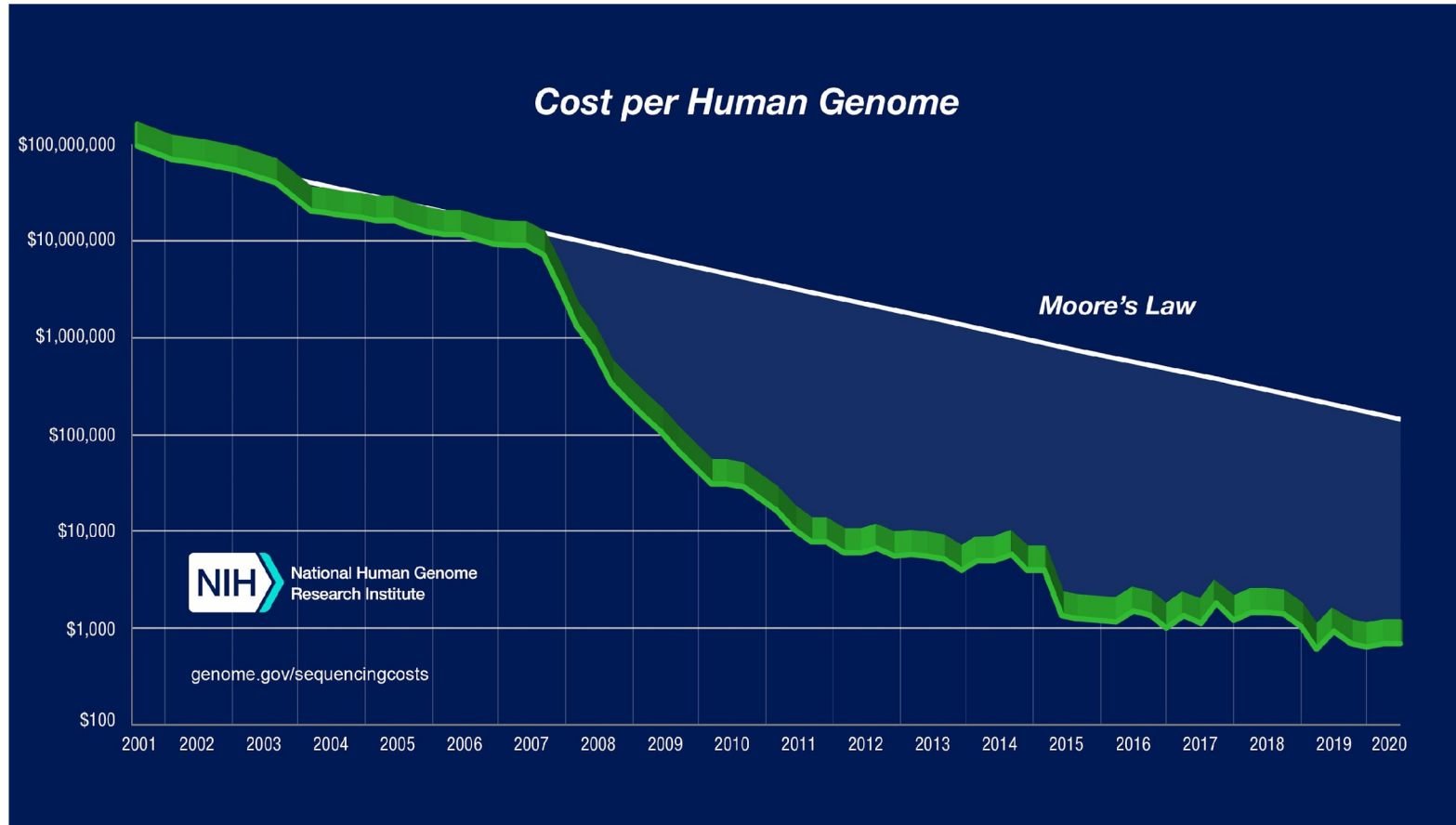


When to use genomic selection

Sequencing cost!

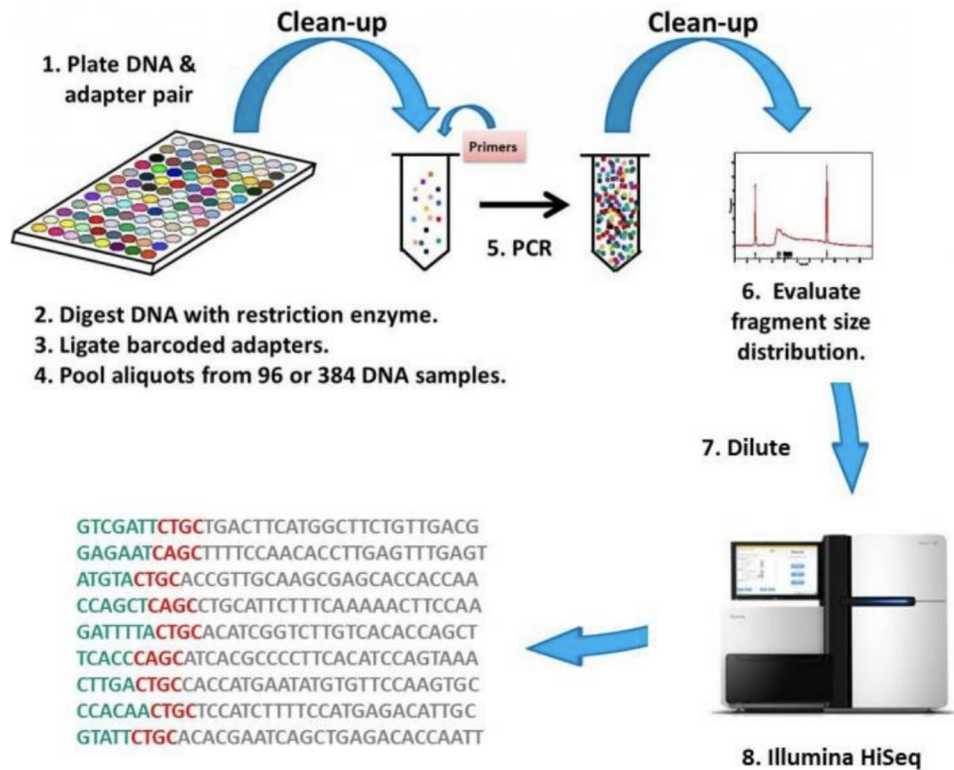


Sequencing cost!

