Genomic Selection for Public Cotton Breeding

Amanda M Hulse-Kemp

USDA Agricultural Research Service
U.S. DEPARTMENT OF AGRICULTURE

"Cotton Produced by Genomic Selection"
Generative AI

Meet the Hulse-Kemp Lab

Dr. Emily Delorean
Postdoc
Chili pepper Genomics

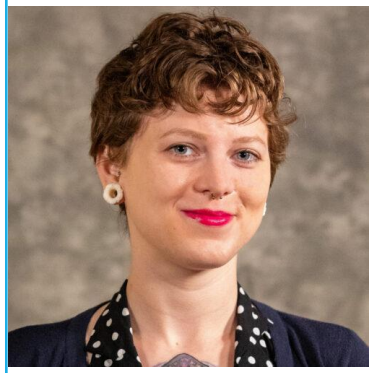
Jonathan Zirkel
PhD Student
Functional Genetics

Laide Rasaki
PhD Student
Advancement of Orphan Crops

Matthew Willman
PhD Student
Wheat Genomics

Grant Billings
PhD Student
Cotton Genomics

Dr. Keo Corak
Associated Scientist
Breeding Informatics



Dr. Ash Yow
Postdoc
Hybrid Genomics

Software Development Team

Jordan James
PhD Student
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Ameaza Rodrigues
Intern

Romil Shah
Intern

Chandler Wilson
Intern

Dr. Heather Manching
Research Associate
Breeding Informatics

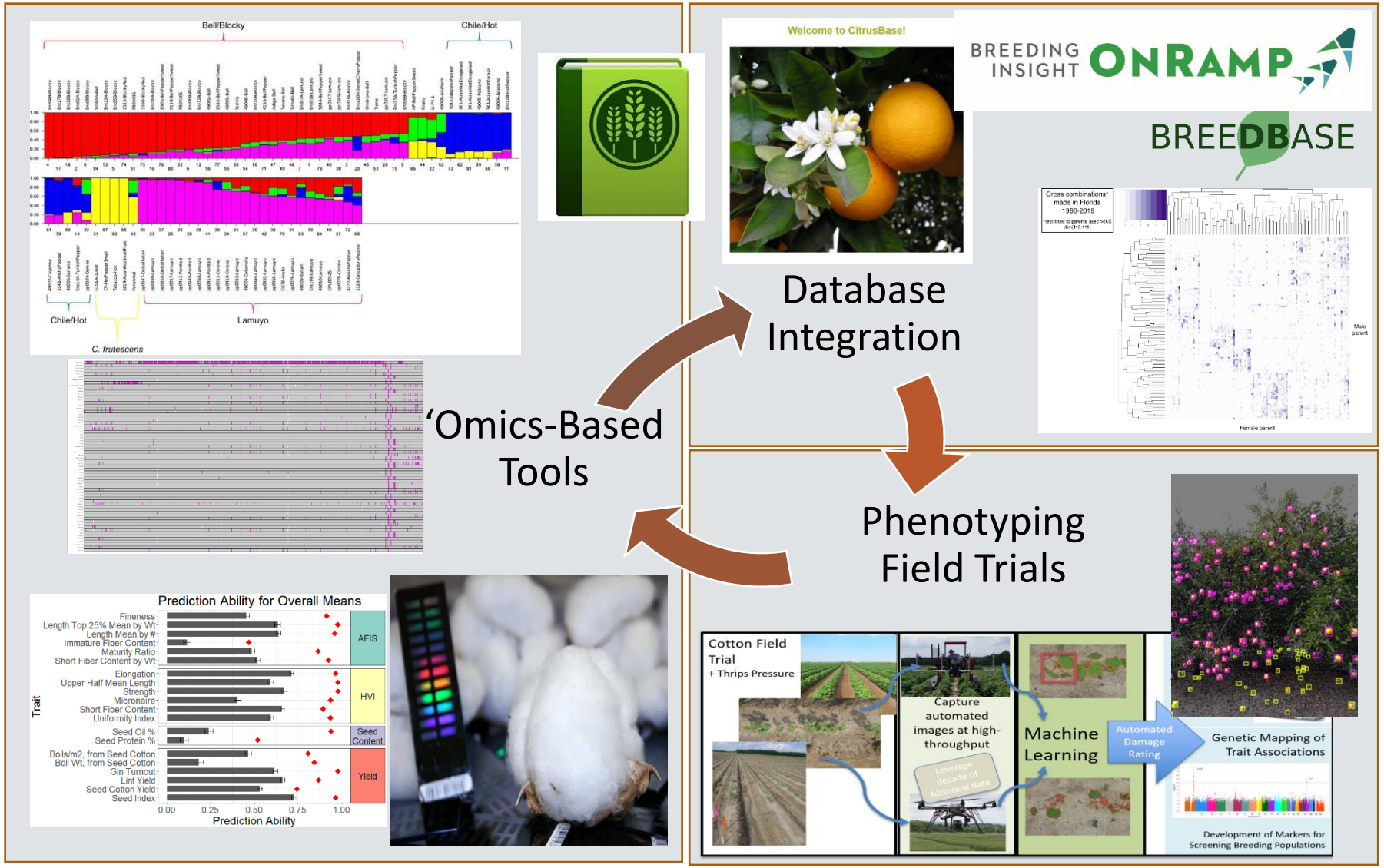
USDA Agricultural Research Service
U.S. DEPARTMENT OF AGRICULTURE

NC STATE UNIVERSITY

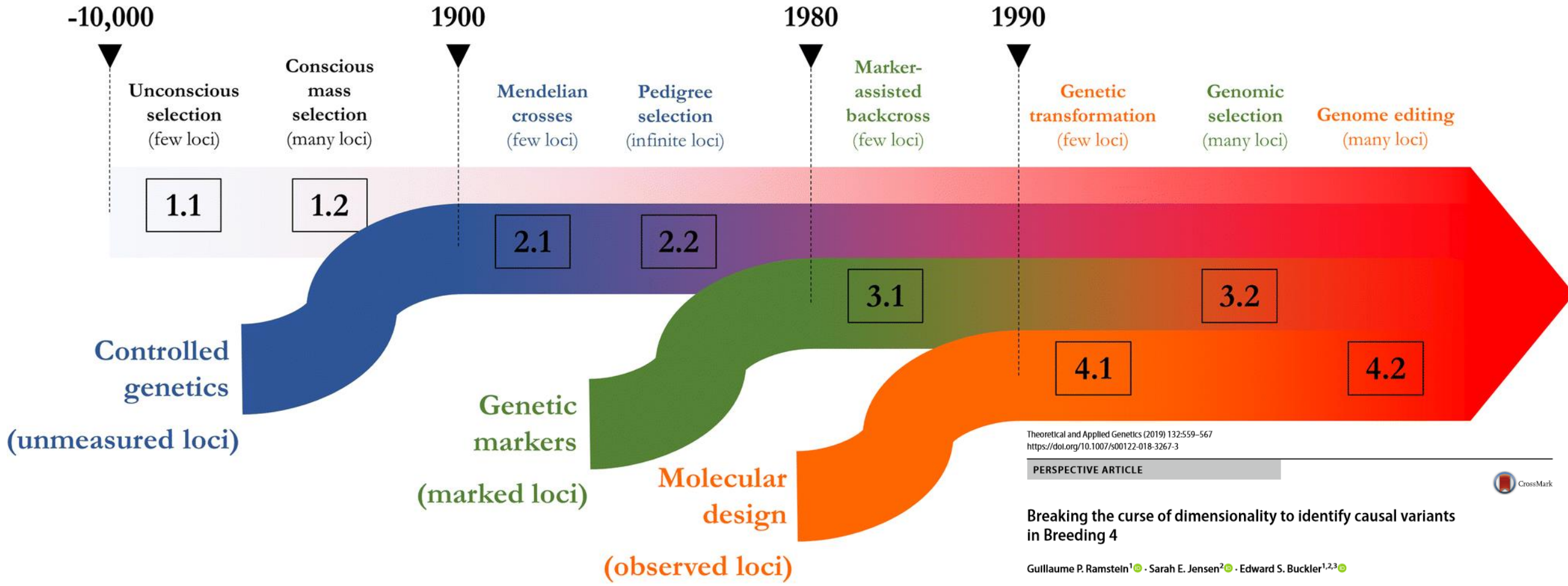
Cotton Team

As of July 2024

Developing Tools Across Crops for Breeders



TECHNOLOGICAL PHASES OF PLANT BREEDING



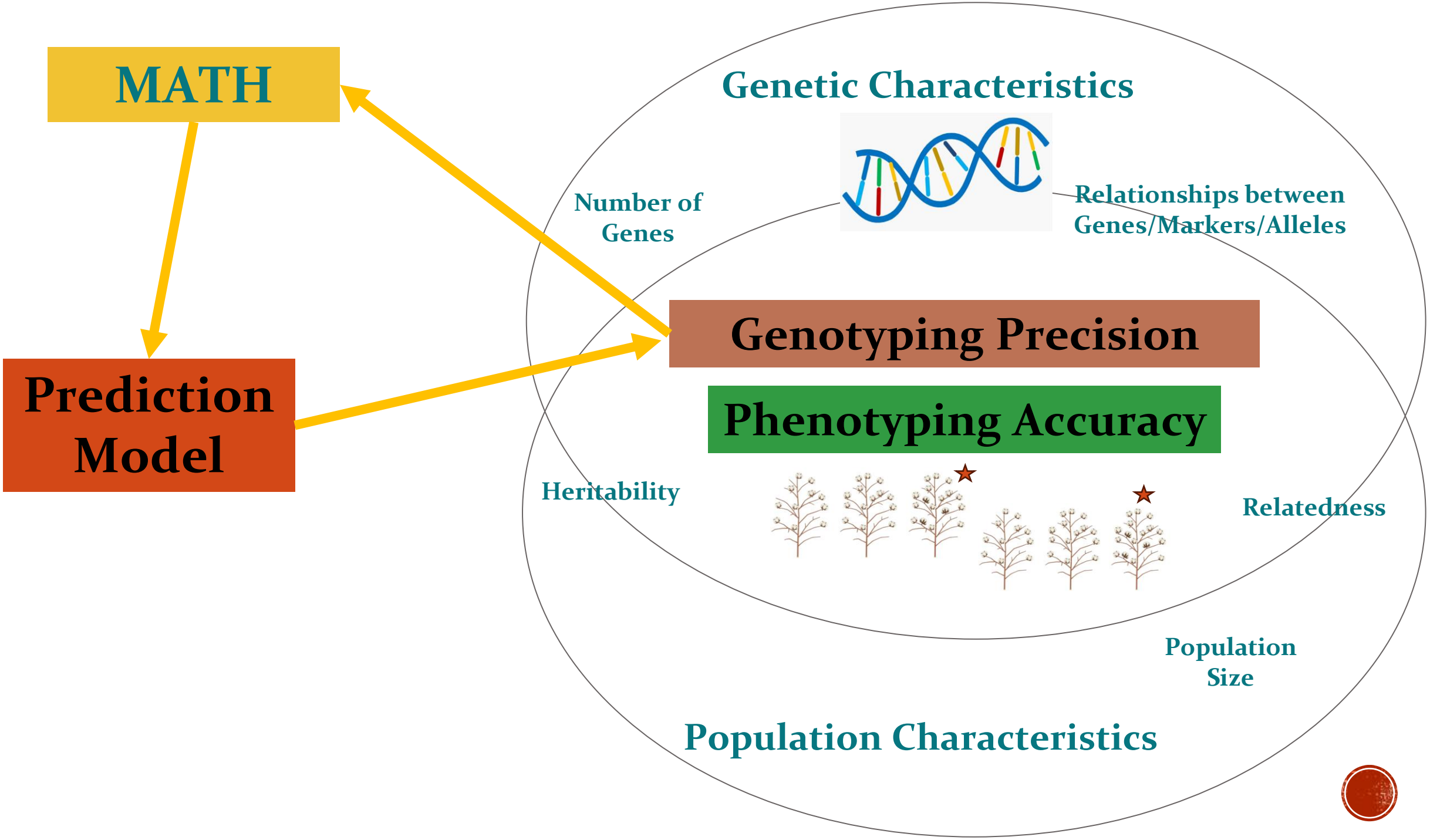
Theoretical and Applied Genetics (2019) 132:559–567
https://doi.org/10.1007/s00122-018-3267-3

PERSPECTIVE ARTICLE

Breaking the curse of dimensionality to identify causal variants in Breeding 4

Guillaume P. Ramstein[1] · Sarah E. Jensen[2] · Edward S. Buckler[1,2,3]

Received: 15 November 2018 / Accepted: 7 December 2018 / Published online: 13 December 2018


MATH
Prediction Model
Genetic Characteristics
Number of Genes
Relationships between Genes/Markers/Alleles
Genotyping Precision
Phenotyping Accuracy
Heritability
Relatedness
Population Size
Population Characteristics

GENOMIC SELECTION IN BREEDING PROGRAMS

Genome Wide Association Model:

$$\boldsymbol{Y} = \mu + \boldsymbol{X_S\beta_S} + \boldsymbol{Zu} + \boldsymbol{\varepsilon}$$

