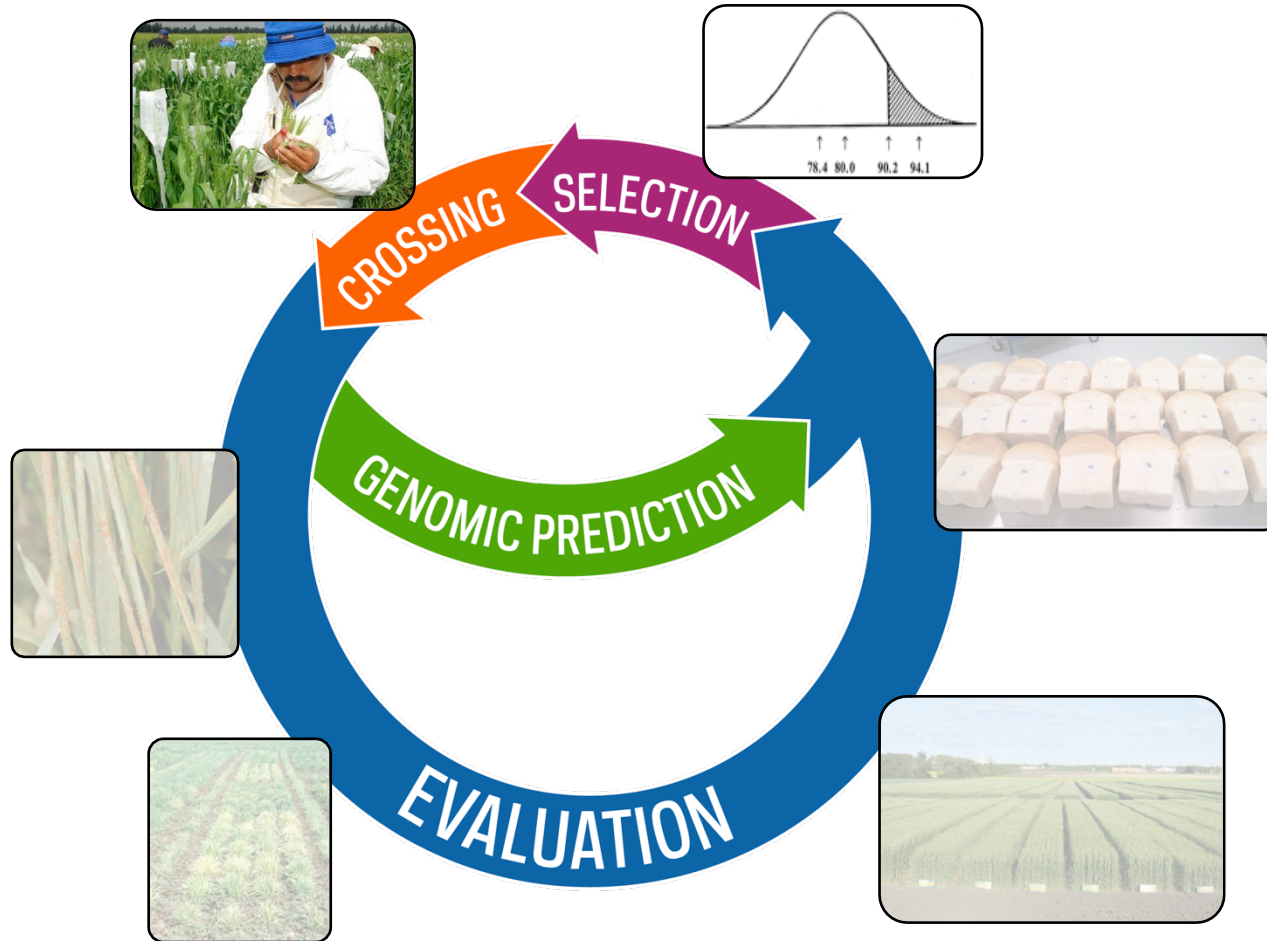
	RESPONSE			
	h^2	$r_{P:GS}$	CR / R	Increase in response
TKW	0.60	0.485	1.78	78%
TESTWT	0.56	0.343	1.35	35%
GRNHRD	0.41	0.322	1.73	73%
FLRYLD	0.43	0.399	2.04	104%
GRNPRO	0.55	0.545	2.18	118%
FLRPRO	0.57	0.530	2.04	104%
FLRSDS	0.62	0.550	1.95	95%
MIXTIM	0.68	0.620	2.01	101%
MP	0.63	0.619	2.16	116%
ALVW	0.65	0.583	1.97	97%
ALVPL	0.46	0.516	2.47	147%
LOFVOL	0.63	0.486	1.70	70%



The Breeding Cycle



(accelerating) The Breeding Cycle



Where it all began....

