

Applications of genomic selection in poultry

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- Specific features of poultry industry
- History of molecular information in poultry breeding
- Genomic selection experiment in layers
- Genomic selection implementation in layers
- Genomic selection implementation in broilers

- Short generation interval
(overlapping generations every 6 weeks in broilers, non-overlapping generations every year in layers)



GS has to be fast and accurate

- Very high number of selection candidates and high selection intensity
- Low marginal revenue from a single individual
- No cryopreservation
- Multiplication pyramid of the progress



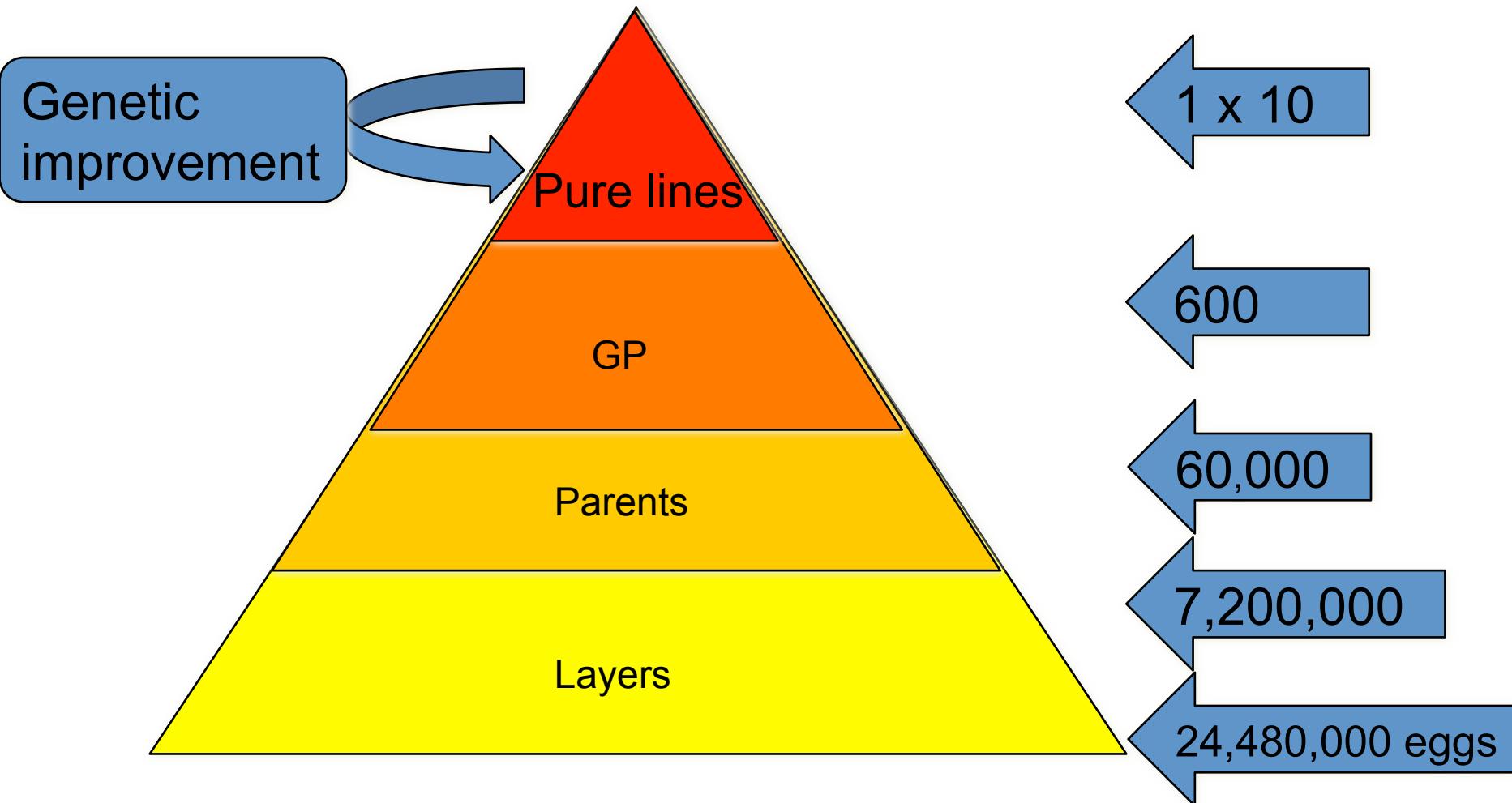
GS has to be cheap
Can't afford HD genotyping or sequencing



Small changes have big impact

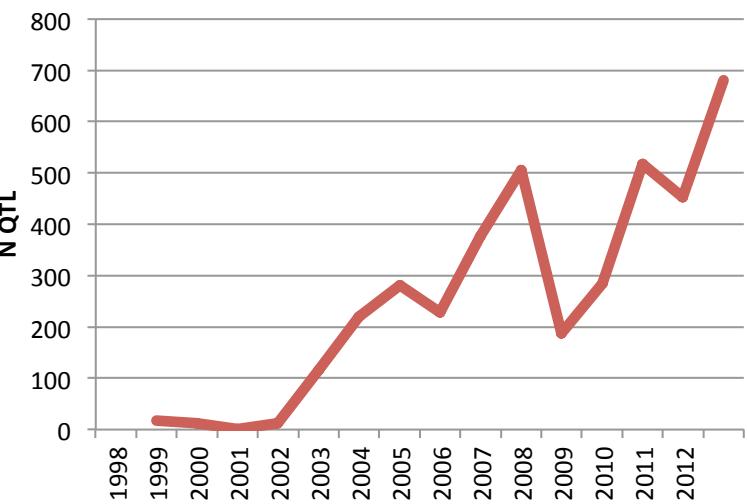
Breeding pyramid

– small improvements have large impact

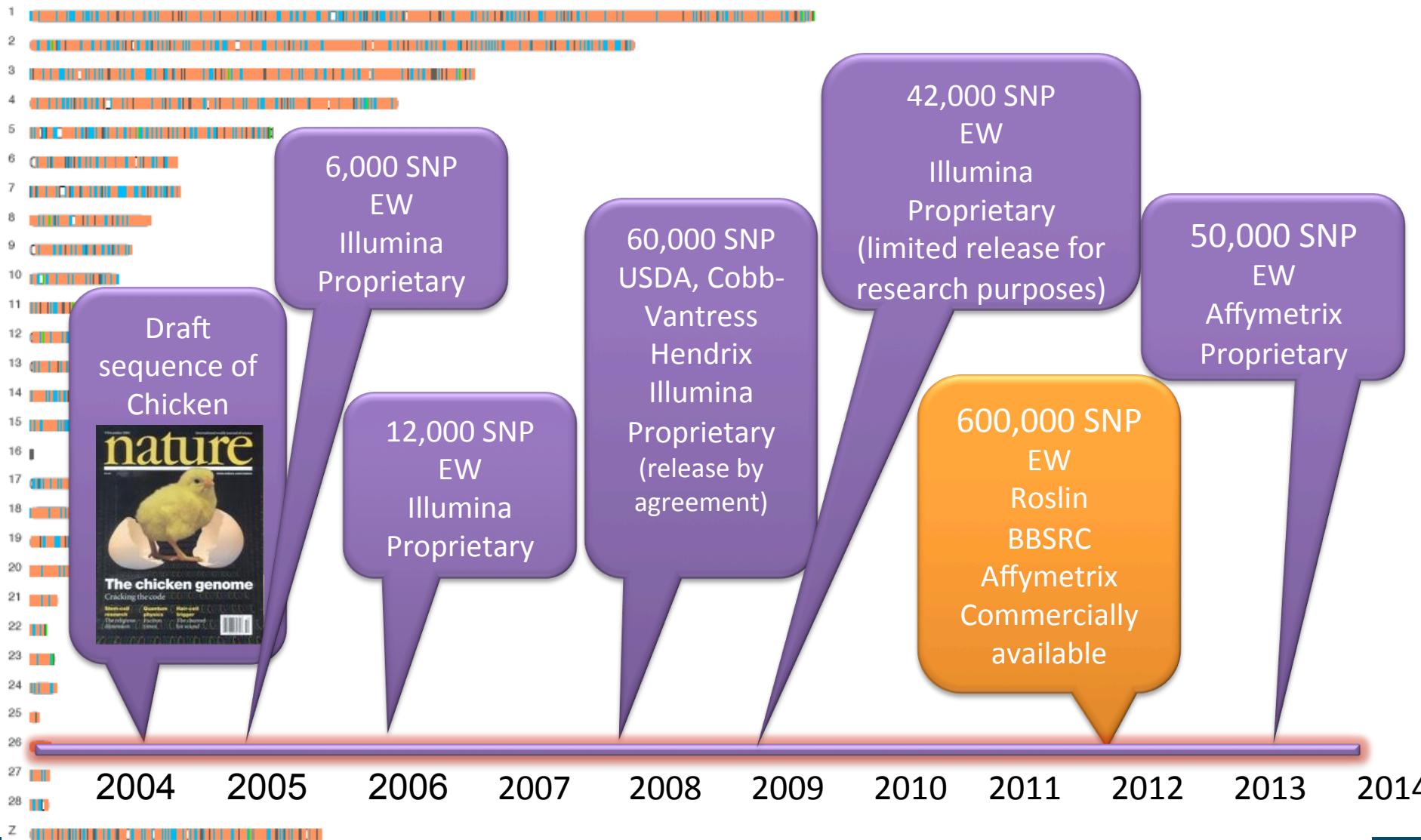


History

- 1960s – B blood group used to select for disease resistance
 - **Microsatellites and RFLPs** – about 2,000 markers known, not all mapped
 - Explosion of **QTL mapping** – 4,525 QTLs from 215 publications in animalgenome.org



Evolution in Chicken SNP Panels



Microsatellites

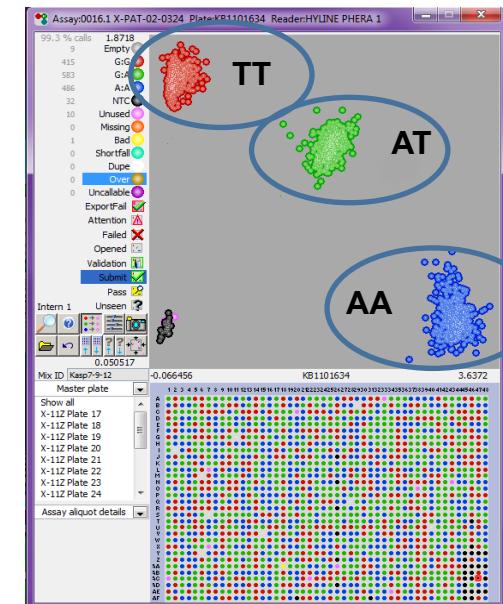
- 1,500 available
- \$1.50 per test
- 5,000 per week