Interest is in SNP effect $\widehat{\boldsymbol{\beta}}_S$

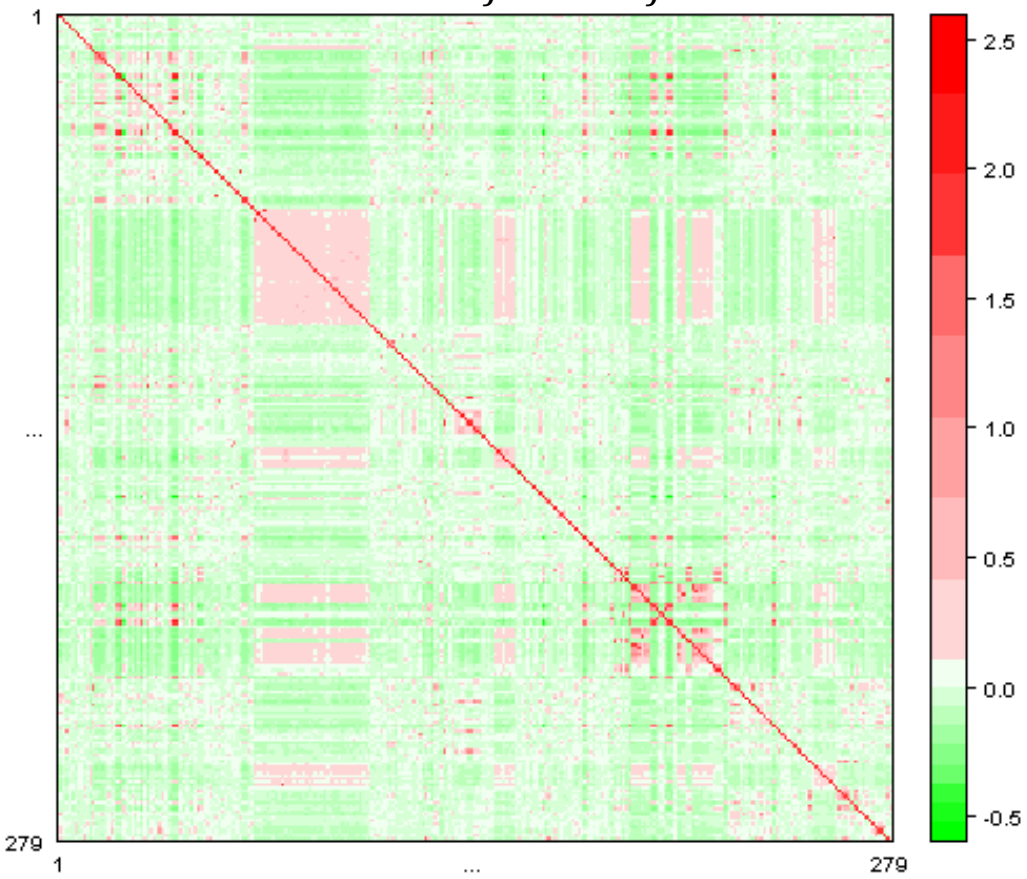
Genomic Prediction Model:

$$\boldsymbol{Y} = \mu + \boldsymbol{Zu} + \boldsymbol{\varepsilon}$$

Interest is in prediction of u: $\widehat{\boldsymbol{u}}$

Similar models, different objectives
Best approach for breeding depends on genetic architecture

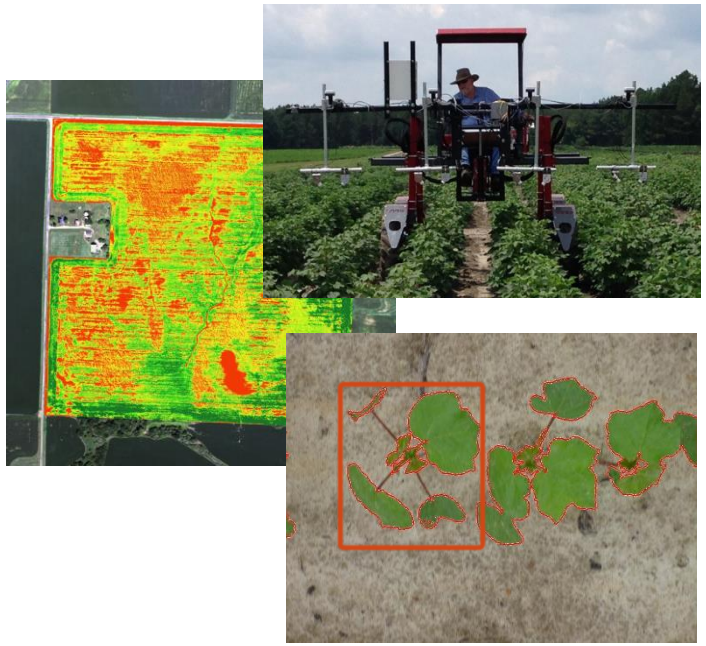
$$u \sim N(0, G\sigma_A^2)$$
$$G_{ij} = 2\theta_{ij}$$



Pairwise realized genomic relationship matrix for 279 maize inbreds

Courtesy of Jim Holland et al.

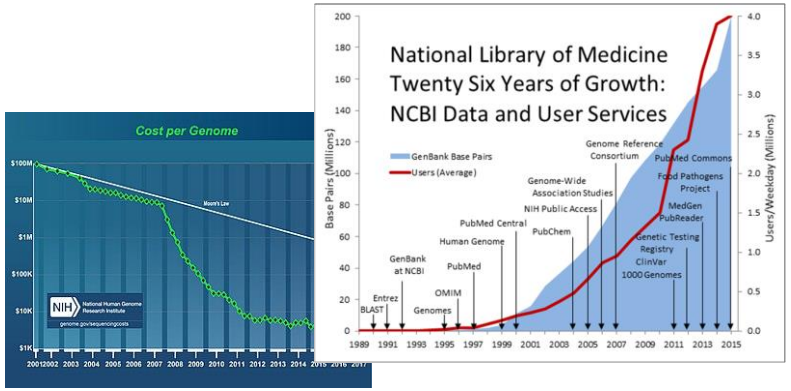
INPUTS INTO GENOMIC SELECTION



Bioinformatics for High-throughput Phenotyping

R Statistical Software

Genomic Estimated Breeding Values (GEBV) for Selection



Bioinformatics to Obtain Inputs

Tassel Software

Many custom pipelines

Predictive Breeding

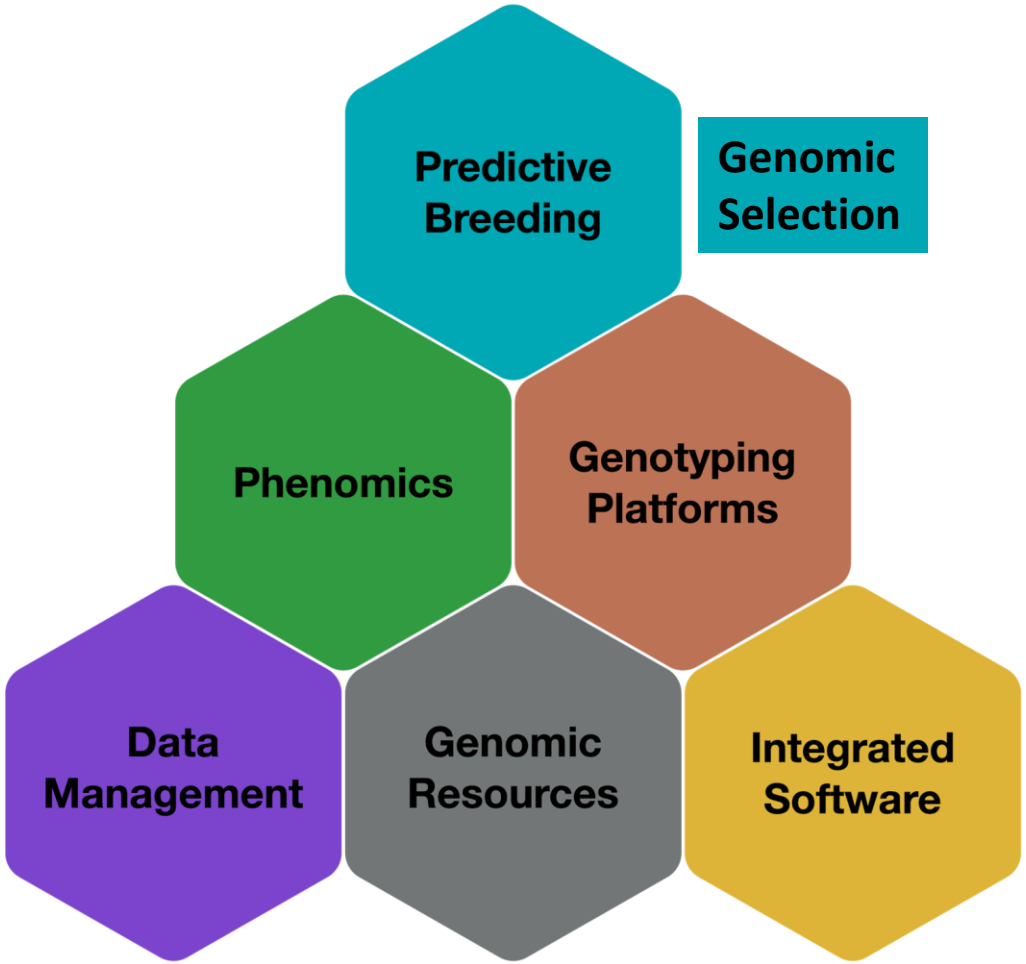
Single experiment - Estimating ability to estimate traits WITHIN the same experiment (same set of materials) = GENOMIC PREDICTION

- **Usually gives an idea of theoretical maximums of many situations you may face - simplest path forward**

Estimating traits across experiments - ie. in a breeding program (related, but NOT the same set of materials); THEN using those estimates to select what individuals to retain = GENOMIC SELECTION

- **May be empirically similar or potentially very different in practice than Genomic Prediction**
- **Difficult to measure success until put in practice**

Plant Breeding - Advanced Technologies



Advanced Breeding Technologies = Methods to Manipulate Breeders Equation

- Reduce generation intervals
- Improve genetic gain
- Standardized genotyping
- Advanced standardized phenotyping methods
- Data management systems to integrate multiple field trials

$$\text{Response } R_t = h^2 S = \frac{i\, r\, \sigma_A}{L}$$

$h^2 = Narrow\ sense\ heritability$
$S = Difference\ between\ selected\ parents\ and\ population$
$i = Selection\ intensity$
$r = Selection\ accuracy$
$\sigma_A = Genetic\ Variance$
$L = Generational\ interval$

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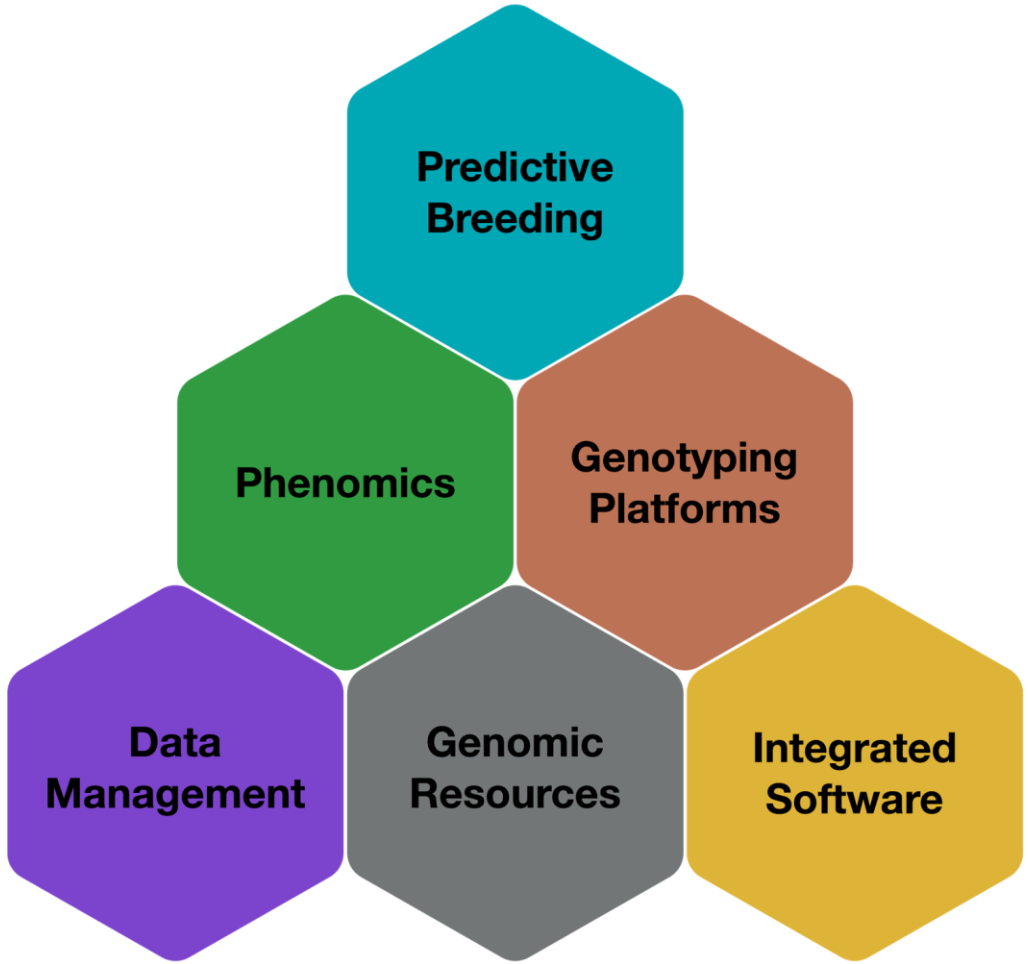
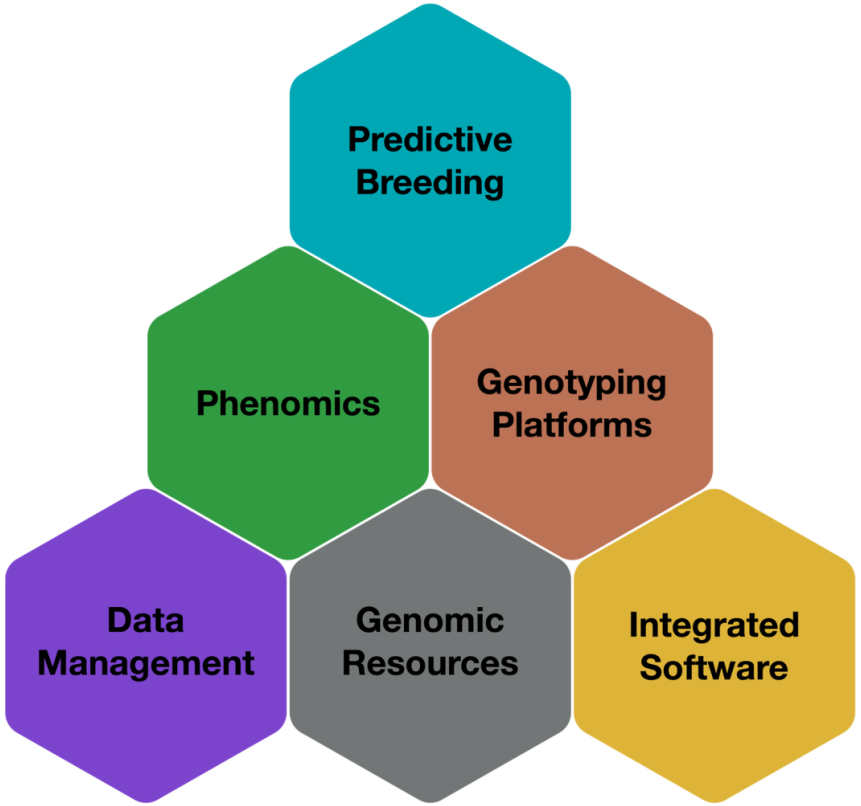


All of these aspects can play into the various components of the breeders equation!

