

***Genetic gain for quantitative traits  
by genomic selection – a simulation study***

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## Motivation and Purpose

1. Successful genetic selection in livestock species;  
genetic trend must reflect in phenotypic trend (final products)
2. How much more efficient in genomic selection?
3. Not easy to investigate the efficiency in field data
4. Comparing genetic trends in various simulation scenarios
5. Focusing on realized accuracy in Genetic Gain ( $\Delta G$ )

# Maximizing genetic gain in genomic selection

$$\Delta G = \frac{\text{*Accuracy} \times \text{Genetic variation (SD)} \times \text{Selection intensity}}{\text{Generation interval}}$$

**\*Accuracy** ↑ more information on phenotypes, pedigrees, genotypes

**Additive genetic variation** ↑ more genomic information, migration, mutation, genetic drift, ...

**Selection intensity** ↑ more genotypes and phenotypes => more individuals

**Generation interval** ↓ producing offspring before maturity;  
selecting animals before producing phenotypes

# Comparing ssGBLUP and ABLUP

- **ssGBLUP** (single-step genomic breeding values) = **phenotypes**
  - + pedigree( $A^{-1}$ )
  - + genomic ( $G^{-1}$ )
  - pedigree ( $A_{22}^{-1}$ ) => subtracting double counting in pedigreehere ( $G^{-1} - A_{22}^{-1}$ ) > 0 => additional genomic information
- **ABLUP** (pedigree-based breeding values) = **phenotypes**
  - + pedigree ( $A^{-1}$ )
- **IBLUP** (animal effects) = **phenotypes** + no pedigree ( $A^{-1} = I$ )

## SOFTWARE

- QMSim – (Sargolzaei & Schenkel, 2009) - Simulation
- BLUPF90 – (G)EBV calculation (running inside QMSim)
- AIREMLF90 – (Co)variance component estimation
- PREGSF90 – QC and calculating eigenvalues in G
- POSTGSF90 – calculating SNP effects and variances, and p-values

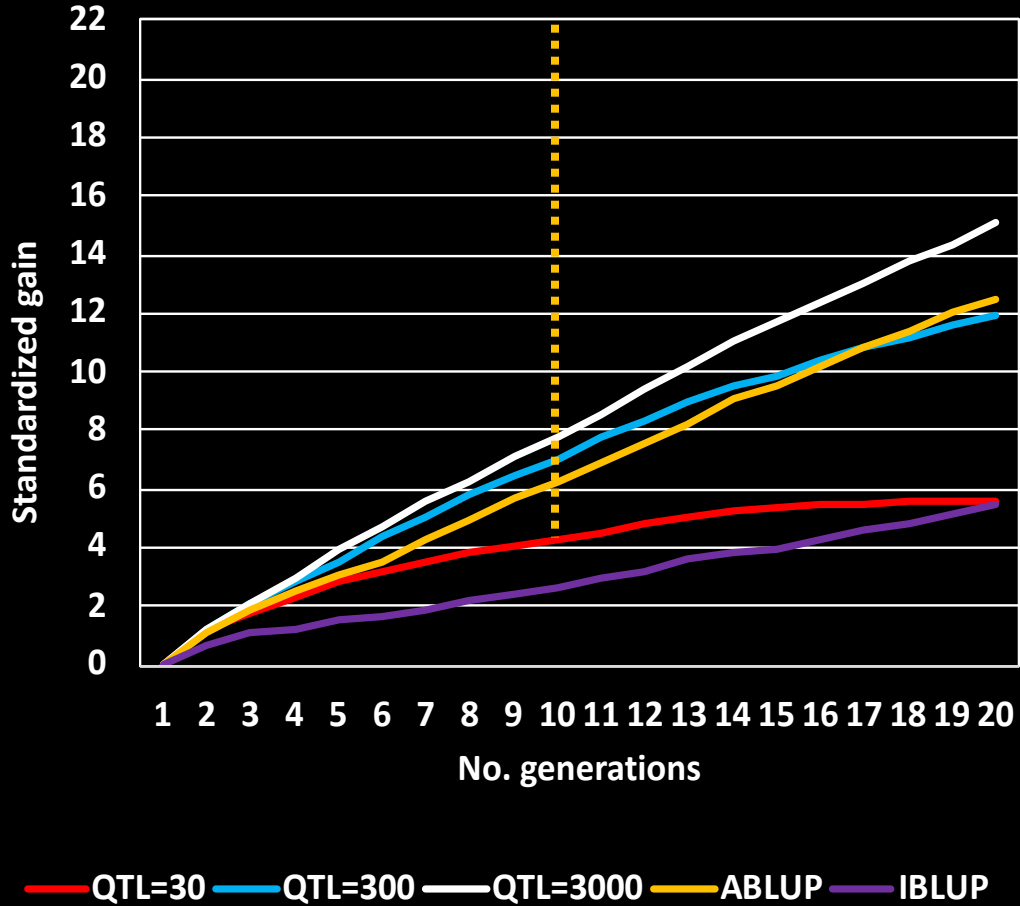
\*BLUPF90 programs available at <http://nce.ads.uga.edu/software/>

# Simulation scenarios

Variables	Parameters
Additive genetic variance, $\text{Var}(g)$	50 (fixed)
Heritability	0.50 (fixed)
Effective population size	40 (fixed)
No. chromosomes (autosomes)	30 (fixed)
No. SNP markers	30,000 (fixed)
<b>No. QTL</b>	<b>30, 300, 3000</b> 1, 10, 100 / chromosome
QTL explained in $\text{Var}(g)$ , %	100% (=no polygenic) (fixed)
No. generations with phenotypes	20 (fixed)
<b>No. animals</b>	<b>400, 2000, 20,000, 60,000</b>
<b>Full-sib family size</b>	<b>1, 10, 30</b>
No. genotyped generations	Last 10 (fixed)
<b>No. genotyped animals</b>	<b>200, 1000, 10,000, 30,000</b>
Selection by ssGBLUP, ABLUP, or IBLUP	Male: top 10% Female: top 50% (fixed)

