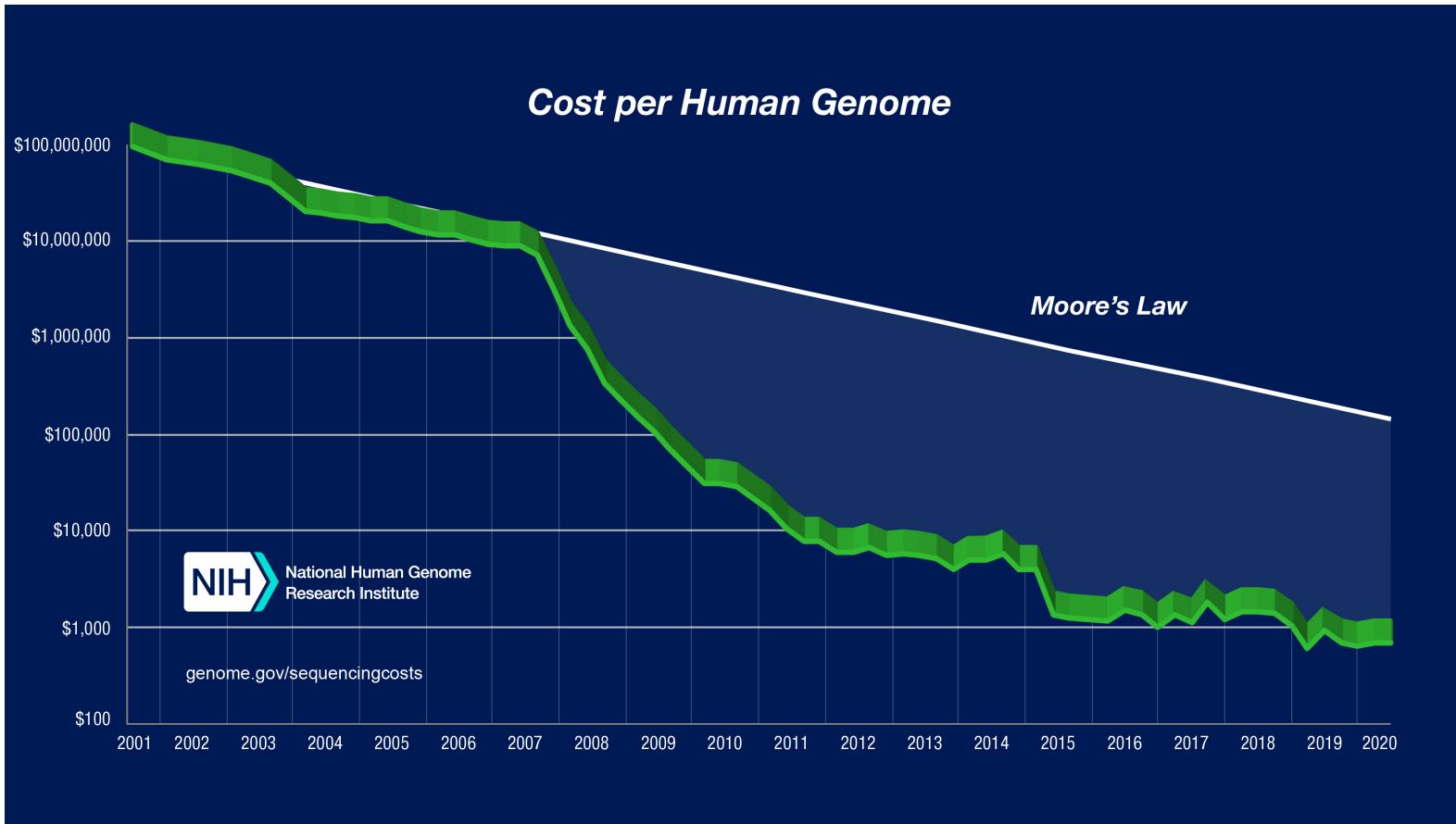


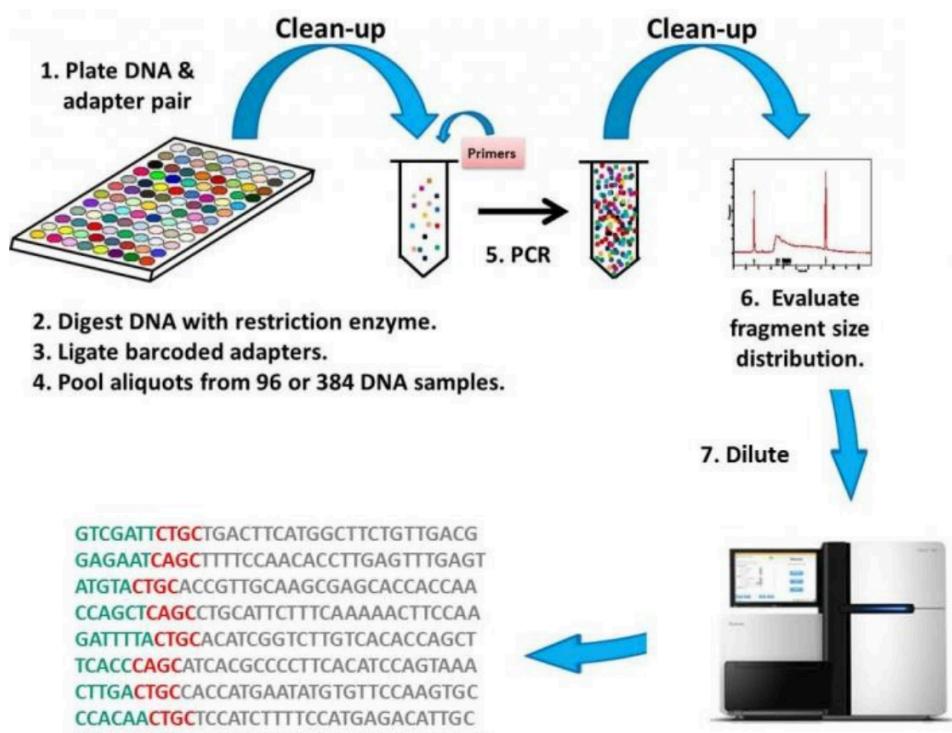
When to use genomic  
selection

# Sequencing cost!



# Sequencing cost!

2020



Elshire et al 2011

$$\sim \$ 1,500 / 384 \text{ samples} = 3.9 + 6 = \$10$$

\$25 = 1 plot, 1 environment



# Sequencing cost!

Field

1 plot , 1 env = ~\$25

Minerals:

1 sample, 1 env = ~\$10

Cooking time:

1 sample, 1 env = ~\$15

....