Plant Breeding - Advanced Technologies



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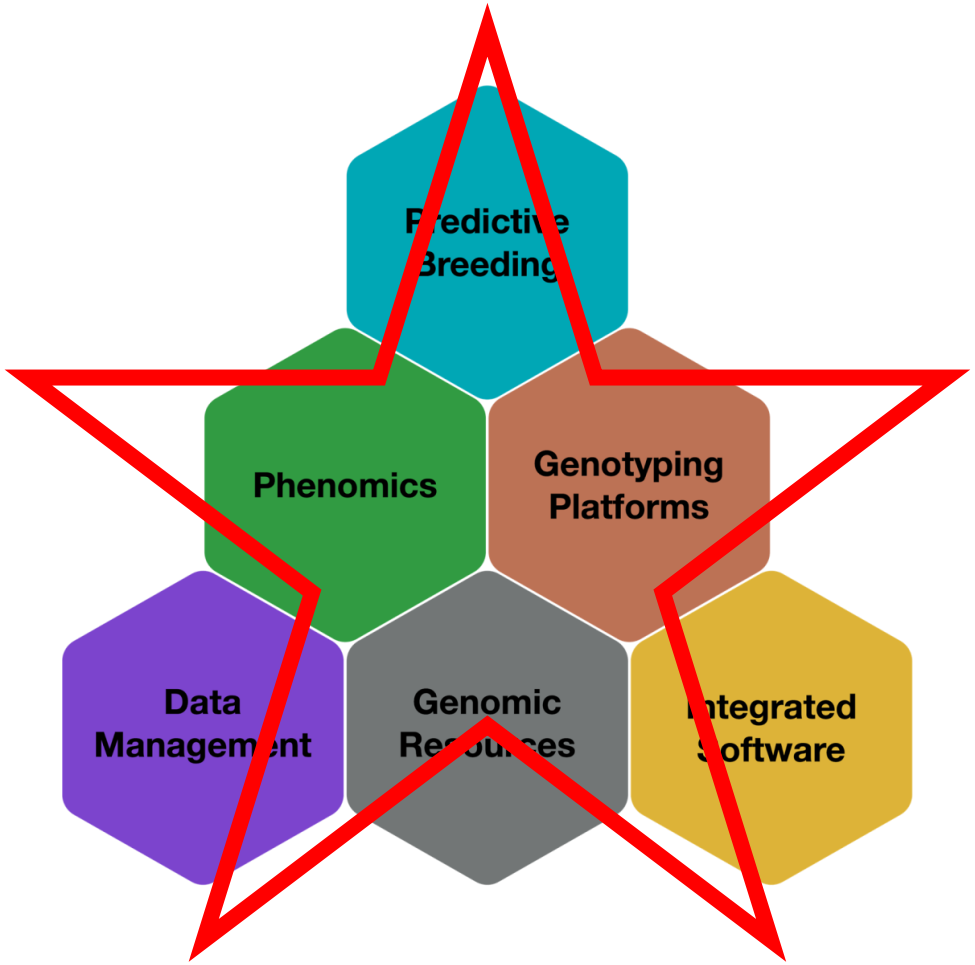
Biological aspect can measure - changes depending on how you measure traits of interest

Plant Breeding - Advanced Technologies



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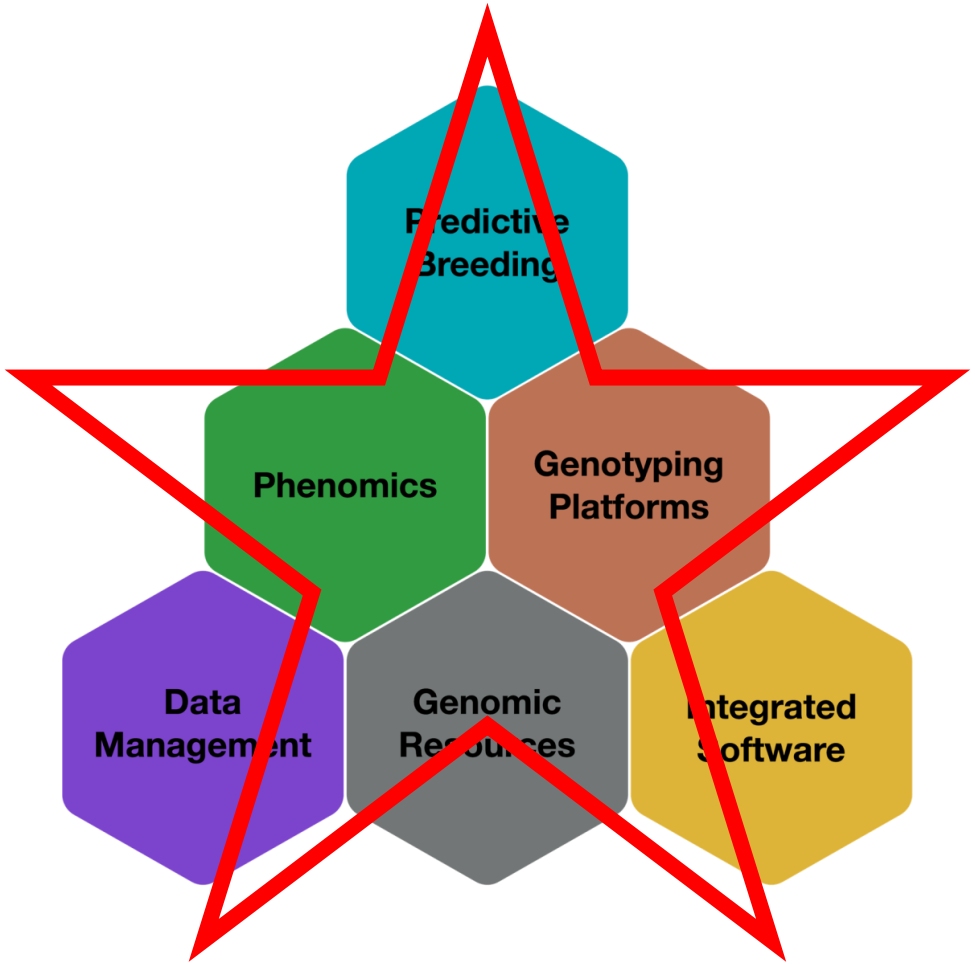
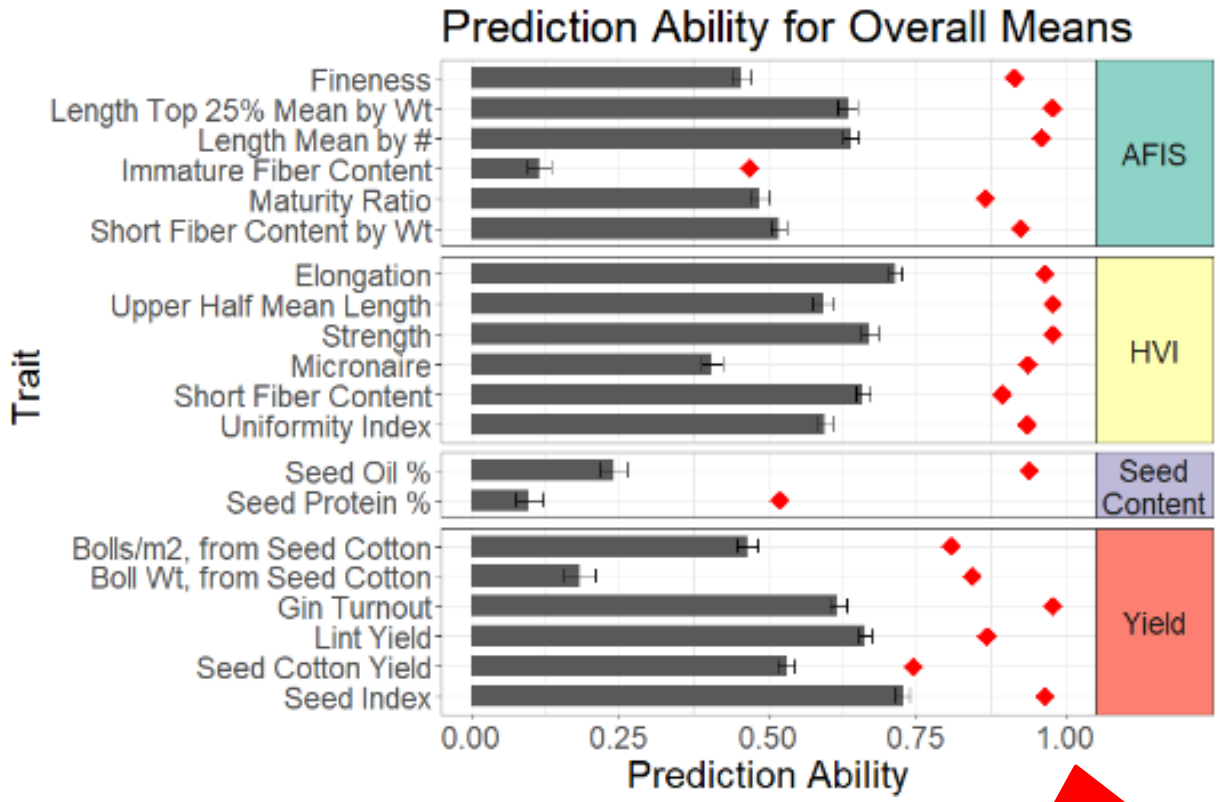
ACCURACY!!!!
Important in ALL aspects of the system
Affects our ability to reach theoretical maximums

Prediction Accuracies





Response $R_t = h^2 S = \frac{i\, r\, \sigma_A}{L}$

$h^2 = Narrow\ sense\ heritability$

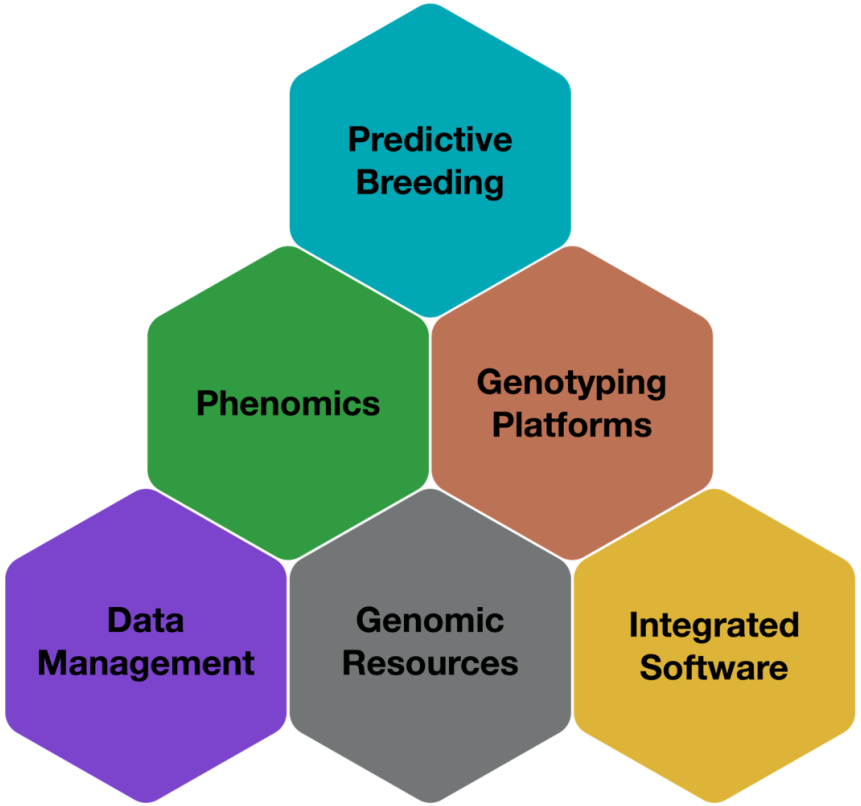
Theoretical maximum on prediction = h^2

Changes per trait!

Difference can be many things but impacted by models developed and accuracy on measurements - genotype & phenotype

Billings et al. (2022) Outlook for Implementation of Genomics-Based Selection in Public Cotton Breeding Programs

Plant Breeding - Advanced Technologies



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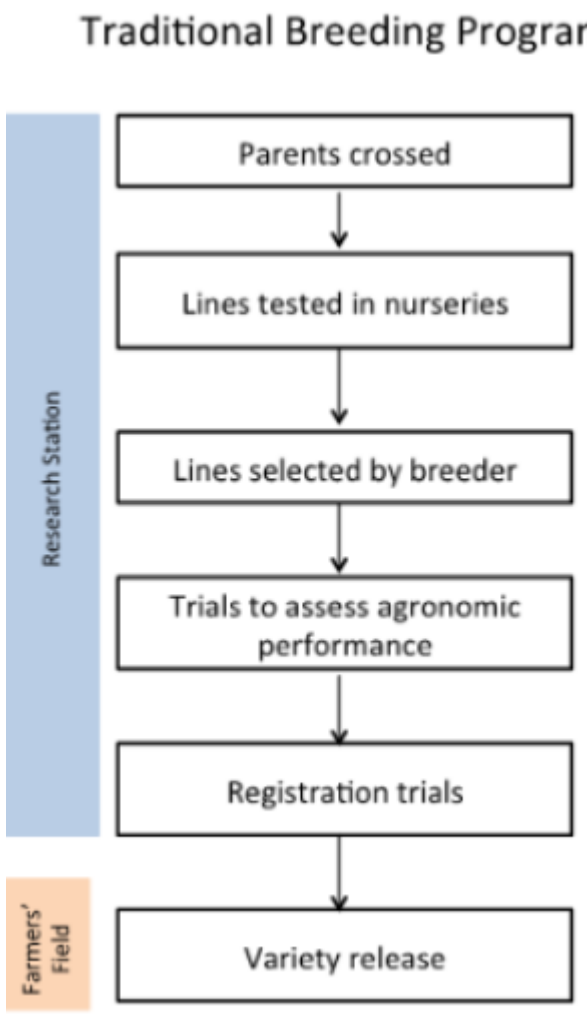
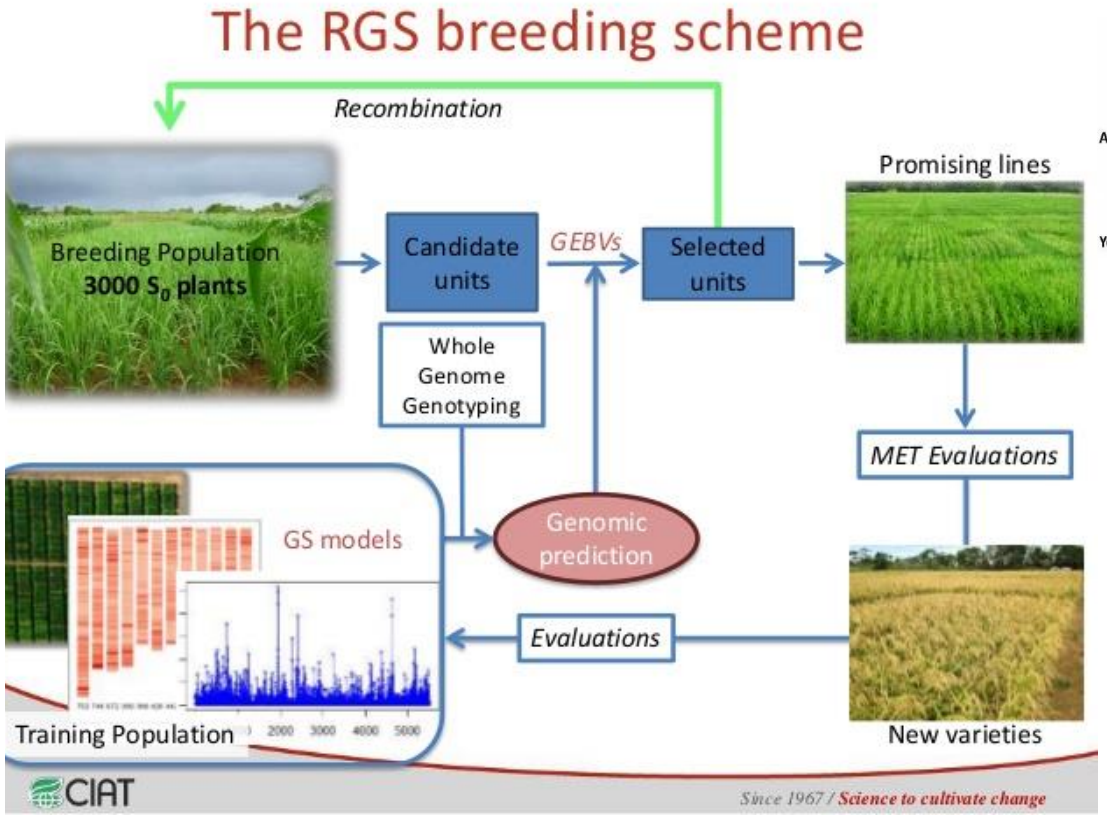
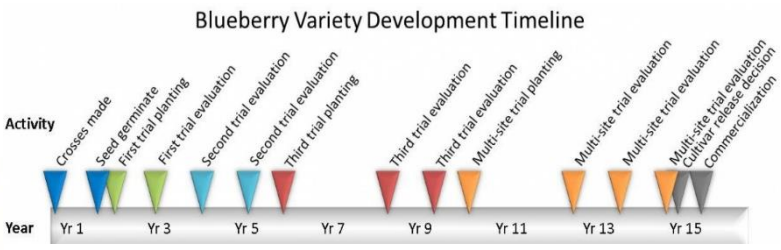
Quickest way to increase gain
Biggest effect on whole equation -> <u>spend a lot of time here</u>

