

Animal breeding in the genomics era: challenges and opportunities for the maintenance of genetic diversity

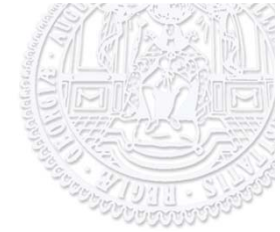
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Introduction

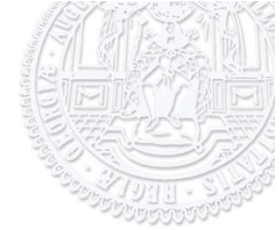
Severe loss of genetic variability in conventional dairy cattle breeding programs, primarily through concentration on few bulls used via AI as cow- and bull sires

„Parametric“ consequences:

- low **effective population size** ($N_e \sim 50$)
- high **inbreeding rate** ($\Delta F \sim 1$ per cent) per generation

„Physical“ consequences:

- Repeated „outbreaks“ of **recessive defects** (e.g. BLAD, CVM)
 - Erosion in functional traits (**inbreeding depression**)
 - (Expected) loss of **genetic variability** available for selection
- } massive impact regarding economy and animal welfare

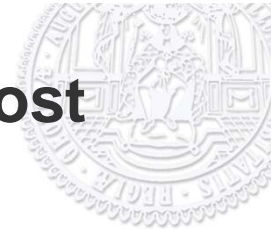


Introduction

Dairy cattle breeding enters the 'genomic era' – what effect will this have

- on the parameters (ΔF , N_e)
- on the physical consequences of inbreeding

How should breeding programs react?



Doubled genetic progress for eight per cent of the cost (Schaeffer, 2006)

Conventional dairy cattle breeding scheme with progeny testing

Path	Sel.%	i	r_{TI}	$i \times r_{TI}$	ΔT
Bull Sire	5	2.06	0.99	2.04	6.50
Cow Sire	20	1.40	0.75	1.05	6.00
Bull Dam	2	2.42	0.60	1.45	5.00
Cow Dam	85	0.27	0.50	0.14	4.25

~ 25 mio \$



12.5 : 1

Genomic selection of bulls and bull dams

Path	Sel.%	i	r_{TI}	$i \times r_{TI}$	ΔT
Bull Sire	5	2.06	0.75	1.54	1.75
Cow Sire	20	1.40	0.75	1.05	1.75
Bull Dam	2	2.42	0.75	1.82	2.00
Cow Dam	85	0.27	0.50	0.14	4.25

~ 2 mio \$

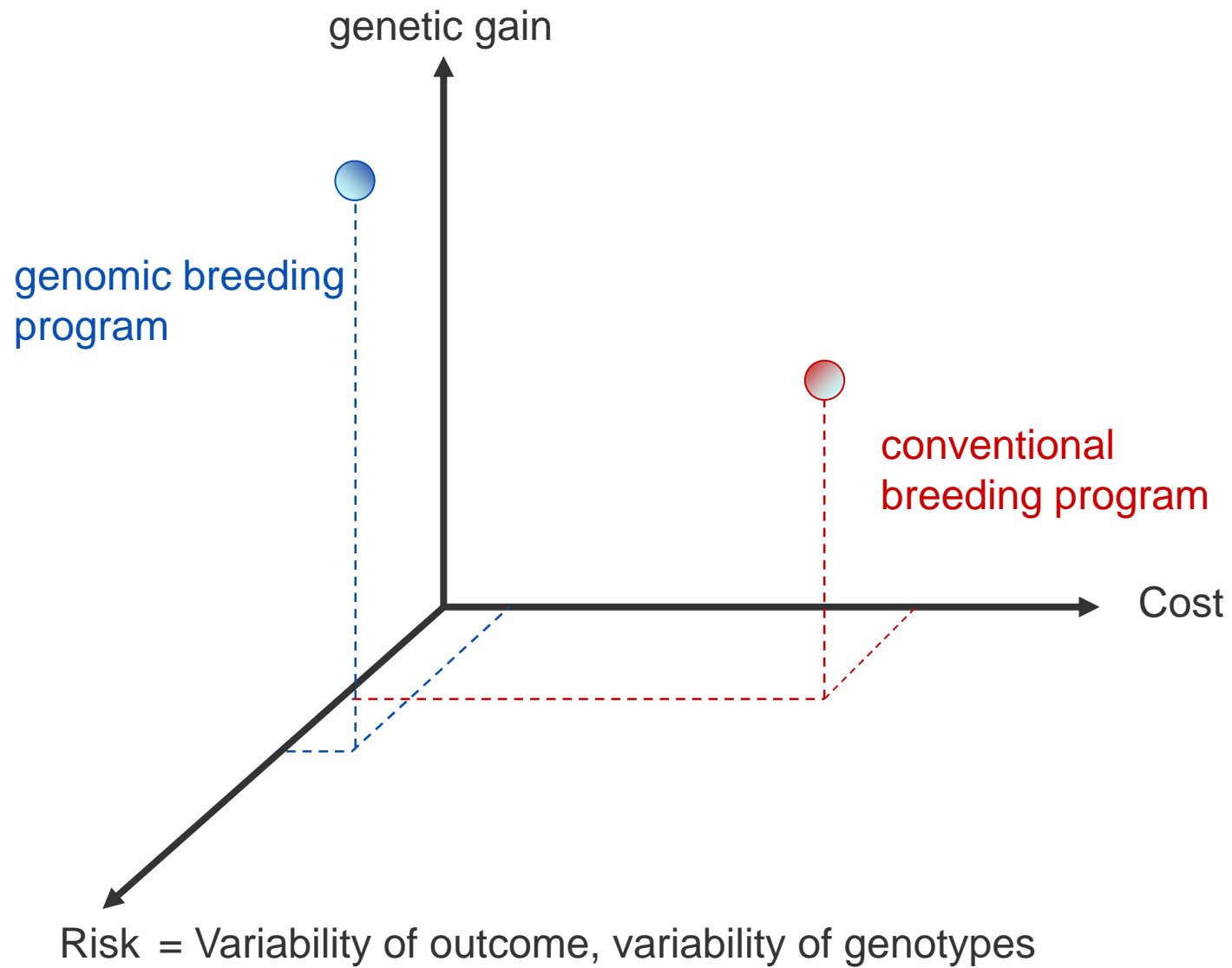
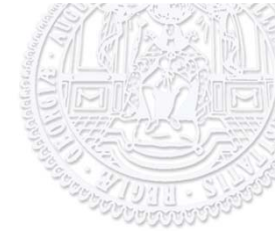