Individual SNP

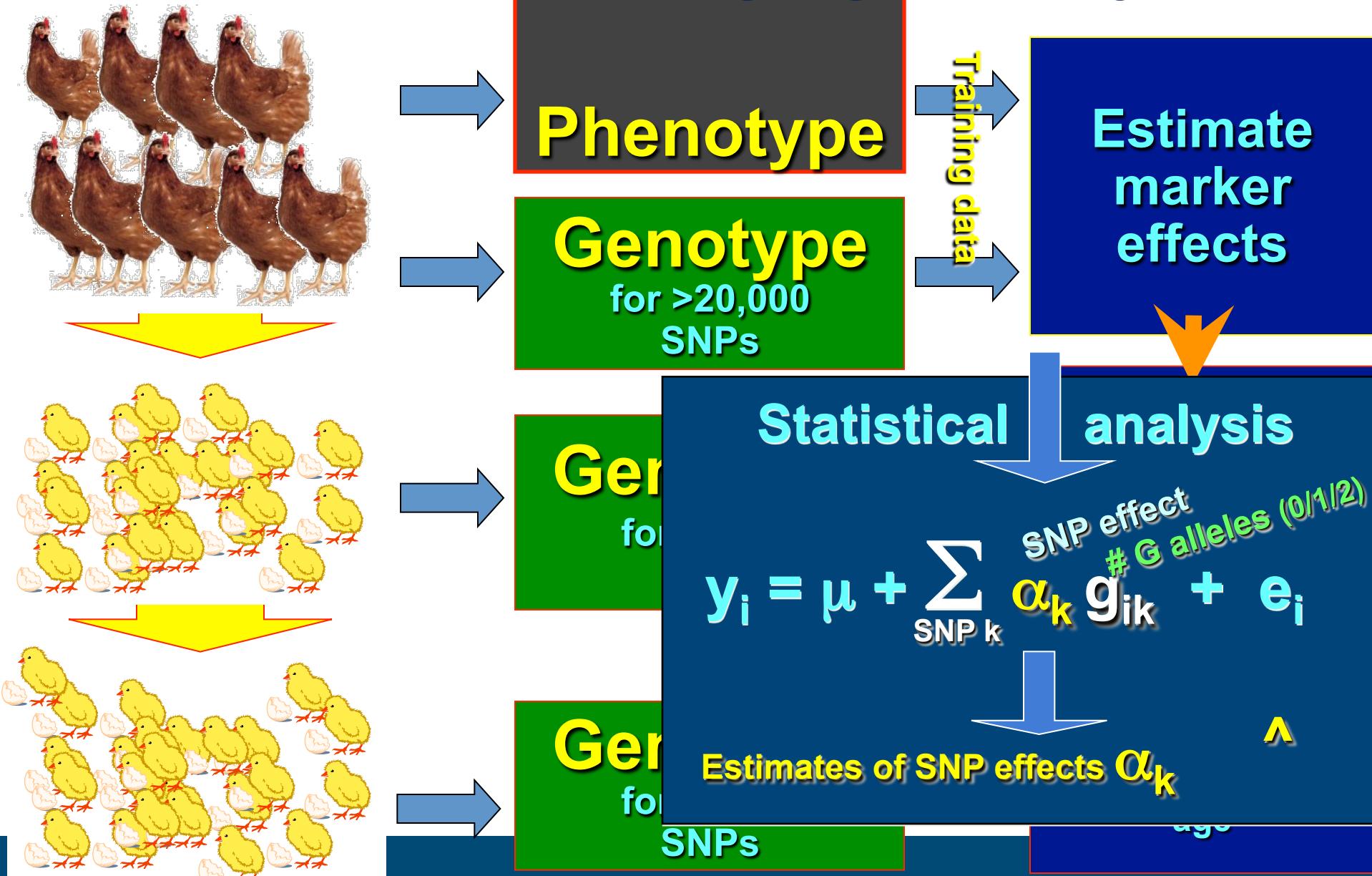
- 39 million available
- \$.022 per test
- 129,000 per week

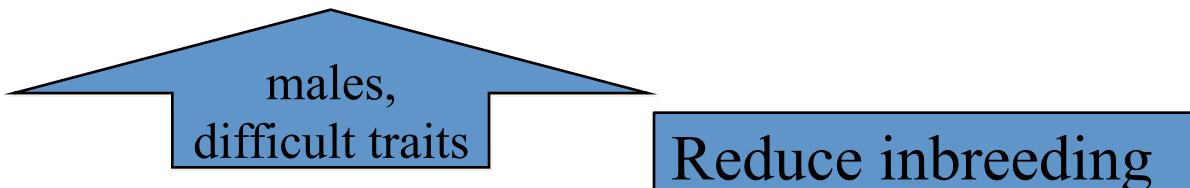
SNP chip

- 600 000
- \$.0003 per test
- 57,600,000 per run



Genetic Evaluation using high-density SNPs



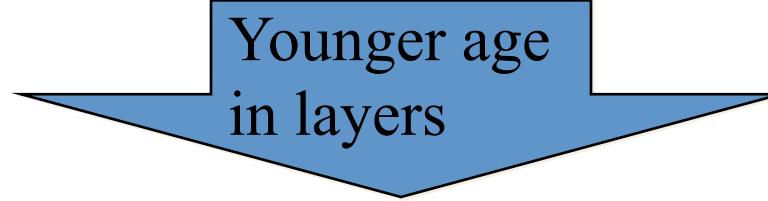


males,
difficult traits

Reduce inbreeding

Intensity x accuracy x genetic s.d.

Generation interval



Younger age
in layers

Experimental Implementation of GS in Layers with Program Redesign

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Jesus Arango
HY-LINE INTERNATIONAL**

**Anna Wolc, Chris Stricker, Rohan Fernando,
Dorian Garrick,
David Habier, Sue Lamont, Jack Dekkers
IOWA STATE UNIVERSITY**

Objective

Develop and compare Genomic Selection programs
that capitalize on opportunities to reduce generation intervals
Using layer chickens as an example

Breeding Program Goal

A Genomic Selection program for layer chickens

- that doubles response per year
- by reducing generation interval from 12 to 6 months
- but at the same rate of inbreeding per year
- and with a much smaller breeding program

Approach

1. Screen a large number of possible Genomic Selection programs by selection index methods.
2. Evaluate the program that meets the Goal by stoch.simul

Selection parameters for Traditional and Genomic Selection

Selection strategy	Traditional		Genomic	
Selection parameters	♂♂	♀♀	♂♂	♀♀
# candidates/gener.	1,000	3,000	N ?	N ?
# phenotyped	0	3,000	0	0
# selected	60	360	?	?
Generation interval	12 mo	12 mo	6 mo	6 mo
Accuracy of selection	0.44	0.62	0.6 / 0.7	0.6 / 0.7
Response / yr	0.48 σ_P		?	
Inbreeding / yr	1.4 %		?	

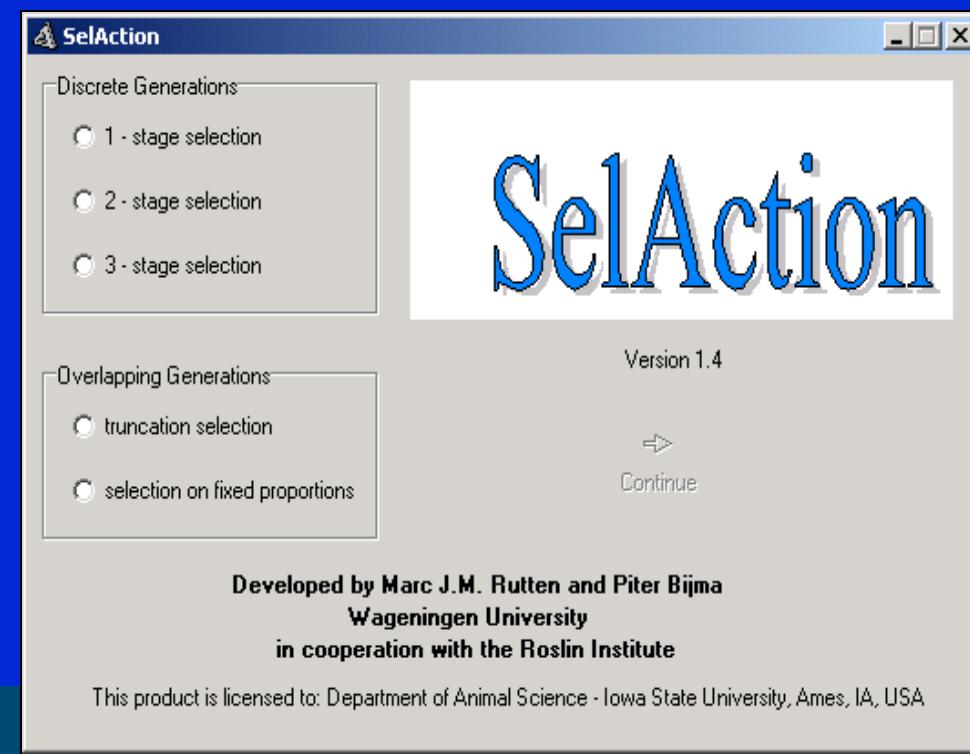

Obtained by SelAction with $h^2=0.3$
Assumed accuracy of G-EBV

Prediction of Response and Inbreeding from Genomic Selection by Selection Index Methods

Include G-EBV as a correlated trait in SelAction with:

(Dekkers, JABG 2008)

- $h^2 = 1$
- $r_g = \text{accuracy}$
of G-EBV
(assumed value)



Choice of selection parameters

Step 1:

Deterministic prediction of response and inbreeding (SelAction) for TS and GS

Trait $h^2=0.3$

Initial accuracy of GS EBV = 0.8

Aim to find GS program with similar ΔG but 50% lower ΔF per generation

Such that halving the generation interval would result in doubling ΔG at similar ΔF per year

	## selected Sires	## selected Dams	Progeny per # female			Accuracy		In SigP		TOTAL PROJECT genotypes	28,880 SNPs	
			Male	Female	genoty	Males	Females	Response per gener.	Inbreeding per gener.		All in sample	cost per
BLUP	60	360	3	8	0	0.437	0.618	0.46	1.38			
	60	360	3	8	8	0.709	0.709	0.59	0.29	25,820	\$181	\$4,673
1	25	100	4	4	4	0.704	0.704	0.53	0.71	6,860	\$215	\$1,475
2	25	100	4	3	3	0.706	0.706	0.50	0.70	6,260	\$234	\$1,465
3												
4	30	60	5	5	5	0.704	0.704	0.51	0.73	5,660	\$234	\$1,324
5	30	90	6	6	6	0.702	0.702	0.57	0.66	8,540	\$201	\$1,717
6	30	120	4	4	4	0.704	0.704	0.53	0.59	7,820	\$215	\$1,681
7												
8	40	40	5	5	5	0.707	0.707	0.46	0.73	4,460	\$301	\$1,342
9	40	40	8	8	8	0.704	0.704	0.53	0.78	5,900	\$234	\$1,381
10	40	80	5	5	5	0.704	0.704	0.51	0.55	6,860	\$215	\$1,475
11	40	80	4	4	4	0.706	0.706	0.48	0.53	5,900	\$234	\$1,381
12	40	120	3	3	3	0.707	0.707	0.46	0.46	6,380	\$234	\$1,493
13	40	120	4	4	4	0.705	0.705	0.51	0.48	7,820	\$215	\$1,681
14	40	120	5	5	5	0.703	0.703	0.54	0.49	9,260	\$190	\$1,759
15												
16	45	45	6	6	6	0.705	0.705	0.49	0.67	5,300	\$261	\$1,383
17	45	45	7	7	7	0.704	0.704	0.51	0.68	5,840	\$234	\$1,367
18	45	45	8	8	8	0.703	0.703	0.53	0.69	6,380	\$234	\$1,493
19	45	45	9	9	9	0.702	0.702	0.55	0.70	6,920	\$215	\$1,488
20	45	45	10	10	10	0.702	0.702	0.57	0.71	7,460	\$215	\$1,604
21												
22	45	90	3	3	3	0.709	0.709	0.43	0.45	5,300	\$261	\$1,383
23	45	90	4	4	4	0.706	0.706	0.48	0.48	6,380	\$234	\$1,493
24	45	90	5	5	5	0.704	0.704	0.51	0.49	7,460	\$215	\$1,604
25	45	90	6	6	6	0.703	0.703	0.54	0.50	8,540	\$201	\$1,717
26												
27	50	50	5	5	5	0.706	0.706	0.46	0.58	5,060	\$261	\$1,321
28	50	50	6	6	6	0.705	0.705	0.49	0.60	5,660	\$234	\$1,324
29	50	50	7	7	7	0.704	0.704	0.51	0.61	6,260	\$234	\$1,465
30	50	50	8	8	8	0.703	0.703	0.53	0.62	6,860	\$215	\$1,475
31	50	50	9	9	9	0.702	0.702	0.55	0.63	7,460	\$215	\$1,604
32	50	50	10	10	10	0.702	0.702	0.57	0.64	8,060	\$201	\$1,620
33												
34	50	100	3	3	3	0.709	0.709	0.43	0.41	5,660	\$234	\$1,324
35	50	100	4	4	4	0.706	0.706	0.48	0.43	6,860	\$215	\$1,475
36	50	100	5	5	5	0.704	0.704	0.51	0.44	8,060	\$201	\$1,620
37												
38	60	60	5	5	5	0.706	0.706	0.46	0.49	5,660	\$234	\$1,324