2020

~\$ 1,500 / 384 samples = 3.9 + 6 = \$10

\$25 = 1 plot, 1 environment



Elshire et al 2011



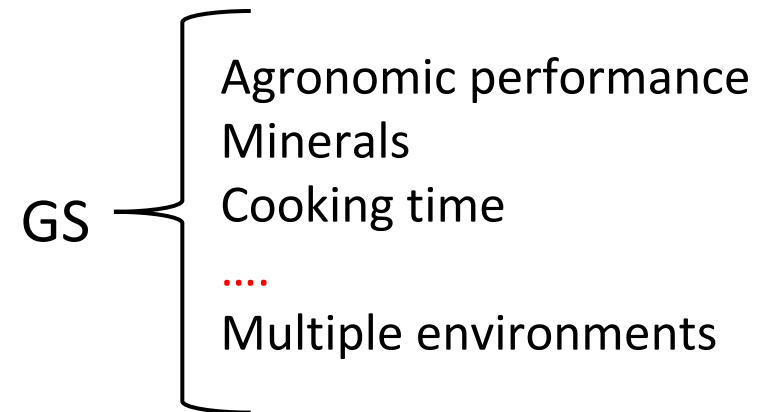
Sequencing cost!

Field
1 plot , 1 env = ~\$25

Minerals:
1 sample, 1 env = ~\$10

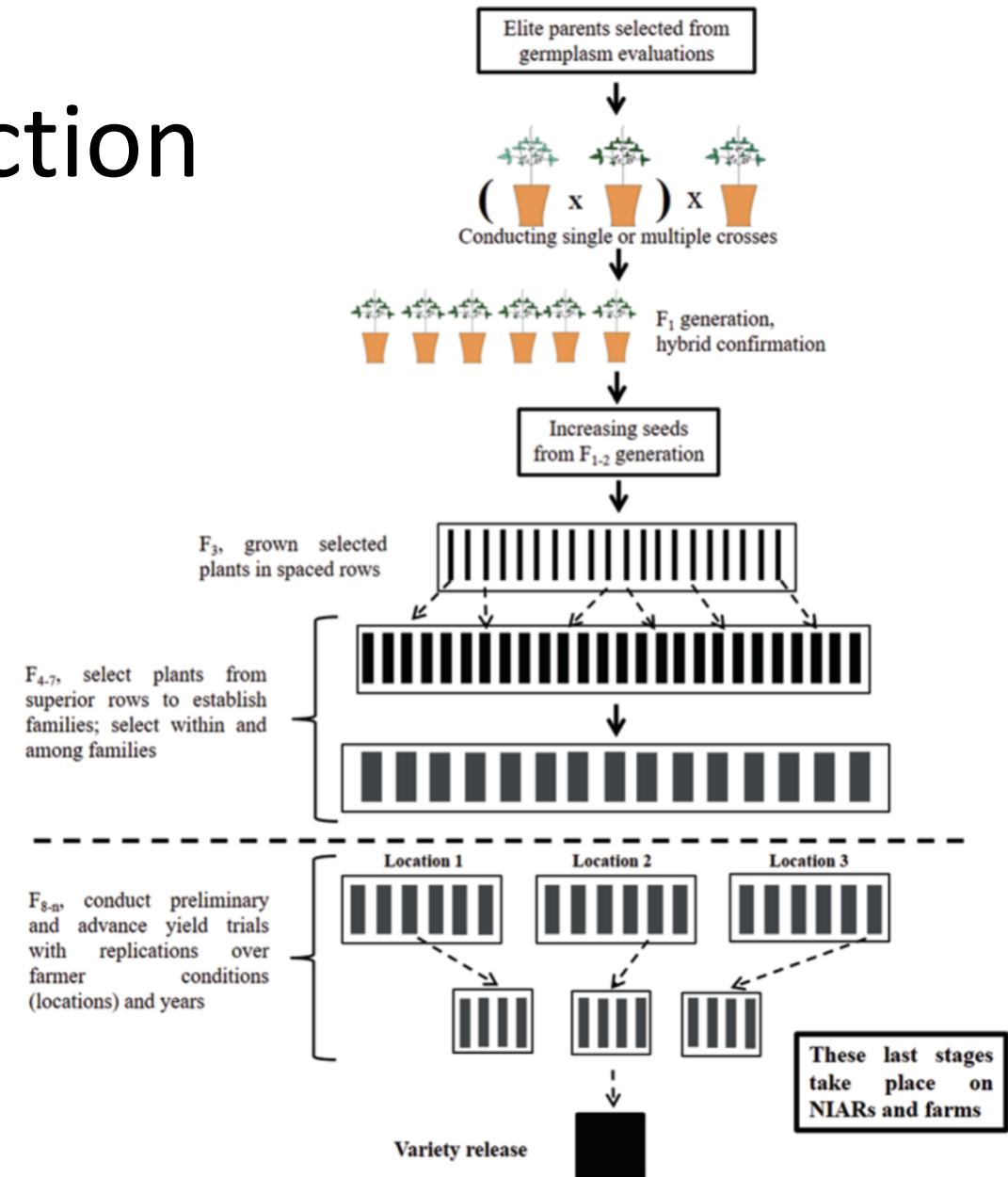
Cooking time:
1 sample, 1 env = ~\$15

.... ~\$50 vs ~ \$10 Sequencing →



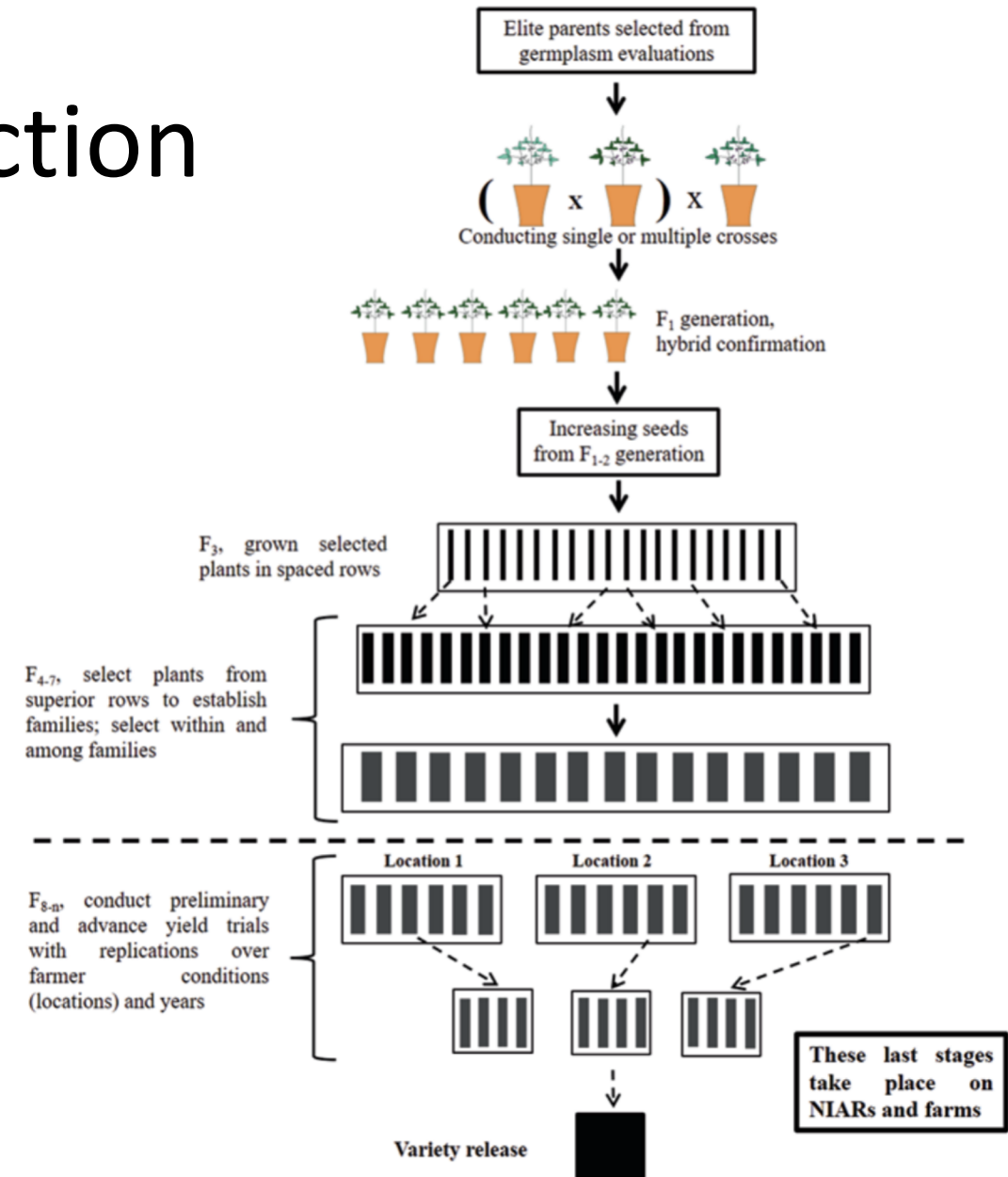
When to use genomic selection

1. When phenotypic selection is ineffective



When to use genomic selection

1. When phenotypic selection is ineffective
2. To increase gain per unit time



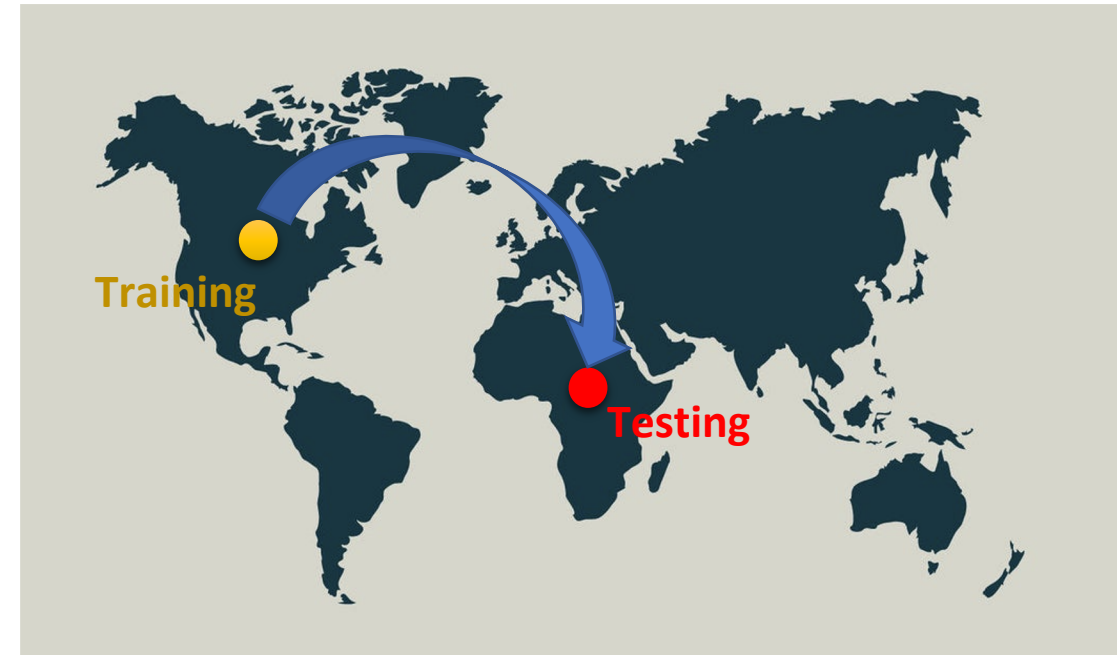
When to use genomic selection

1. When phenotypic selection is ineffective