Implementation of Genomic Selection

Outline of breeding programs







Evaluations/Selections Made Each Year

20,000 — Total number of potential plant varieties evaluated in first trail. These are evaluated for early flower development and fruit quality characteristics to select the top 10%.

2,000 — Number of potential plant varieties being evaluated in second trials (plantings from 3 successive years). These remain in place and are evaluated an average of 2 years for yield, harvest timing, disease susceptibility, and fruit quality to select the top 10%.

200 — Number of potential varieties being evaluated in third trials under commercial production conditions. These multi-plant trials are evaluated an average 2 years for yield, harvest timing, disease susceptibility, fruit quality, and growth habit to select the top 10%.

20 — Number of potential plant varieties being evaluated at multiple testing locations in North Carolina and worldwide. Yield, harvest timing, disease susceptibility, fruit quality, growth habit, and environmental adaptation are evaluated for 3 years to select potential varieties for release and commercialization.

Cultivar

Predictive Breeding

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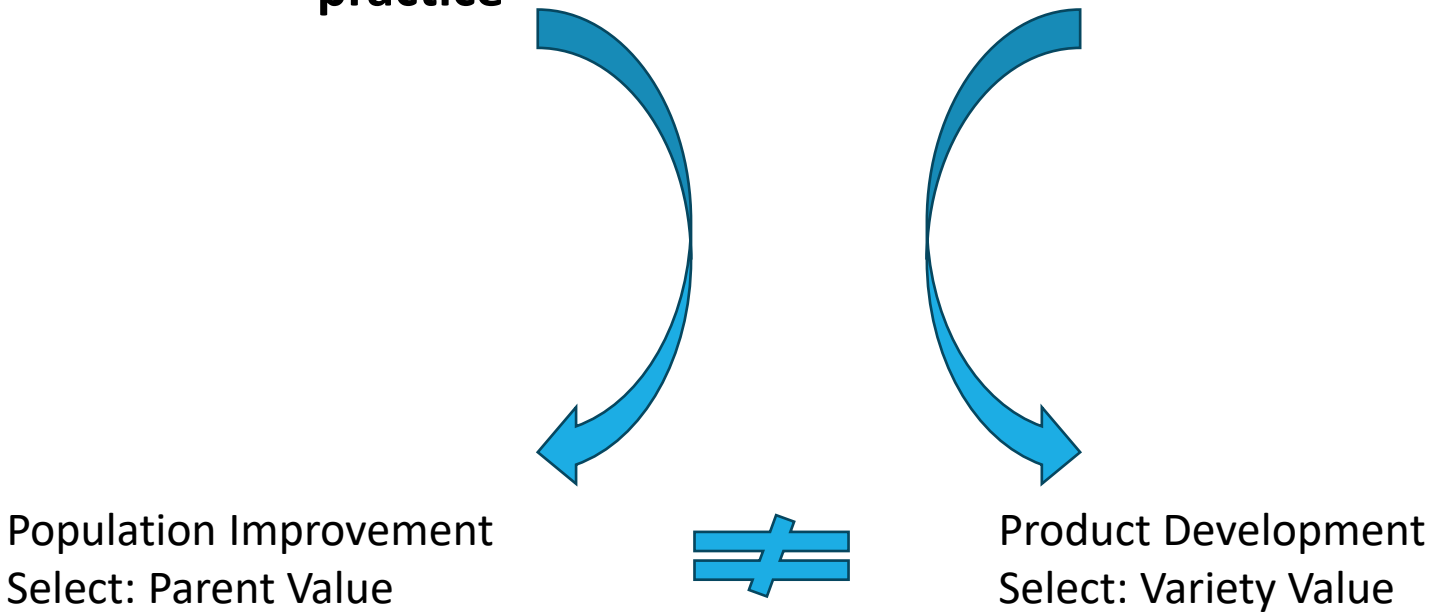
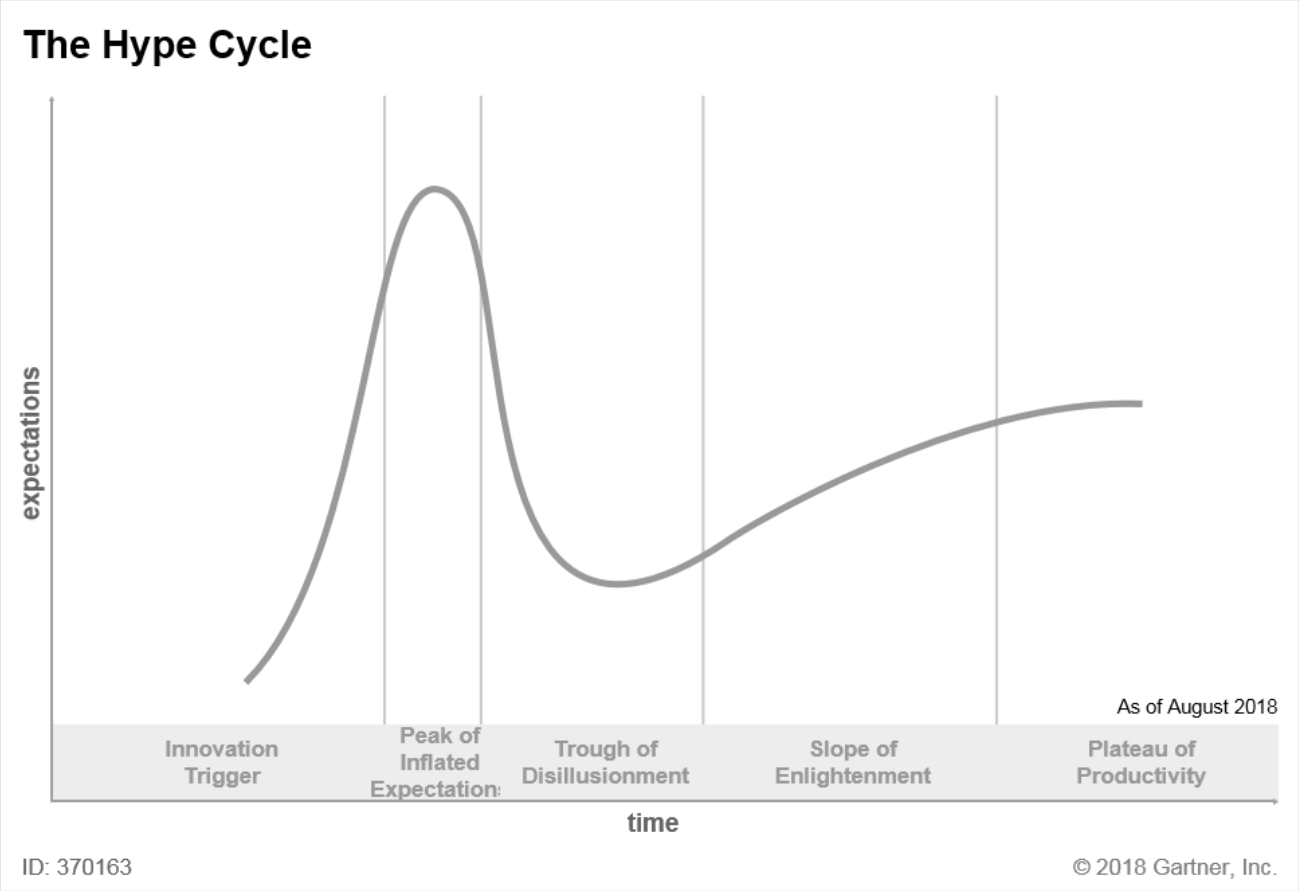


Technology Researchers -
Generalists Evaluating and Developing Any Type of Technology

- Evaluate emerging technology
- Research to investigate integration of tools into breeding programs
- Develop new tools to fit holes where nothing is available



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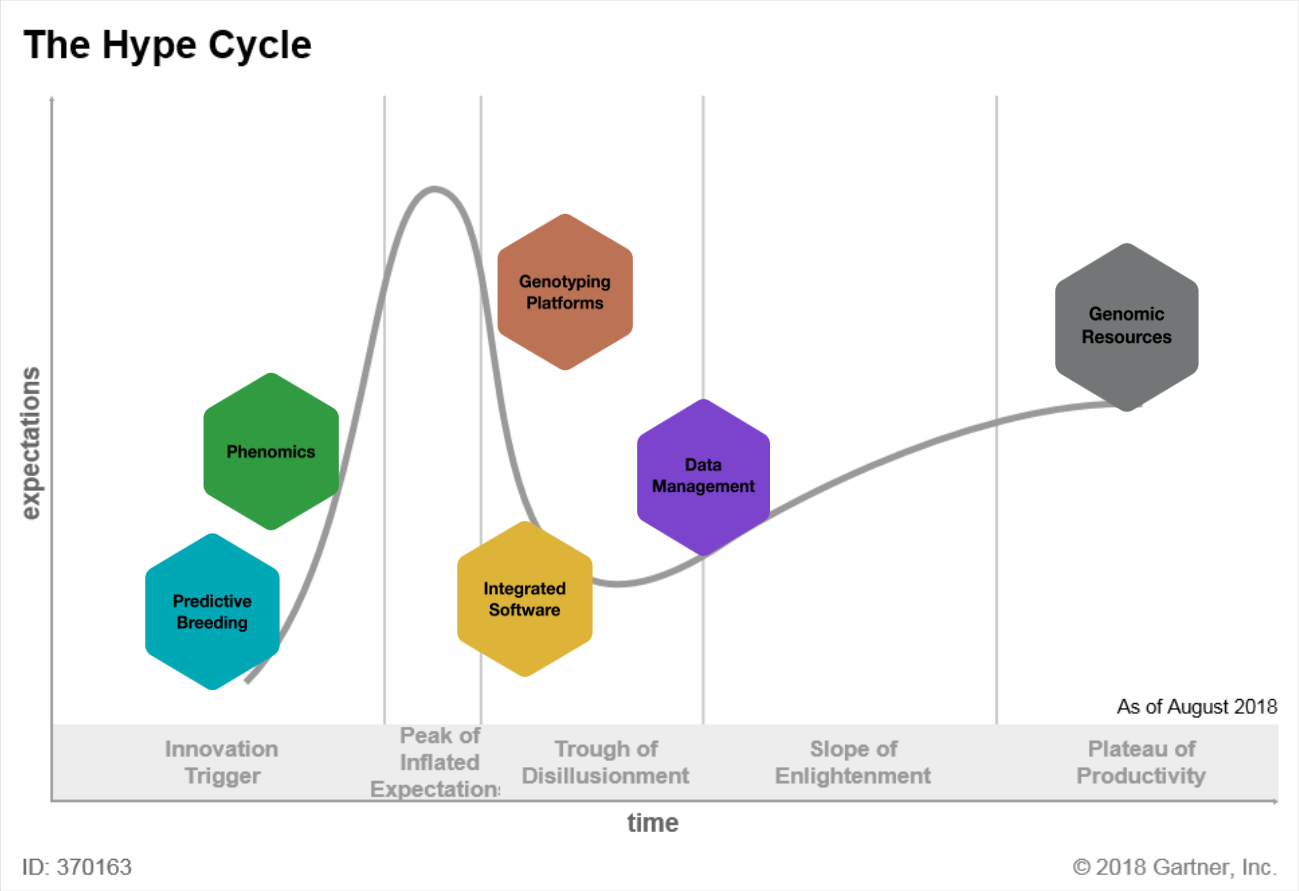