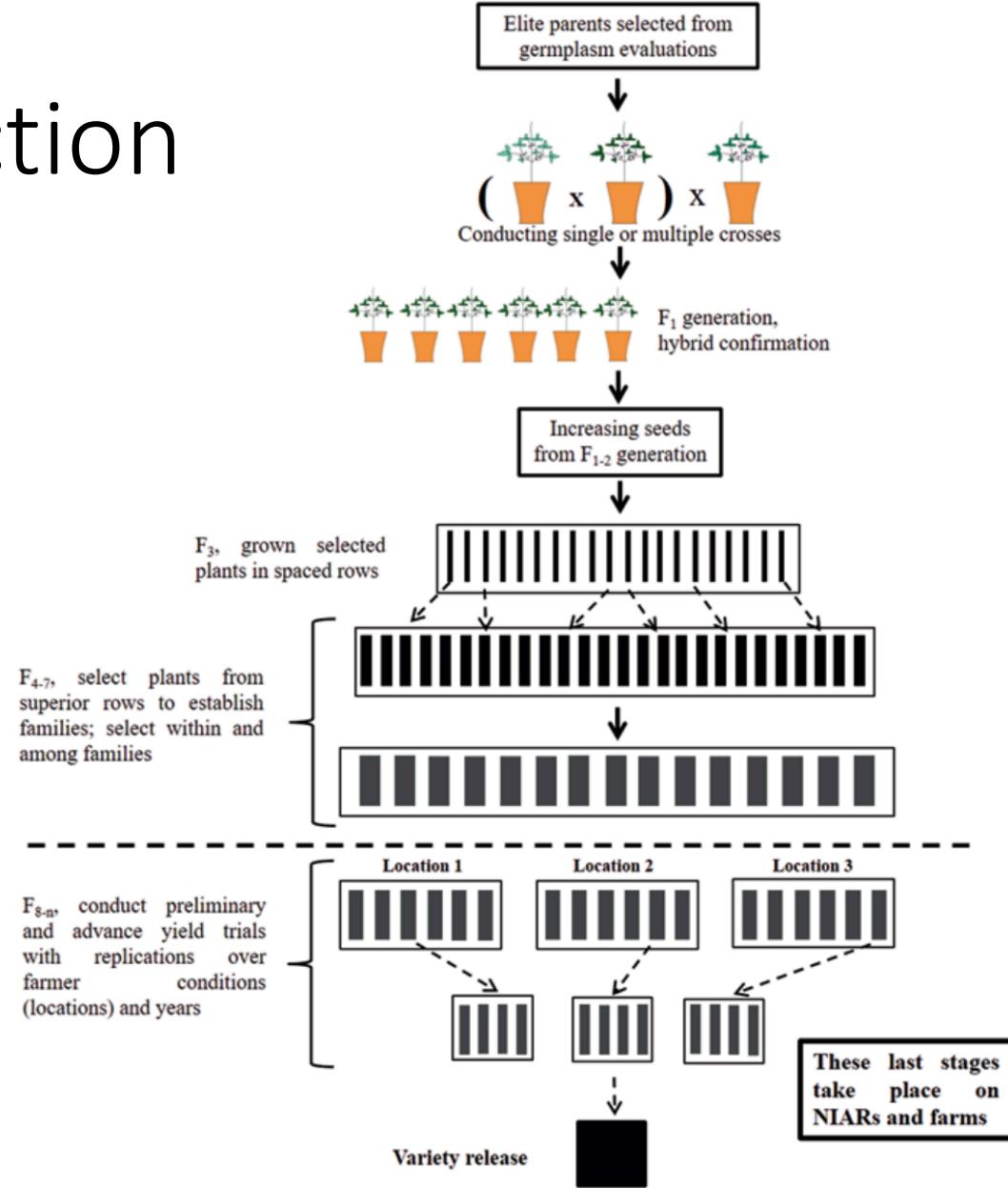
~\$50 vs ~ \$10 Sequencing ➔ GS



A agronomic performance  
Minerals  
Cooking time  
....  
Multiple environments

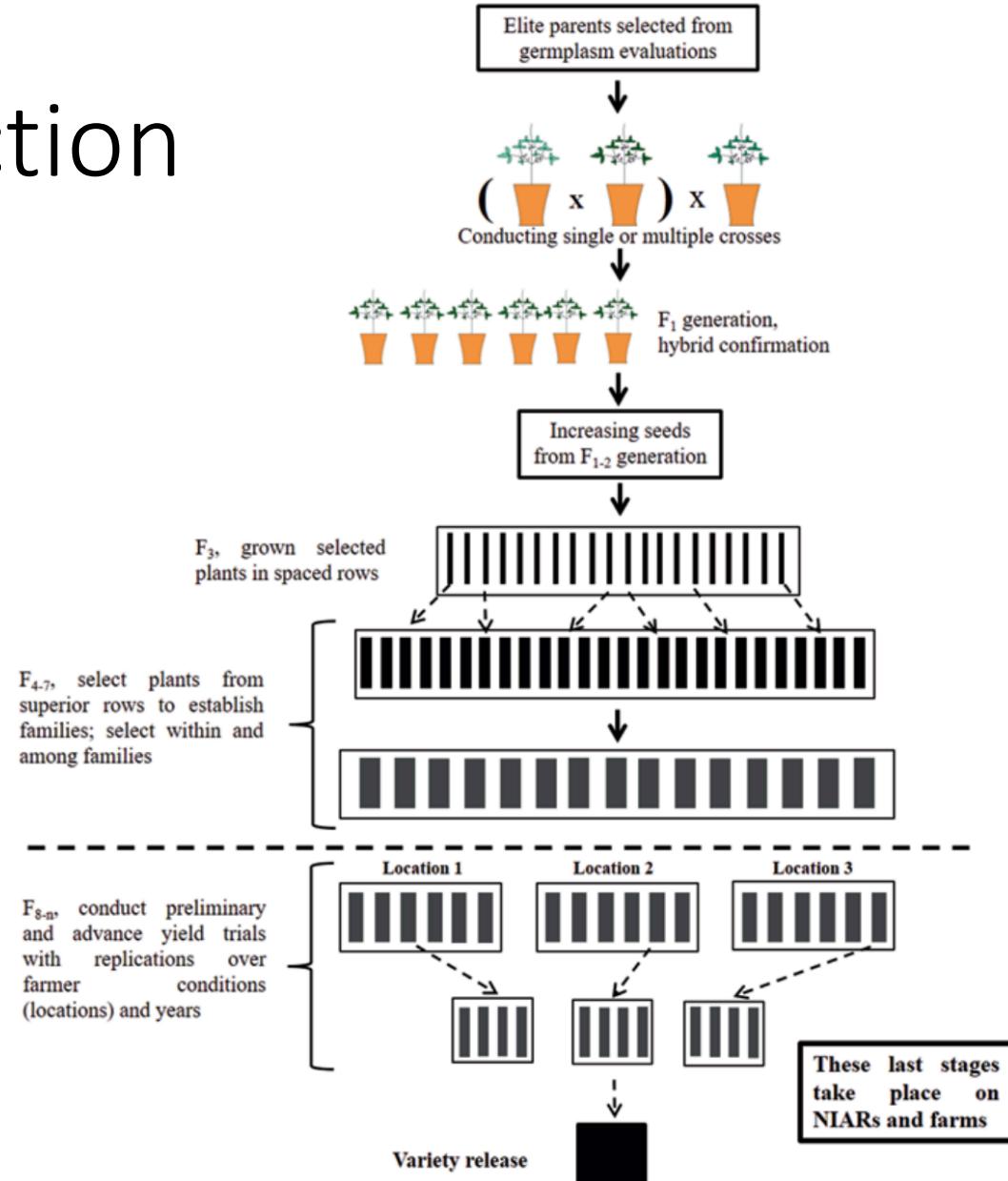
# When to use genomic selection

## 1. When phenotypic selection is ineffective



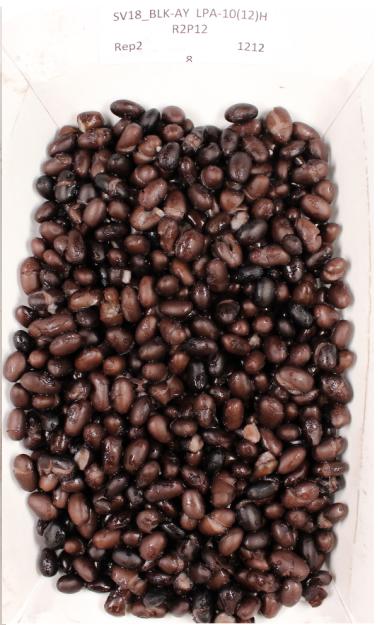