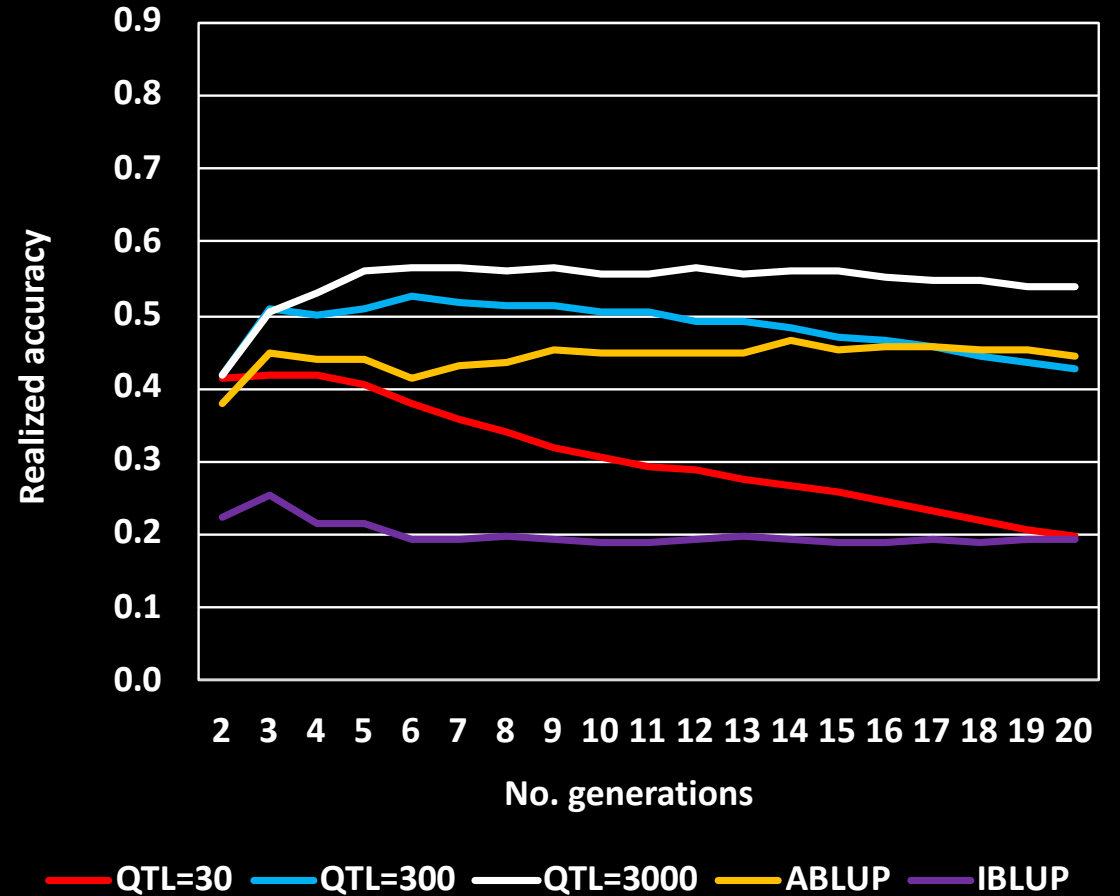
# Genetic trend by #QTL

No. genotyped animals=30000

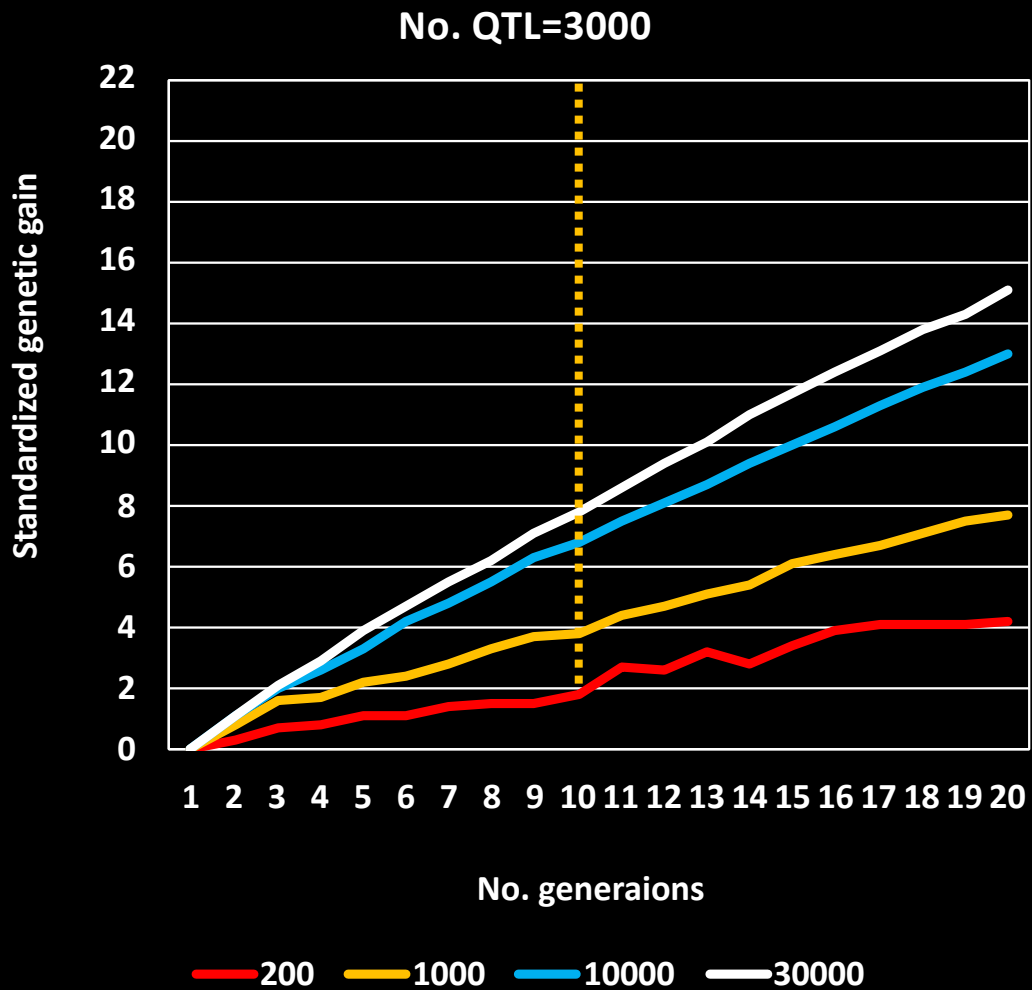


# Realized accuracy

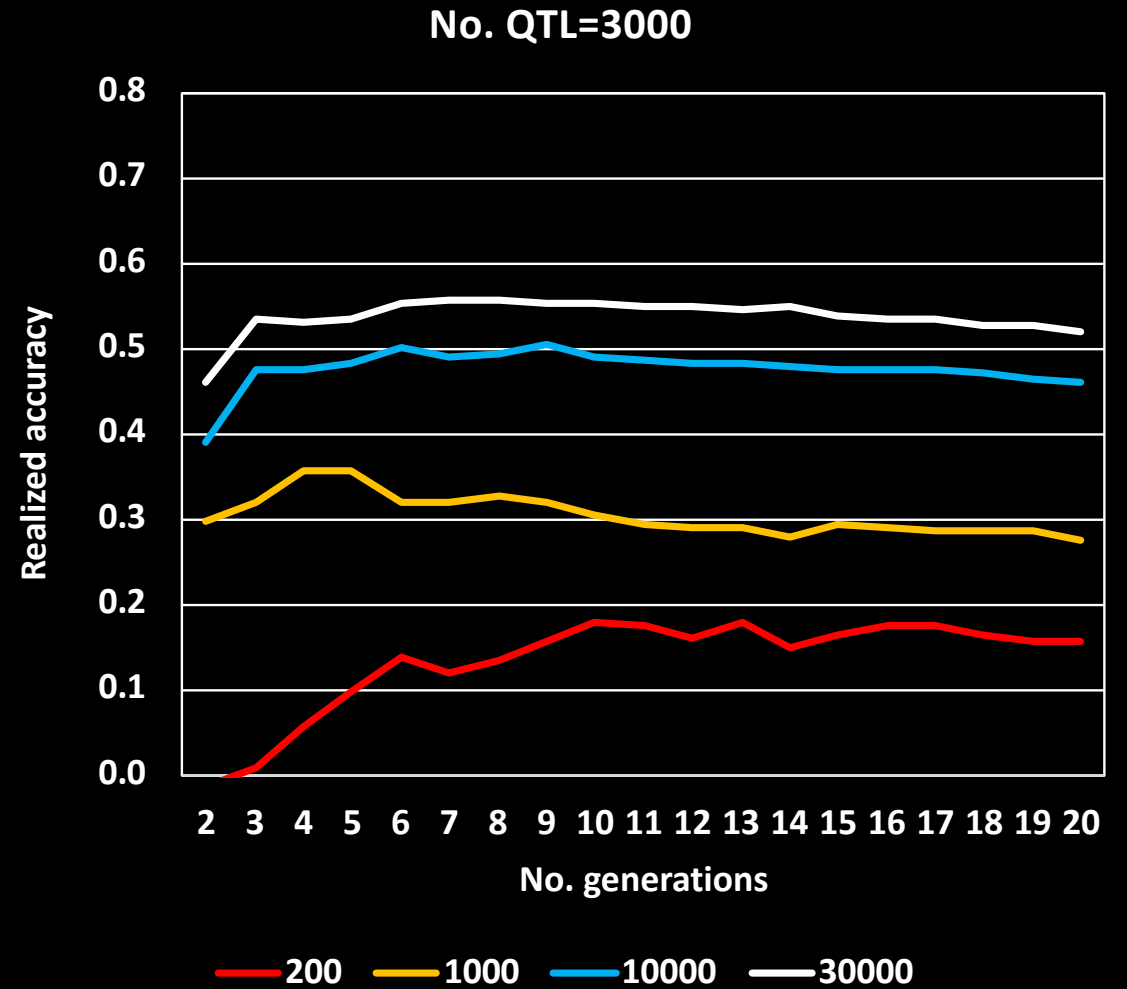