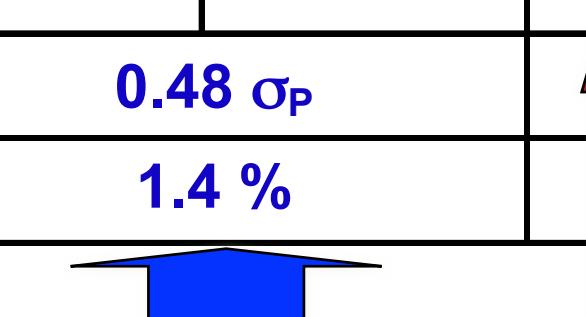
Choice of selection parameters

Initial accuracy of GS EBV = 0.7

BLUP	## selected		Progeny per # female		Accuracy		In SigP		TOTAL	28,880 SNPs		
	Sires	Dams	Male	Female	genoty	Males	Females	Response	Inbreeding	PROJECT	All in	
	60	360	3	8	0	0.437	0.618	0.48	1.38	genotypes	cost per	Total
1	25	100	4	4	4	0.589	0.589	0.46	0.70	6,860	\$215	\$1,475
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3												
4	30	60	5	5	5	0.589	0.589	0.45	0.72	5,660	\$234	\$1,324
5	30	90	6	6	6	0.587	0.587	0.50	0.65	8,540	\$201	\$1,717
6	30	120	4	4	4	0.589	0.589	0.46	0.59	7,820	\$215	\$1,681
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8	40	40	5	5	5	0.592	0.592	0.40	0.71	4,460	\$301	\$1,342
9	40	40	8	8	8	0.588	0.588	0.47	0.76	5,900	\$234	\$1,381
10	40	80	5	5	5	0.589	0.589	0.45	0.54	6,860	\$215	\$1,475
11	40	80	4	4	4	0.591	0.591	0.42	0.52	5,900	\$234	\$1,381
12	40	120	3	3	3	0.593	0.593	0.40	0.45	6,380	\$234	\$1,493
13	40	120	4	4	4	0.590	0.590	0.44	0.47	7,820	\$215	\$1,681
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20	45	45	10	10	10	0.586	0.586	0.50	0.70	7,460	\$215	\$1,604
21												
22	45	90	3	3	3	0.594	0.594	0.37	0.45	5,300	\$261	\$1,383
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24	45	90	5	5	5	0.589	0.589	0.45	0.48	7,460	\$215	\$1,604
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32	50	50	10	10	10	0.587	0.587	0.50	0.63	8,060	\$201	\$1,620
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39	60	60	6	6	6	0.59	0.59	0.43	0.49	6,380	\$234	\$1,493

Selection parameters for Traditional and Genomic Selection

Selection strategy	Traditional		Genomic	
Selection parameters	♂♂	♀♀	♂♂	♀♀
# candidates/gener.	1,000	3,000	250	250
# phenotyped	0	3,000	0	0
# selected	60	360	50	50
Generation interval	12 mo	12 mo	6 mo	6 mo
Accuracy of selection	0.44	0.62	0.6 / 0.7	0.6 / 0.7
Response / yr	0.48 σ_P		0.80 / 0.92 σ_P	
Inbreeding / yr	1.4 %		1.14 / 1.16 %	



Obtained by SelAction Assumed accuracy
with $h^2=0.3$ of G-EBV

Evaluation by Stochastic Simulation

Generation

0

.

$N_e = 500$

900

.

$N_e = 100$

1000

1001

1002

.

1012

20 chr of 37.5 cM

120,000 SNPs (freq. = $\frac{1}{2}$, LE)

Random mating → LD by drift, mutation

Allocate 200 loci with MAF>0.1 as QTL and 6000 as SNPs

Training data: Expand to 1000 indiv. – phenotype + genotype

Estimate marker effects by Bayes-B ($\pi=0.05$)

Mate random 50 males to random 50 females

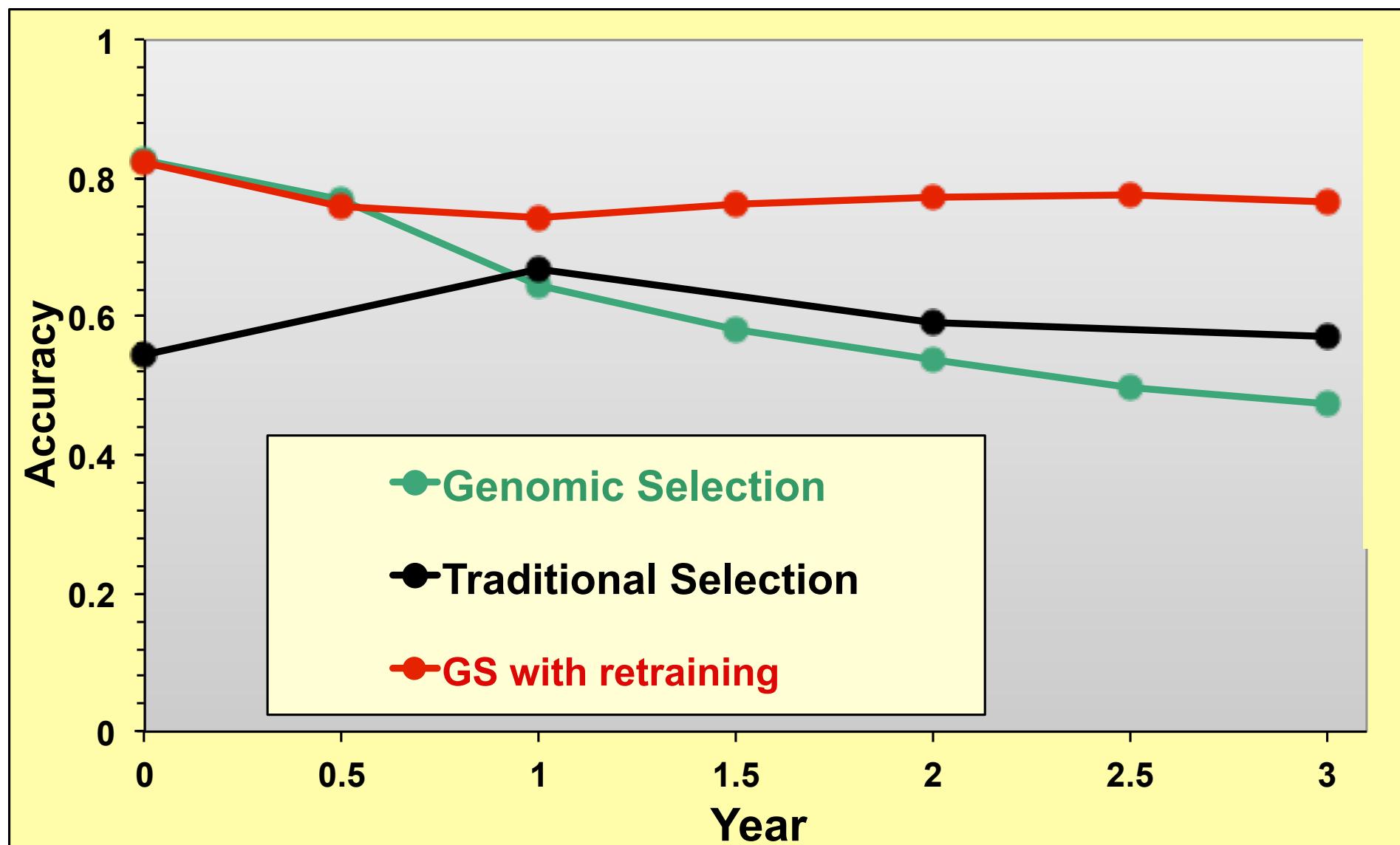
Select 50/250 males 50/250 females

Select Without / with retraining

Replicate 100 times

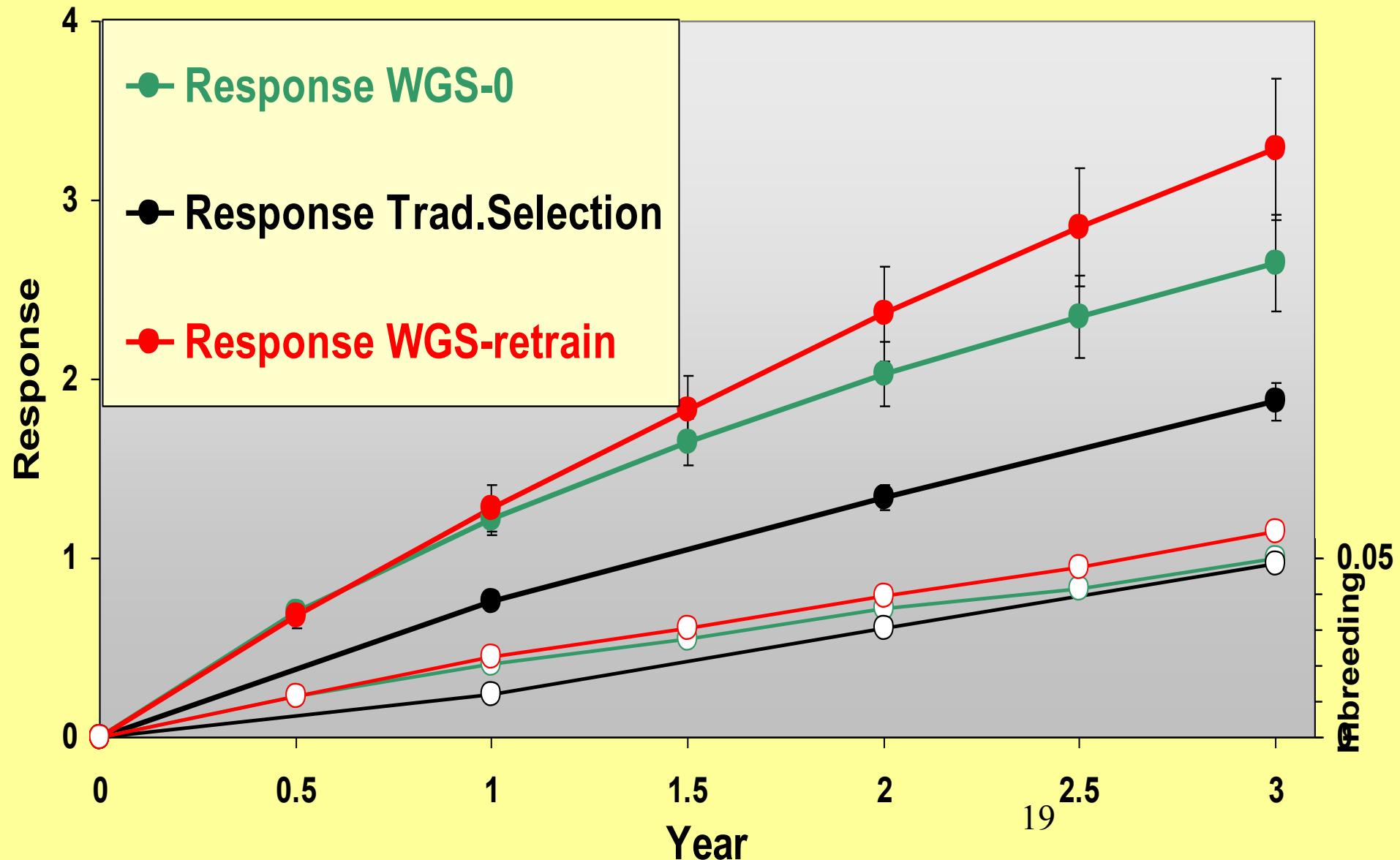
Accuracy of selection (50 replicates)