# When to use genomic selection

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. For other target populations or environments



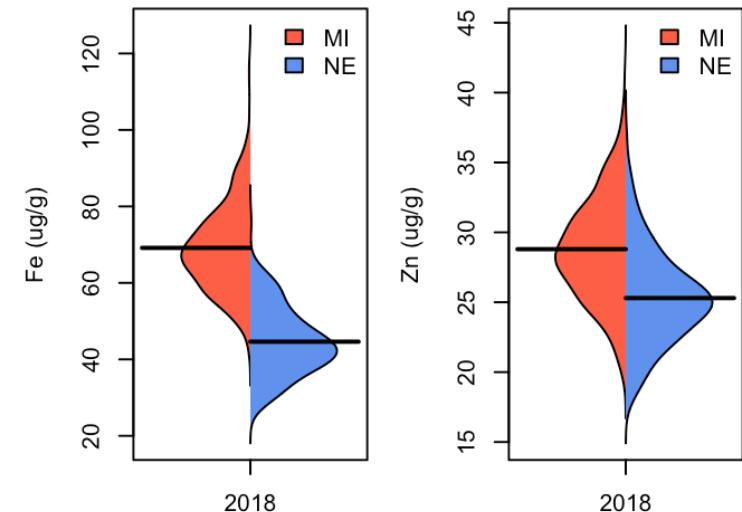
# When to use genomic selection

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

~24 samples per day

n = 700

30 days milling!