No. genotyped animals=30000



# Genetic trend by #animals

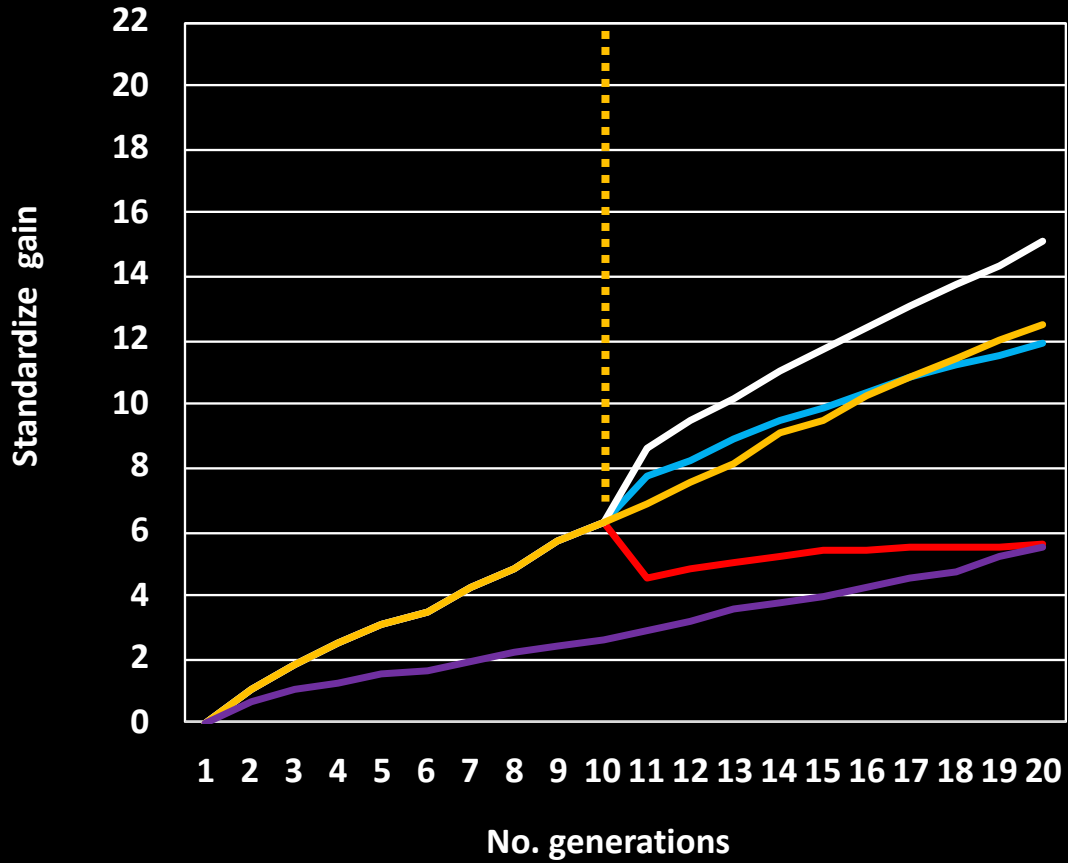


# Realized accuracy



# Genetic trend by #QTL

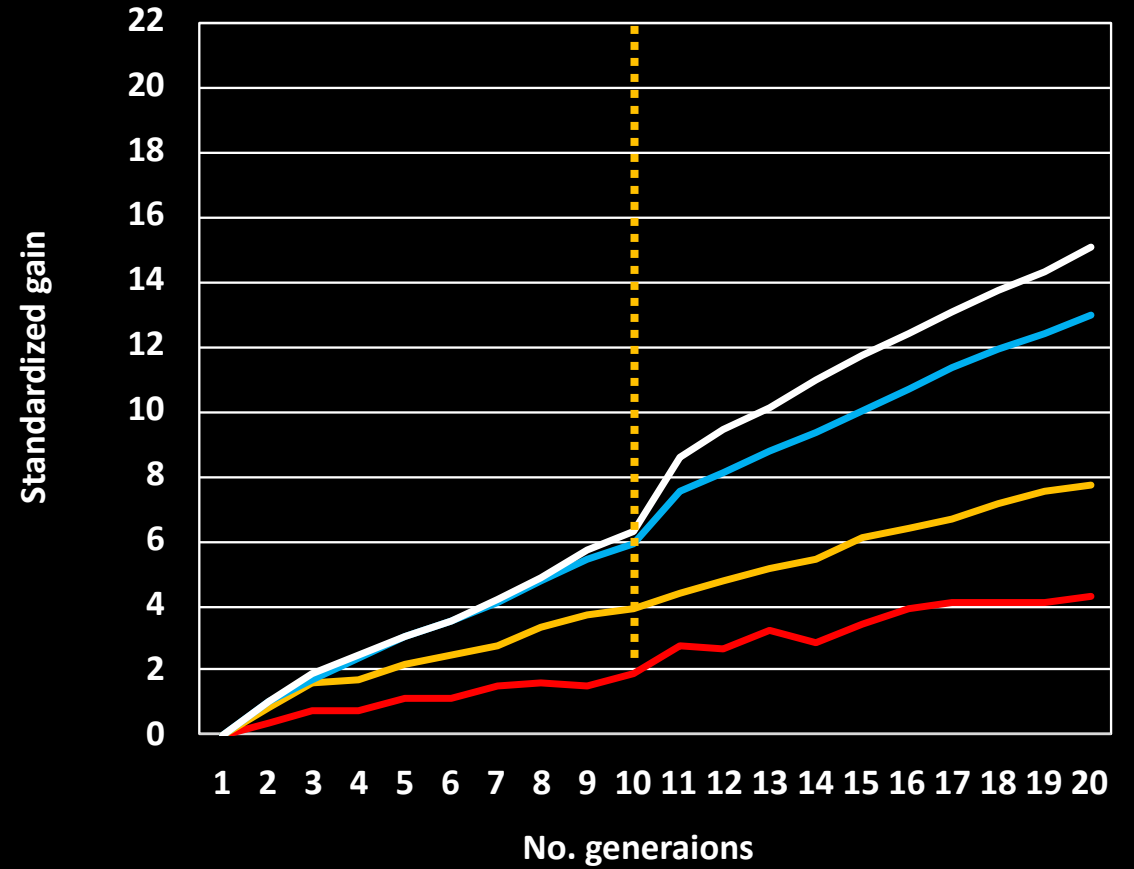