2. To increase gain per unit time
3. For traits that are difficult to measure
eg. root characteristics, canning quality



When to use genomic selection

1. When phenotypic selection is ineffective
2. To increase gain per unit time
3. For traits that are difficult to measure
4. Assess agronomic performance in other environments



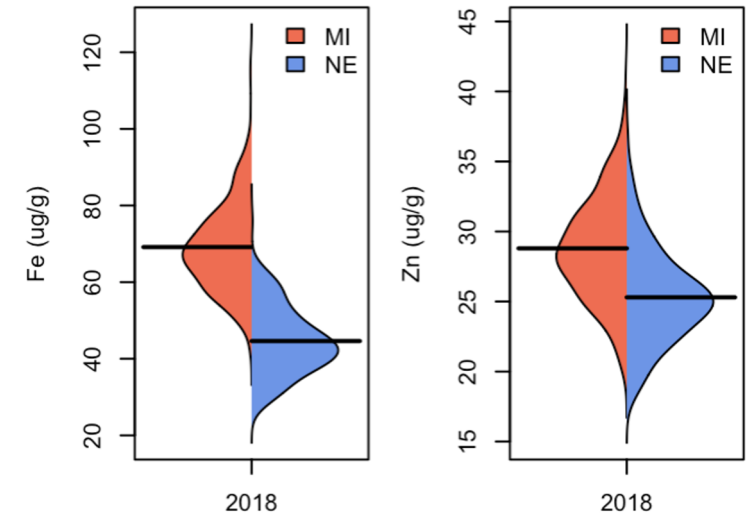
When to use genomic selection

1. When phenotypic selection is ineffective
2. To increase gain per unit time
3. For traits that are difficult to measure
4. Assess agronomic performance in other environments
5. To reduce phenotyping

~24 samples per day

n = 700

30 days milling!