GS program with 50 sires and 50 dams

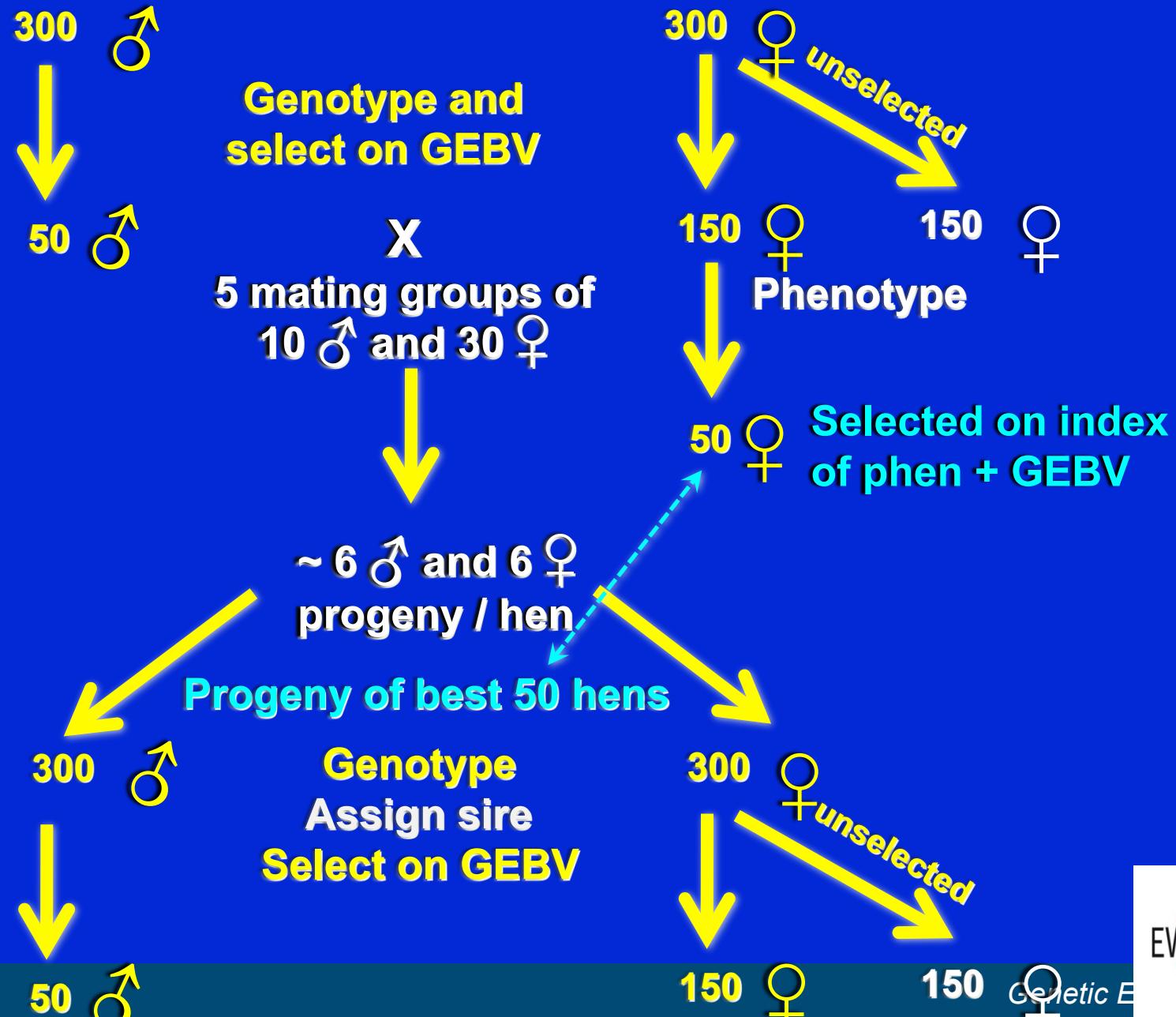


Response and Inbreeding (50 replicates)