No. genotyped animals=30,000



— QTL=30 — QTL=300 — QTL=3000 — ABLUP — IBLUP

# Genetic trend by #animals

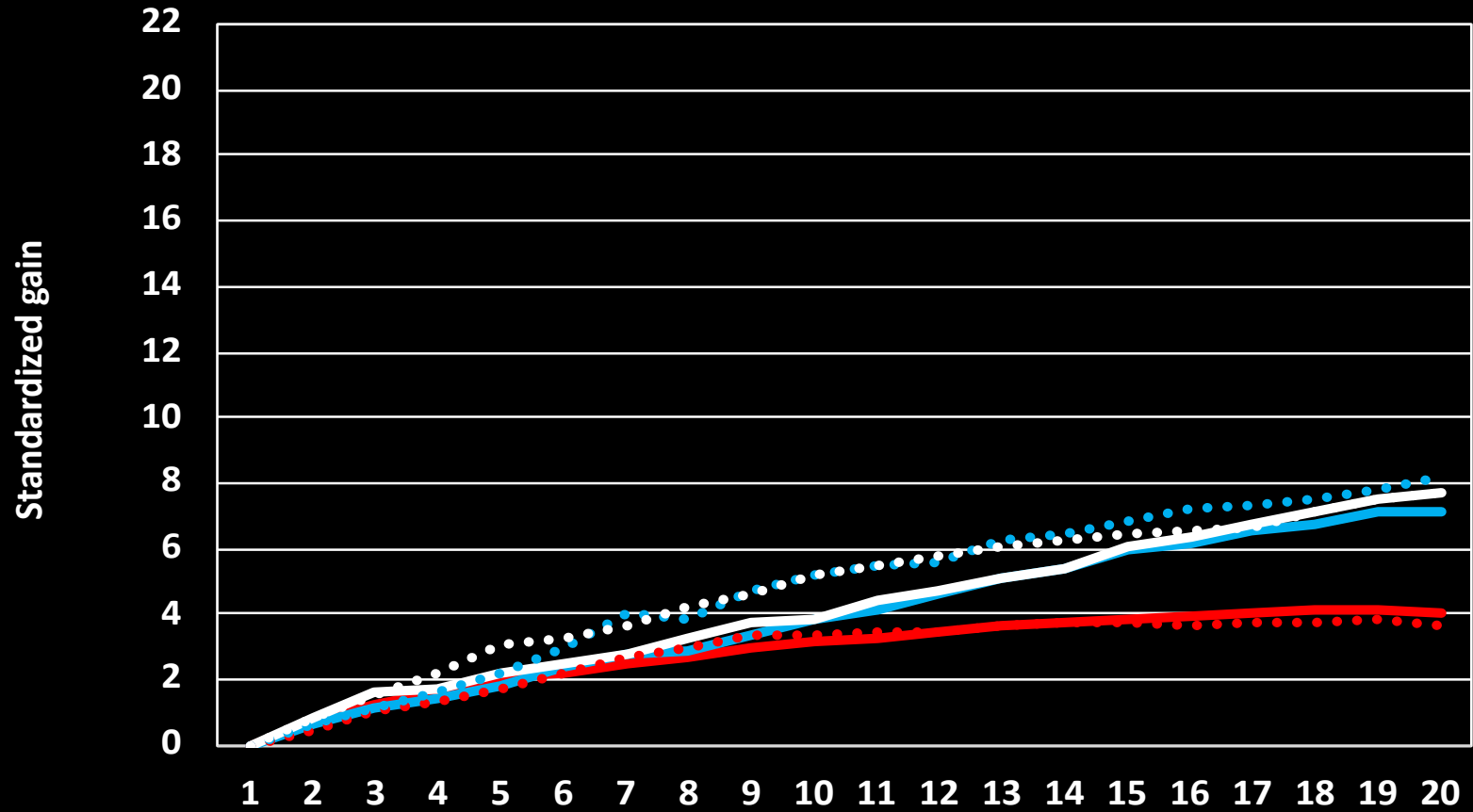
No. QTL=3000



— 200 — 1000 — 10000 — 30000