50%
Training

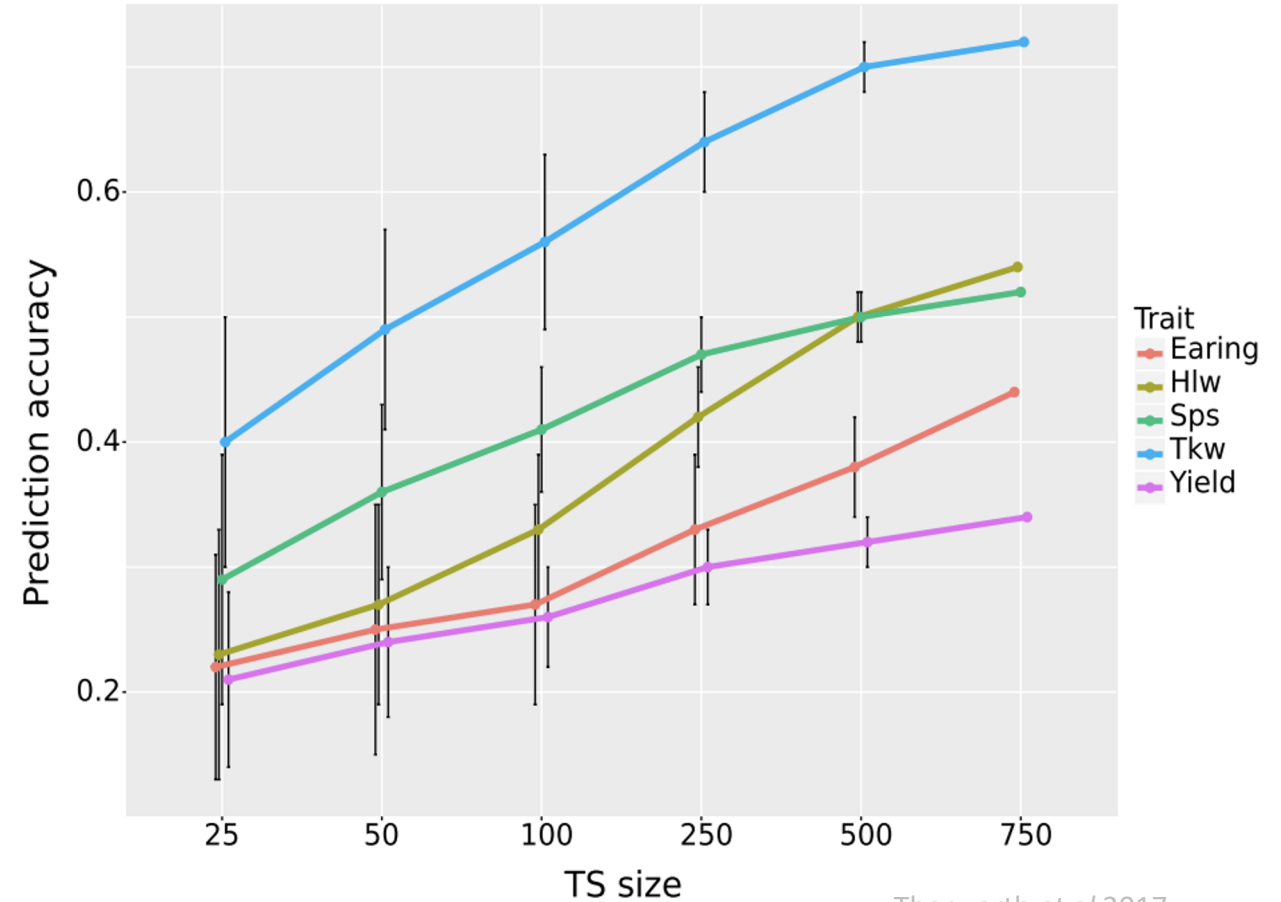
50%
Testing

Factors affecting predictive ability

1. h^2 and population size of TP

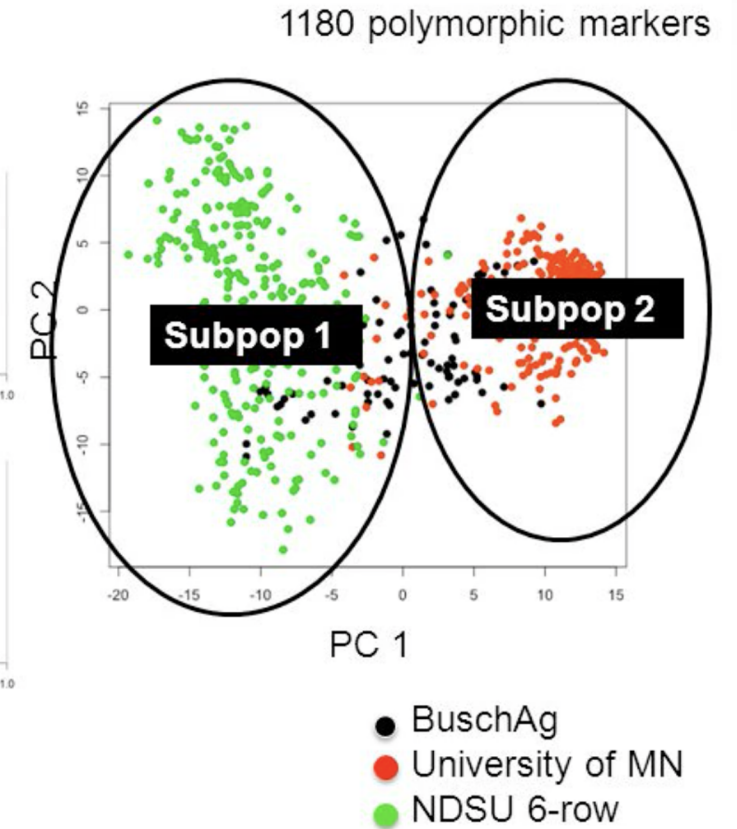