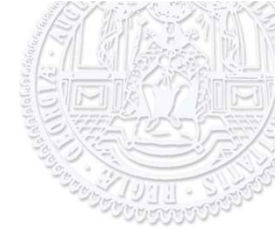
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Genetic progress per year

$$4.68 / 21.75 = 0.215\sigma_A$$

$$4.55 / 9.75 = 0.467\sigma_A$$

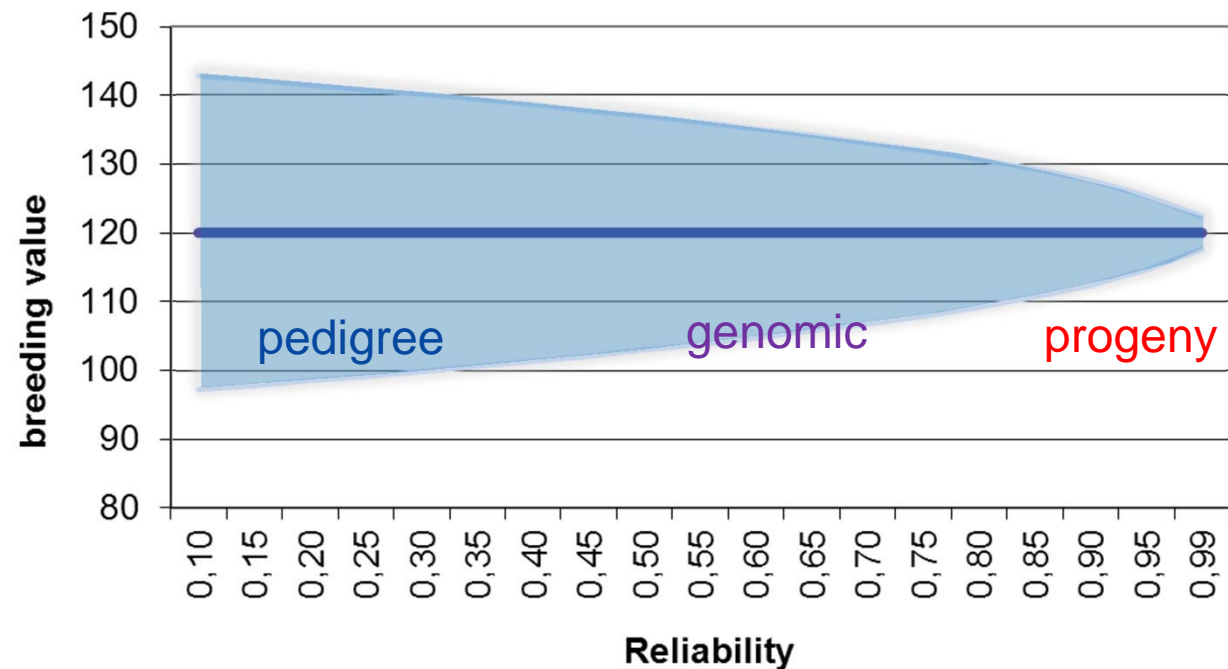




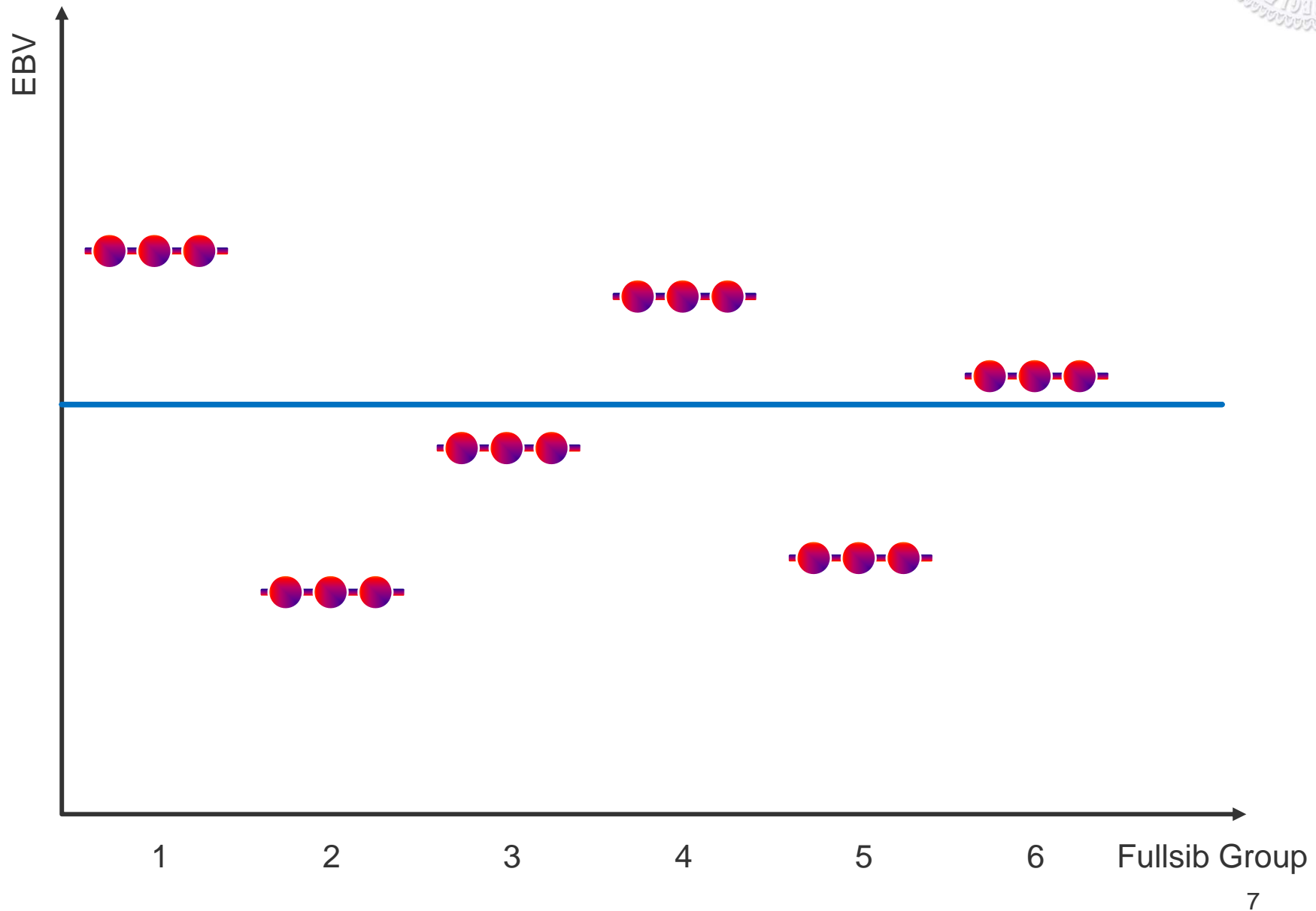
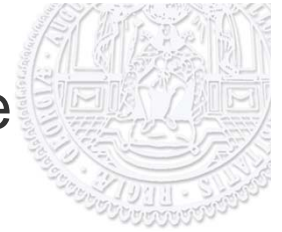
Extra genetic progress comes from