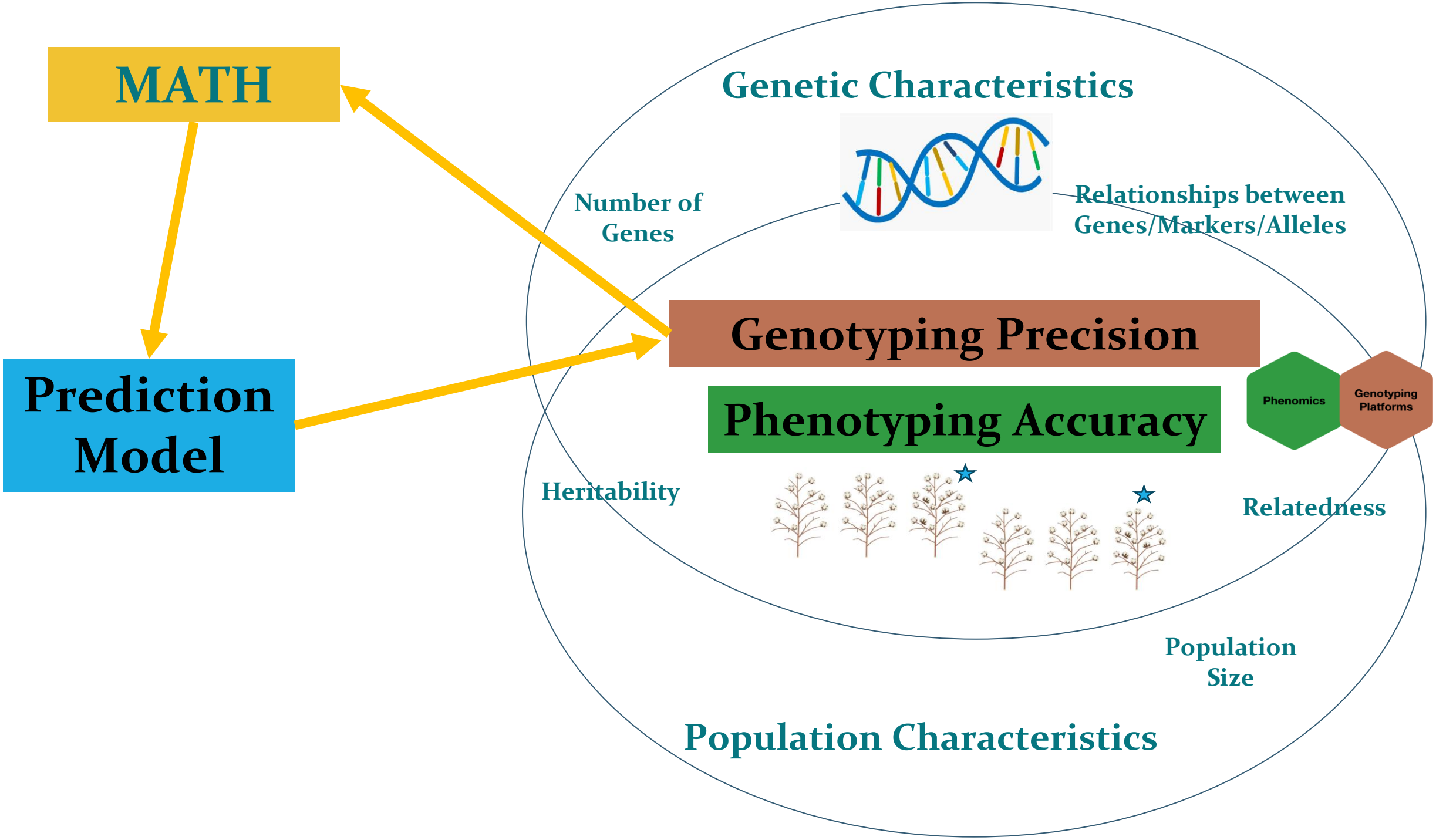
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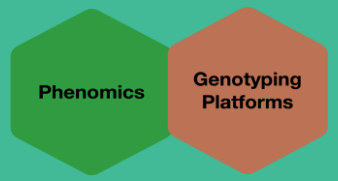
Predictive Breeding = 

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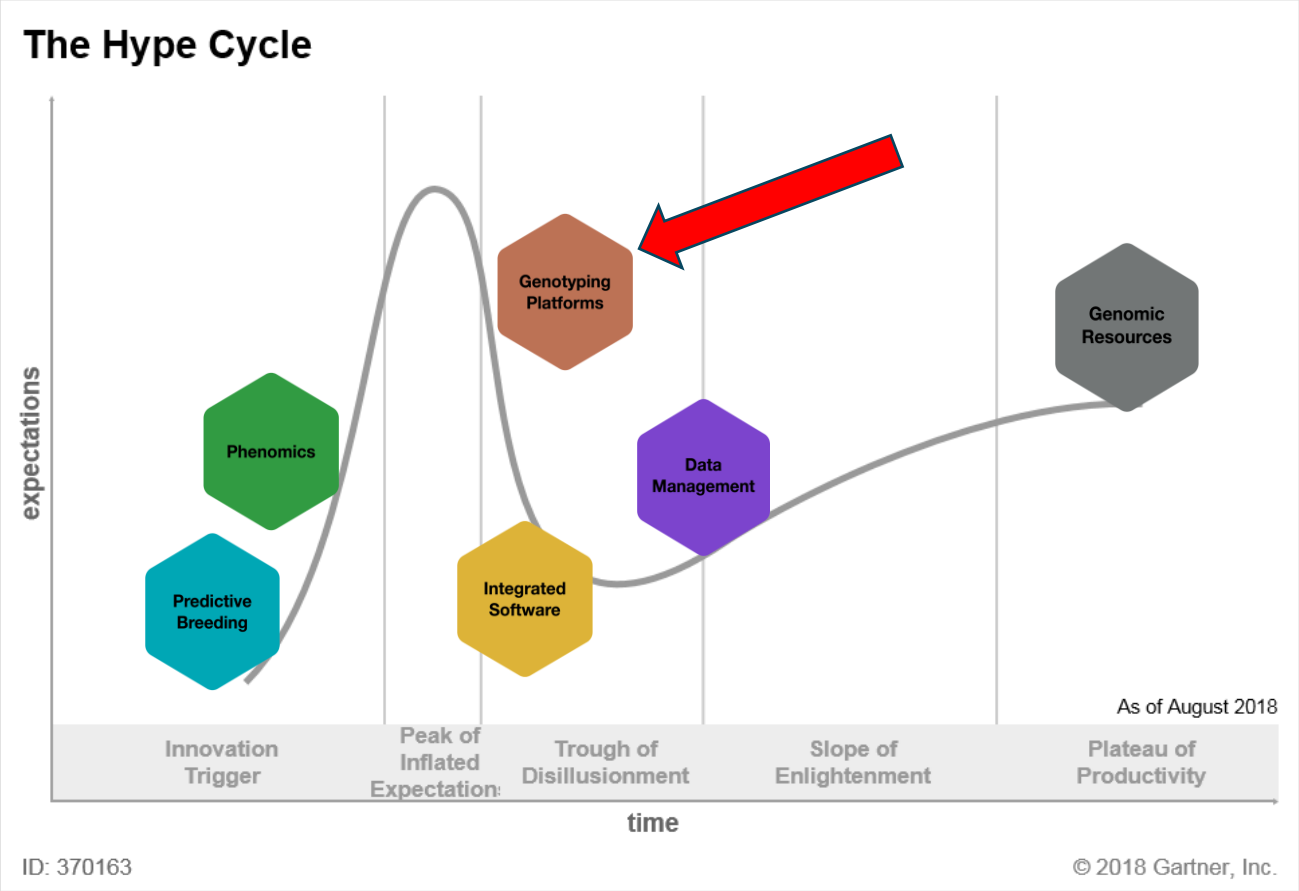


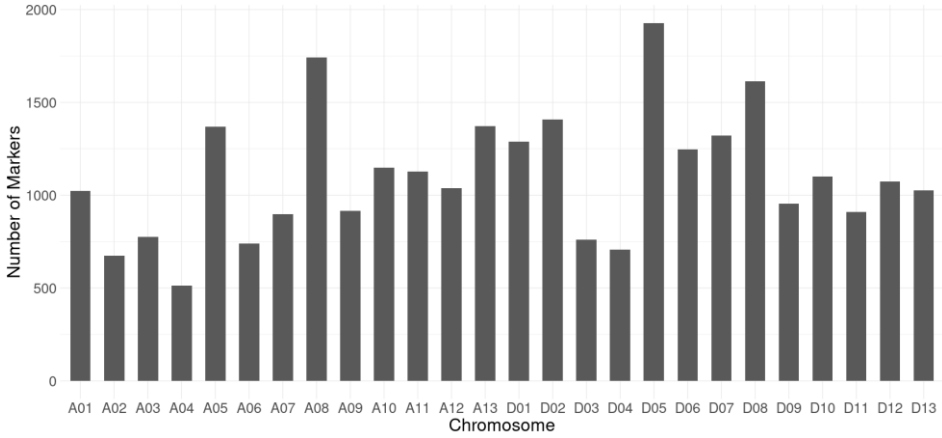
Genotyping Platforms

Various Options

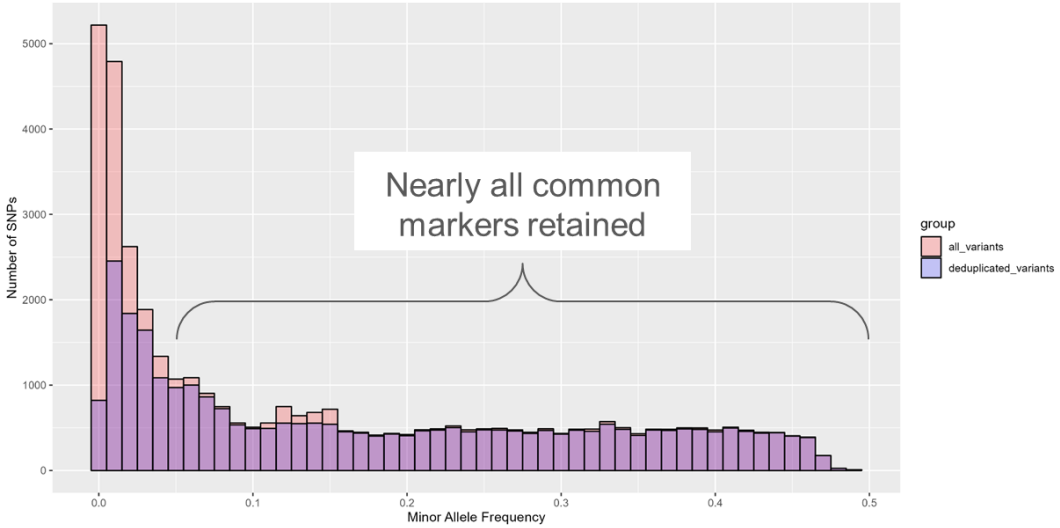
- ~~CottonSNP63K (Available 2015-2023)~~
- CottonSNP30K
  - Public – should be available by end of 2024
- 18K XT Infinium Cotton Array
  - Available now through SGS

CottonSNP30K

- $32/sample + processing
- Includes all markers on SGS 18K
- Like the old array, add-on content is available for private use
- Currently producing cluster file
- ~100 markers for agronomic traits provided by breeders and geneticists



CottonSNP30K



Trait-Specific Markers - Pending Validation

CottonSNP30K

Pulled from Publications

- A10 Cotton blue disease (Fang et al, 2010a - 1 [A/T] type)
- D01 Okra leaf locus (Andres et al, 2016)
- D02 Bacterial blight (Fang et al, 2010b - 4 [A/T])
- D03 FOV4 resistance gene (Liu et al, 2021)
- D06 markers for photopheriodicity (Gowda et al, 2023)

Contributed Confidentially Pre-Publication by Various Collaborators

- 95 markers for various agronomic/fiber quality traits (Billings/Hulse-Kemp et al, unpub. - [A/T] and [C/G] type)
- 13 other markers retained from 63K due to suggestive mapping results (Chee et al, unpub.; Kuraparthy et al, unpub.)
- Other markers (Thyssen/Fang et al.) for:
  - Reniform Nematode
  - STR/UI/SFI
  - Root Knot Nematode
  - Immature Fiber Content, Elongation, Micronaire, Upper Half Mean Length, Fiber Strength

Public Resources along with CottonSNP30K

CottonSNP30K

- Genetic map positions for each marker (from publications on old array)
- Physical TETRAPLOID genome positions on Coker 312
- Cluster file to enable automated processing like the old array
- "Immortal set" of 24 lines - data public
  - Enabling future development of new technologies and technology integration
- R/Shiny App for streamlined analysis & deposition of data to CottonGen
  - https://gbru-ars.shinyapps.io/iCottonQTL/

plants MDPI

Article

Detecting Cotton Leaf Curl Virus Resistance Quantitative Trait Loci in *Gossypium hirsutum* and iCottonQTL a New R/Shiny App to Streamline Genetic Mapping

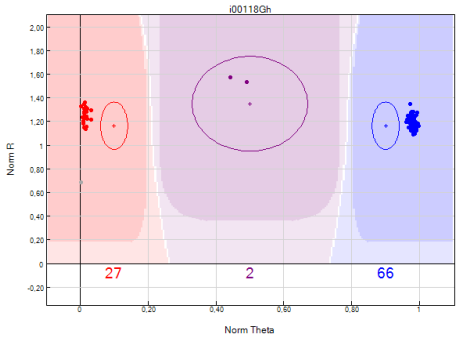
Ashley N. Schoonmaker [1,2], Amanda M. Hulse-Kemp [1,2,3,*], Ramey C. Youngblood [4], Zainab Rahmat [5,6], Muhammad Atif Iqbal [6], Mehboob-ur Rahman [6], Kelli J. Kochan [7], Brian E. Scheffler [8] and Jodi A. Scheffler [9,*]

*Disclaimer – slide received from SGS

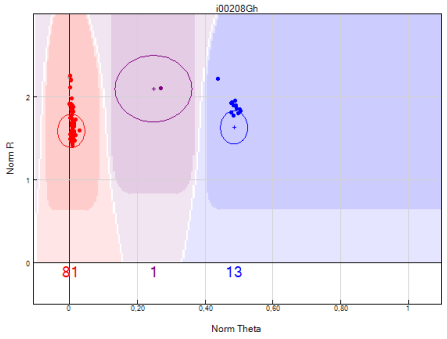
Design Illumina 18K XT Infinium Cotton Array

- **18,438** SNP markers were selected from the 63K HD Infinium Array based on Indian and North-American material
- Selection criteria: marker quality (cluster resolution), genome distribution and redundancy

