Intro to Genomic Breeding

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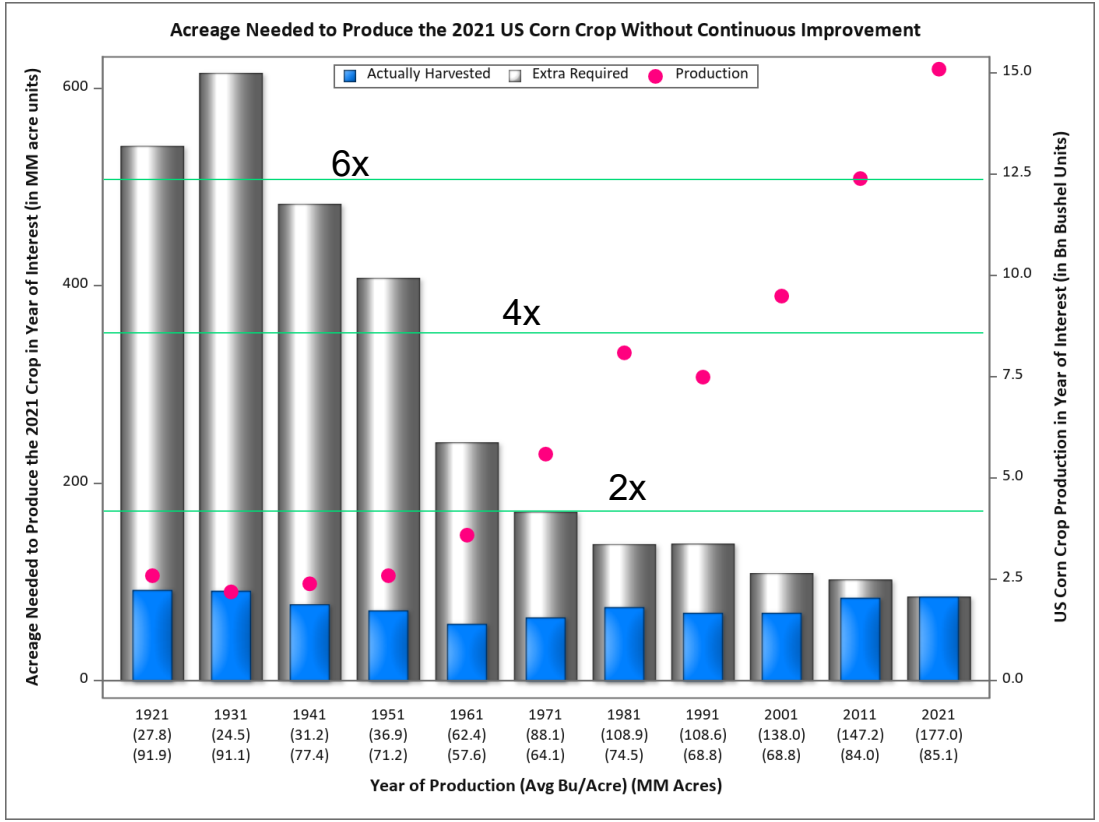
What are some implications of continuous Corn Improvement?