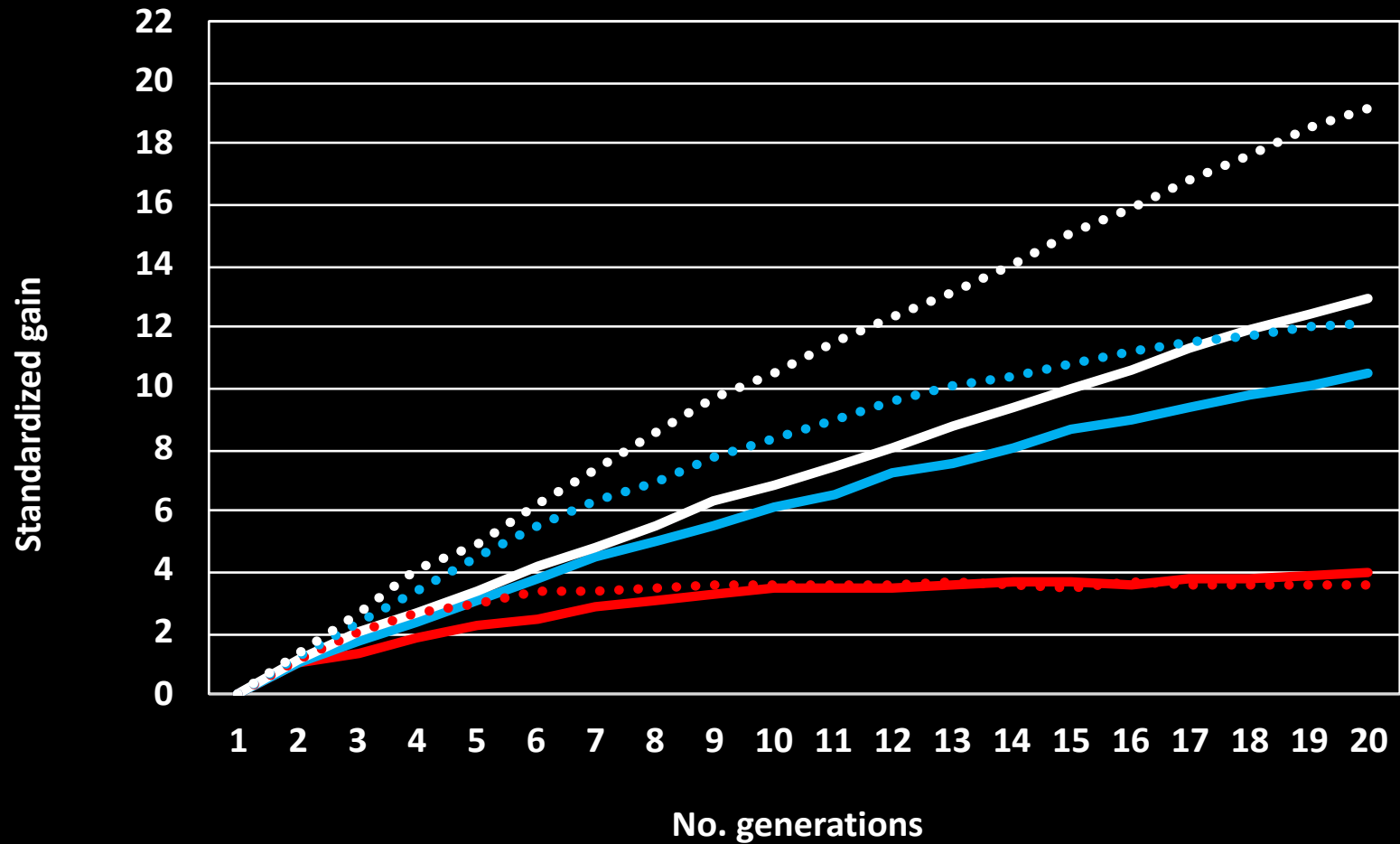


No. genotyped animals=1000 : Full sib = 1 vs 10



Full sib = 1 : — QTL=30 — QTL=300 — QTL=3000  
Full sib = 10 : ..... QTL=30 ..... QTL=300 ..... QTL=3000