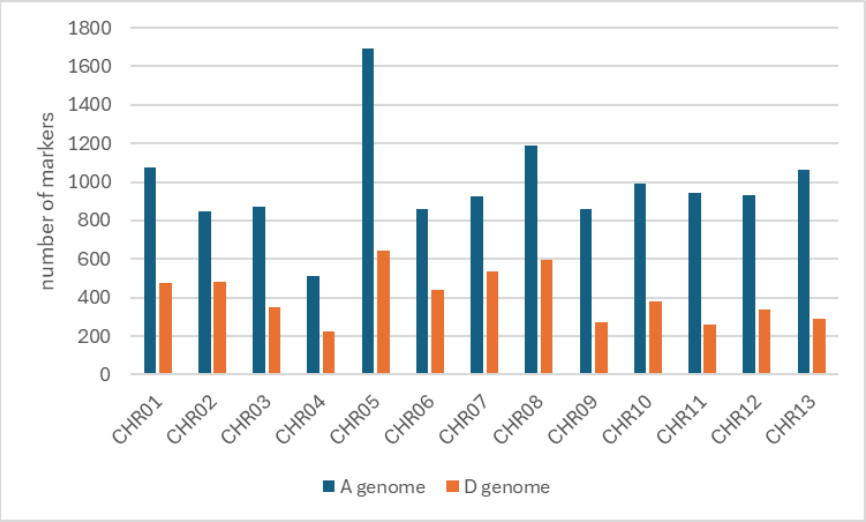
	A genome	D genome
CHR01	1074	477
CHR02	847	480
CHR03	874	352
CHR04	509	223
CHR05	1695	641
CHR06	858	437
CHR07	924	538
CHR08	1187	594
CHR09	859	270
CHR10	991	379
CHR11	946	259
CHR12	933	336
CHR13	1066	290
sum	12763	5276
unmapped	399	



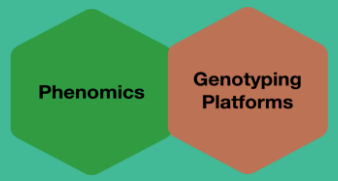
genome specific marker



marker detecting both genomes



Martin Ganal martin.ganal@sgs.com
Edward Bruggemann edward.bruggemann@sgs.com

Predictive Breeding = 

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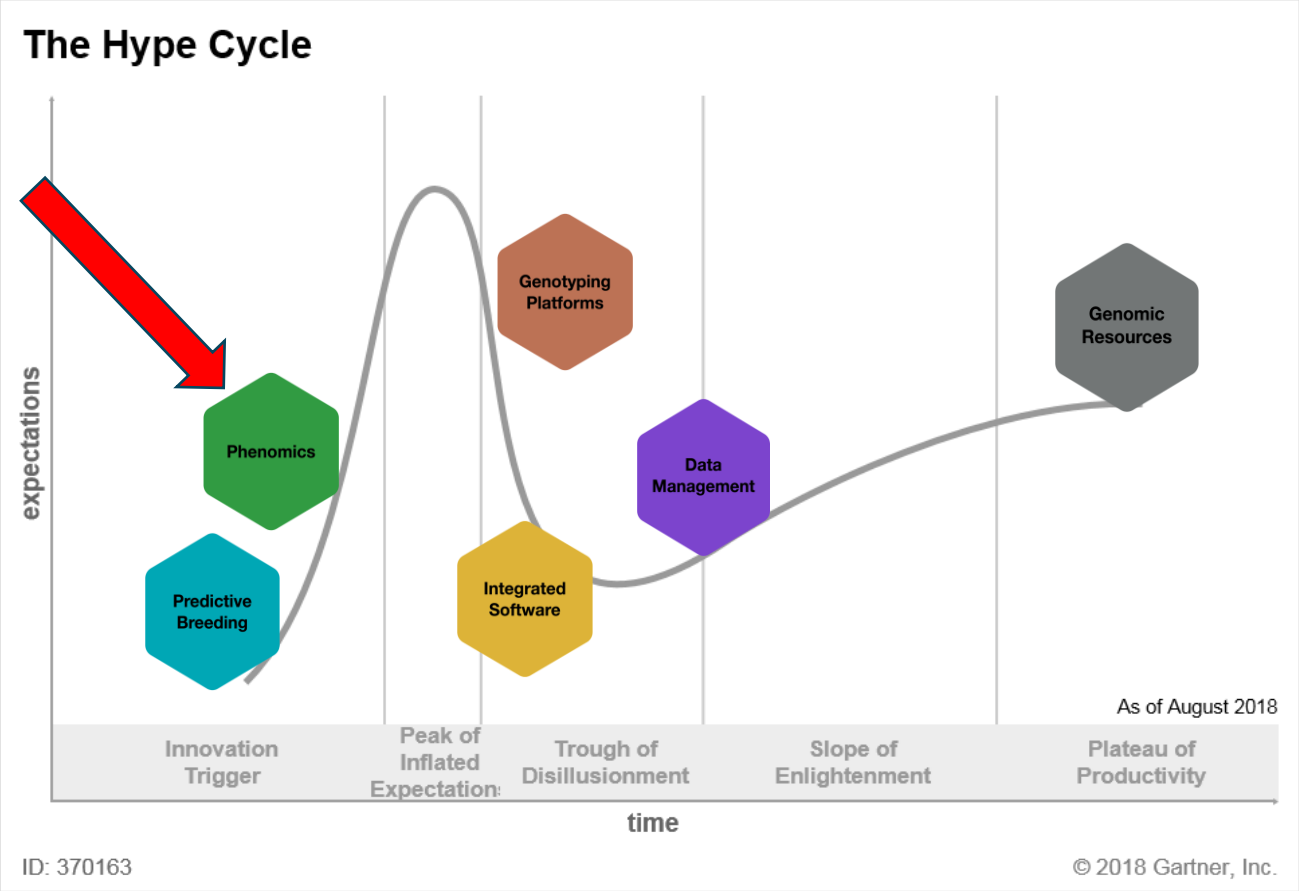


Phenomics

What would be helpful

- Capturing additional trait-specific markers
  - QTL/Fine-mapping
- Validating function of identified loci
  - Transformation, VIGS

VALIDATED FUNCTION -> FIXED EFFECTS

Genome Wide Association Model:

$$Y = \mu + X_S\beta_S + Zu + \varepsilon$$

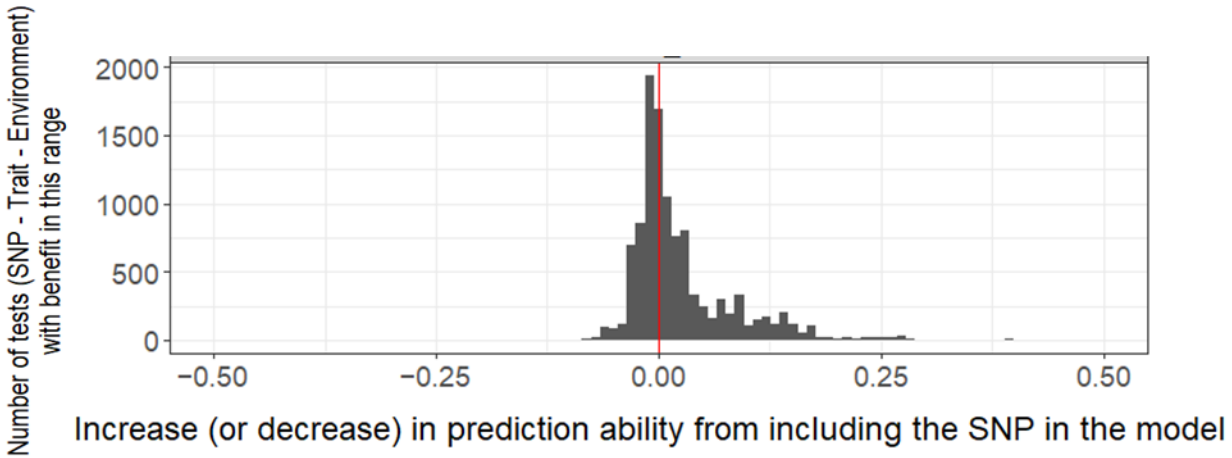
Interest is in SNP effect $\widehat{\beta}_S$

Can add fixed effects to the model for loci with known function

Genomic Prediction Model:

$$Y = \mu + Zu + \varepsilon$$

Interest is in prediction of u: $\widehat{u}$



Billings et al. (2022) Outlook for Implementation of Genomics-Based Selection in Public Cotton Breeding Programs

Phenomics

What would be helpful

- Capturing additional trait-specific markers
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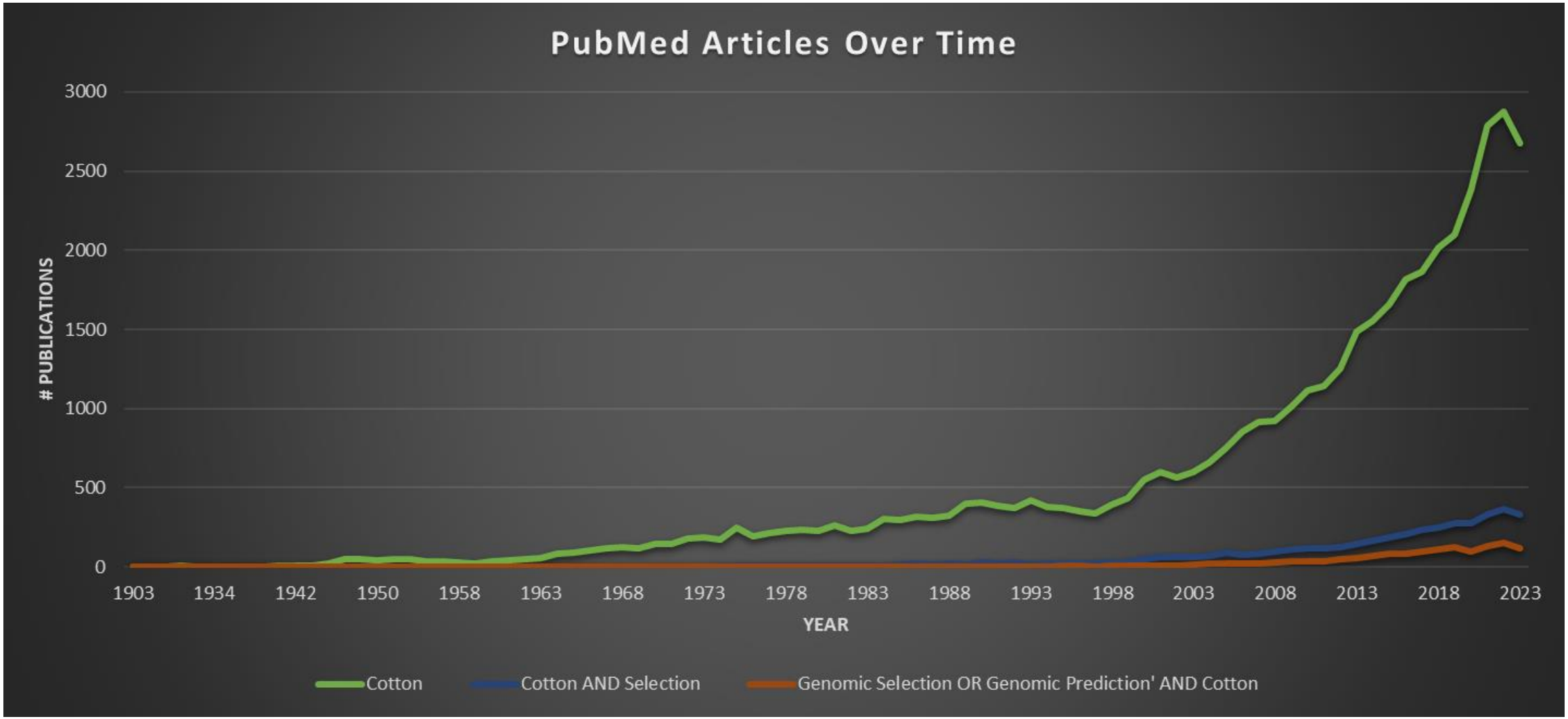
- Validating function of identified loci
  - Transformation, VIGS
- Standardized formatting of publication results

WHY?


PubMed Articles Over Time
PUBLICATIONS
3000
2500
2000
1500
1000
500
0
1903
1934
1942
1950
1958
1963
1968
1973
1978
1983
1988
1993
1998
2003
2008
2013
2018
2023
YEAR
Cotton
Cotton AND Selection
Genomic Selection OR Genomic Prediction' AND Cotton

FORMATTING ENABLES BIOINFORMATICS

aka...
Helping
ourselves!!!

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- Full summary statistics for any analysis (GWAS or differential expression)
- Supplemental tables listing each differentially expressed gene
- Clearly indicate genome version utilized in analysis
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BONUS -> Work directly with CottonGen as a part of your publication process and ensure result is available through that avenue directly

CottonGen
Cotton Database Resources

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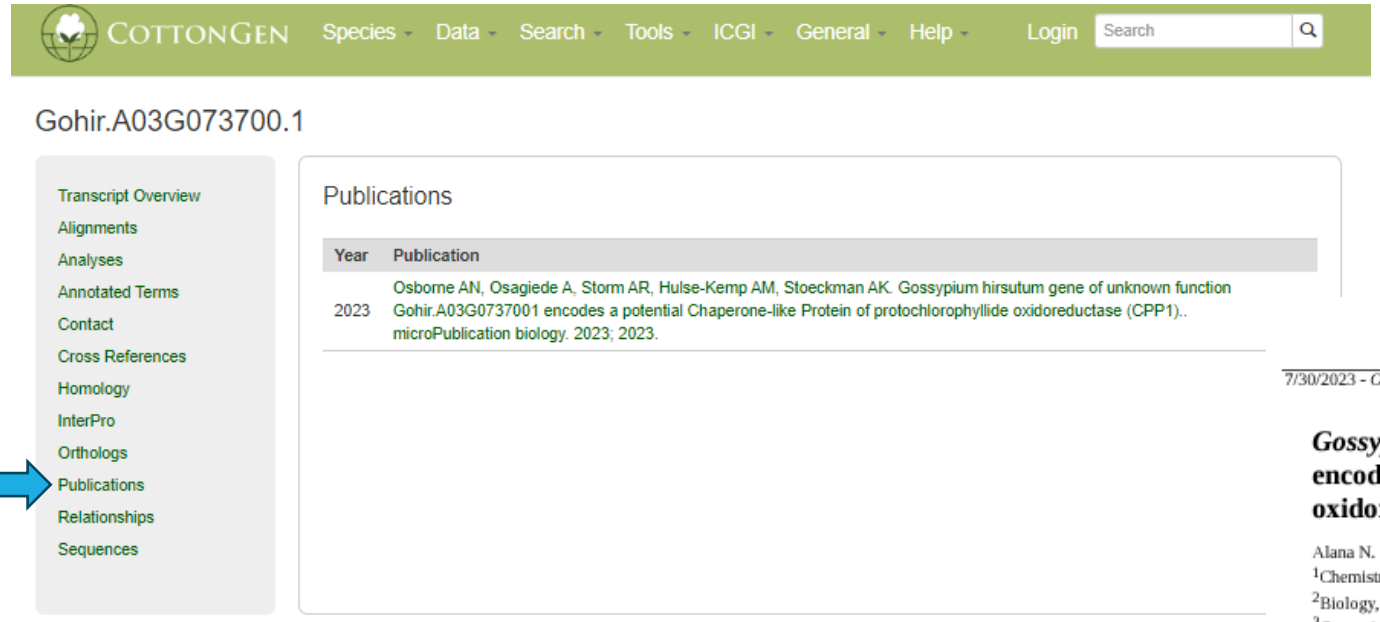