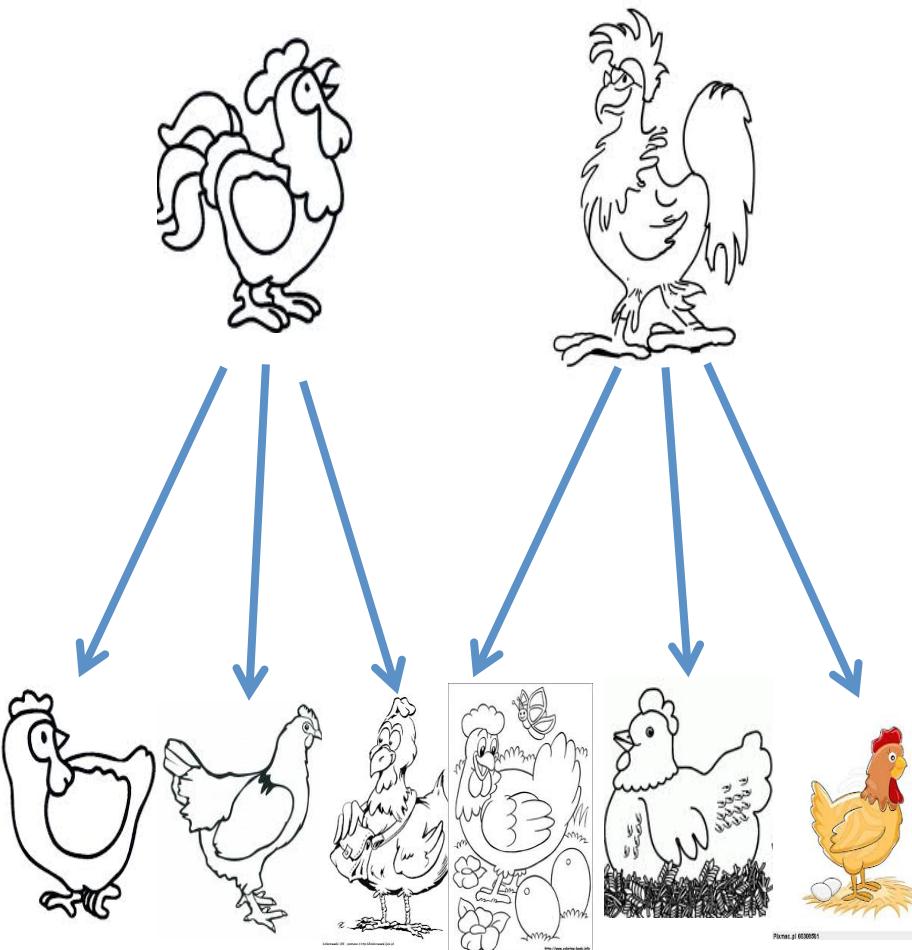
GS program with 50 sires and 50 dams



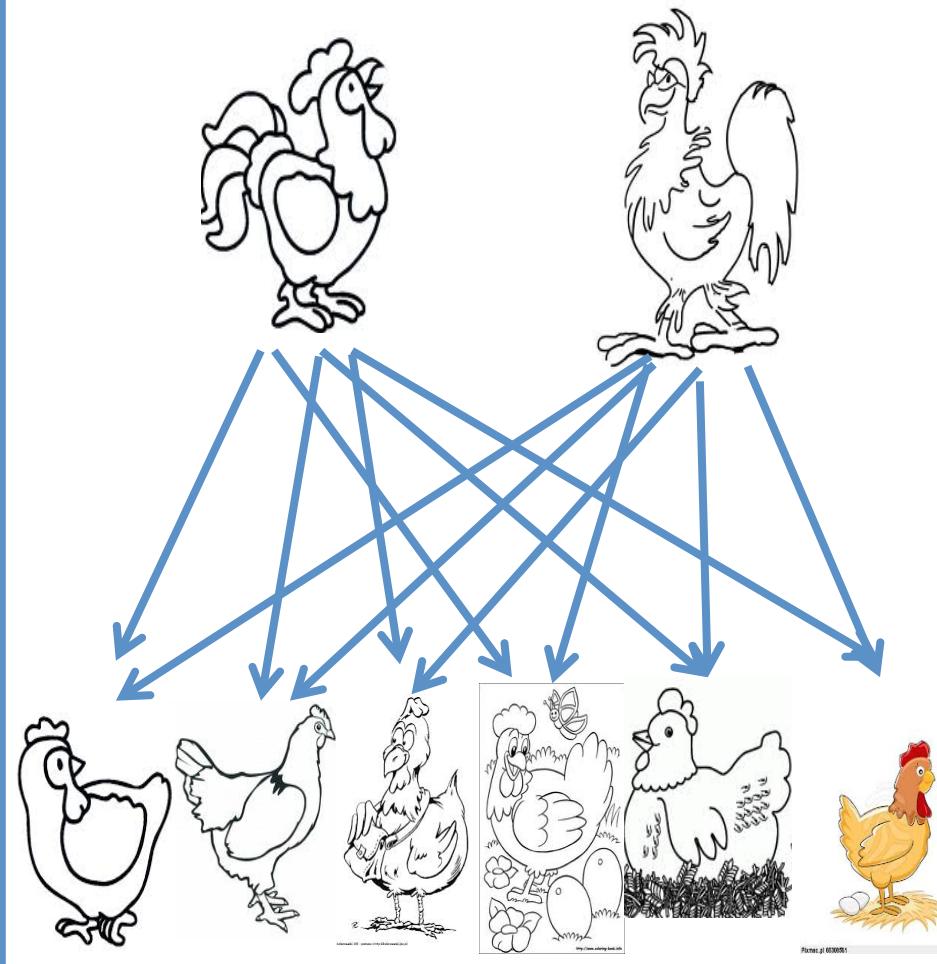
Modified Genomic Selection Program



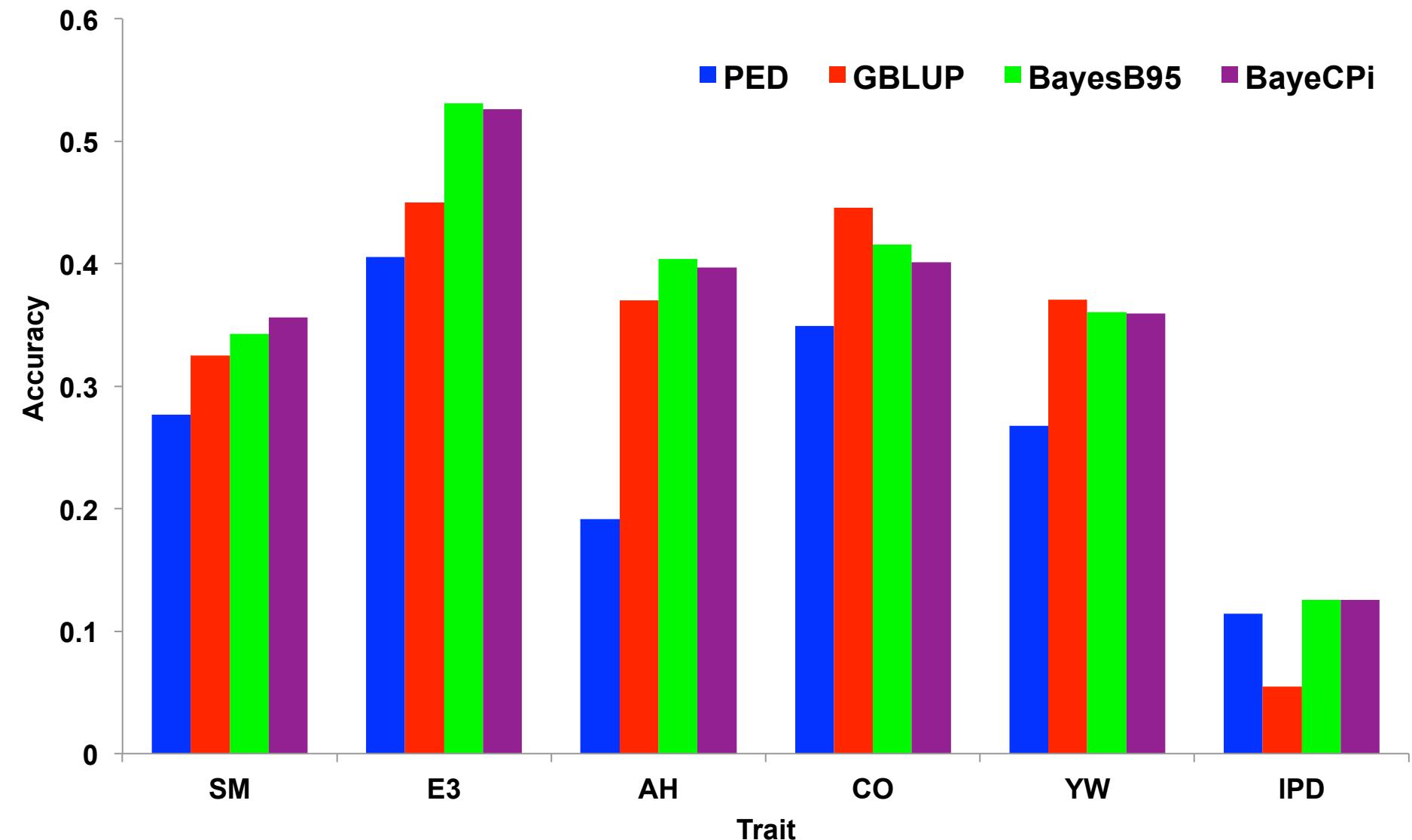
Nested mating

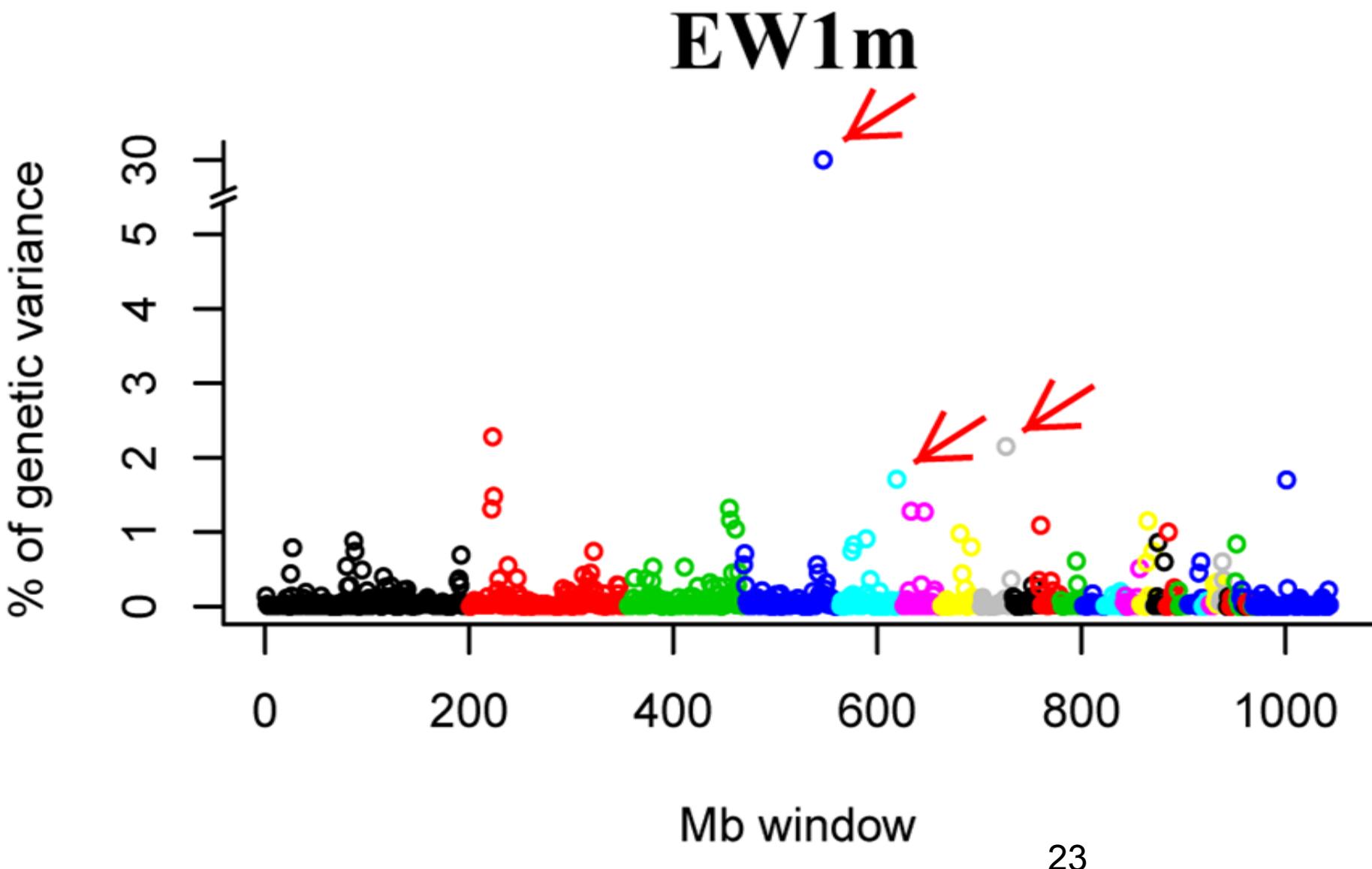


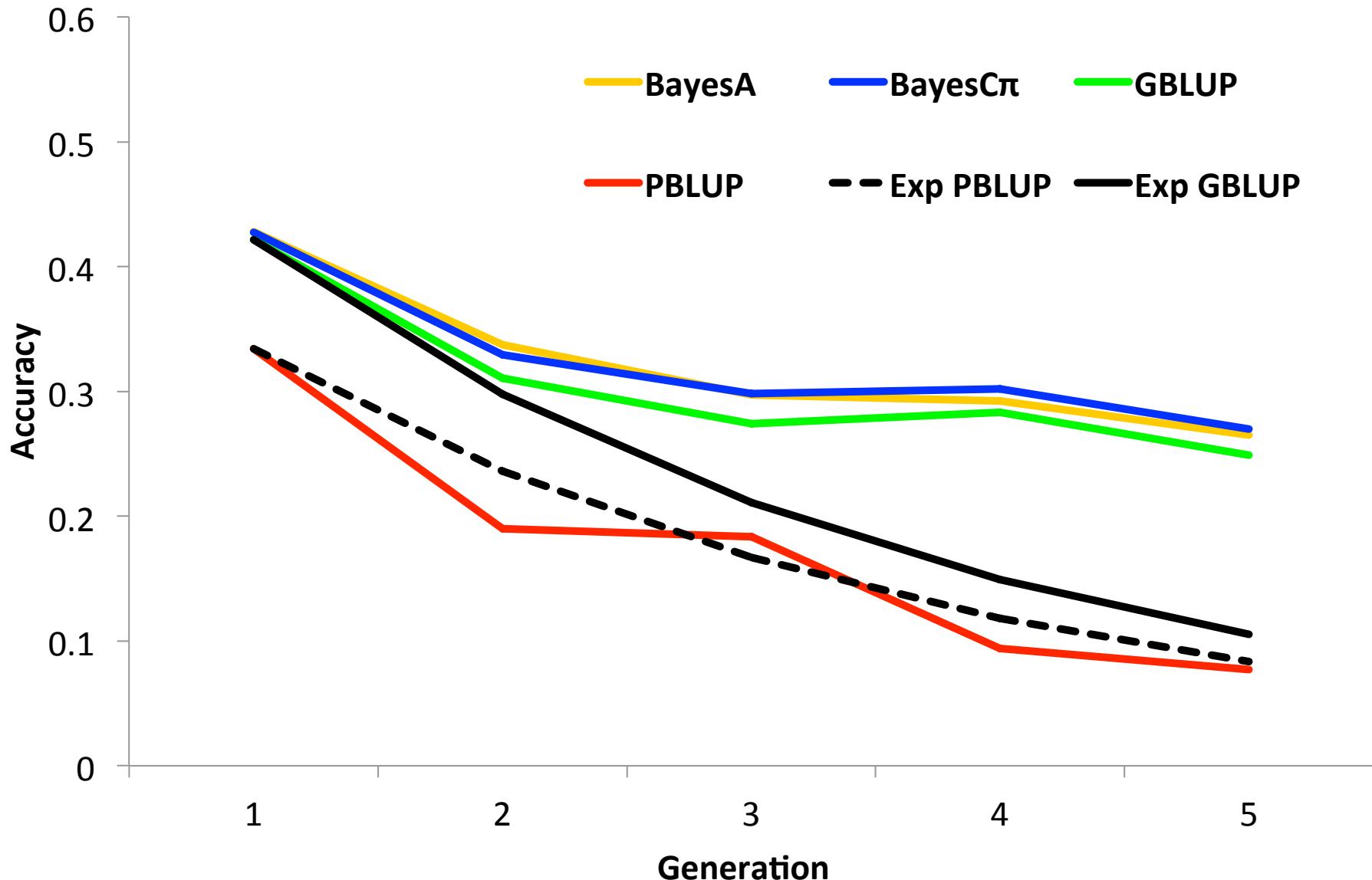
Cross-classified mating



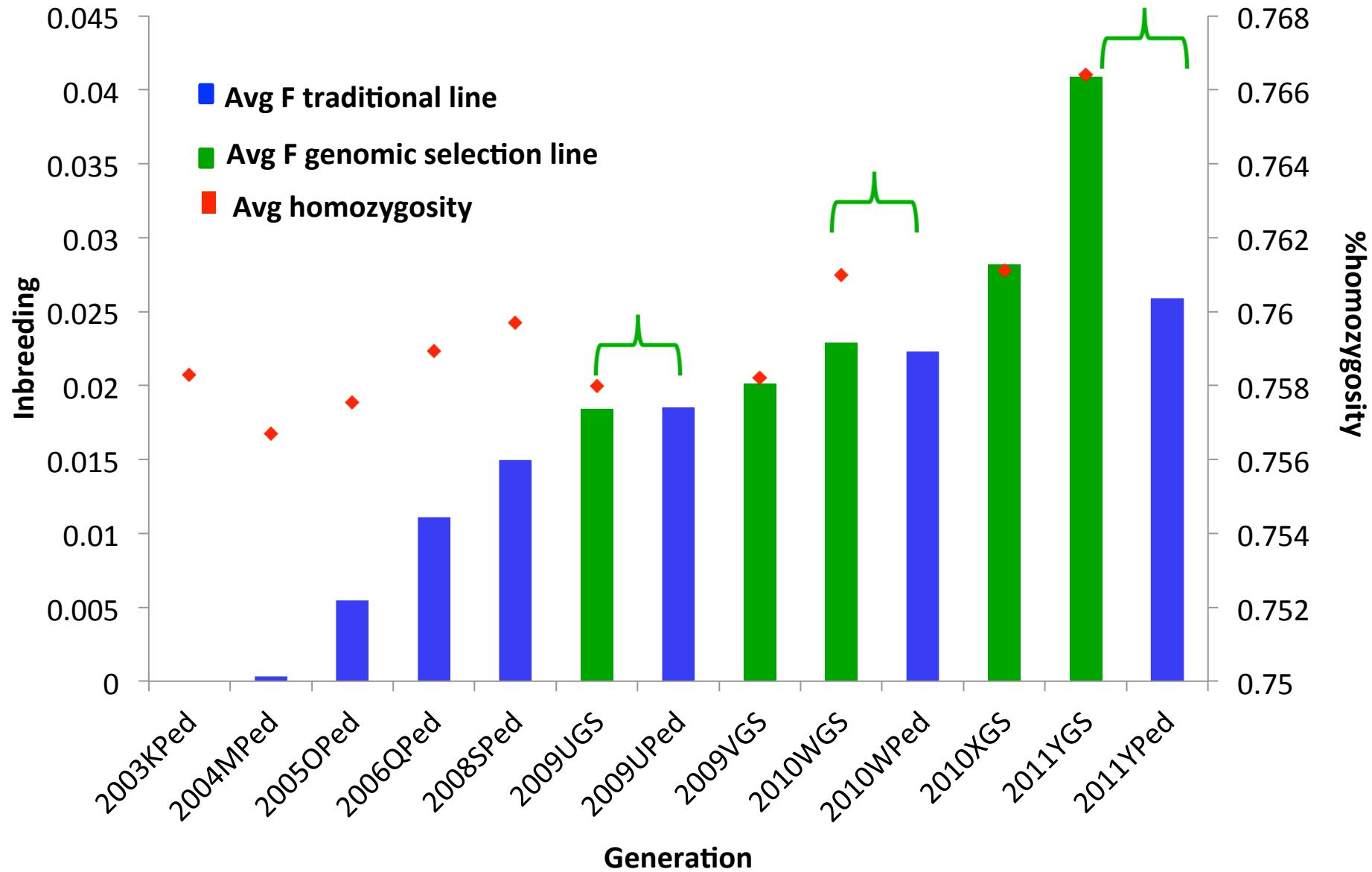
Different methods for genomic prediction