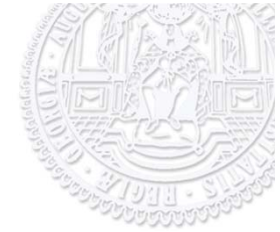
- early selection of young bulls
 - based on breeding values that are
 - more accurate than pedigree breeding values, but
 - less accurate than progeny based breeding values
- more ‚residual variability‘ around genomic breeding values

95% CI of a breeding value 120 estimated with different reliability (Reinhardt, 2011)

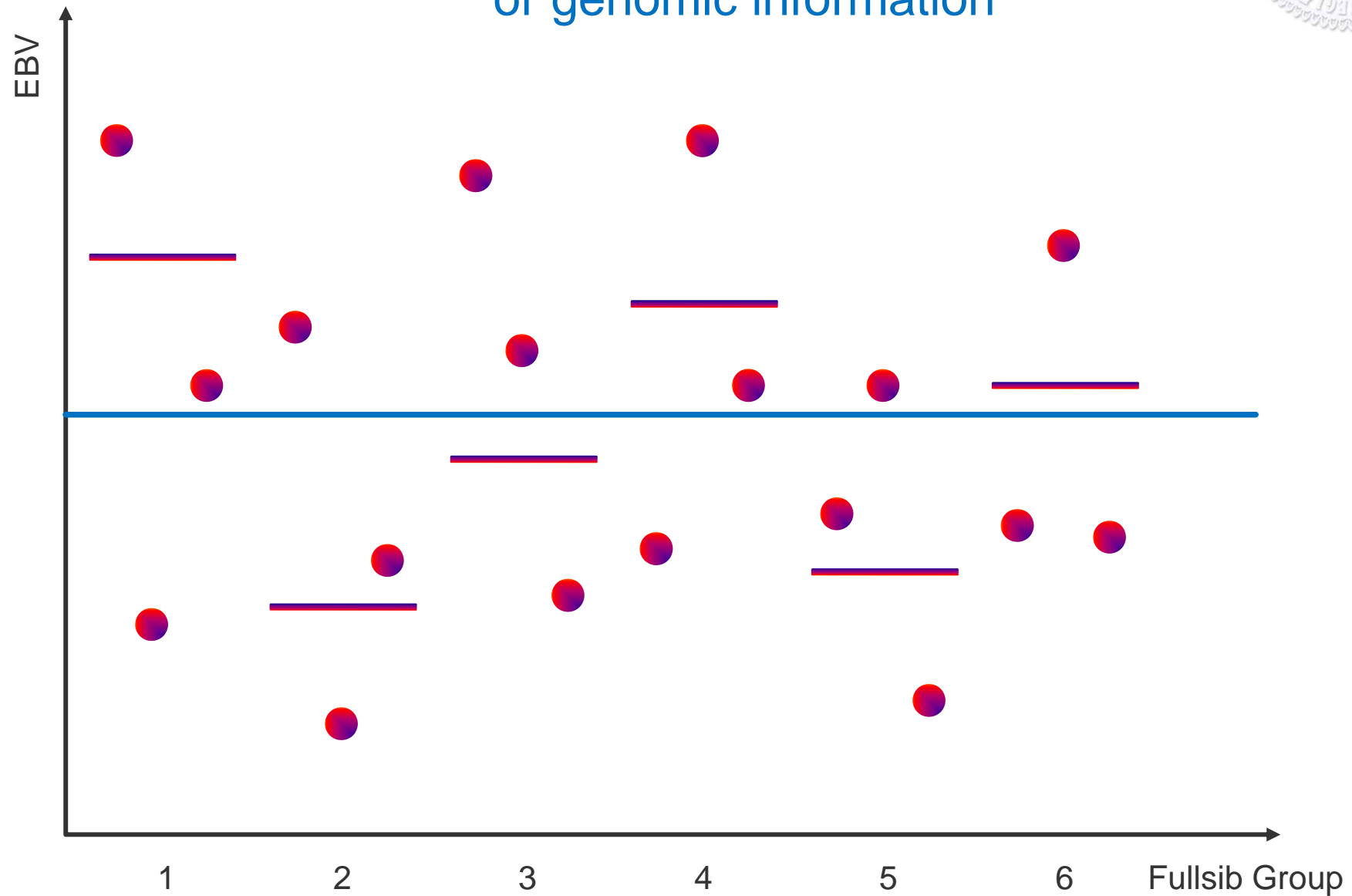


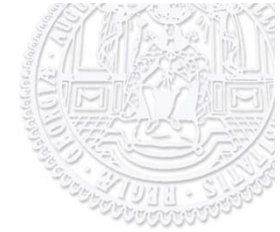
Conventional BLUP – without own/progeny performance