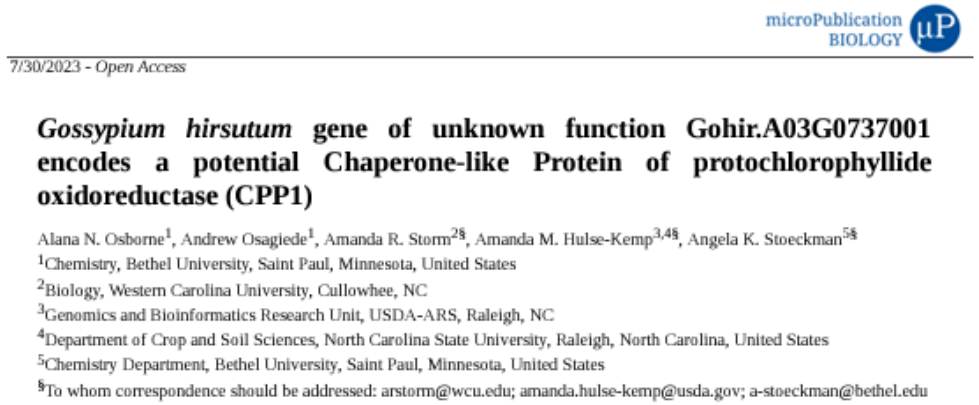

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Phenomics

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- Capturing additional trait-specific markers
  - QTL/Fine-mapping
- Validating function of identified loci
  - Transformation, VIGS
- Standardized formatting of publication results
- Movement to digital data and databases

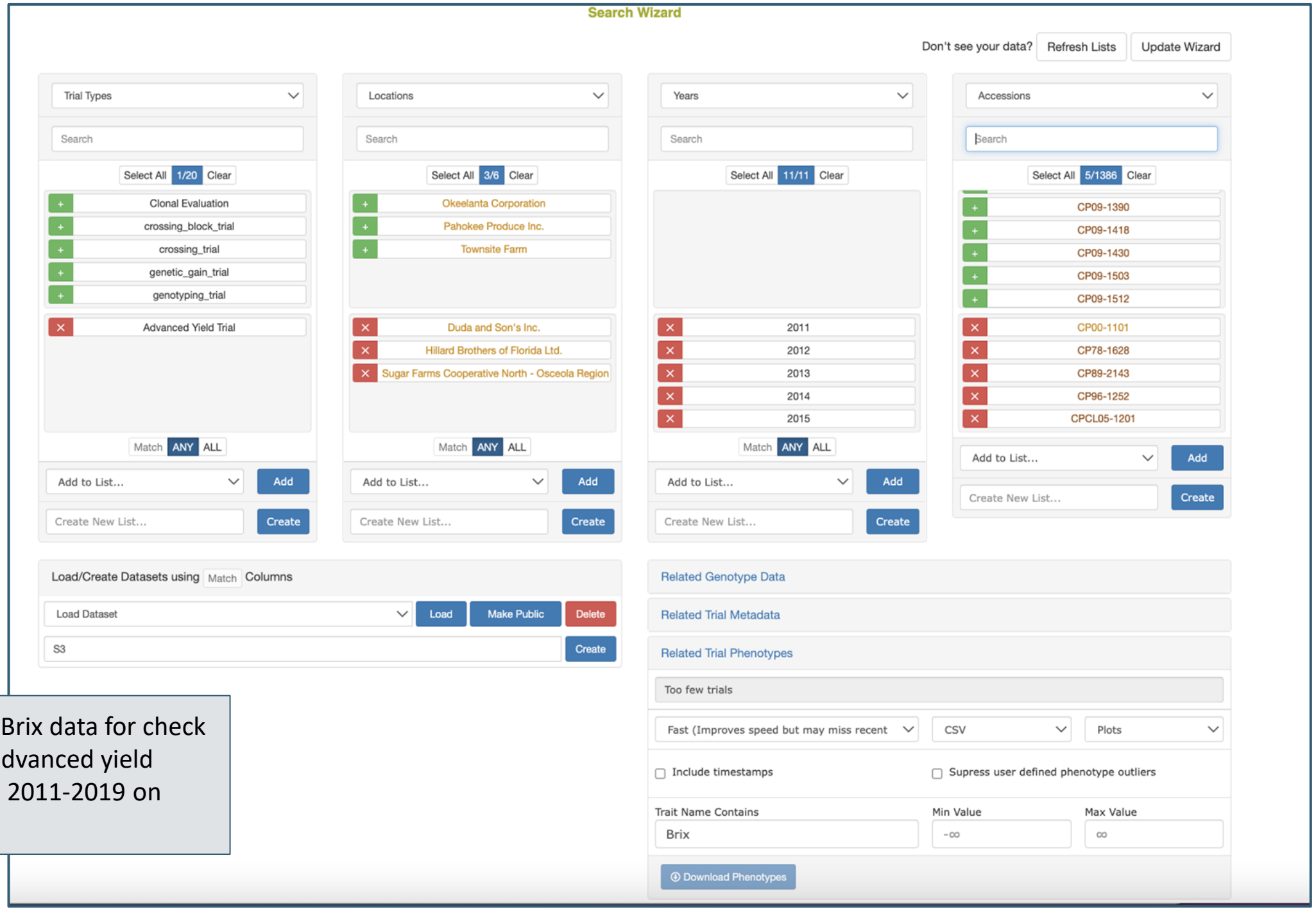
BREEDBASE

BREED WITH BIMS

COTTONGEN
COTTON DATABASE RESOURCES

Field Book

Breedbase allows fast data queries without advanced programming knowledge!



"I want to analyze Brix data for check varieties used in advanced yield trials conducted in 2011-2019 on muck soils"

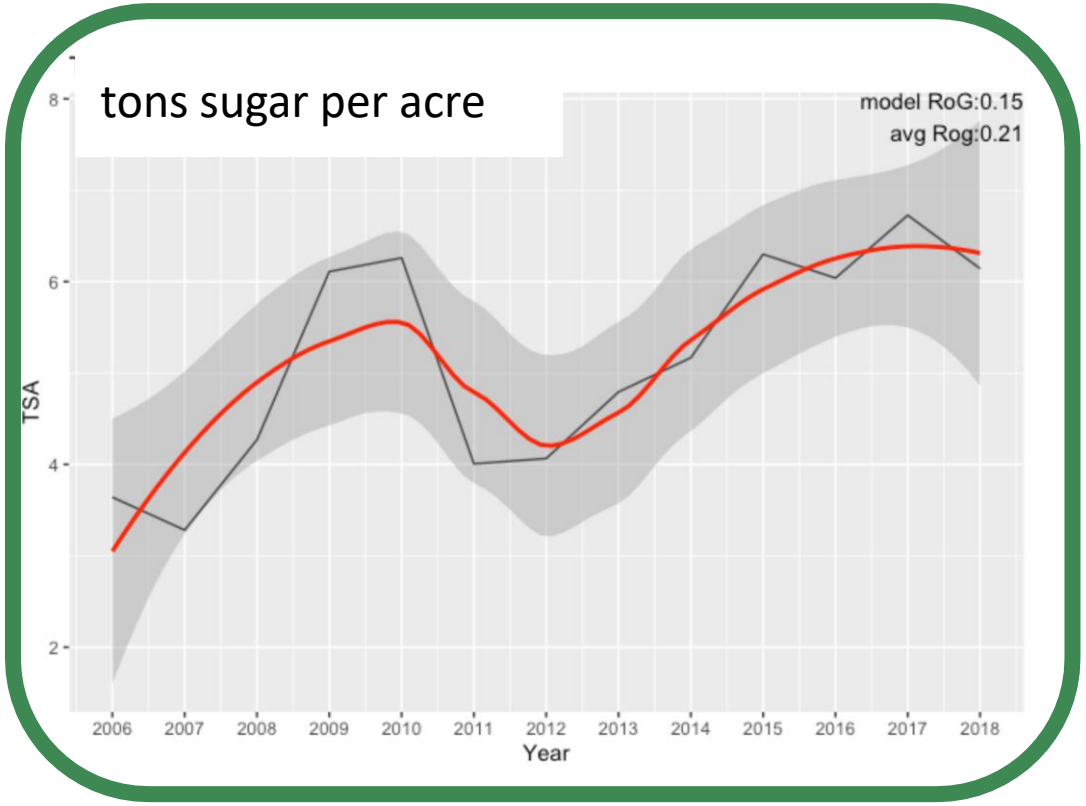
Phenomics

What would be helpful

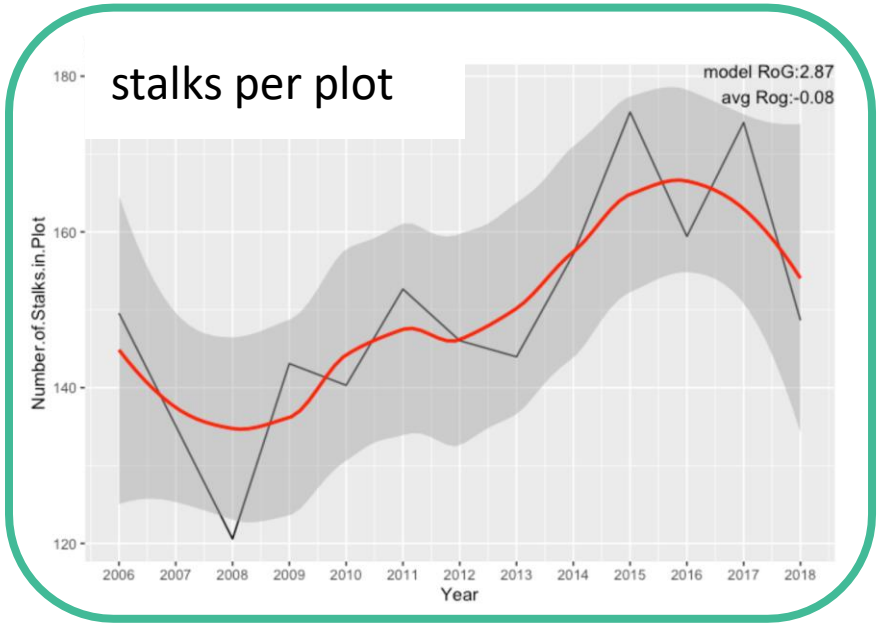
- Capturing additional trait-specific markers
  - QTL/Fine-mapping
- Validating function of identified loci
  - Transformation, VIGS
- Standardized formatting of publication results
- Movement to digital data and databases
- Increased shared use of checks
  - Enable cross location comparison of early generation materials
  - Use transformation lines as checks