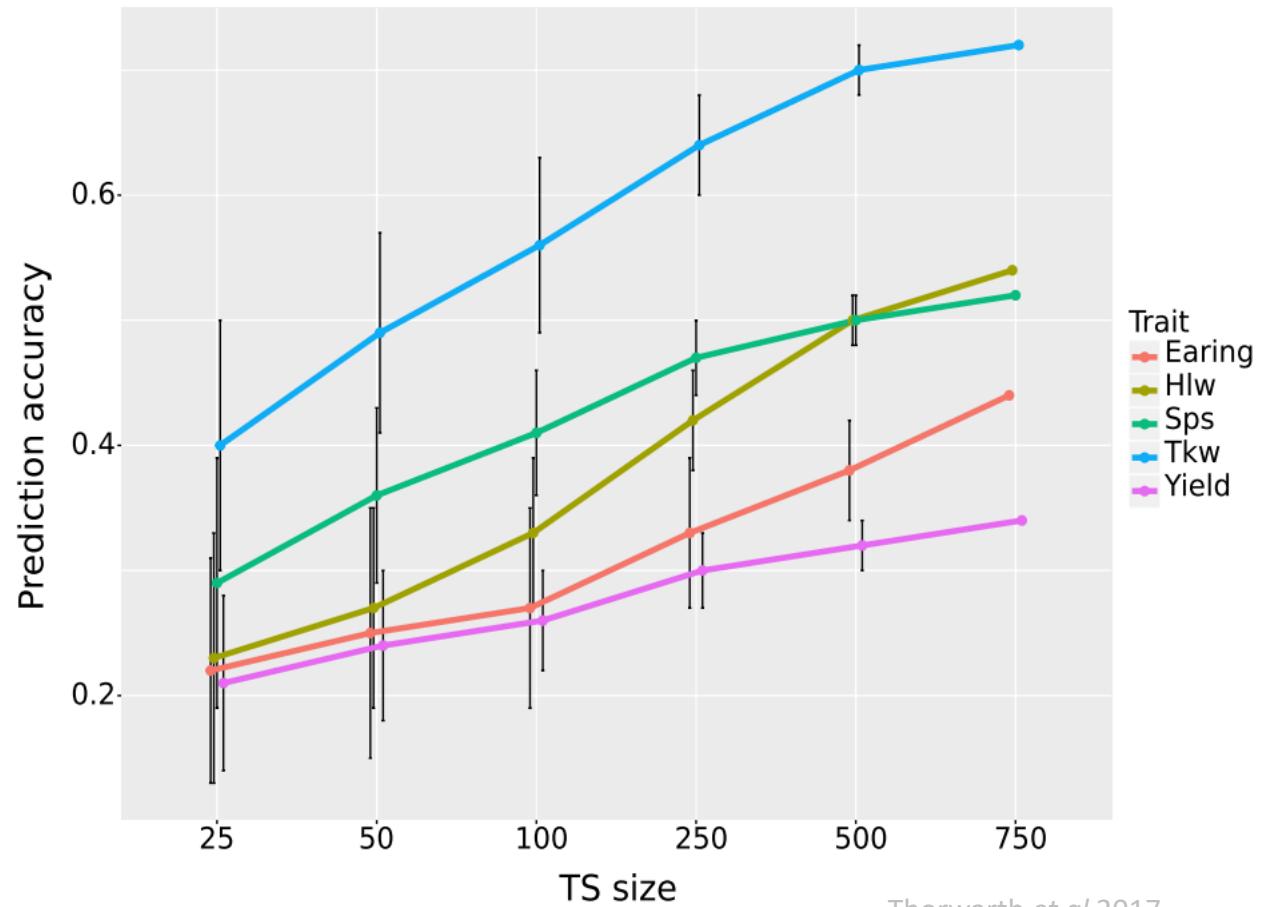


# Factors affecting predictive ability

## 1. $h^2$ and population size of TP

$Nh^2$

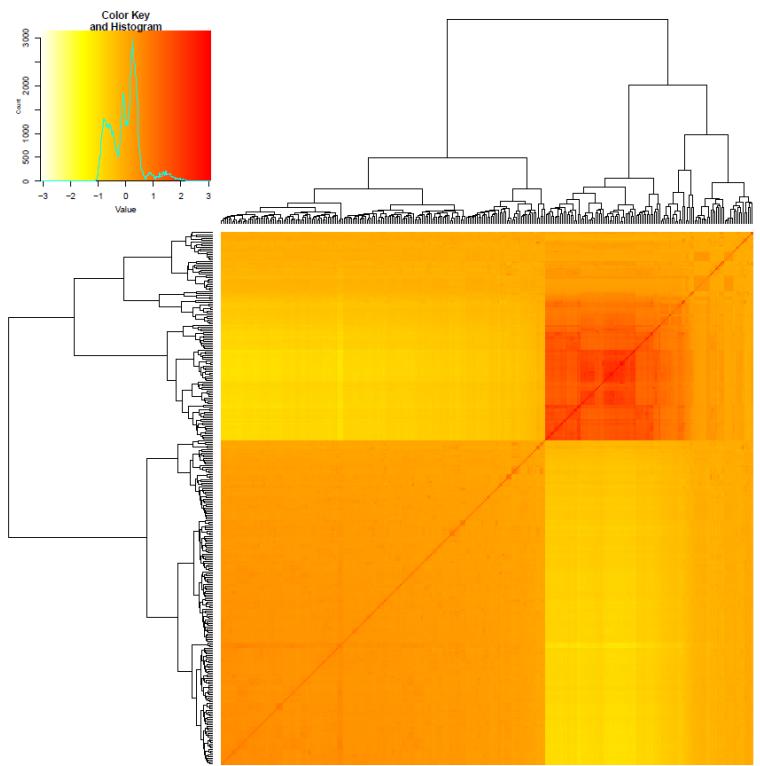
$N$  and  $h^2$  affects both the power to detect QTL and the accuracy of GS!