*Based on 2021 USDA NASS data

Source: Totir 2021, ASTA

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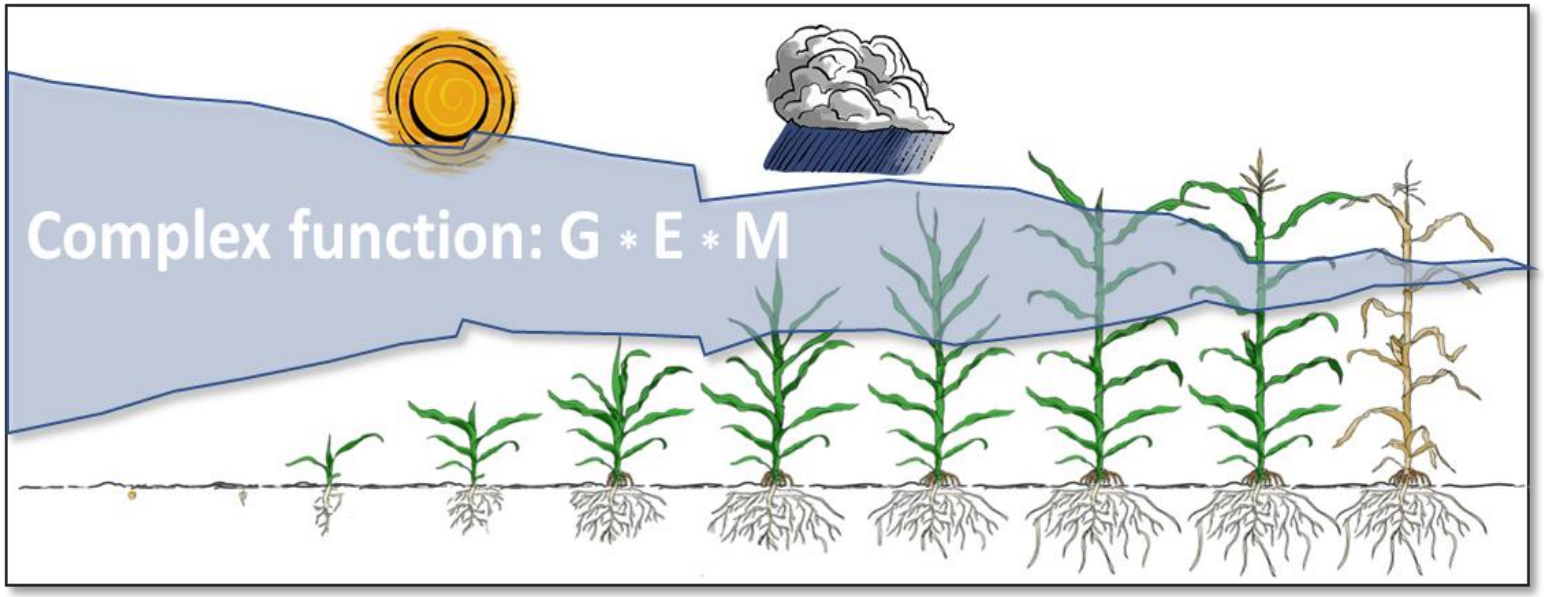
Challenges in Corn Improvement