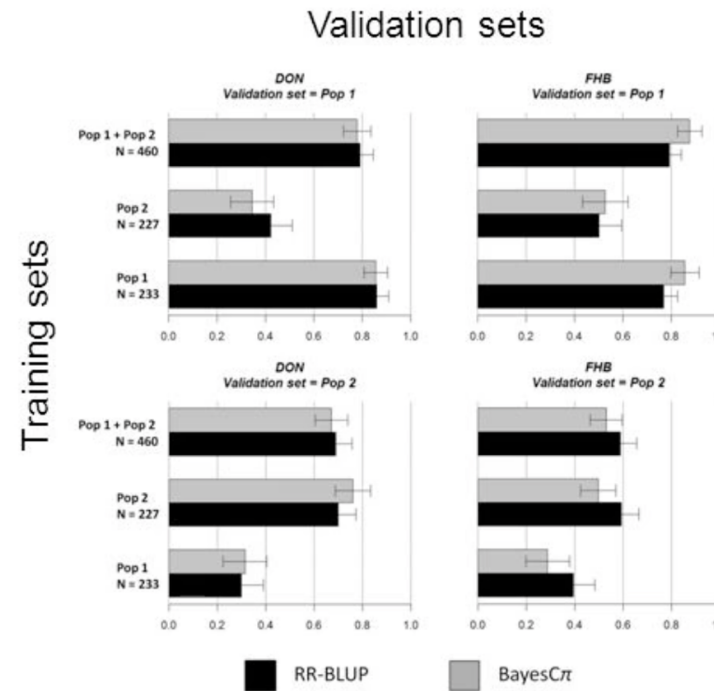
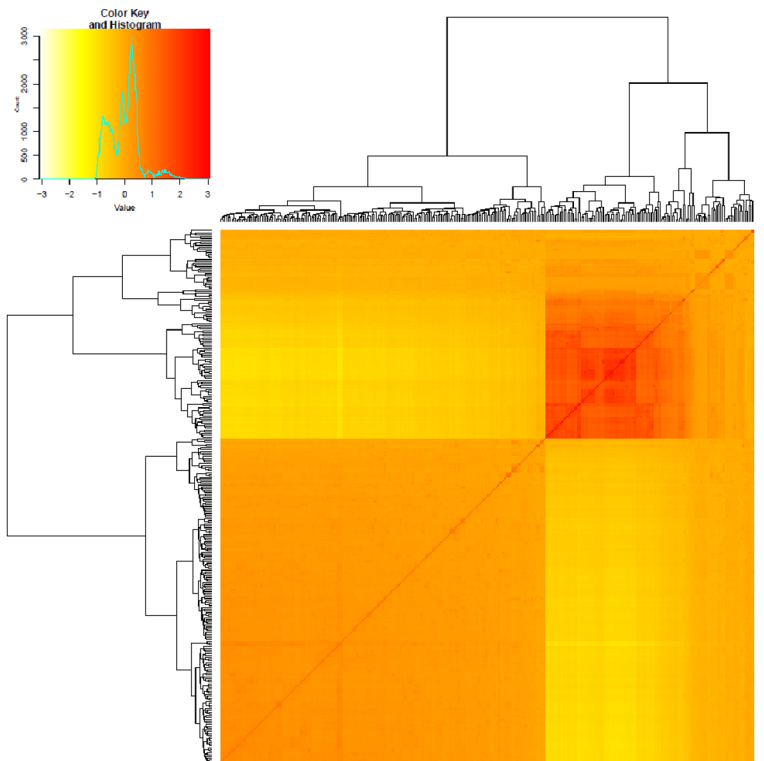
Nh^2

N and h^2 affects both the power to detect QTL and the accuracy of GS!