No. genotyped animals=10000 : Full sib = 1 vs 10



Full sib = 1 : — QTL=30    — QTL=300    — QTL=3000  
Full sib = 10 : ..... QTL=30    ..... QTL=300    ..... QTL=3000

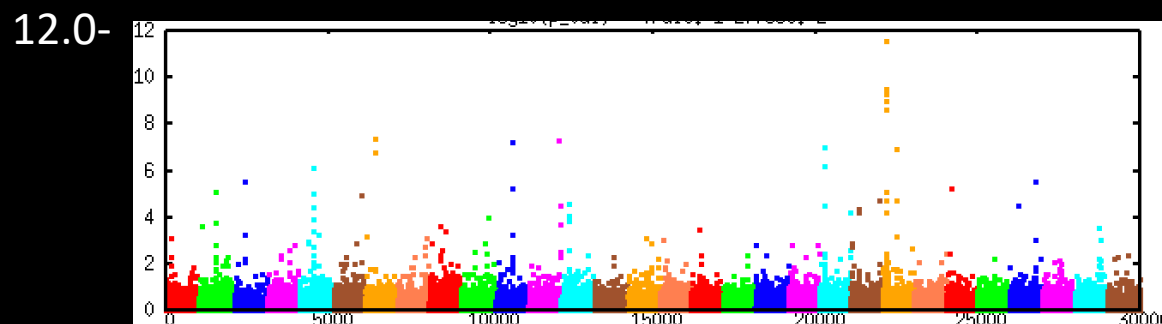
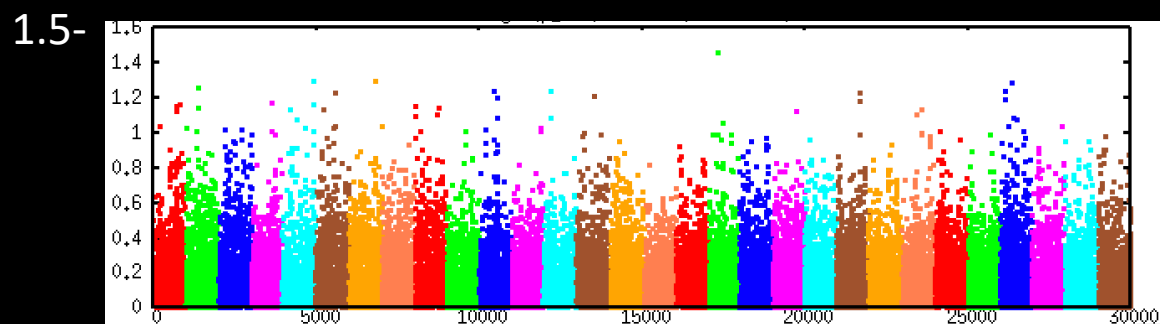
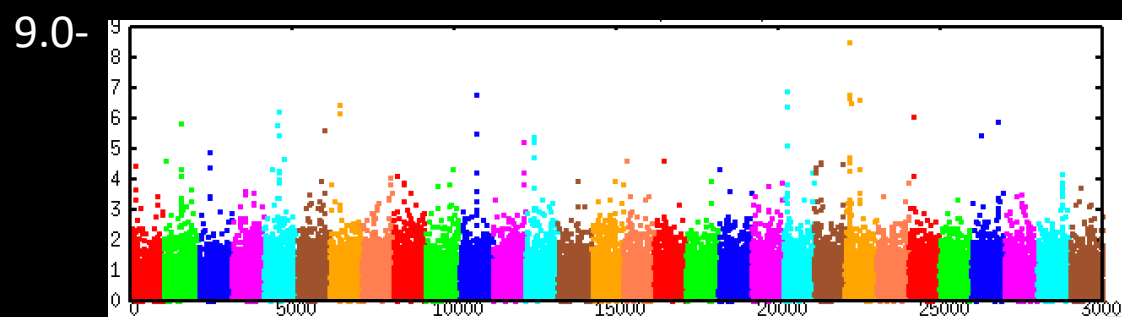
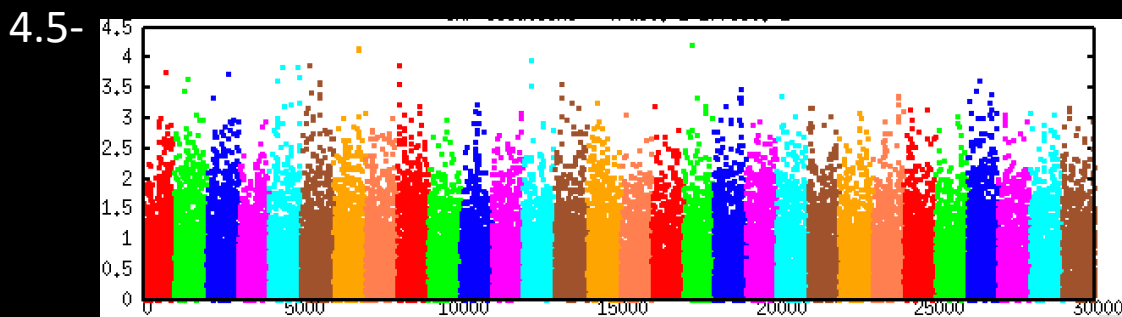
# Genetic gain (average in last 10 gen)

No. genotyped animals	No. QTL	Genetic gain /generation	ssGBLUP /ABLUP	Accuracy	$G^{-1} - A_{22}^{-1}$
200	ABLUP	0.2	-	0.12	-
	30	0.1	0.4	0.11	0.3
	3000	0.2	1.0	0.17	0.3
	<b>3000: weighted</b>	<b>0.3</b>	<b>2.3</b>	<b>0.16</b>	<b>0.5</b>
30,000	ABLUP	0.6	-	0.19	-
	30	0.1	0.2	0.25	19.5
	<b>3000</b>	<b>0.7</b>	<b>1.1</b>	<b>0.54</b>	<b>21.4</b>
	3000: weighted	0.6	1.0	0.53	21.3
	<b>3000: full sib=10</b>	<b>1.0</b>	<b>1.5</b>	<b>0.83</b>	<b>47.1</b>