G = Genetics; E = Environment; M = Management

Source: Totir 2021, ASTA

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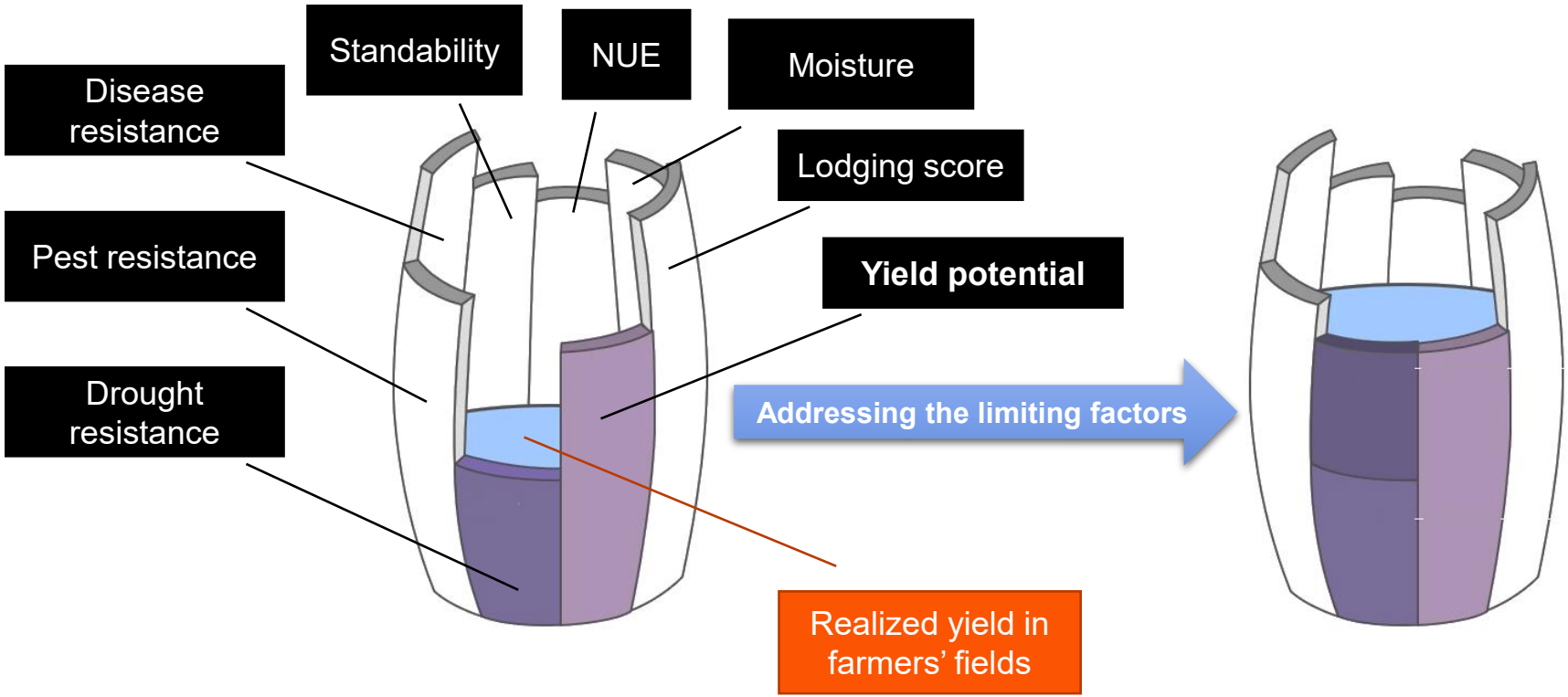
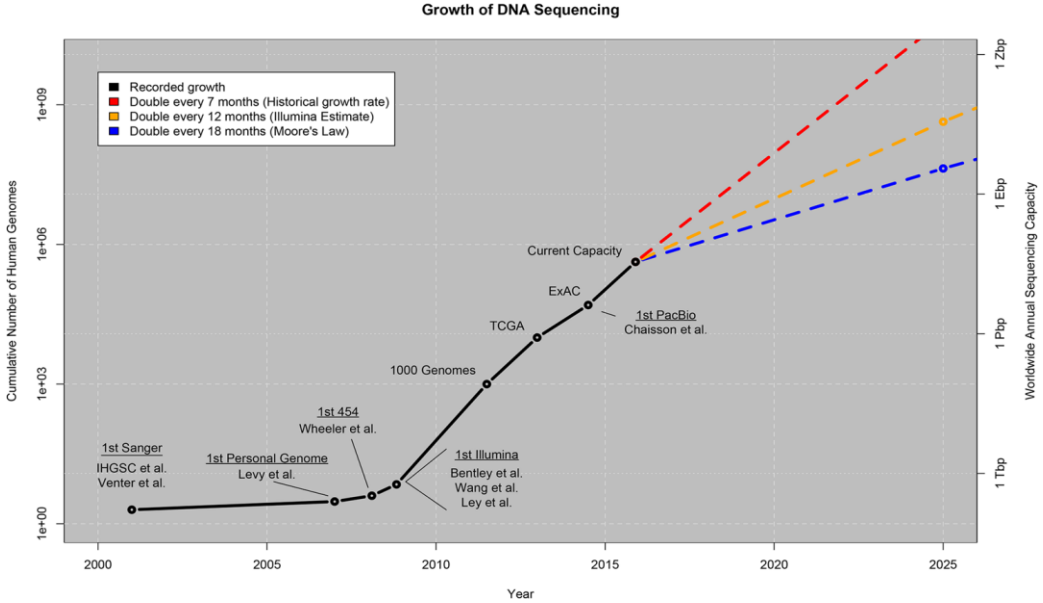
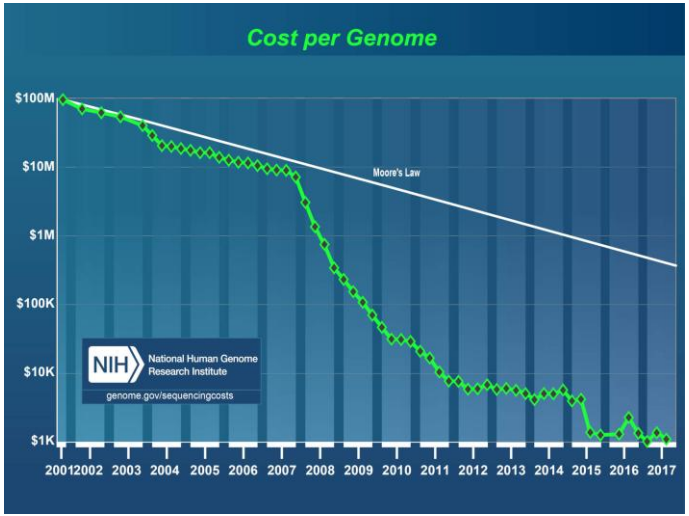
Law of the minimum