Factors affecting predictive ability

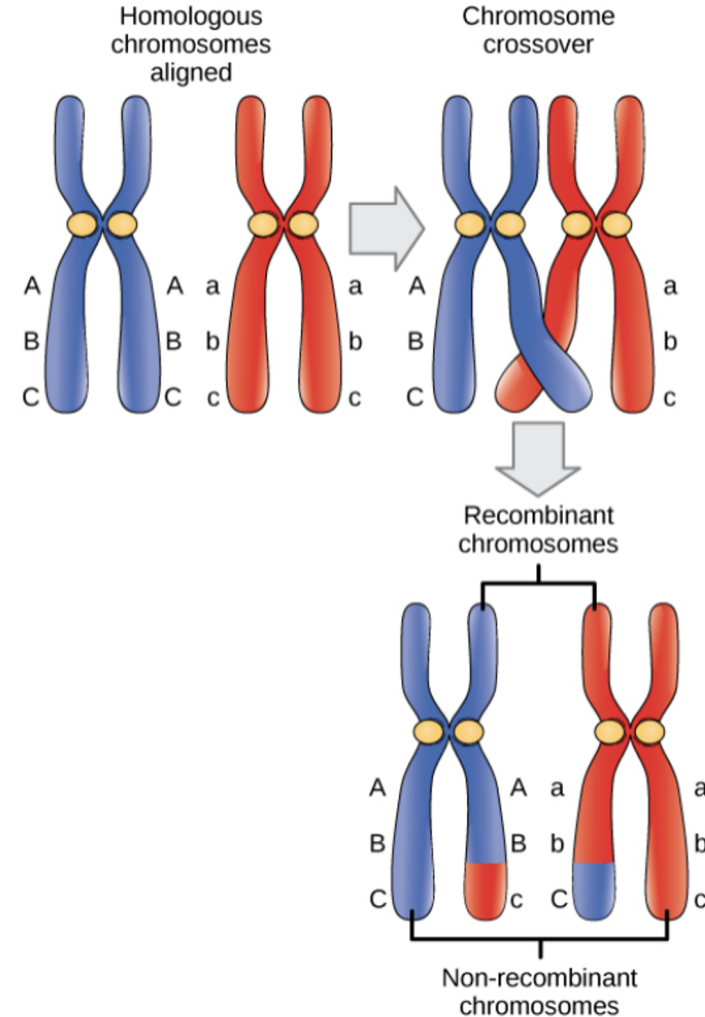
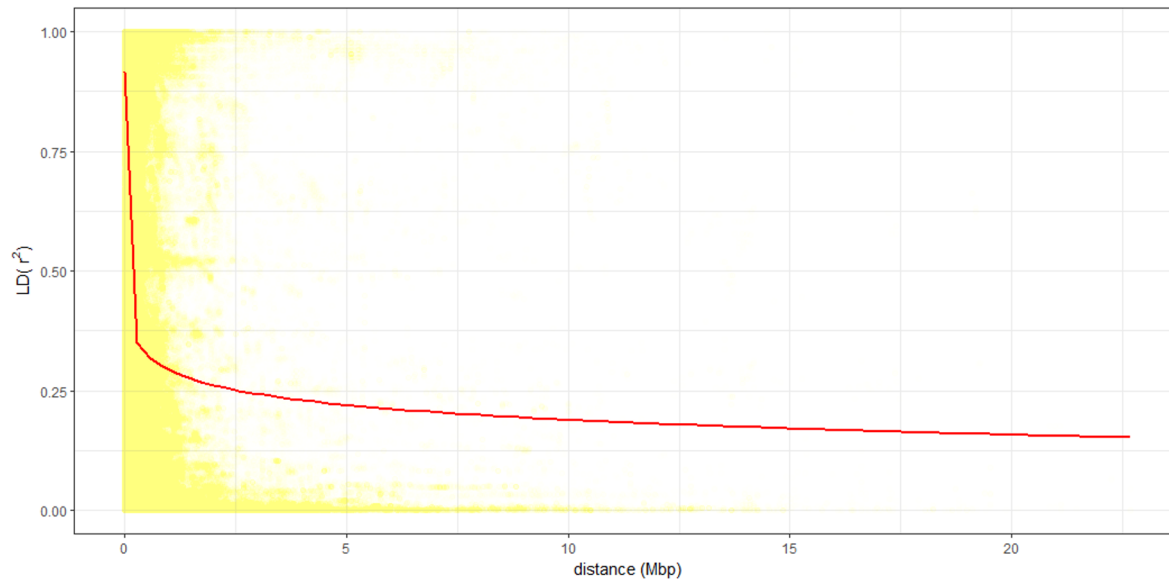
1. h^2 and population size of TP
2. Genetic relationship