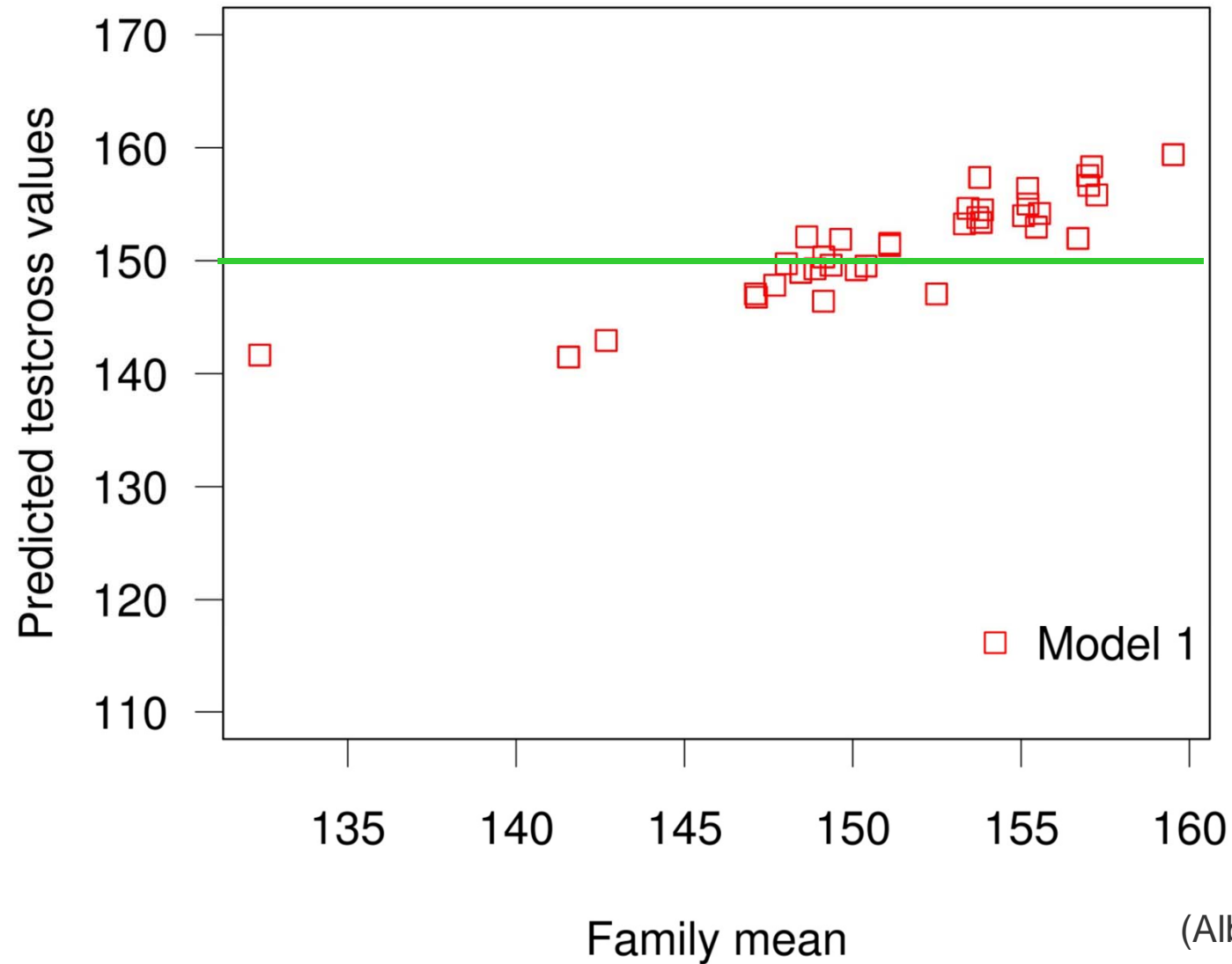


Conventional BLUP – with own/progeny performance or genomic information



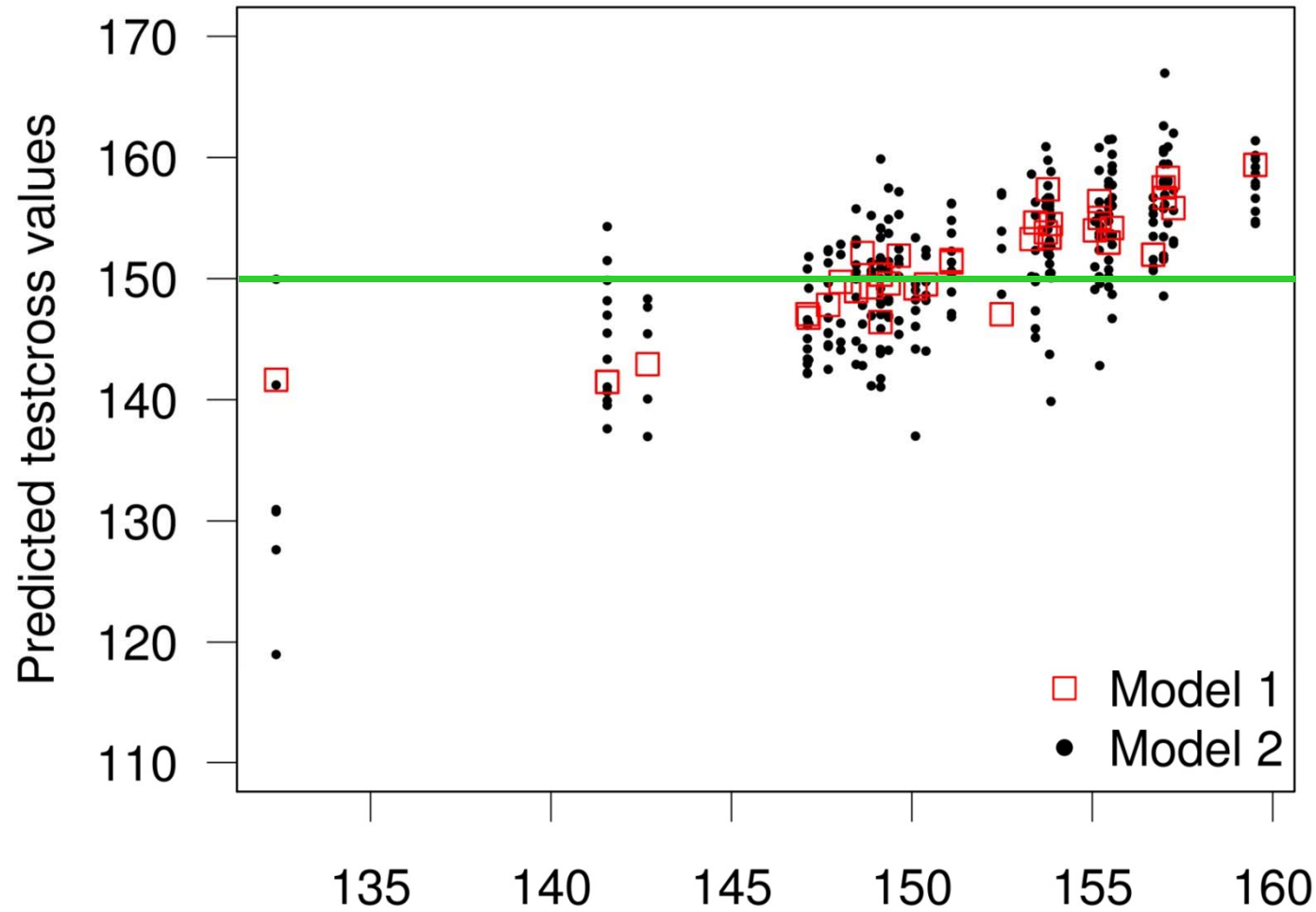
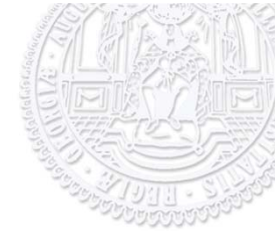