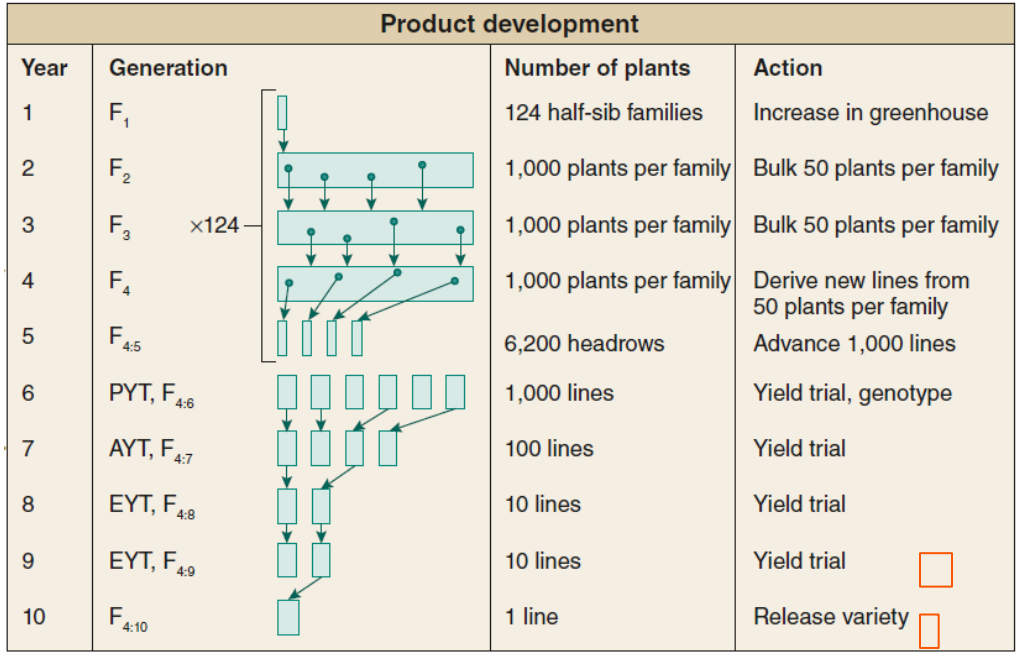
Stephens, Z. D.et al. (2015). Big data: astronomical or genomical? *PLoS biology*, *13*(7), e1002195.



The Cost of Sequencing a Human Genome. NIH. https://www.genome.gov/27565109/the-cost-of-sequencing-a-human-genome/

PLANT BREEDING PIPELINE

Example from one program, one geography - Varietal Wheat



Product development			
Year	Generation	Number of plants	Action
1	F_1	124 half-sib families	Increase in greenhouse
2	F_2	1,000 plants per family	Bulk 50 plants per family
3	F_3 ×124	1,000 plants per family	Bulk 50 plants per family
4	F_4	1,000 plants per family	Derive new lines from 50 plants per family
5	$F_{4:5}$	6,200 headrows	Advance 1,000 lines
6	PYT, $F_{4:6}$	1,000 lines	Yield trial, genotype
7	AYT, $F_{4:7}$	100 lines	Yield trial
8	EYT, $F_{4:8}$	10 lines	Yield trial
9	EYT, $F_{4:9}$	10 lines	Yield trial
10	$F_{4:10}$	1 line	Release variety

Hickey et al. (2017) *Nature genetics* 49(9):1297

Main types of plant breeding

1. Varietal (soy, wheat)
2. Hybrid (corn, sunflower)
3. Clonal (potato, sugar cane)
4. Population (alfalfa, red clover)

“Breeding objective”

$f(\text{market segment, farming systems})$

- Set of traits of interest (**TOI**) bred into a
  WHAT

  Yield, moisture, maturity, disease resistance, stability, producibility

- Target population of genetics (**TPG**) for a given
  WHO

  Corn 110-112, soybean MG2, winter wheat

- Target population of environments (**TPE**) and management (**TPM**) practices
  WHERE
  HOW, WHEN

  Drought, irrigation, early planting, varying levels of disease pressure, different soil types

$$\rho_{\text{GxExM}} = \rho_{\text{TPG}} \times \rho_{\text{TPE}} \times \rho_{\text{TPM}}$$

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What is genomic prediction?