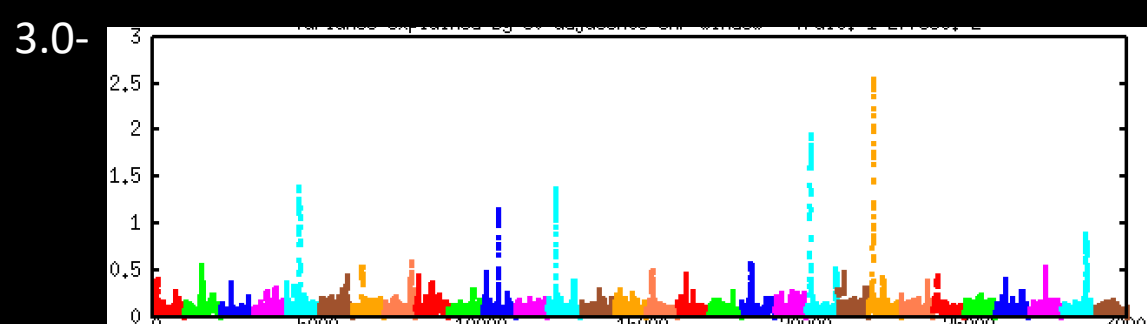
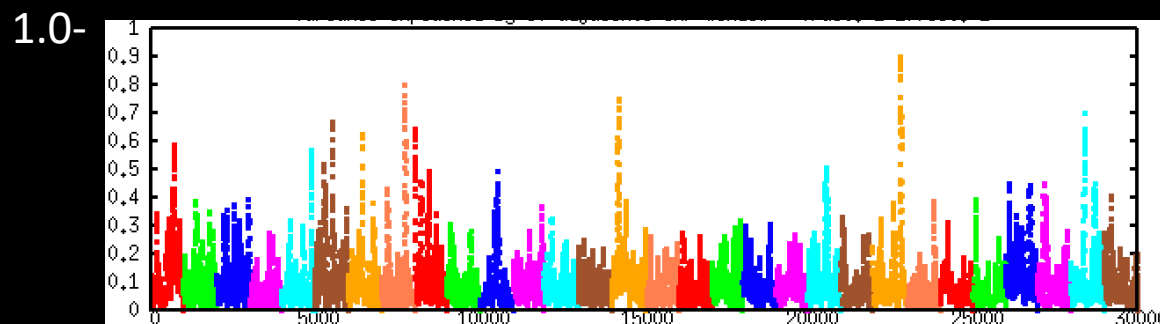
30 QTL / 200 animals