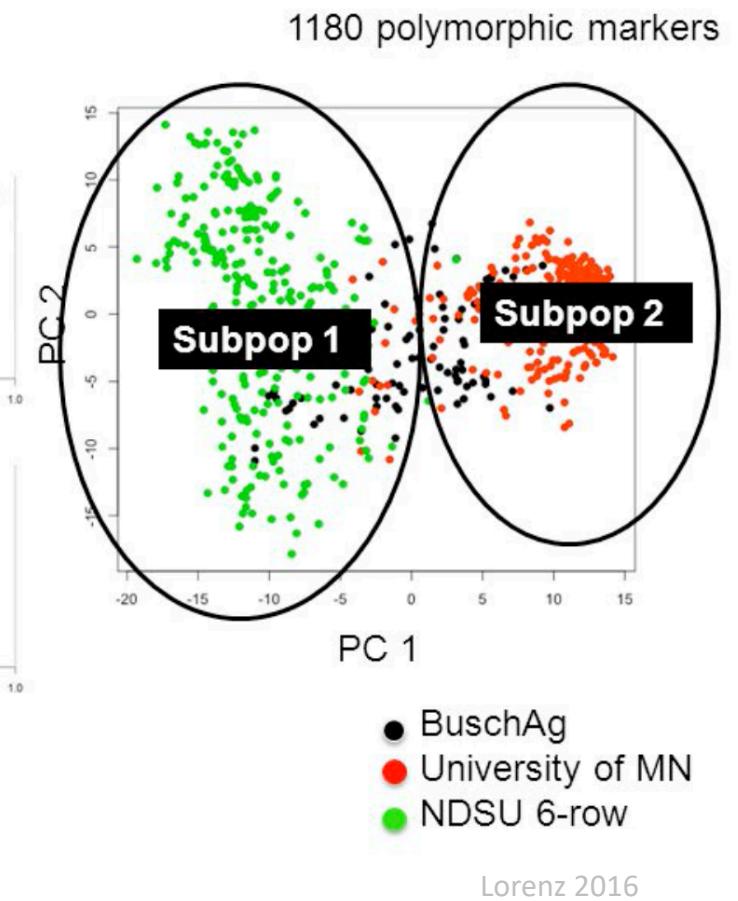
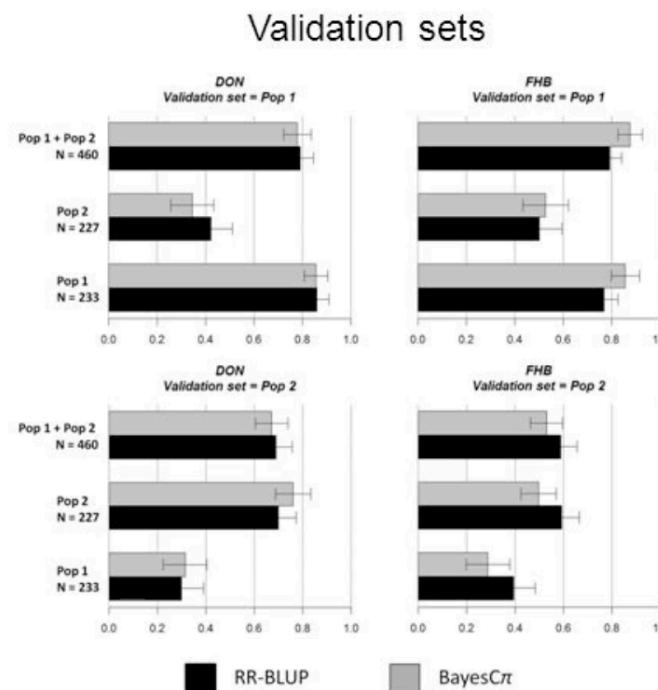
Thorwarth *et al* 2017