DATASET	GENOTYPES	PHENOTYPES
TRAINING POPULATION	YES	YES
PREDICTION TARGET	YES	NO

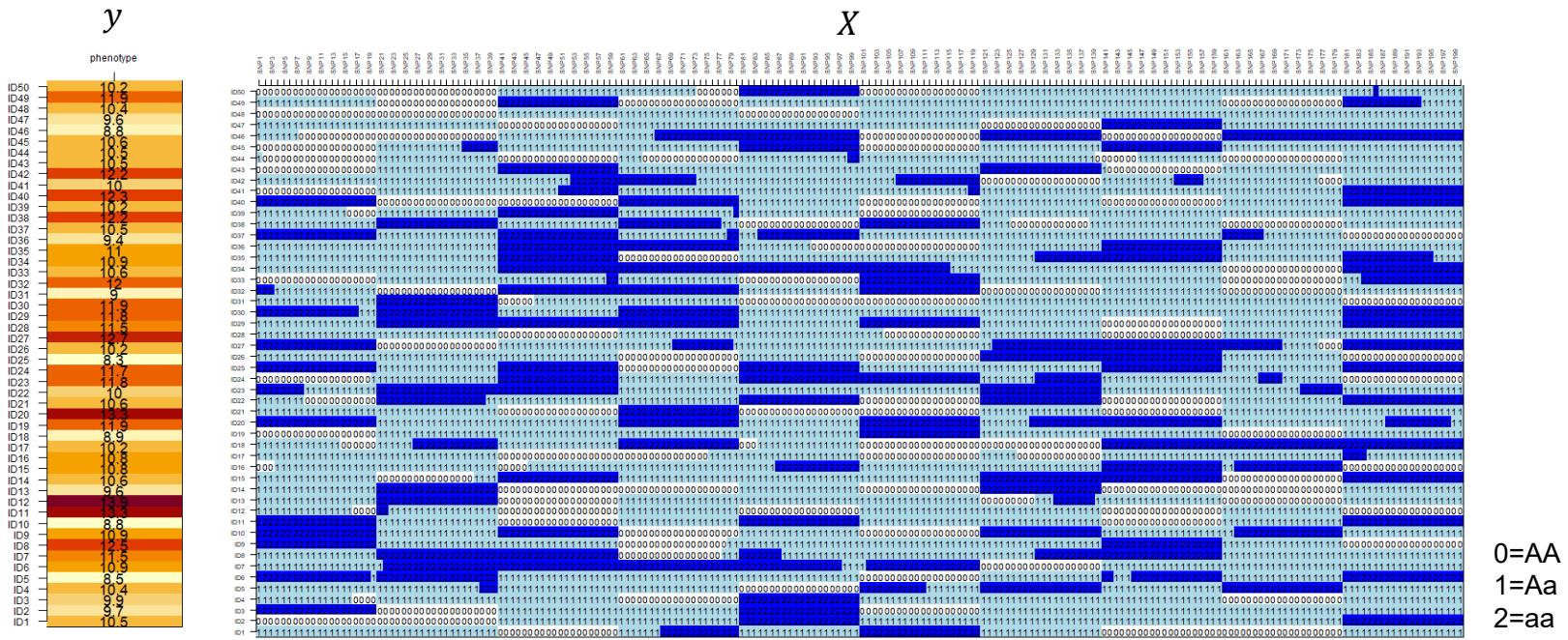
Purpose of GS:

- Improve selection accuracy
- Select material without phenotypes
- Selection of new parents
- Prediction of cross combinations
- Optimize resources
- Stability and genetic architecture

Genomic prediction accuracy is a function of

- Heritability of the trait
- Relationship training-prediction population
- GxE between training-prediction environment

How does GS work?



Regression problem: $y = \mu + X\beta + \epsilon$

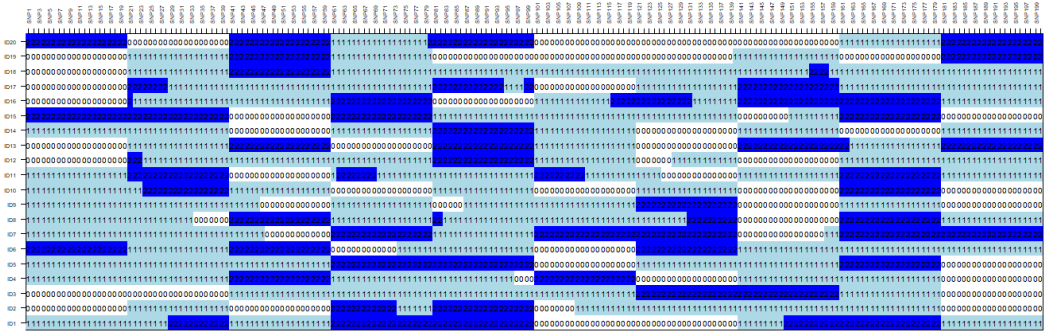
How does GS work?