Factors affecting predictive ability

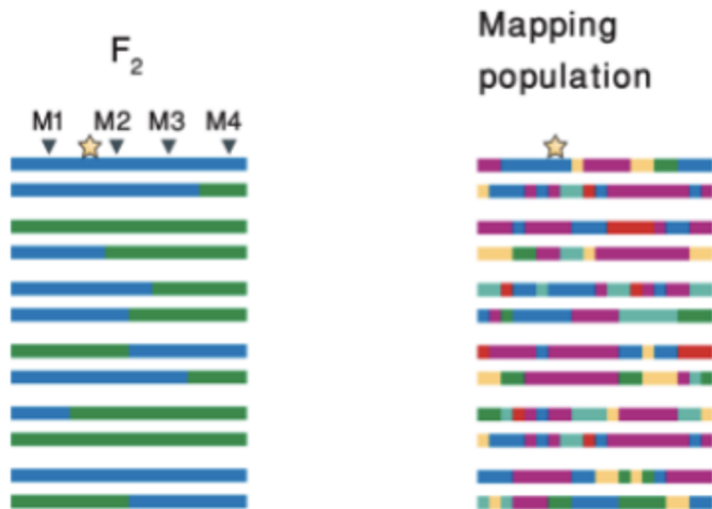
1. h^2 and population size of TP
2. Genetic relationship
3. Linkage disequilibrium

How many markers are needed?

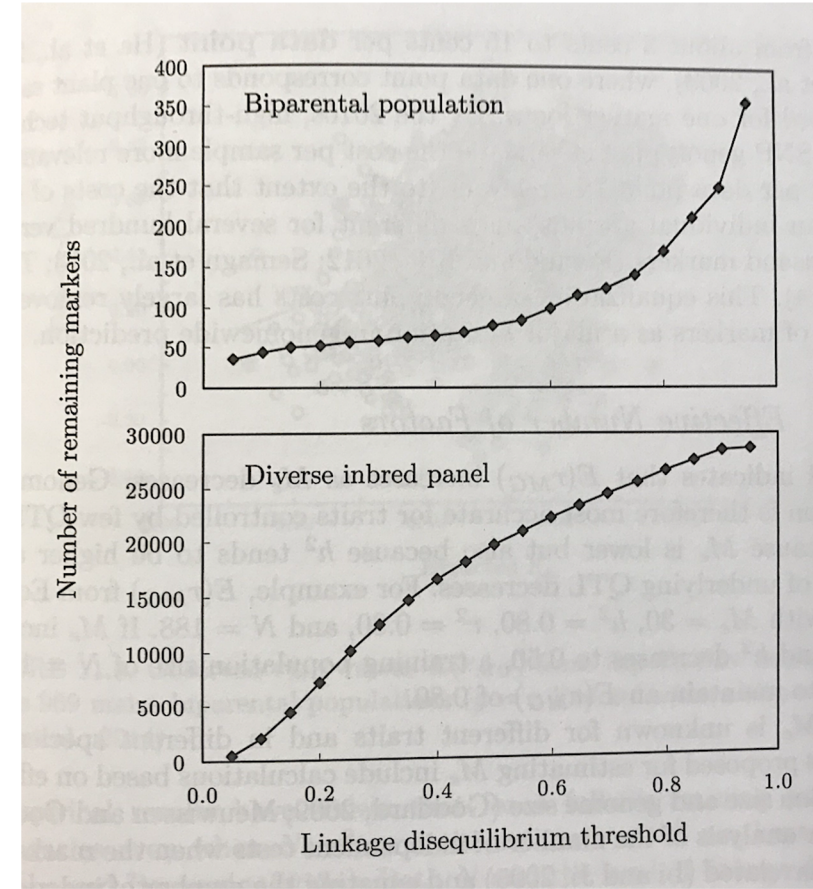


Factors affecting predictive ability

1. h^2 and population size of TP
2. Genetic relationship
3. Linkage disequilibrium