SNP effects

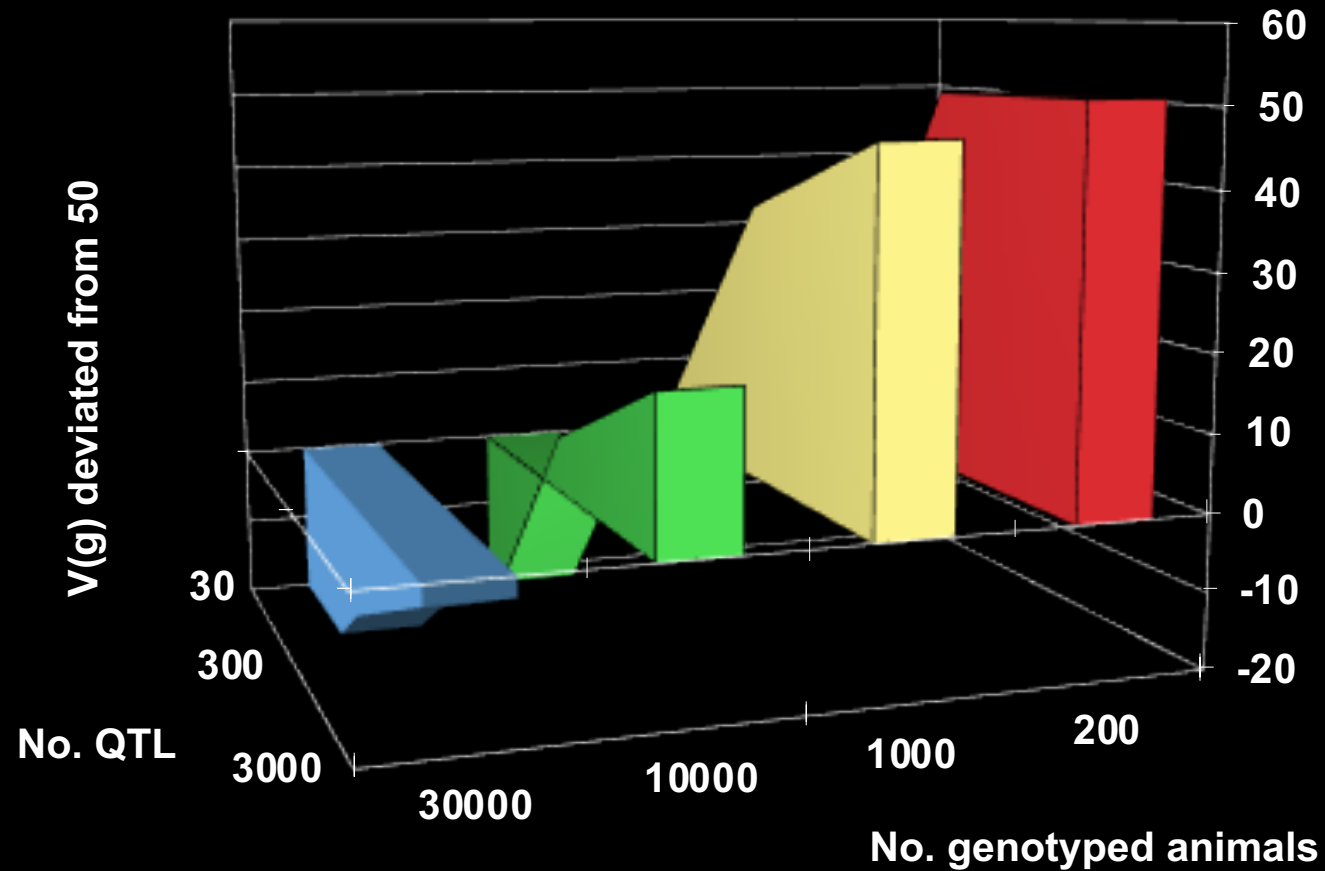
3000 QTL / 30,000 animals



SNP variances

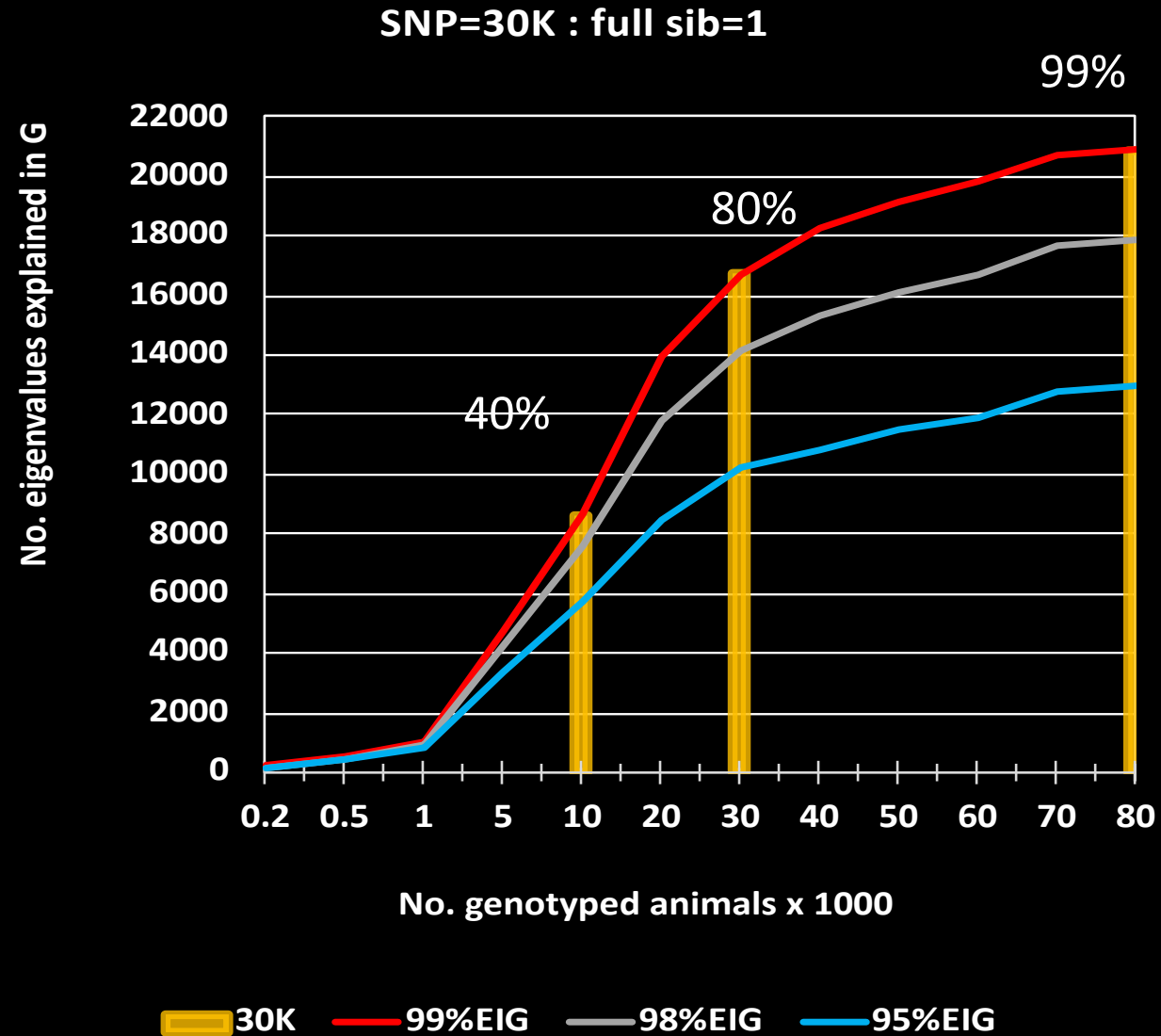


## Overestimation of additive genetic variance



With fewer animals for a polygenic (more QTL) trait >>>> biased  $V(g)$ ?

# Independent Chromosome Segments ( $\approx$ Independent Individuals)

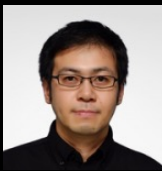
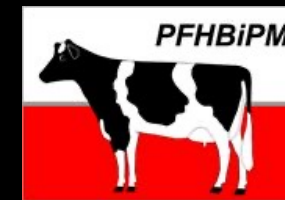
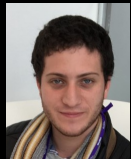
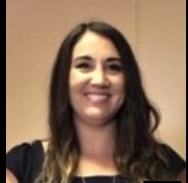


# Summary

To maximize  $\Delta G$  in genomic selection

1. More genotyped animals  $\Rightarrow \Delta G \uparrow$
2. More polygenic inheritance (more QTL)  $\Rightarrow \Delta G \uparrow$
3. More full-sibs  $\Rightarrow \Delta G \uparrow$
4. In a small population, weighted ssGBLUP more effective
5. Biased  $V(\hat{\mathbf{g}})$  using few genotyped animals for polygenic traits  
>>>> biased GEBV and SNP effects???

# Acknowledgments





*Thank you*

## Additional comments on genetic trend

1. Only animals with phenotypes (of progeny) should be included in genetic trend because we can use only those animals for validation over the generations  
===>>> when selecting animals before producing phenotypes, we need to wait until they have phenotypes
2. Genetic trends under different selection pressure should be created separately
3. Genetic trends calculated from EBV and GEBV should be similar unless they are biased
4. In a long-term selection, breeding values for polygenic traits could be confounded with gene interactions (dominance and epistasis)