# Factors affecting predictive ability

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



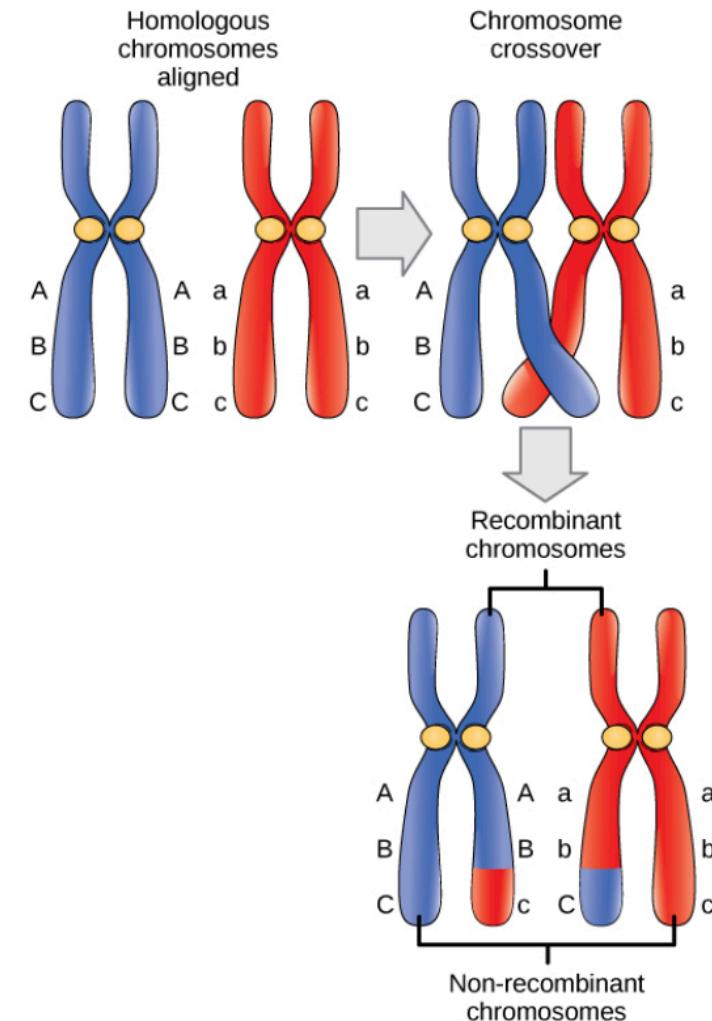
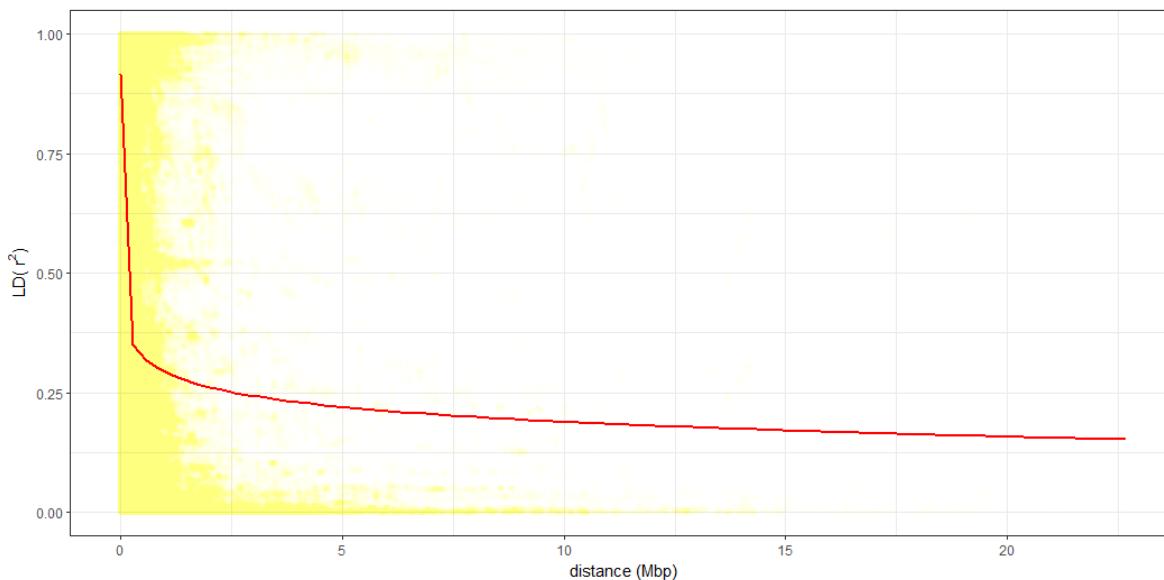
Training sets



# Factors affecting predictive ability

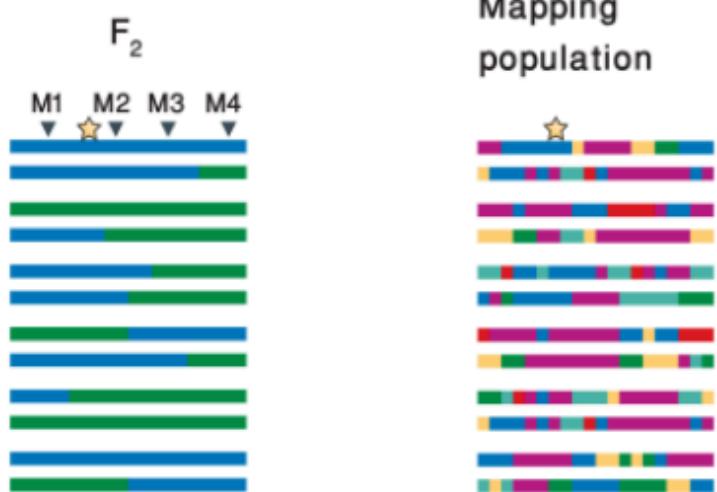
1.  $h^2$  and population size of TP
2. Genetic relationship
3. Linkage disequilibrium

How many markers are needed?