Conventional BLUP – without genomic information



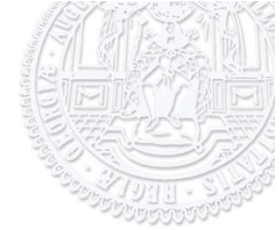
(Albrecht et al., 2011)

Conventional BLUP – with genomic information



Family mean

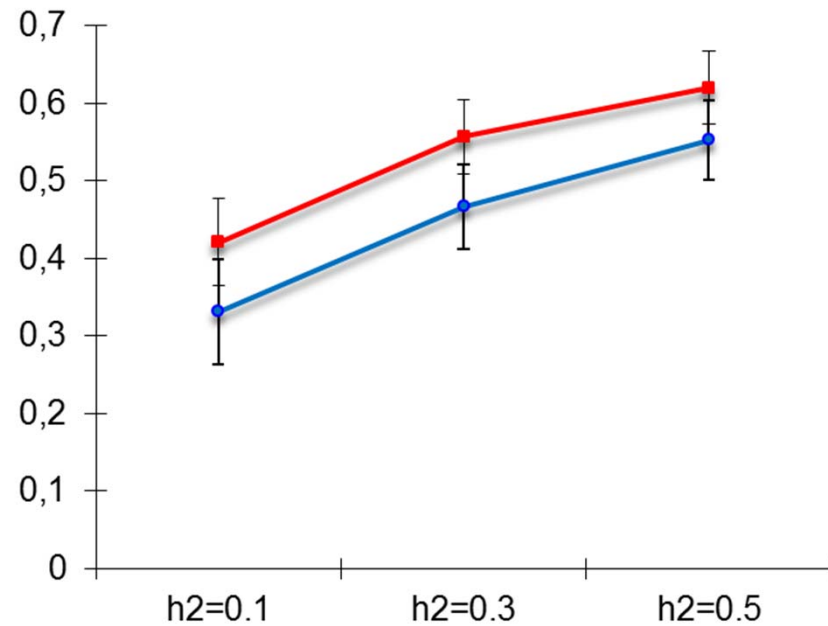
(Albrecht et al., 2011)



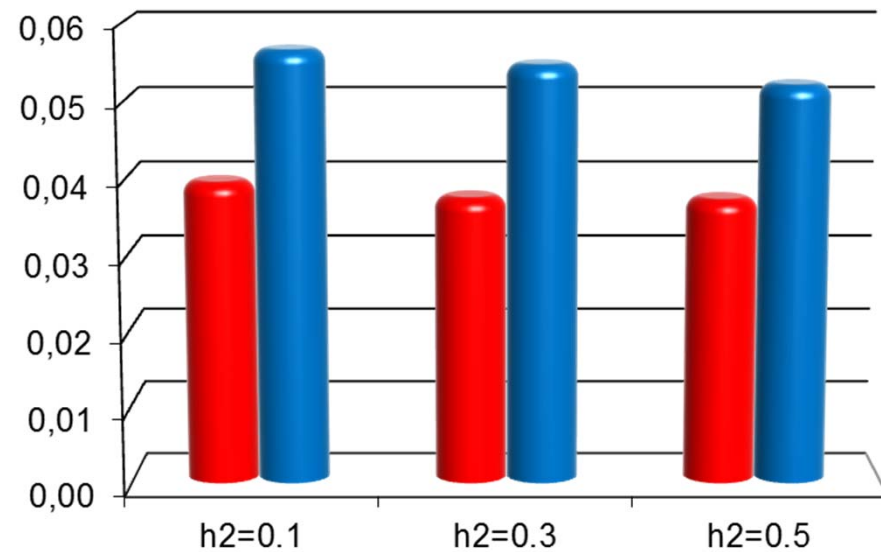
Relationship under genomic selection

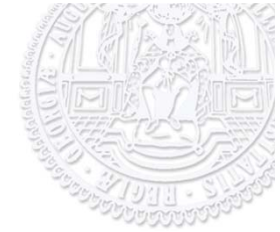
Simulation study (Chen et al., 2011): 5 generations of selection on pedigree-based BLUP or on genomic breeding values