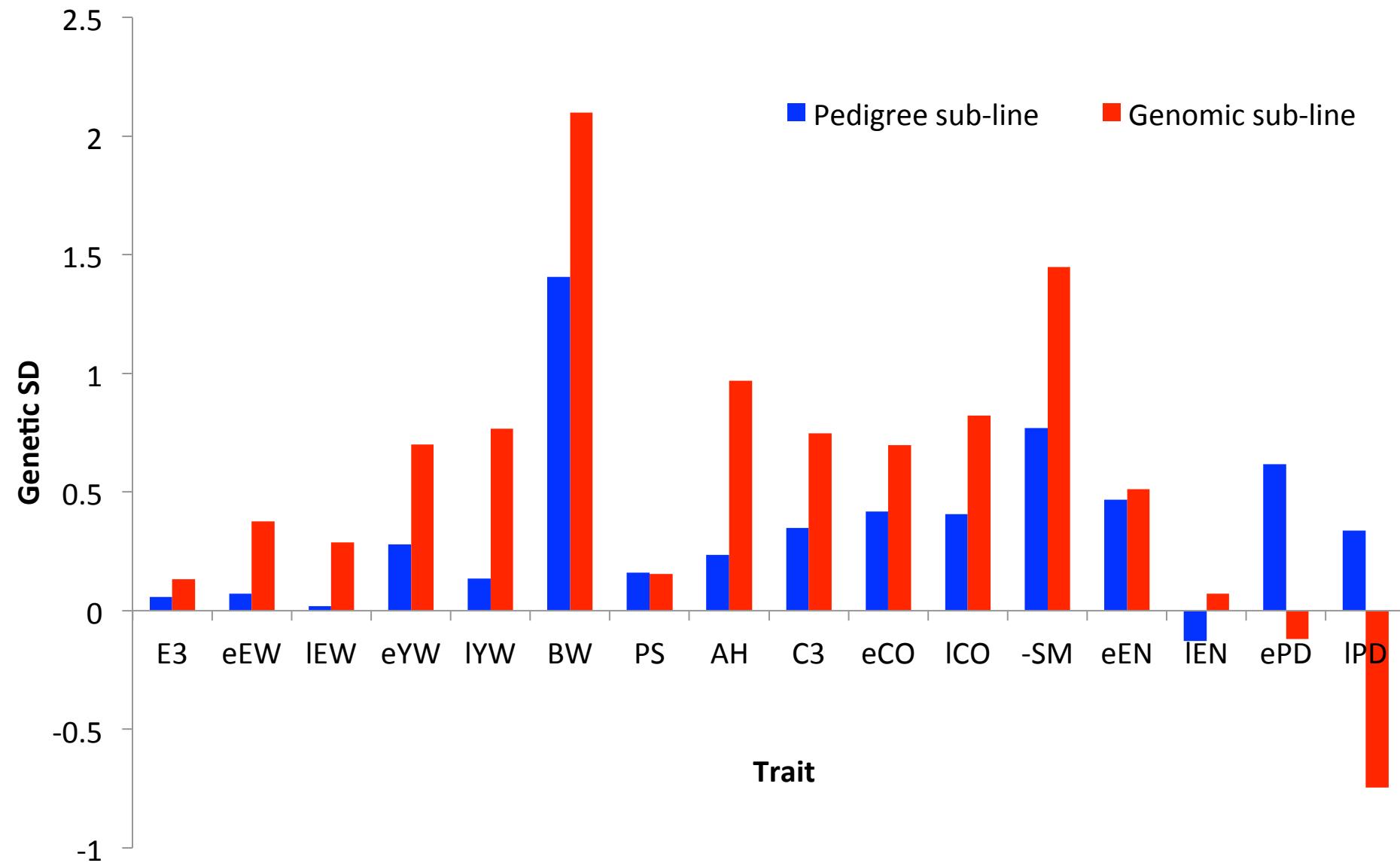


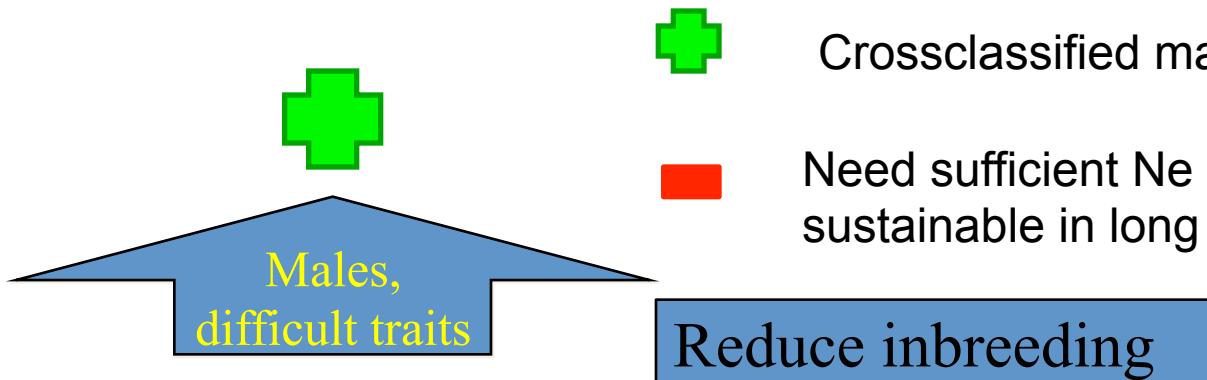




How has inbreeding changed?





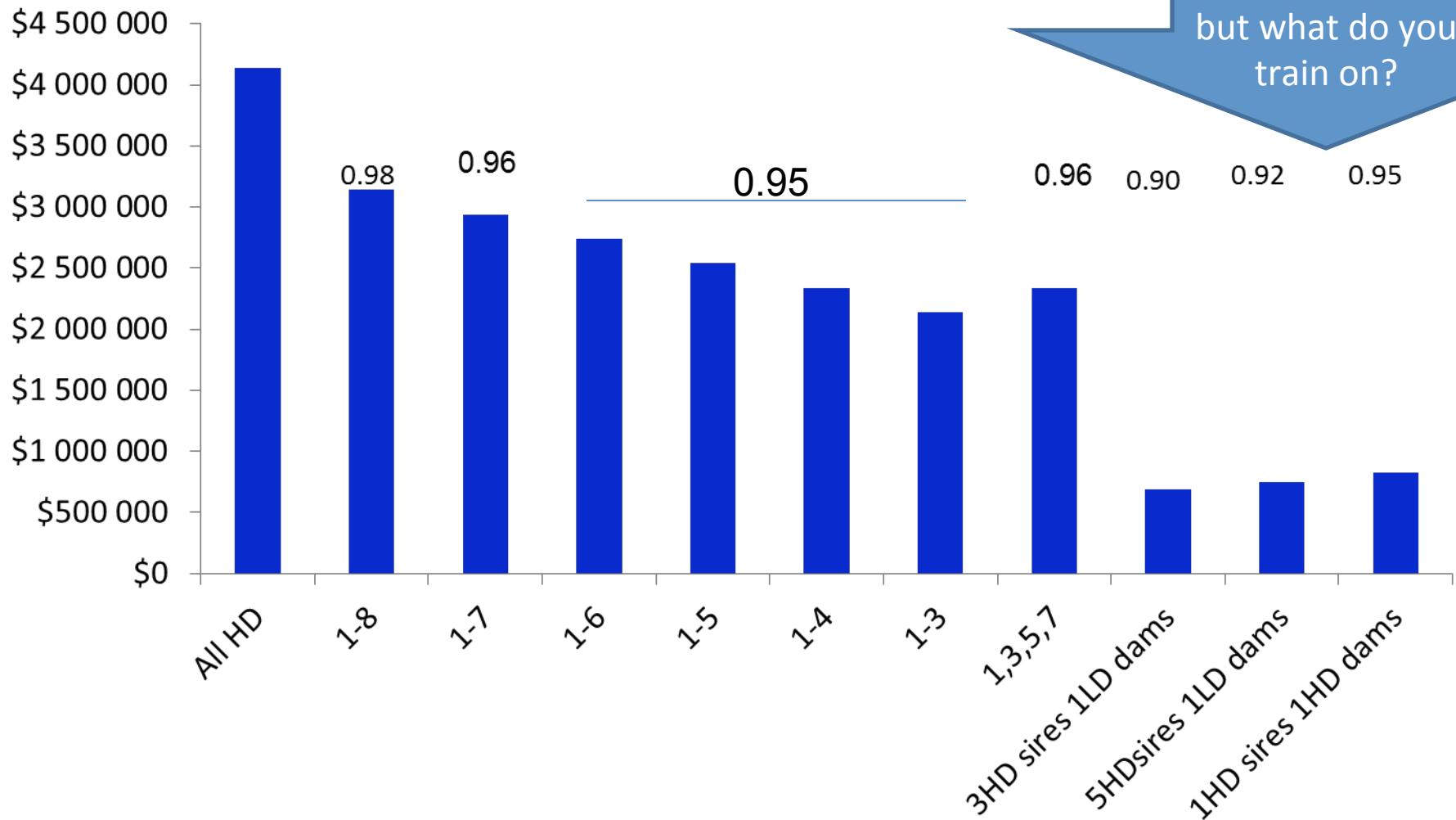


Intensity x accuracy x genetic s.d.