Regression problem:

$$y = \mu + X\beta + \epsilon$$

```
> fit = bWGR::mrr(Y,X)
> fit$mu # intercept
[1] 10.80188
> head( fit$b ) # coefficients
            [,1]
[1,] 0.01093033
[2,] 0.01169121
[3,] 0.01169235
[4,] 0.01126376
[5,] 0.01126586
[6,] 0.01126662
> fit$h2 # heritability
[1] 0.1917349
```

New set of individuals, genotyped but not phenotype?



Regression model (SNP-BLUP) →

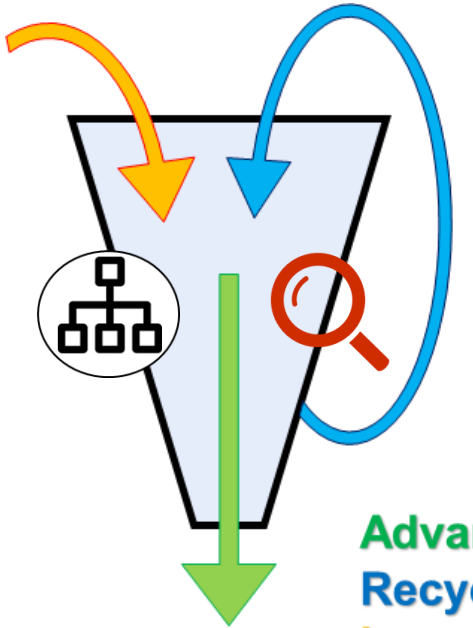
Intercept: $\hat{\mu}$
Coefficients: $\hat{\beta}$
Heritability: $\hat{h}^2$
Breeding values: $\hat{g} = X\hat{\beta}$

→

$$\hat{g}_{new} = \hat{\mu} + X_{new}\hat{\beta}$$

APPLICATIONS

Where is genomic information used for breeding?



Advancement
Recycling
Incorporation

Monitoring

Classification

Where is genomic information used for breeding?

- Germplasm classification (***PCA, Clustering, Unsupervised ML, F_{ST}***)
- Incorporation (***GWAS, haplotype analysis***)
- Genomic selection (***BayesABC, Supervised ML, etc.***)
- Recycling (***Simulation and optimization***)
- Quantitative assessment (***Variance component analysis***)

Where is genomic information used for breeding?

- Germplasm classification (***PCA, Clustering, Unsupervised ML, F_{ST}***)
  - **Characterization** – Characterize diversity using unsupervised learning methods.
  - **Heterotic group** – Classify (if known) or infer (if unknown) heterotic groups on individuals and populations.
  - **Signatures of selection** – Use F_{ST} (or related methods) to identify signatures of selection, adaptation and domestication.
- Incorporation (***GWAS, haplotype analysis***)
- Genomic selection (***BayesABC, Supervised ML, etc.***)
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Where is genomic information used for breeding?

- Germplasm classification (***PCA, Clustering, Unsupervised ML, F_{ST}***)
- Incorporation (***GWAS, haplotype analysis***)
  - **Trait discovery** – Finding new QTLs via association analysis on breeding data and designed populations.
  - **Introduction of diversity** – Screening non-elite (or elite from elsewhere) germplasm for pre-breeding.
  - **Haplotype enrichment** – Assess genome of non-elite material to add diversity to regions where elite germplasm is fixed.
- Genomic selection (***BayesABC, Supervised ML, etc.***)
- Recycling (***Simulation and optimization***)
- Quantitative assessment (***Variance component analysis***)

Where is genomic information used for breeding?

- Germplasm classification (***PCA, Clustering, Unsupervised ML, F_{ST}***)
- Incorporation (***GWAS, haplotype analysis***)
- Genomic selection (***BayesABC, Supervised ML, etc.***)
  - **F2 enrichment (WF)** – Entire population is genotyped with few markers and selected for specific QTL (e.g. disease resistance)
  - **Pre-selection (WF/AF)** – Entire population is genotyped and 0% is phenotyped. Selection is based on the genomic merit estimated a predefined estimation set that is either made by design or using breeding data.
  - **Test-and-shelf (WF/AF)** – Entire population is genotyped and X% is phenotyped. Within-season selection is based on the genomic merit estimated with a genomic model from phenotyped individuals.
  - **Advancement (WF/AF)** – Entire population is genotyped and phenotyped. Selection is based on the genetic merit of the individuals using one or more seasons of data from those individuals.
  - **Product placement (AF)** – Similar to advancement but GxE takes the spotlight from G.
- Recycling (***Simulation and optimization***)
- Quantitative assessment (***Variance component analysis***)