“Recent advances in molecular genetic techniques will make **dense marker maps available** and **genotyping many individuals for these markers feasible.**”

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T. H. E. Meuwissen,* B. J. Hayes[†] and M. E. Goddard^{†,‡}

*Research Institute of Animal Science and Health, 8200 AB Lelystad, The Netherlands, [†]Victorian Institute of Animal Science, Attwood 3049, Victoria, Australia and [‡]Institute of Land and Water Resources, University of Melbourne, Parkville 3052, Victoria, Australia

Manuscript received August 17, 2000
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It was concluded that selection on genetic values predicted from markers **could substantially increase the rate of genetic gain** in animals and plants...”

“... especially if combined with reproductive techniques to **shorten the generation interval.**”





Hybrid wheat!

“...we developed a three-step strategy for **establishing a heterotic pattern**, which was one of the central unsolved challenges for initiating hybrid breeding programs.”

Genome-based establishment of a high-yielding heterotic pattern for hybrid wheat breeding

Yusheng Zhao^a, Zuo Li^a, Guozheng Liu^a, Yong Jiang^a, Hans Peter Maurer^b, Tobias Würschum^b, Hans-Peter Mock^c, Andrea Matros^c, Erhard Ebmeyer^d, Ralf Schachschneider^e, Ebrahim Kazman^f, Johannes Schacht^g, Manje Gowda^{b,1}, C. Friedrich H. Longin^b, and Jochen C. Reif^{a,2}

^aDepartment of Breeding Research, Leibniz Institute of Plant Genetics and Crop Plant Research Gatersleben, 06466 Stadt Seeland, Germany; ^bState Plant Breeding Institute, University of Hohenheim, 70593 Stuttgart, Germany; ^cDepartment of Physiology and Cell Biology, Leibniz Institute of Plant Genetics and Crop Plant Research Gatersleben, 06466 Stadt Seeland, Germany; ^dWheat breeding, KWS LOCHOW GmbH, 29296 Bergen, Germany; ^eWheat breeding, Nordsaat Saatzuchtgesellschaft mbH, 38895 Langenstein, Germany; ^fWheat breeding, Lantmännen SW Seed Hadmersleben GmbH, 39398 Hadmersleben, Germany; and ^gWheat breeding, Limagrain GmbH, 31226 Peine-Rosenthal, Germany

Edited by Edward S. Buckler, Cornell University, Ithaca, NY, and approved November 11, 2015 (received for review July 23, 2015)



The **past** has become the **present** and is the **future**...

...we've been doing GBS
here for a long time...
'genotyping-by-SEEING'!





+

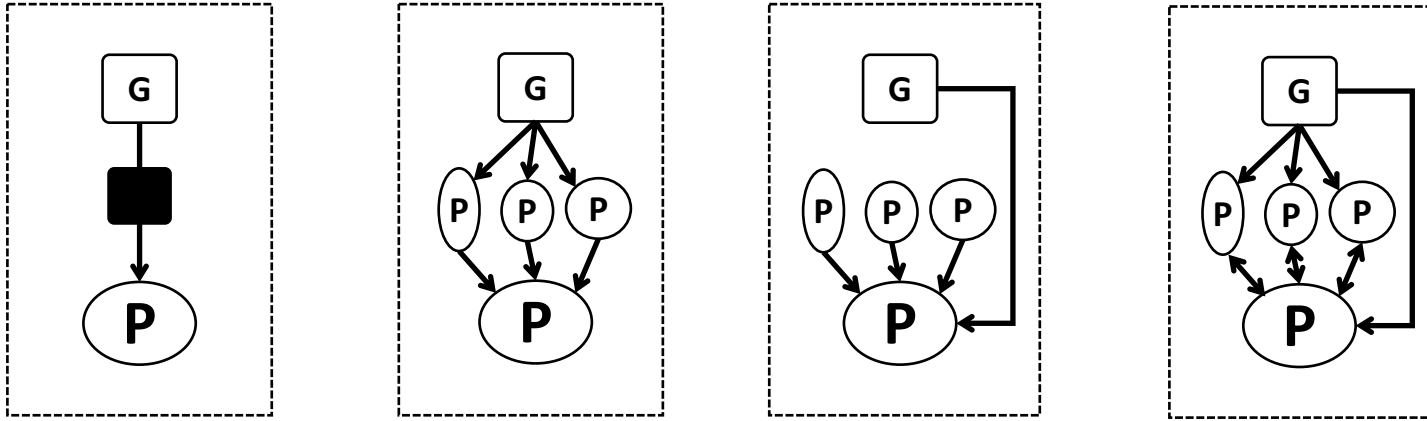


=

genetic
gain



Genomic selection + High-throughput phenotyping



target: measurement of 'secondary traits' that have a genetic and/or phenotypic correlation to yield



*“...secondary traits measured in high-throughput could be used in pedigree and genomic prediction to **improve accuracy**...”*