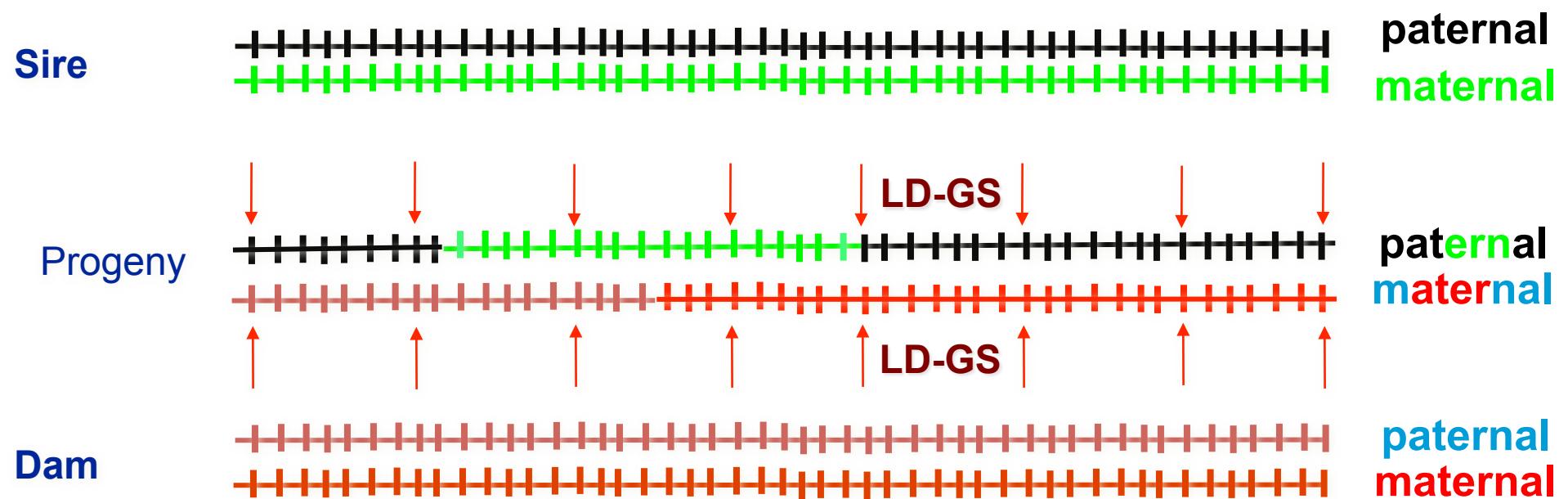
Generation interval



Round math 200 sires, 2000 dams, 10,000 selection candidates, HD 150\$, LD 50\$

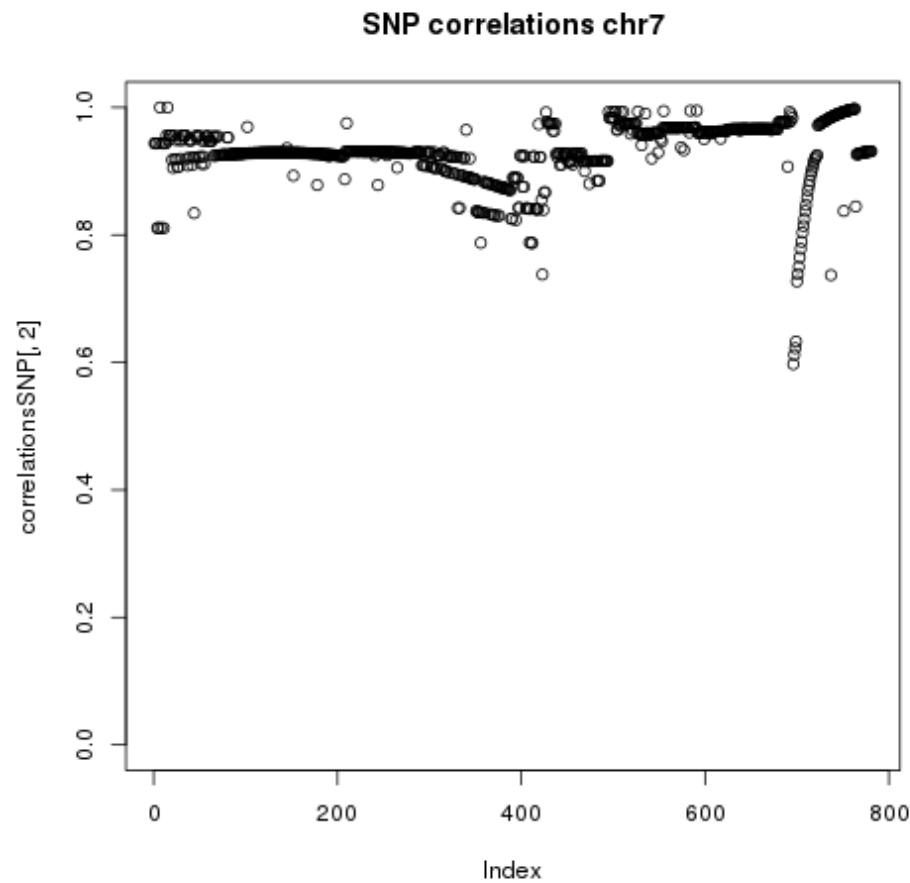
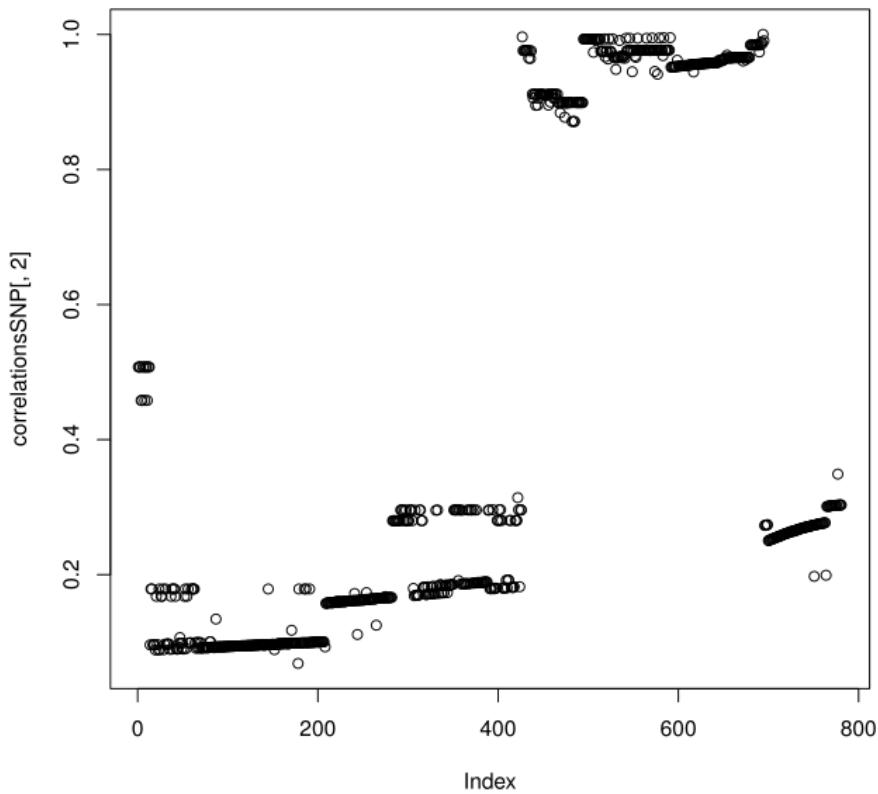


Fair cost to accuracy ratio
but what do you train on?



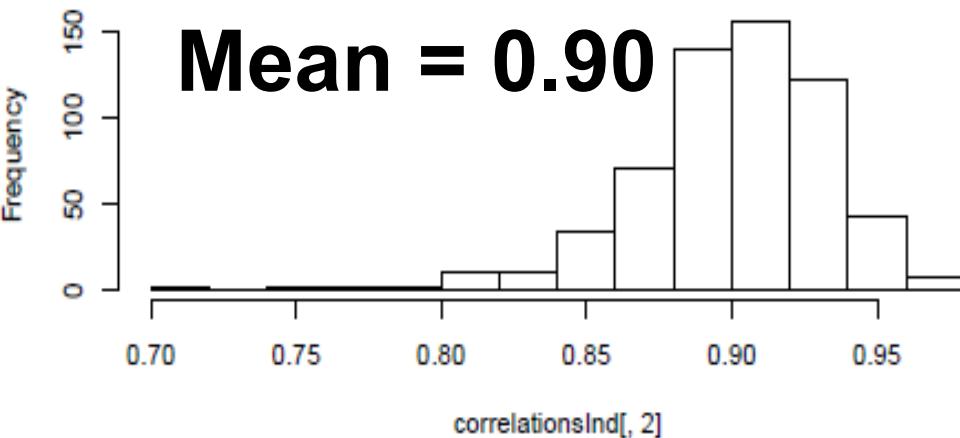
Best hand made improvement

Original panel on the left, the hand made on the right actually has less SNPs



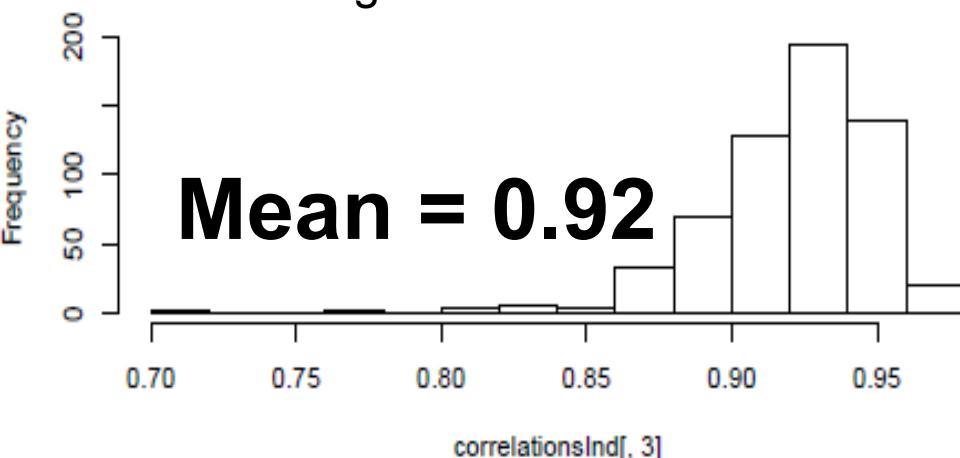
Imputation with reduced HD genotyping of dams

3 gen of HD sires 1 of LD dams



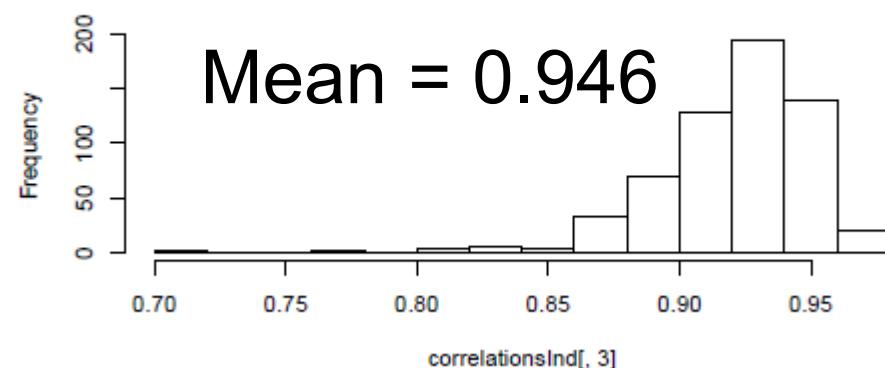
Mean = 0.90

5 gen of HD sires 1 of LD dams



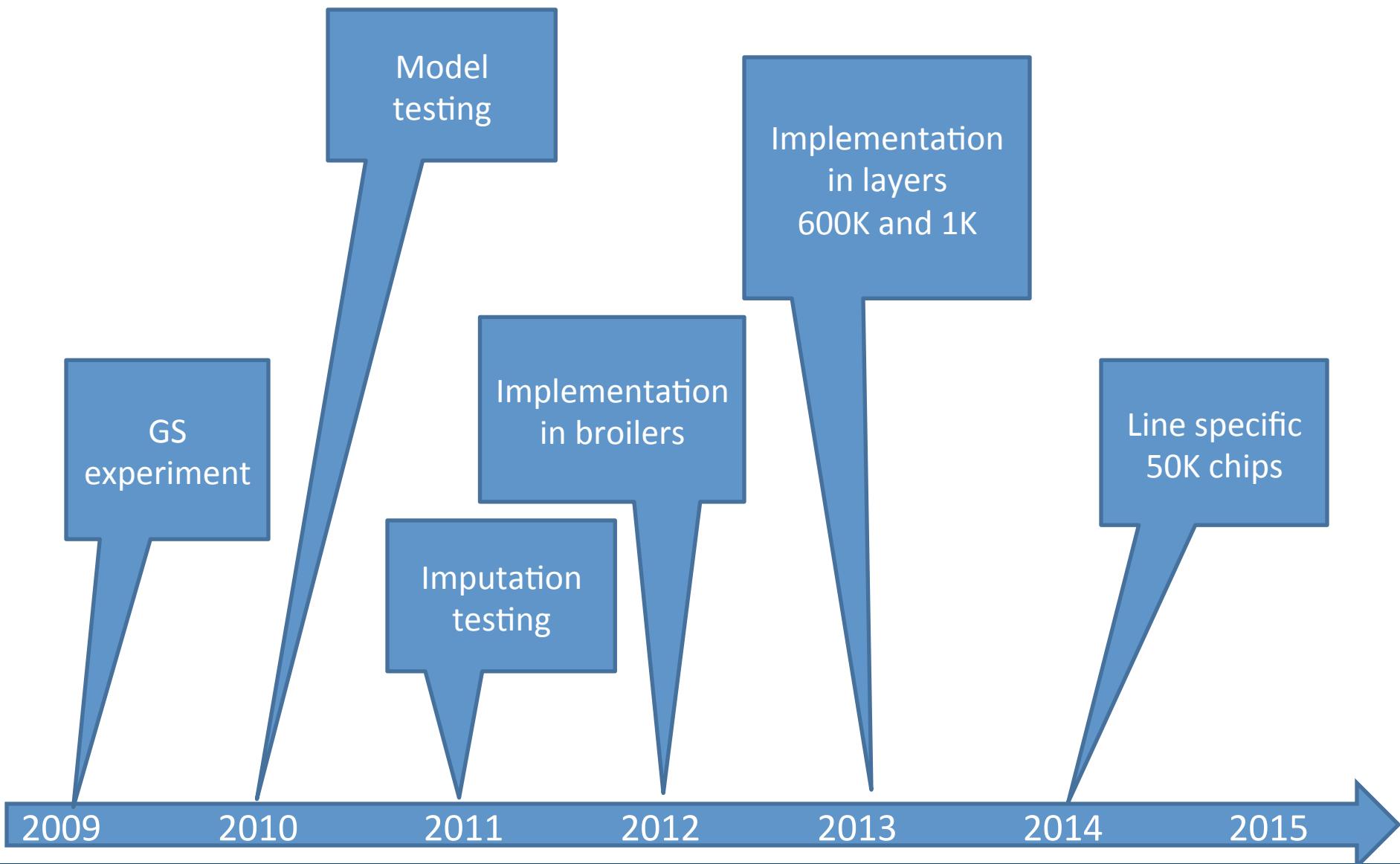
Mean = 0.92

1 gen of HD sires 1 of HD dams

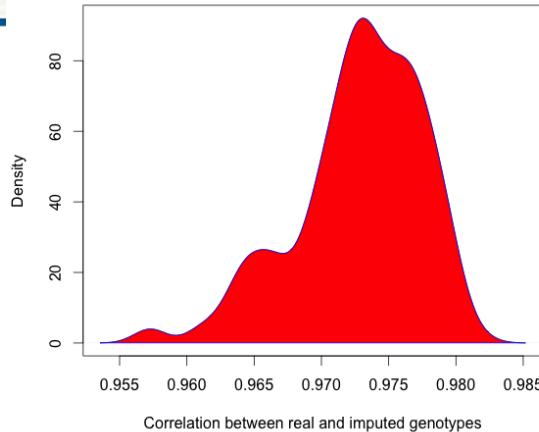


Mean = 0.946

Implementation in layers



- **Imputation** - most animals are genotyped with a sparse panel comprised of equally spaced markers that are imputed to high density
- **Accuracy** of imputation, measured as the correlation between imputed and real high-density genotype, was around **0.97** from 384 SNPs to 42K and **0.99** from 3K to 600K