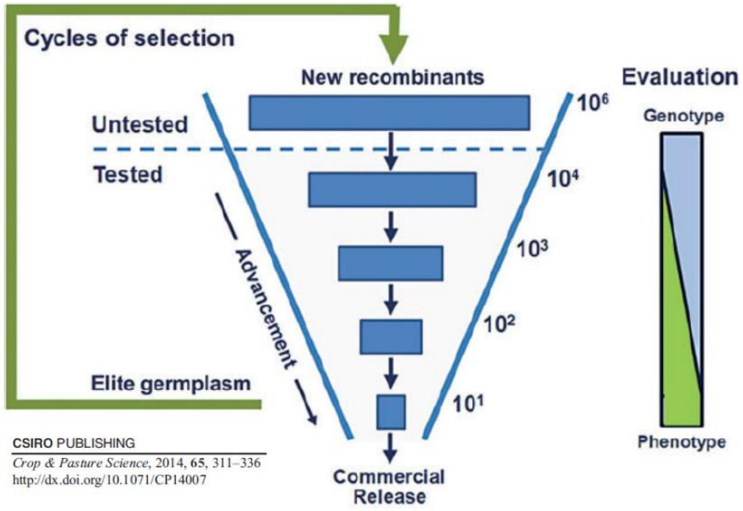
Where is genomic information used for breeding?

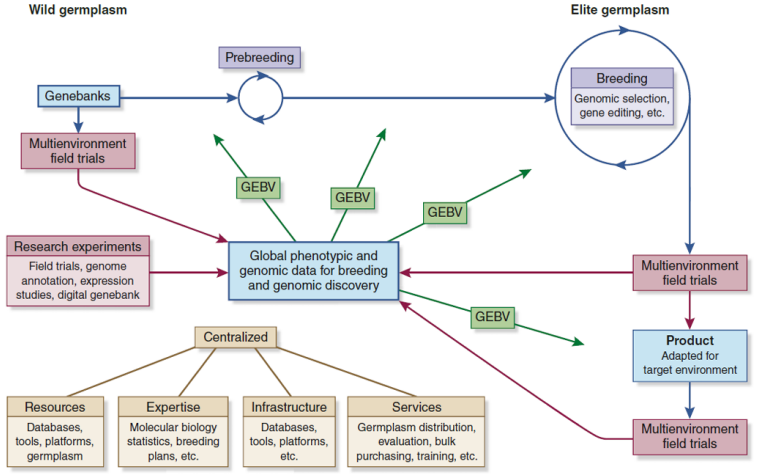
- Germplasm classification (***PCA, Clustering, Unsupervised ML, F_{ST}***)
- Incorporation (***GWAS, haplotype analysis***)
- Genomic selection (***BayesABC, Supervised ML, etc.***)
- Recycling (***Simulation and optimization***)
  - **Selection of parents** – Selection of high BV individuals with complementary polygene or traits.
  - **Select combinations** – Providing a set of candidate parents (100% genotyped), combinations are based on clustering, simulate crosses or predefined criterium (OHV or OPV).
- Quantitative assessment (***Variance component analysis***)

Where is genomic information used for breeding?

- Germplasm classification (***PCA, Clustering, Unsupervised ML, F_{ST}***)
- Incorporation (***GWAS, haplotype analysis***)
- Genomic selection (***BayesABC, Supervised ML, etc.***)
- Recycling (***Simulation and optimization***)
- Quantitative assessment (***Variance component analysis***)
  - **Heritability** – Narrow-sense and GxE (e.g. compound symmetry)
  - **Genetic variance decomposition** – Classic (Vg = Va + Vd + Vi) and hybrid ($Vg = V_{GCA1} + V_{GCA2} + V_{SCA}$)
  - **Genetic correlations** – Across traits or within-trait across environments
  - **Effective population size** – Eigen analysis of the G matrix
  - **Genetic progress and rate of genetic gains** – Assess multiple years
  - **Evaluate breeding strategies** – Simulations and retrospective studies to ask ***what if*** questions