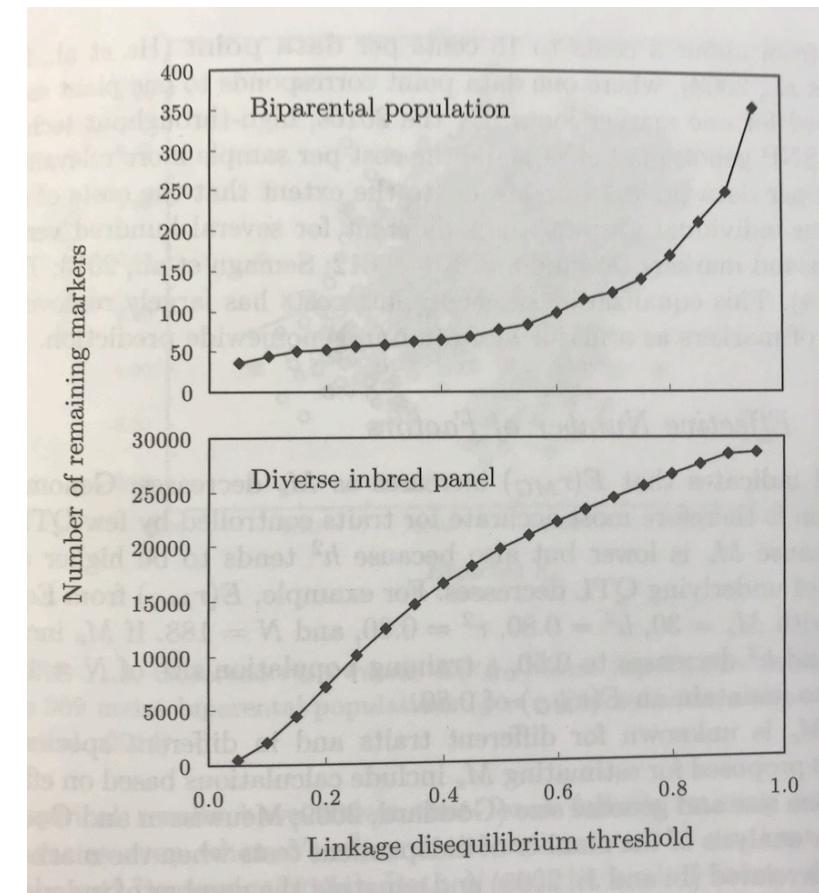


# Factors affecting predictive ability

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



Mackay et al. 2009

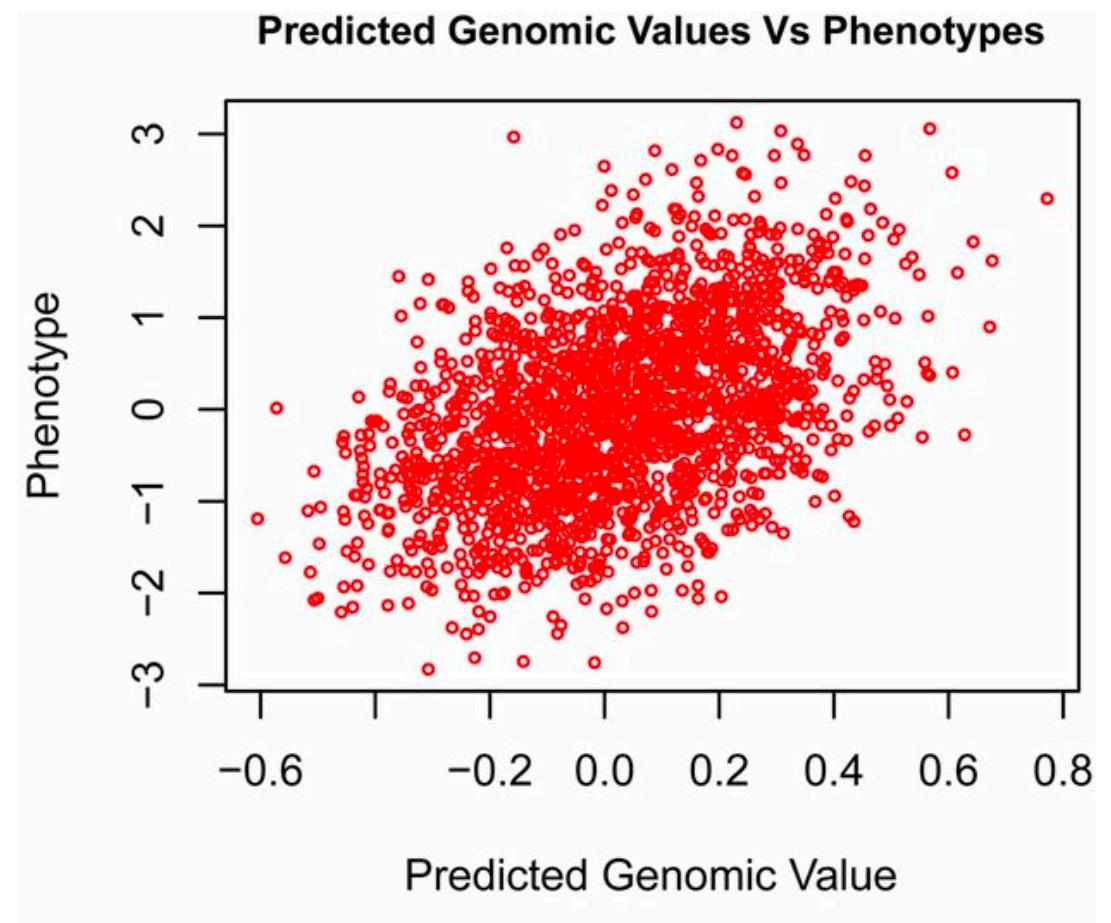


Bernardo 2020, p285

# 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!

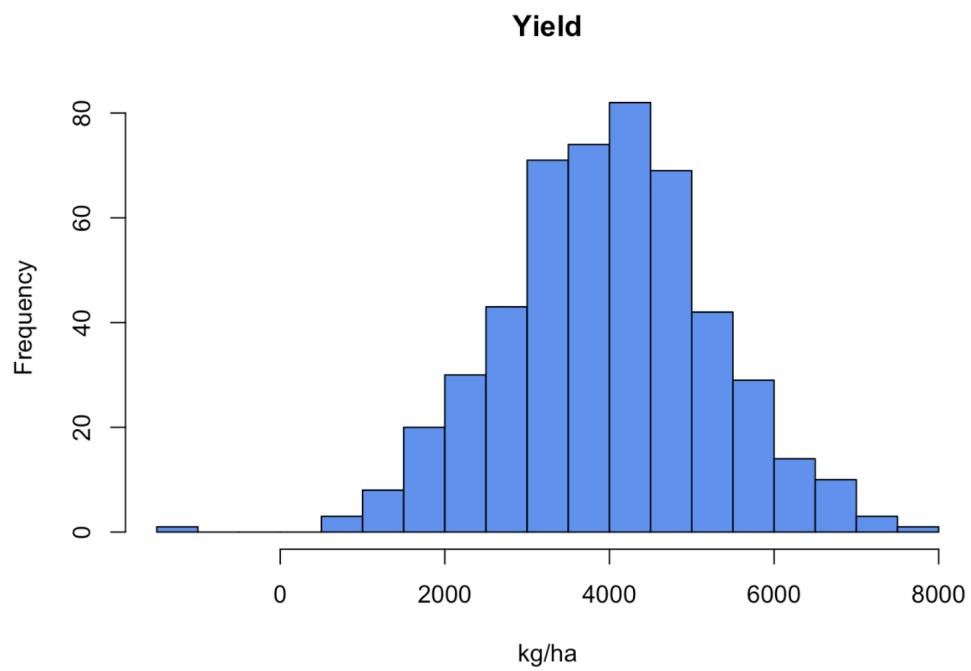
- i) *Each marker explains the same amount of genetic variance*
- ii) *Epistasis is absent*

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.

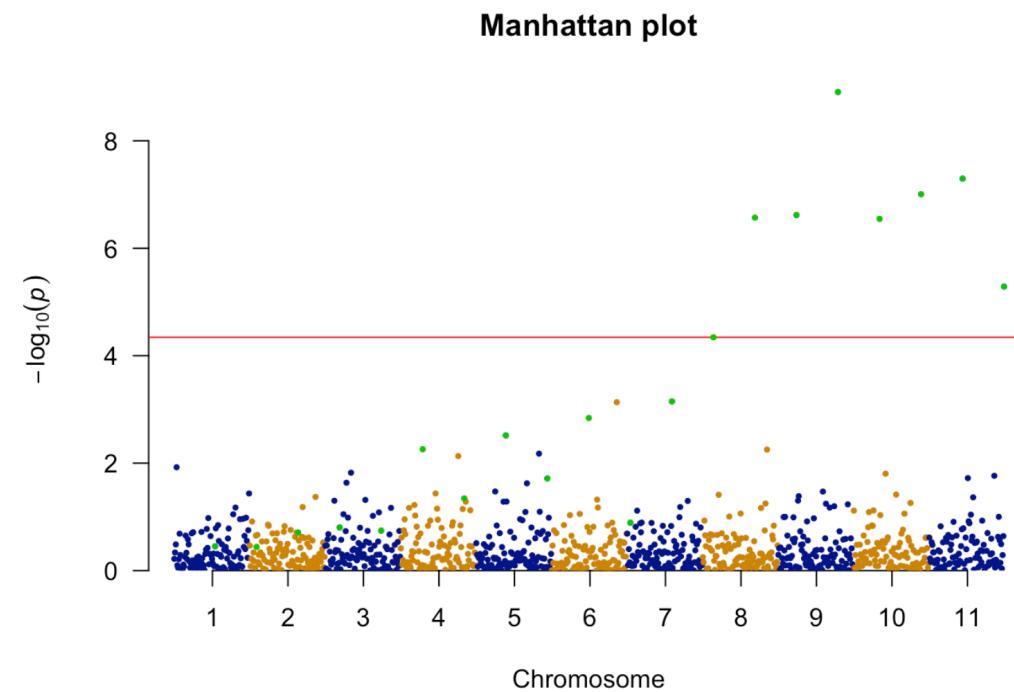
First author (year)	$C$	Prediction method						
		RR <sup>a</sup>	BL	$C\pi$	EB	RK	BA	BB
Lorenzana (2009)	24	0.66				0.62		
Heffner (2011a)	16	0.52		0.53				
Heffner (2011b)	13	0.59		0.58			0.60	0.59
Guo (2012)	25	0.43					0.43	0.37
Heslot (2012)	18	0.56	0.56	0.55	0.54	0.59		
Kumar (2012)	6	0.81	0.81					
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		
Nyne (2018)	30			0.49		0.48	0.50	
de Oliveira (2018)	9	0.77	0.76	0.77			0.77	0.77

<sup>a</sup> 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