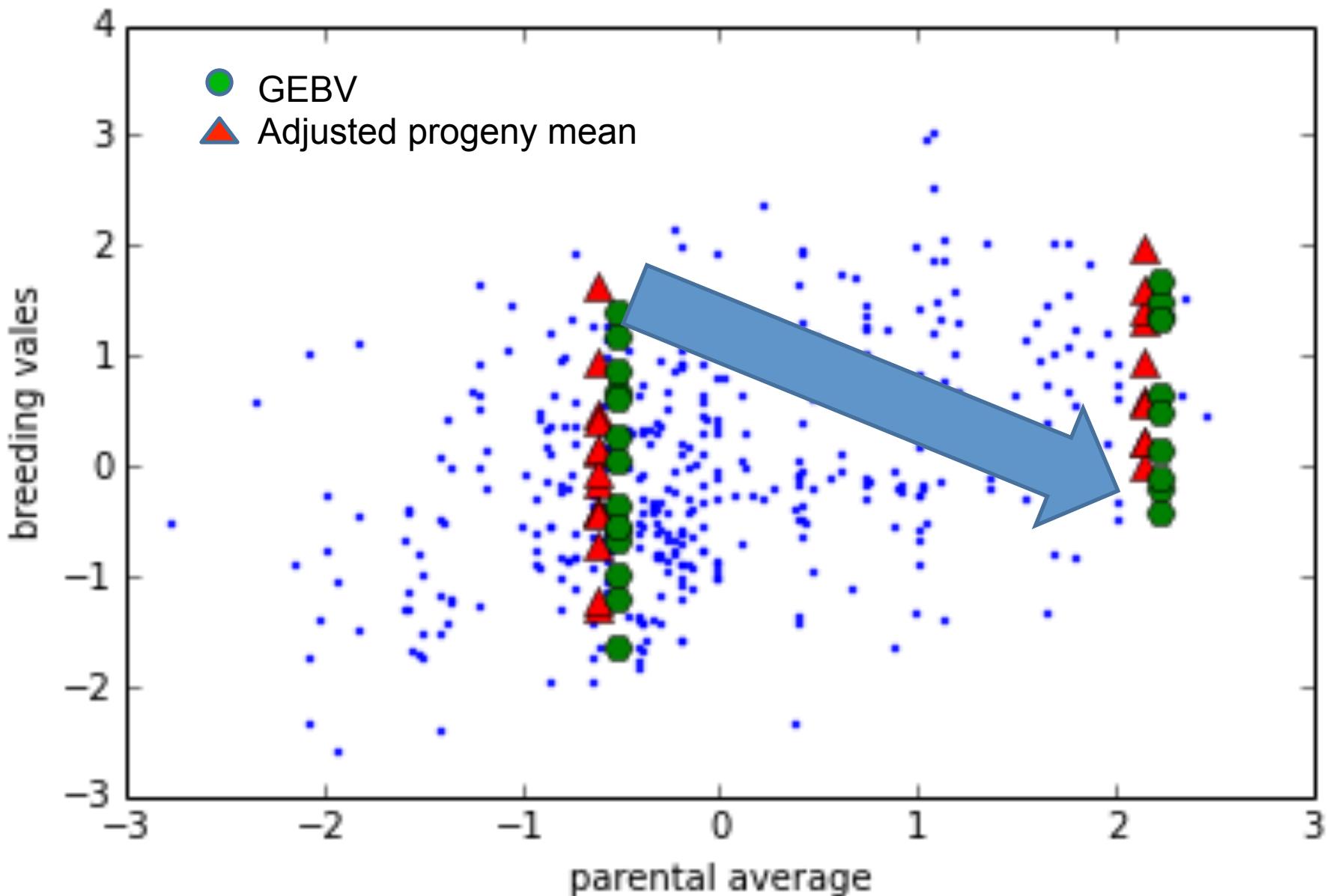
Loss in accuracy of GEBVs by using imputed genotypes

DamHD²

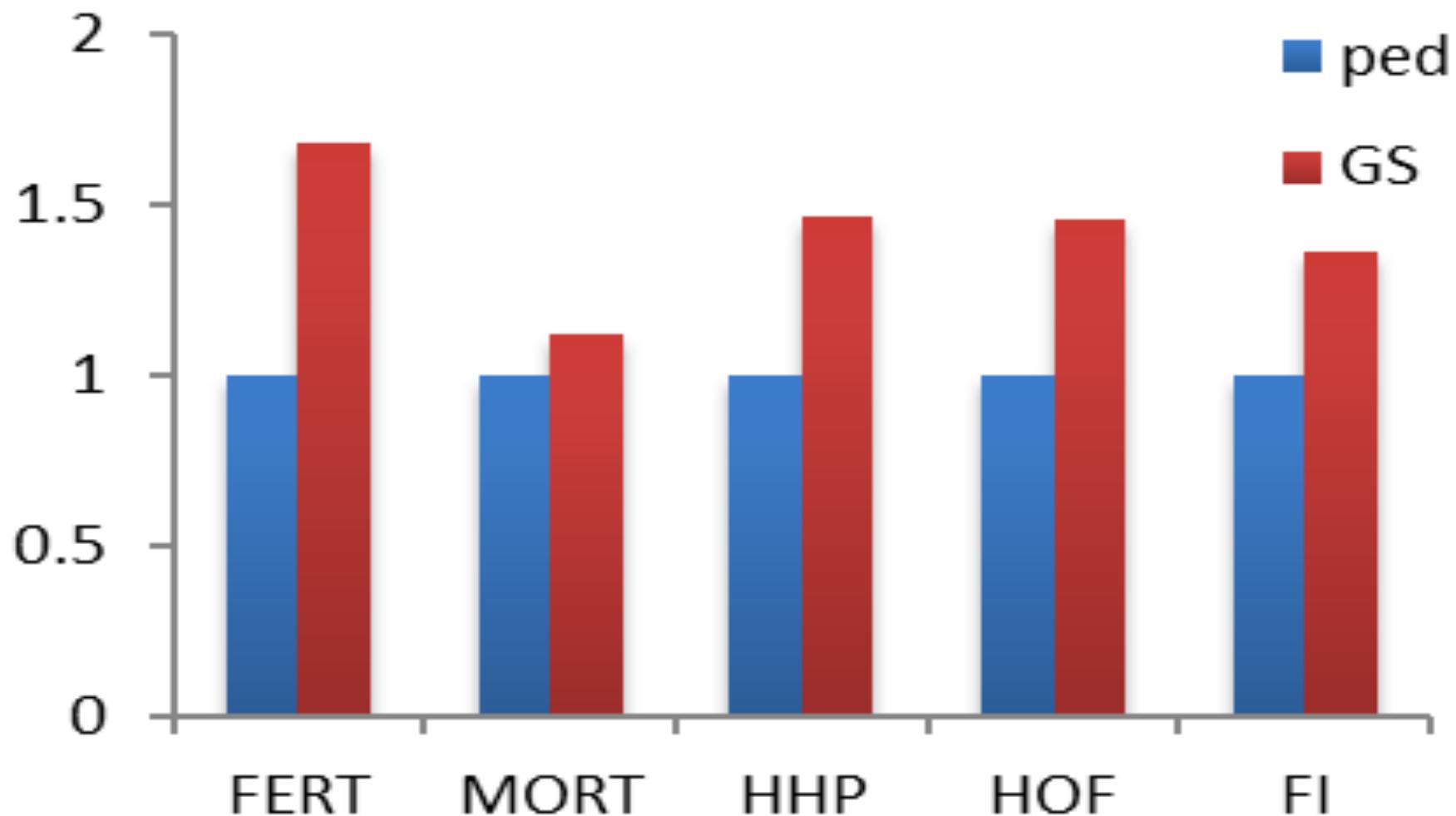
Trait	Method	ELD-1	ELD-2	ELD-1R
BW	Bayes-A	3.6	1.6	4.6
	Bayes-B	5.9	3.0	8.3
	Bayes-C	5.3	2.6	7.4
	GBLUP ⁴	3.4	1.5	4.5
HHP ⁵	Bayes-A	2.3	1.0	2.7
	Bayes-B	2.0	1.0	2.7
	Bayes-C	1.7	0.8	2.2
	GBLUP	1.6	0.6	1.9

Wang et al., 2013

Exploring Mendelian sampling



Relative improvement in accuracy



- Simple
- Fast
- Accurate
- Biases in some populations
- Convergence problems in some populations
- Issues with multiple breeds

From Dr Ignacy Misztal

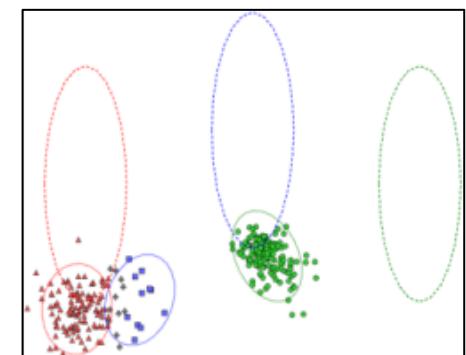
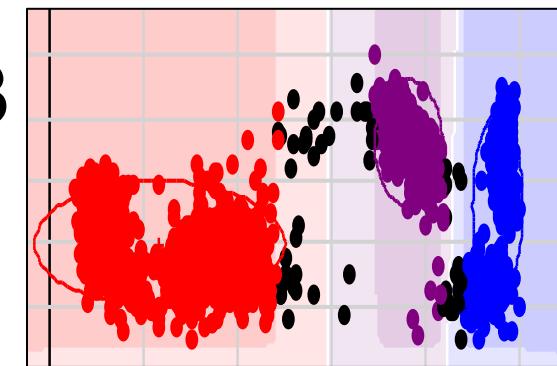
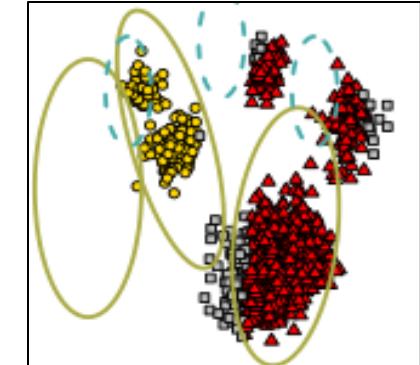
- 240k broiler chicken
- 4 k genotyped with SNP60k chip

Item ²	No genomic information		Genomic			Bayes A SUB	
	BLUP		ssGBLUP		SUB		
	SUB ³	FDS ⁴	SUB	FDS			
Line 1							
BW6	0.46	0.51	0.60	0.61		0.60	
BM	0.30	0.34	0.34	0.40		0.36	
LS	<0	0.28	0.06	0.37		0.09	
Line 2							
BW6	0.39	0.24	0.50	0.44		0.47	
BM	0.27	0.33	0.45	0.51		0.51	
LS	0.24	0.43	0.15	0.73		0.11	

(Chen et al., 2010)

- Models using genomic information are more accurate than using pedigree
- Phenotyping remains essential
- SNP effects are not QTL effects and may be not stable across generations
- SNP effects differ between lines/breeds
- Predictions for unrelated animals/lines/breeds poor
- Genotypes from old data less or not useful
- There is not one model that fits all
- Genomic selection brings new opportunities and new challenges -> We have lots to learn

- Data quality - genotype calling
- Watch data quality, check for outlayers
 - eg. accuracy all data: -0.022 after removing 3 extreme values 0.213
- Check model convergence, more complicated doesn't mean better
- If you are sure it is right, check again
- Simulations and real life are 2 very differnt worlds



- Successfully implemented in layers and broilers on commercial scale
- Cost is still the major challenge
- HD chip and GS under development in turkeys
- New tools under testing
 - Bayesian single-step
 - Genotyping by Sequencing (G-by-S)
 - Non-additive models

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