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

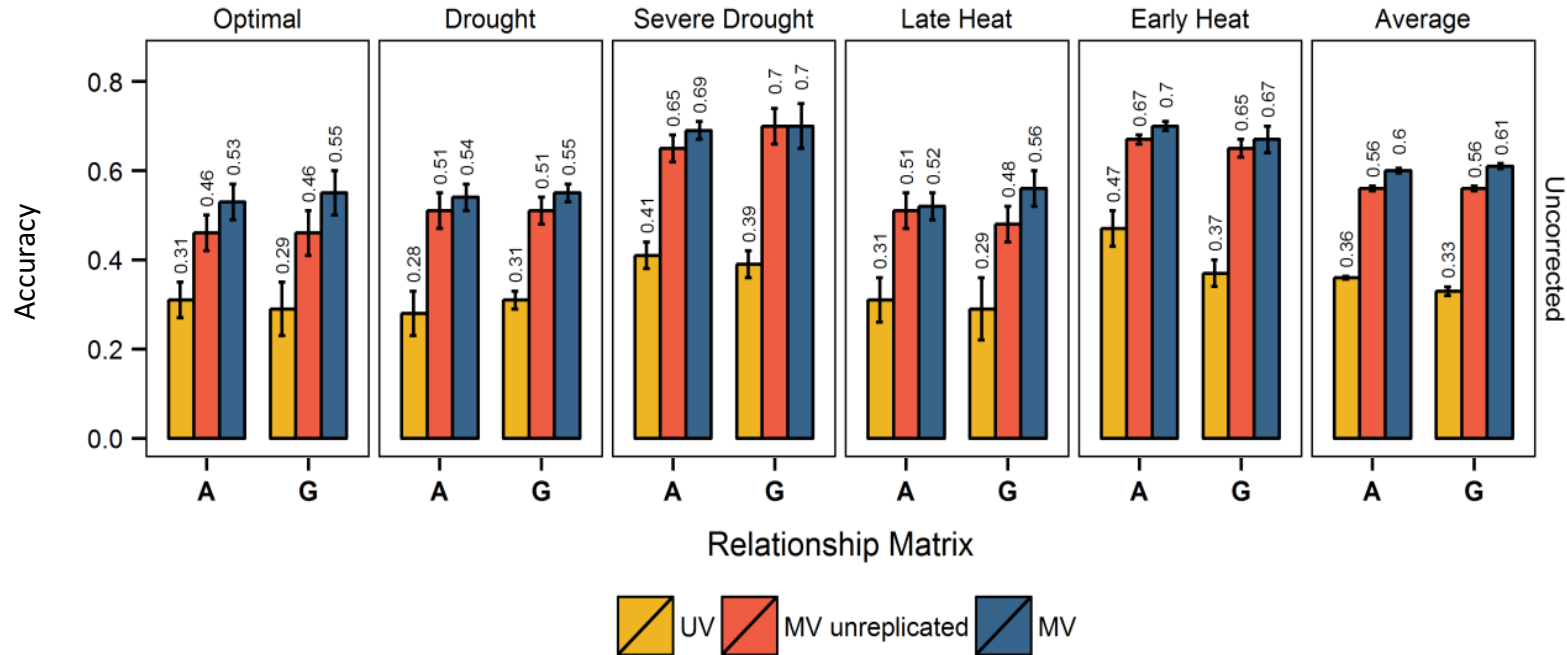
Jessica Rutkoski,^{*,†,‡,1} Jesse Poland,[§] Suchismita Mondal,[‡] Enrique Autrique,[‡] Lorena González Pérez,[‡] José Crossa,[‡] Matthew Reynolds,[‡] and Ravi Singh[‡]

^{*}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



GS + HTP

- ✓ combining high-throughput secondary phenotypes and genomic information increased prediction accuracy



Rutkoski, J., J. Poland, S. Mondal, E. Autrique, L. G. Pérez, J. Crossa, M. Reynolds and R. Singh (2016). "Canopy Temperature and Vegetation Indices from High-Throughput Phenotyping Improve Accuracy of Pedigree and Genomic Selection for Grain Yield in Wheat." G3: Genes | Genomes | Genetics. DOI: 10.1534/g3.116.032888



Conclusions....

- Genomic selection can increase breeding progress through increased selection intensity and decreased cycle time.
- Field-based high-throughput phenotyping is in early stages but maturing quickly and demonstrated potential to measure traits faster and more accurately.
- The combined power of genomics and phenomics will lead to new eras in breeding and functional genomics.



*"Recognize that God and others are responsible
for the successes in your life."*

– Institute in Basic Life Principles / Bill Bockus

POLAND LAB

Shuangye Wu

Byron Evers

Haley Ahlers

Mark Lucas

Jared Crain

Sandra Dunckel

Trevor Rife

Daljit Singh

Narinder Singh

Xu (Kevin) Wang

Megan Calvert

Atena Haghighattalab

Mokhles Rahman

Emily Delorean

Kevin Dorn

Paula Silva

Rich Brown

Bo Winter

Liang Gao

Ravi Singh

Susanne Dreisigacker

Suchismita Mondal

Uttam Kumar

Carlos Guzmán

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Matthew Reynolds

David Bonnett

Rick Ward

M. Imtiaz



Mark Sorells

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