Accuracy of estimated breeding values



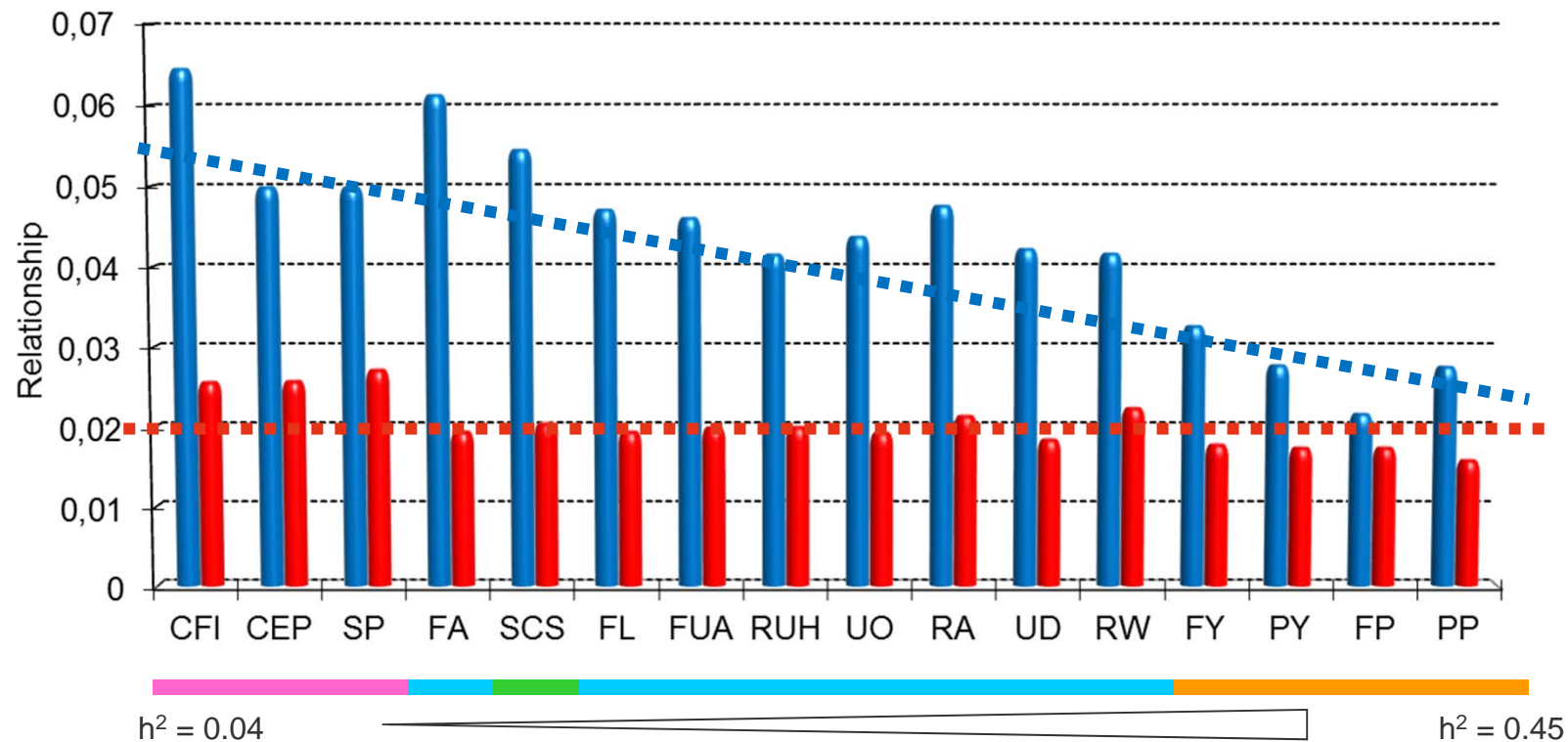
Average relationship of top 10% animals

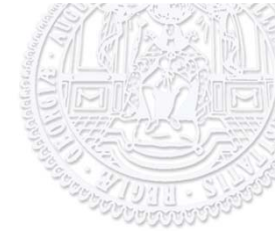




Relationship under genomic selection

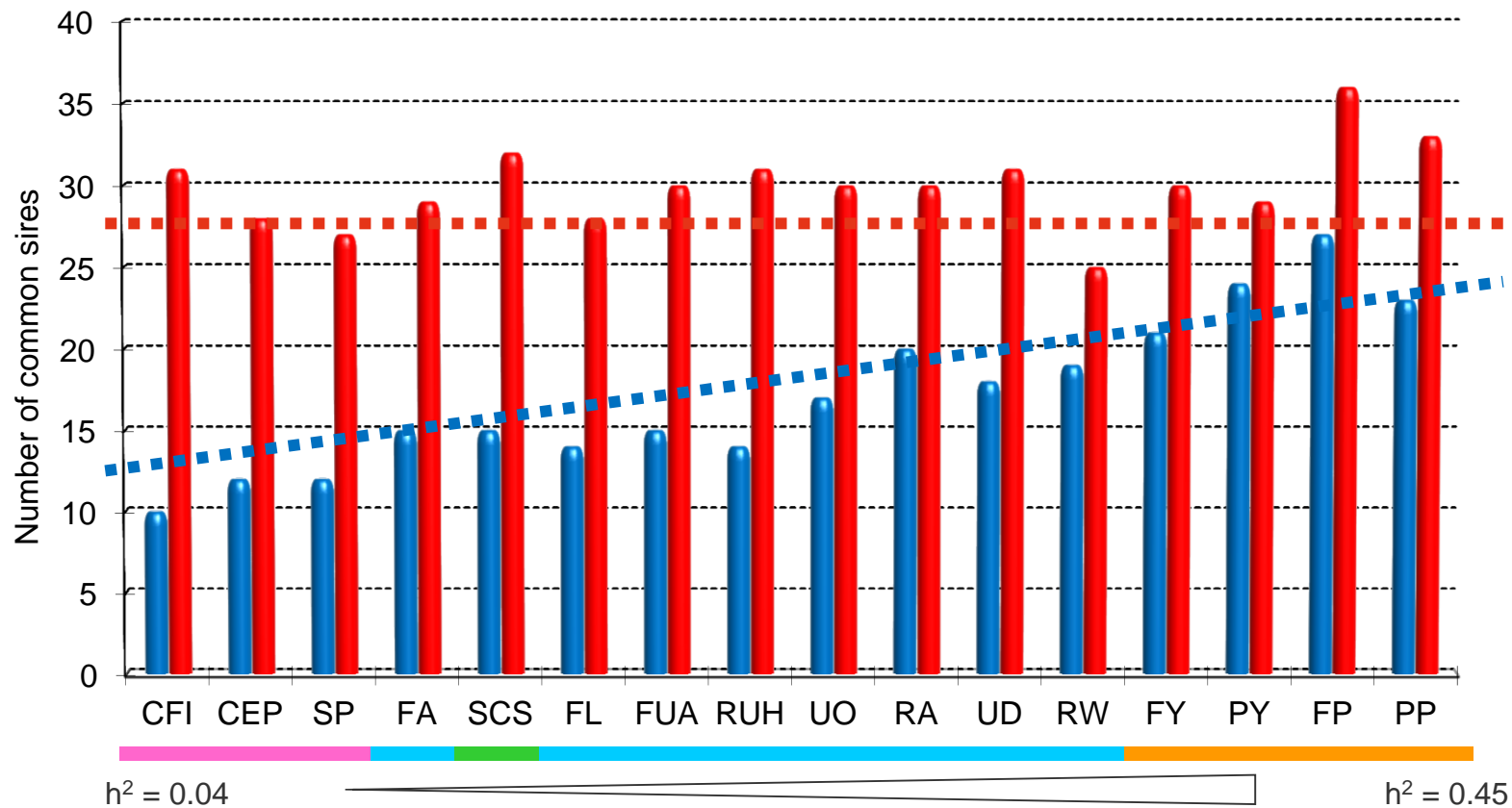
Empirical study (Chen, 2011): **average relationship** of the top 50 out of 816 young Holstein bulls selected based on **pedigree-based BLUP** or on **genomic breeding values** for traits of different heritability