- Mackay et al. 2009

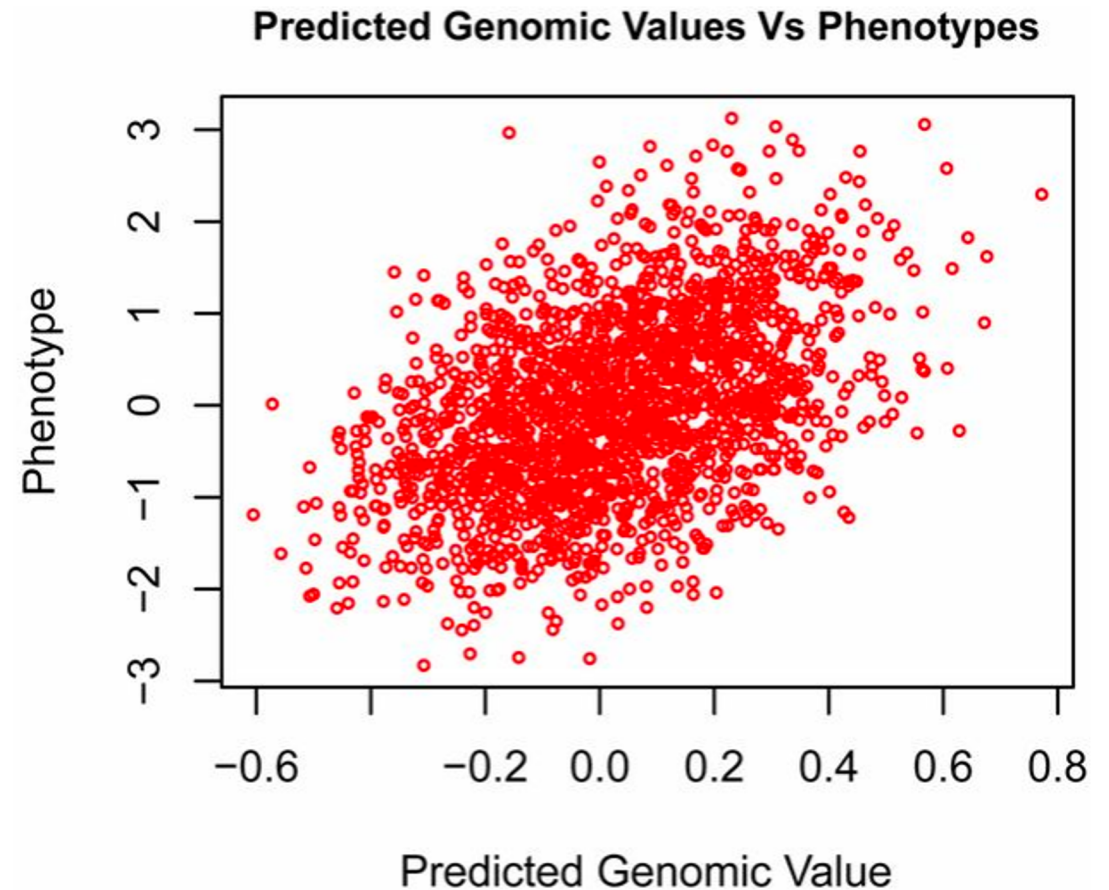


Bernardo 2020, p285

Factors affecting predictive ability

1. h^2 and population size of TP
2. Genetic relationship
3. Linkage disequilibrium
4. Number of QTL

h^2 tend to be higher



Factors affecting predictive ability

1. h^2 and population size of TP
2. Genetic relationship
3. Linkage disequilibrium
4. Number of QTL
5. Prediction models

rrBLUP is wrong!

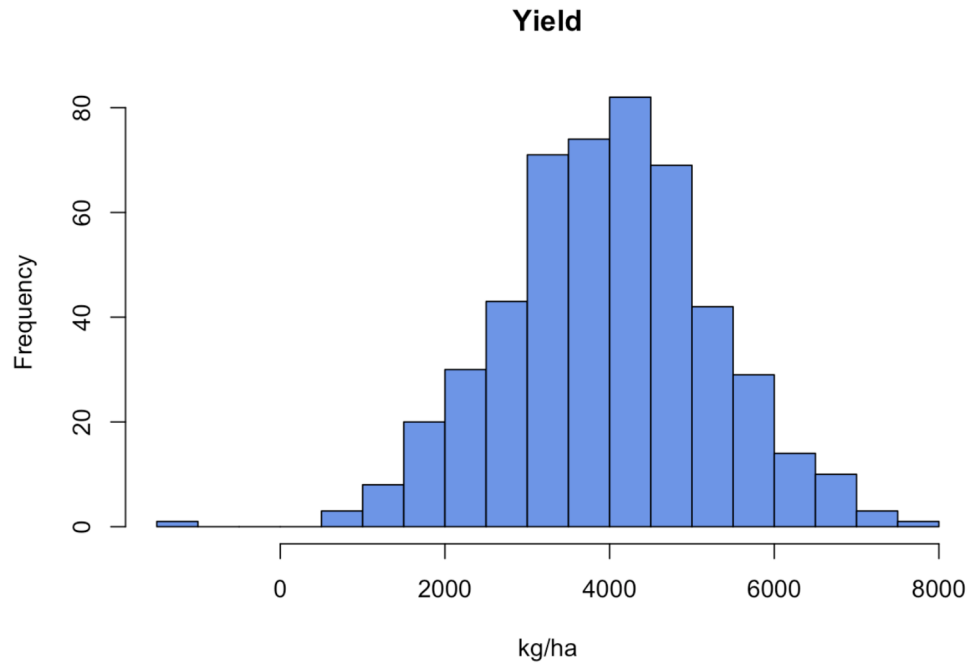
- i) *Each marker explains the same amount of genetic variance*
- ii) *Epistasis is absent*

TABLE 11.5. Prediction accuracy or predictive ability, averaged across C population-trait combinations in each of 22 different studies, with RR-BLUP and other models.

First author (year)	C	Prediction method						
		RR ^a	BL	$C\pi$	EB	RK	BA	BB
Lorenzana (2009)	24	0.66			0.62			
Heffner (2011a)	16	0.52		0.53				
Heffner (2011b)	13	0.59		0.58			0.60	0.59
Guo (2012)	25	0.43					0.43	0.37
Heslot (2012)	18	0.56	0.56	0.55	0.54	0.59		
Kumar (2012)	6	0.81	0.81					
Lorenz (2012)	8	0.61	0.60	0.60				
Riedelsheimer (2012)	6	0.65				0.65		0.63
Gouy (2013)	20	0.33	0.33			0.34		
Zhao (2013)	1	0.63		0.58			0.61	0.62
Grenier (2015)	4	0.30	0.31					
Jiang (2015)	10	0.51				0.53		
Sallam (2015)	4	0.67		0.68				
Tayeh (2015)	3	0.71					0.72	0.72
Conley (2016)	2	0.50	0.51			0.51	0.50	0.50
Duhnen (2017)	6	0.53	0.53	0.53				
Gezan (2017)	5	0.58	0.58	0.61		0.62		0.62
Kwong (2017)	6	0.30	0.29	0.31			0.31	0.31
Wolfe (2017)	21	0.30	0.30	0.30		0.33	0.31	0.31
Yamamoto (2017)	8	0.43	0.44	0.46		0.45		0.50
Nyine (2018)	30			0.49		0.48		
de Oliveira (2018)	9	0.77	0.76	0.77			0.77	0.77

^a Model abbreviations are: RR, RR-BLUP or GBLUP; BL, Bayesian Lasso; $C\pi$, Bayes $C\pi$; EB, empirical Bayes; RK, reproducing kernel Hilbert spaces; BA, BayesA; and BB, BayesB

Genomic selection with Major QTL



$$h^2 = 0.6$$



Genomic selection with Major QTL