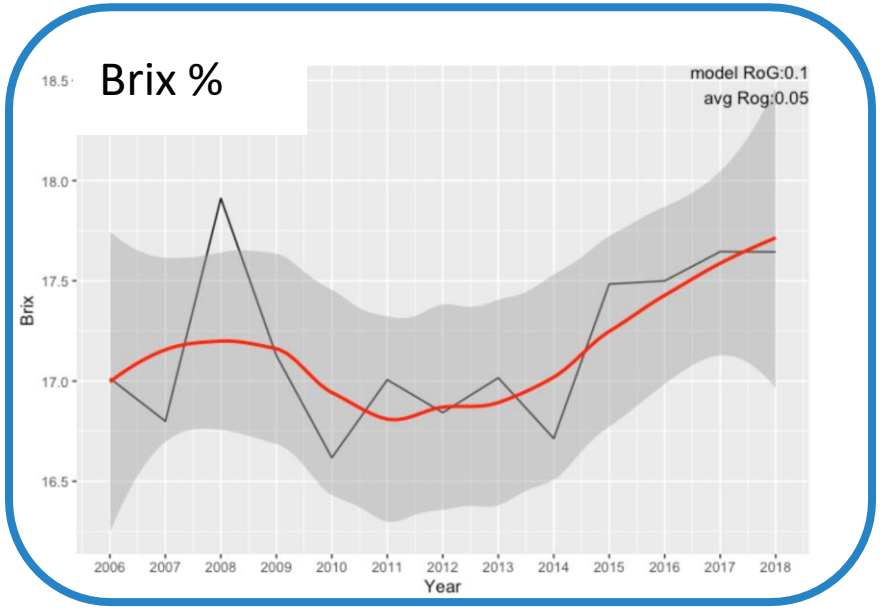
MAKES EVALUATION OVER TIME POSSIBLE

USDA Sugarcane



Yield is up, but that's driven by increases in **biomass**, not **sugar**



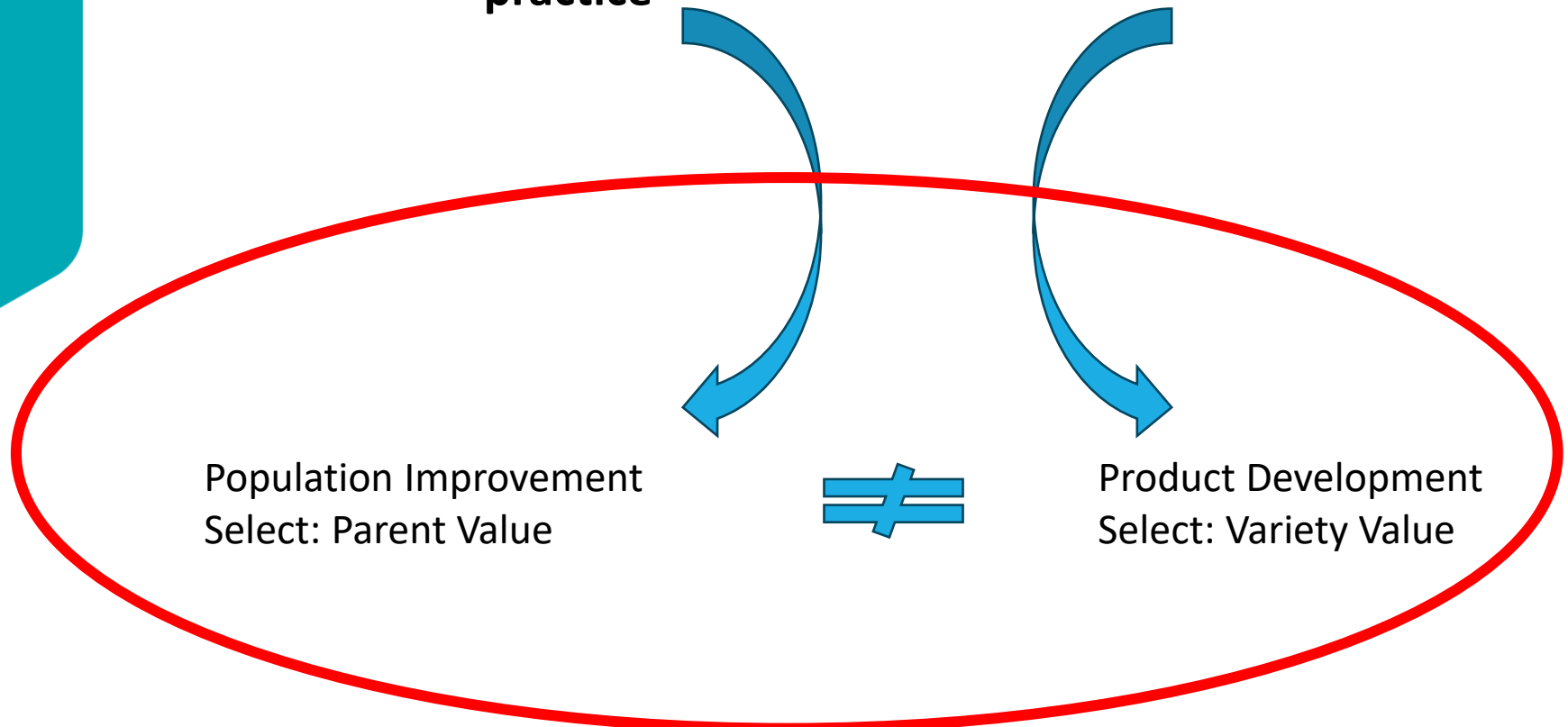


BREEDING INSIGHT ONRAMP

Predictive Breeding

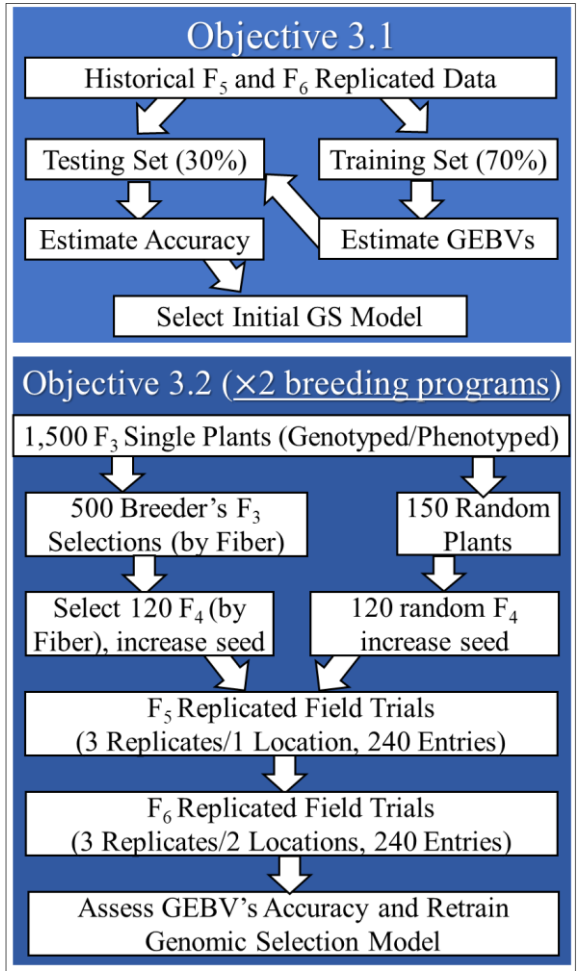
Estimating traits across experiments - ie. in a breeding program (related, but NOT the same set of materials); THEN using those estimates to select what individuals to retain = GENOMIC SELECTION

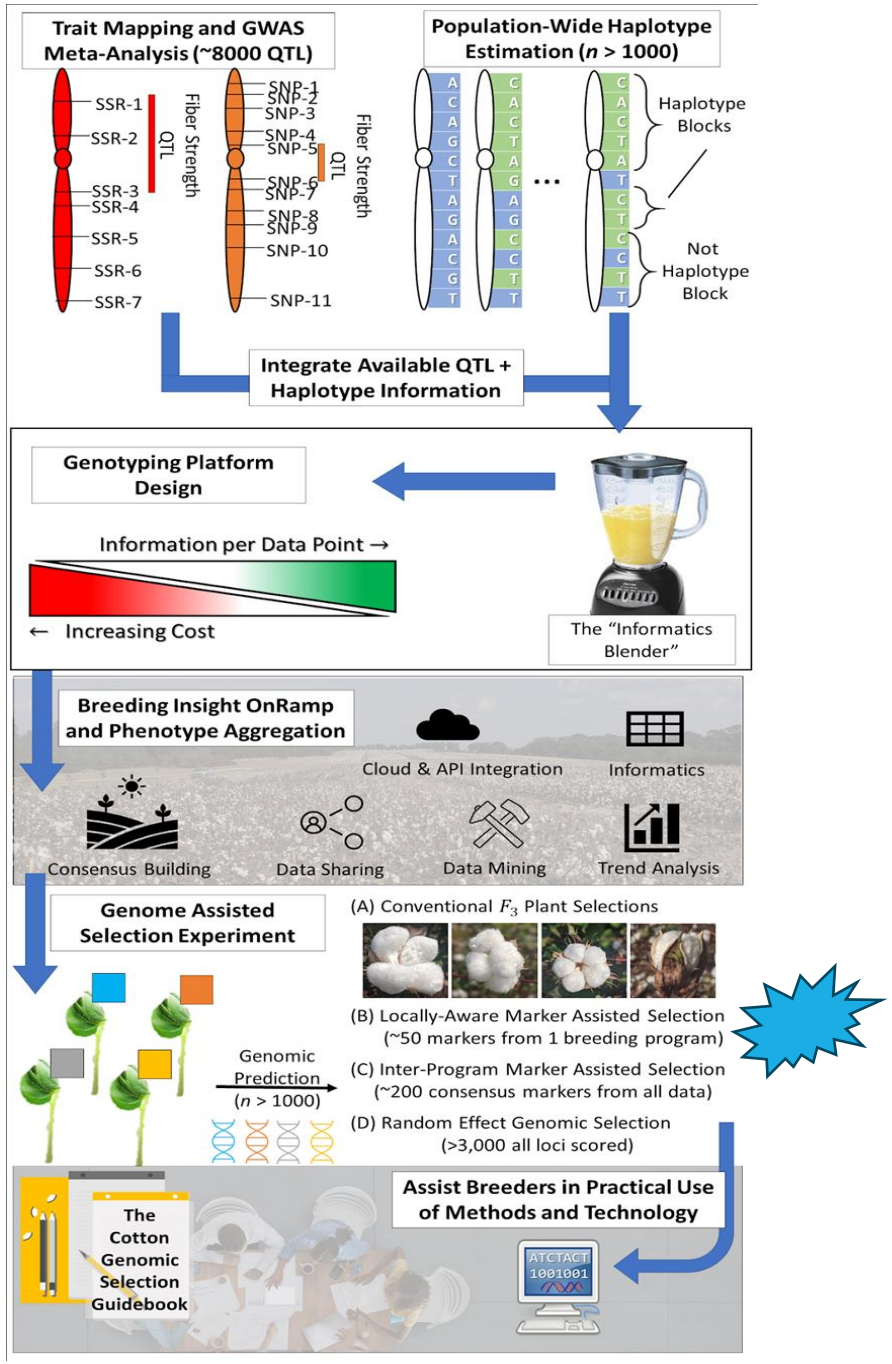
- **May be empirically similar or potentially very different in practice than Genomic Prediction**
- **Difficult to measure success until put in practice**



PRODUCT DEVELOPMENT SELECT: VARIETY VALUE

- Empirically test impact of selection against traditional selection methods
- Initiate and compare genomic selection methods in two US public cotton breeding programs and develop recommendations.



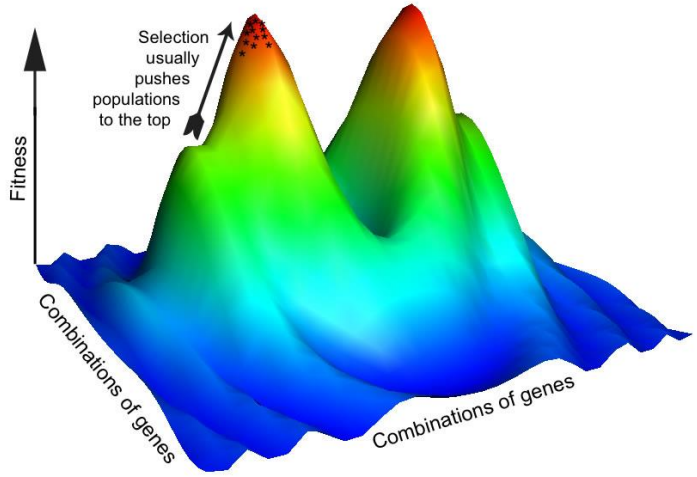


POPULATION IMPROVEMENT
SELECT: PARENT VALUE

- Investigate benefit of earlier recycling of materials for parents
- Are mid-parent values fully predictive of progeny performance?
- Target recombination recalcitrant areas
- General combining ability vs. Specific combining ability

WHAT DOES THE FUTURE LOOK LIKE?

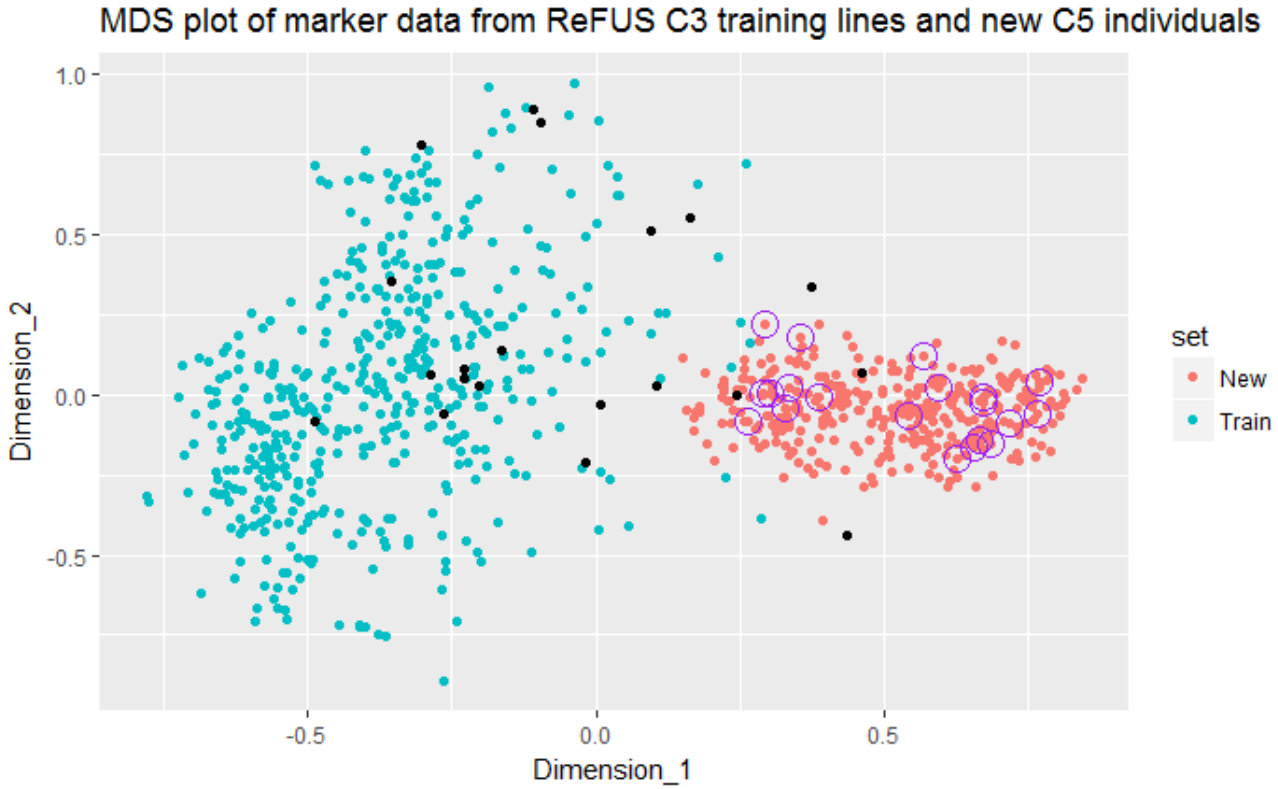
- Moving from single crop function to leveraging across crops
  - Informatics to Identify NEW adaptive peaks

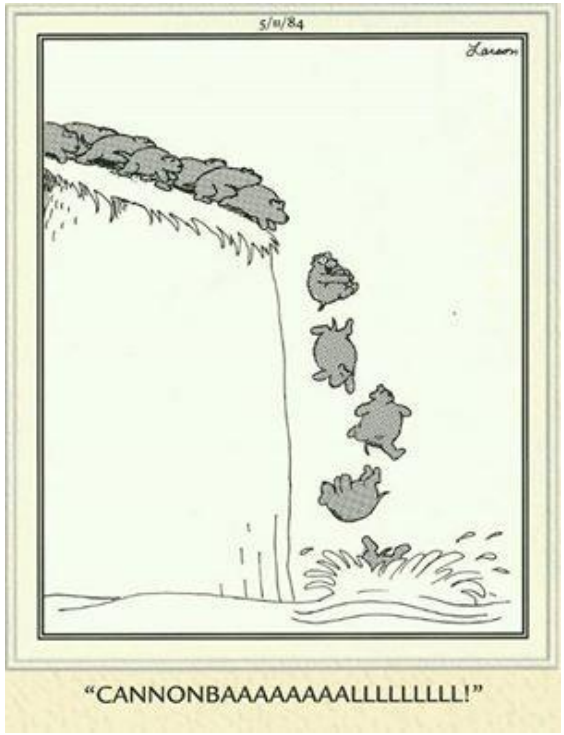


- Advancing Genomic Selection
  - Leverage data across breeding programs
  - Continued access to performant high-quality genotyping platforms

- Better integrated Systems can use in the Field!
  - Sharing phenotyping technologies

GENOTYPIC COMPOSITION OF GS POPULATION IS CHANGING VERY FAST!





Gary Larson

Minimizing inbreeding with 'Optimal Contribution' method and genetic algorithms!

Accuracy of prediction model breaks down over generations

Courtesy of Jim Holland et al.

ACKNOWLEDGEMENTS

Grant Billings
Jonathan Zirkel

SGS (Formerly Trait Genetics) - Martin Ganal, Ed Bruggemann

David Stelly

Kelli Kochan

Gregory Thyssen

David Fang

Vasu Kuraparthy

Anjan Gowda

Peng Chee

Todd Campbell

Jodi Scheffler

USDA Agricultural Research Service

Cotton Incorporated

Nos.18-274, 19-872, 21-734

USDA NIFA

MISW-2021-11369
MISW-2021-07681