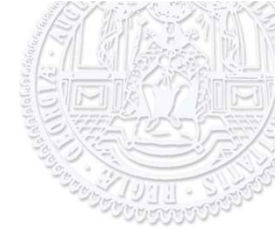




Relationship under genomic selection

Empirical study (Chen et al. 2011): **number of sires** of the top 50 out of 816 young Holstein bulls selected based on **pedigree-based BLUP** or on **genomic breeding values** for traits of different heritability

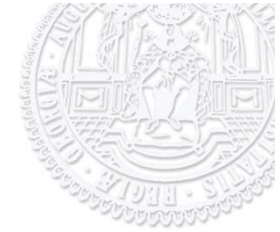




What is expected under genomic selection:

- Due to the limited accuracy it is a rational strategy to **spread the risk** by using a diverse set of genomically selected young bulls
- The top genomically selected young bulls will represent **more families** and will be **less related**
- The limited accuracy of estimated genomic breeding values will result in a **larger variance of true breeding values** in the selected set

 Inbreeding will become less of a problem

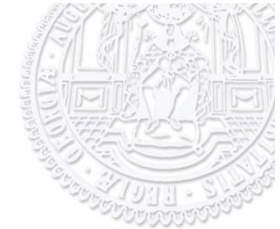


➔ Inbreeding will become less of a problem ...
... depends on the perspective!

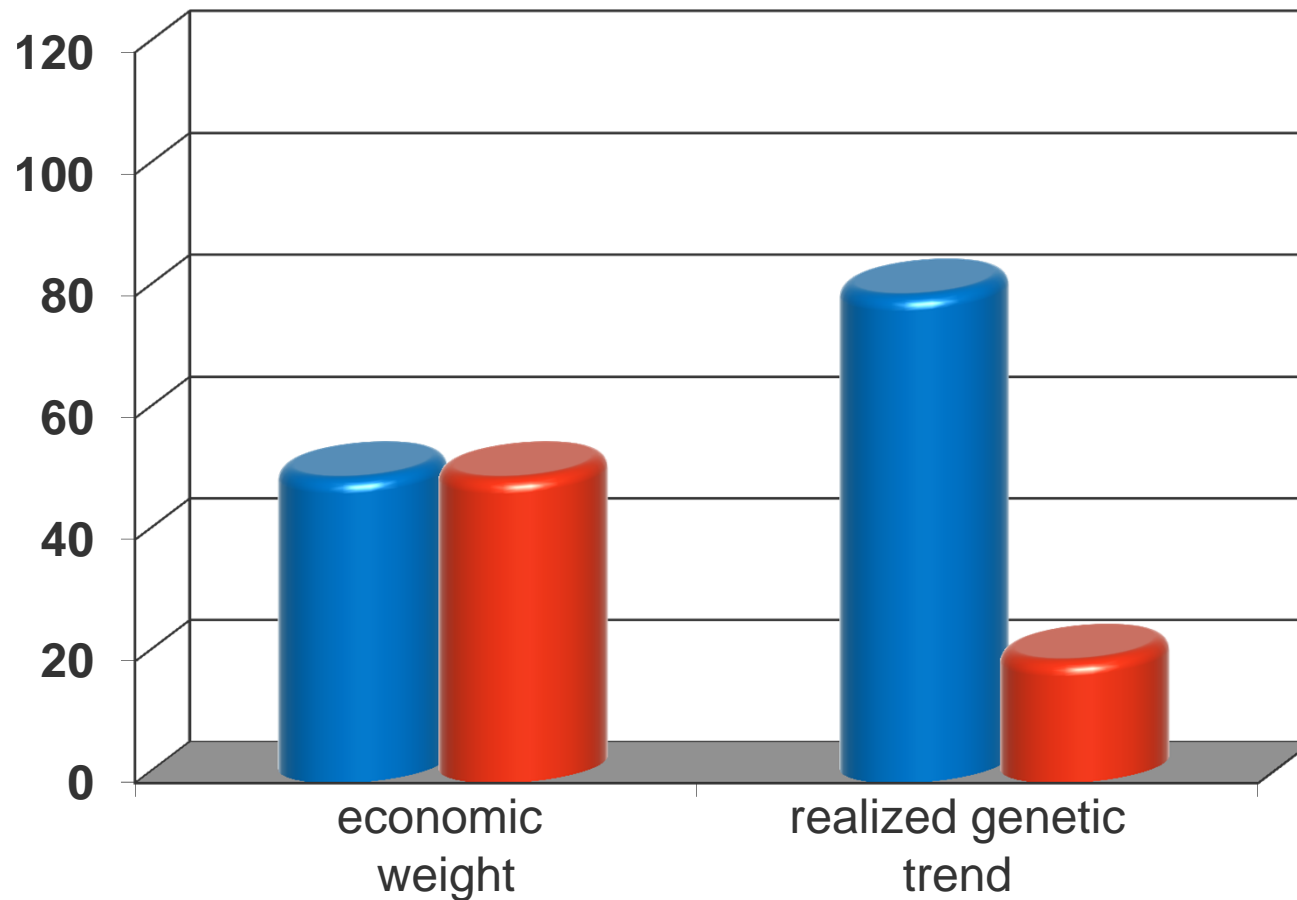
	conventional	genomic
Genetic progress per year	0.20 σ_A	0.40 σ_A
Generation interval	7.50 yr	2.50 yr
Inbreeding rate per generation	1.00 %	0.80 %
Inbreeding rate per unit ΔG	0.66 %	0.80 %
Inbreeding rate per year	0.13 %	0.32 %