Training population theory





Hickey et al. (2017) *Nature genetics* 49(9):1297

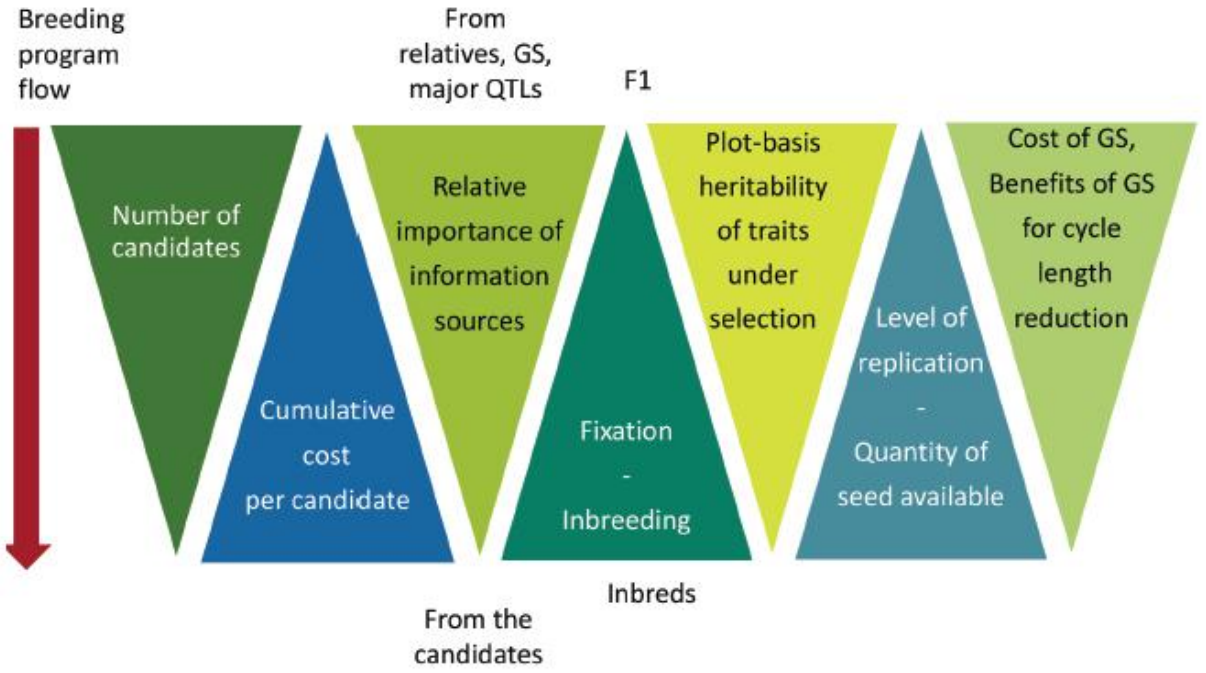


Figure 1. Key parameters and changes during a breeding cycle, to consider in implementing genomic selection (GS). The triangles indicate increase or decrease of the quantity considered. QTL, quantitative trait loci.

Heslot, N., Jannink, J. L., & Sorrells, M. E. (2015). Perspectives for genomic selection applications and research in plants. *Crop Science*, *55*(1), 1-12.

CHALLENGES

KEY CHALLENGES

- Improve accuracy with modeling + pop design + experimental design
- Better use of GxE and better understanding TPEs
- Use environment data (soil, weather, management) in genomic models
- Handle multi-parental crosses
- Collaborate effectively and breed consistently across programs
- Educate breeders on how to use genomic data
- Data management – easy access to any type of data & visualization tools

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Concluding Remarks

1. GS is utilized differently for advancement, recycling, monitoring
2. Experimental settings and breeding design play key role in GS
3. Genomic breeding pipeline is dynamic and constantly improving

Thank you for your attention!

Questions??

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https://alenxav.github.io/

References and additional information

- Variance components - Purdue lecture 2022
- Walking through the statistical black boxes of plant breeding
- Bases for Genomic Prediction
- Genomic selection in plant breeding: from theory to practice
- Perspectives for Genomic Selection Applications and Research in Plants
- Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery
- Prediction-based breeding: Modern tools to optimize and reshape programs
- Genomic selection and reproducibility - are complex models distracting us from true scientific validity?
- Optimizing Plant Breeding Programs for Genomic Selection
- Expanding genomic prediction in plant breeding
- Statistical Approach for Improving Genomic Prediction Accuracy
- Megavariate methods capture complex genotype-by-environment interactions