➔ Problems due to inbreeding will evolve more rapidly

Breeding goals with genomic selection



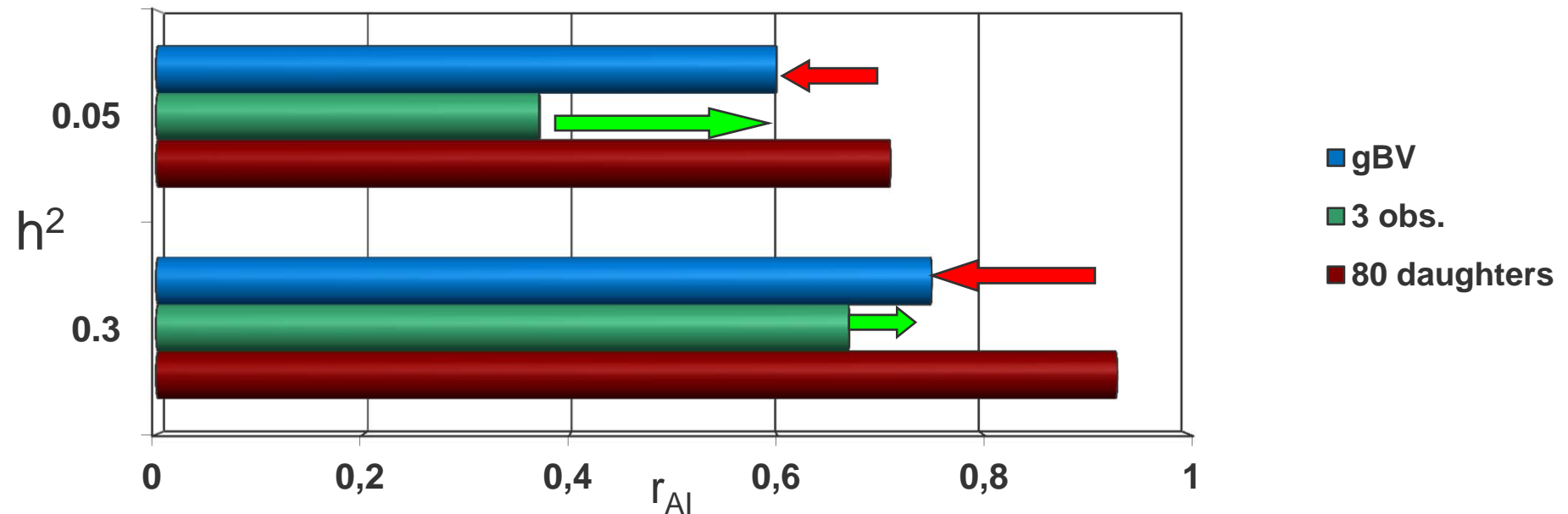
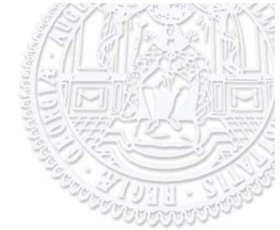
Production traits vs. functional traits in many breeding programs



Why is this so?

- ⇒ low heritability of functional traits
- ⇒ unfavourable genetic correlations to production traits
- ⇒ difference in quantity and quality of performance test data

Breeding goals with genomic selection

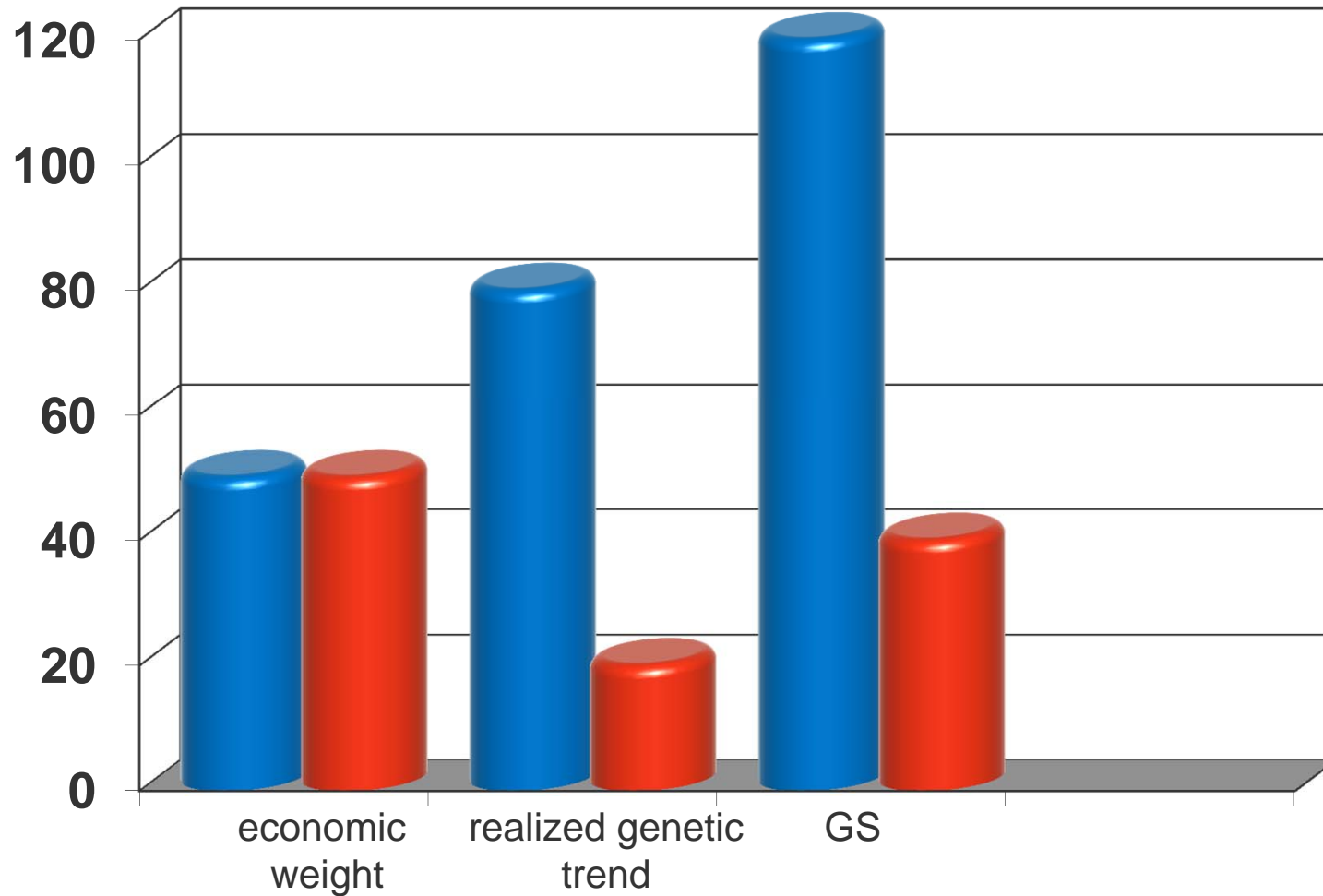


- ⇒ Low heritability traits (fitness, fertility) will benefit relatively more from genomic selection than high heritability traits
- ⇒ May be a bit more complicated in multiple-trait situations

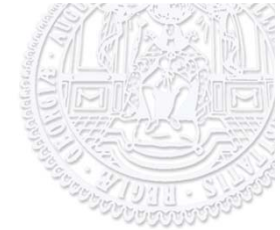
Breeding goals with genomic selection



Production traits vs. functional traits – options for genomic selection



Breeding goals with genomic selection



If genetic progress in production traits is massively increased

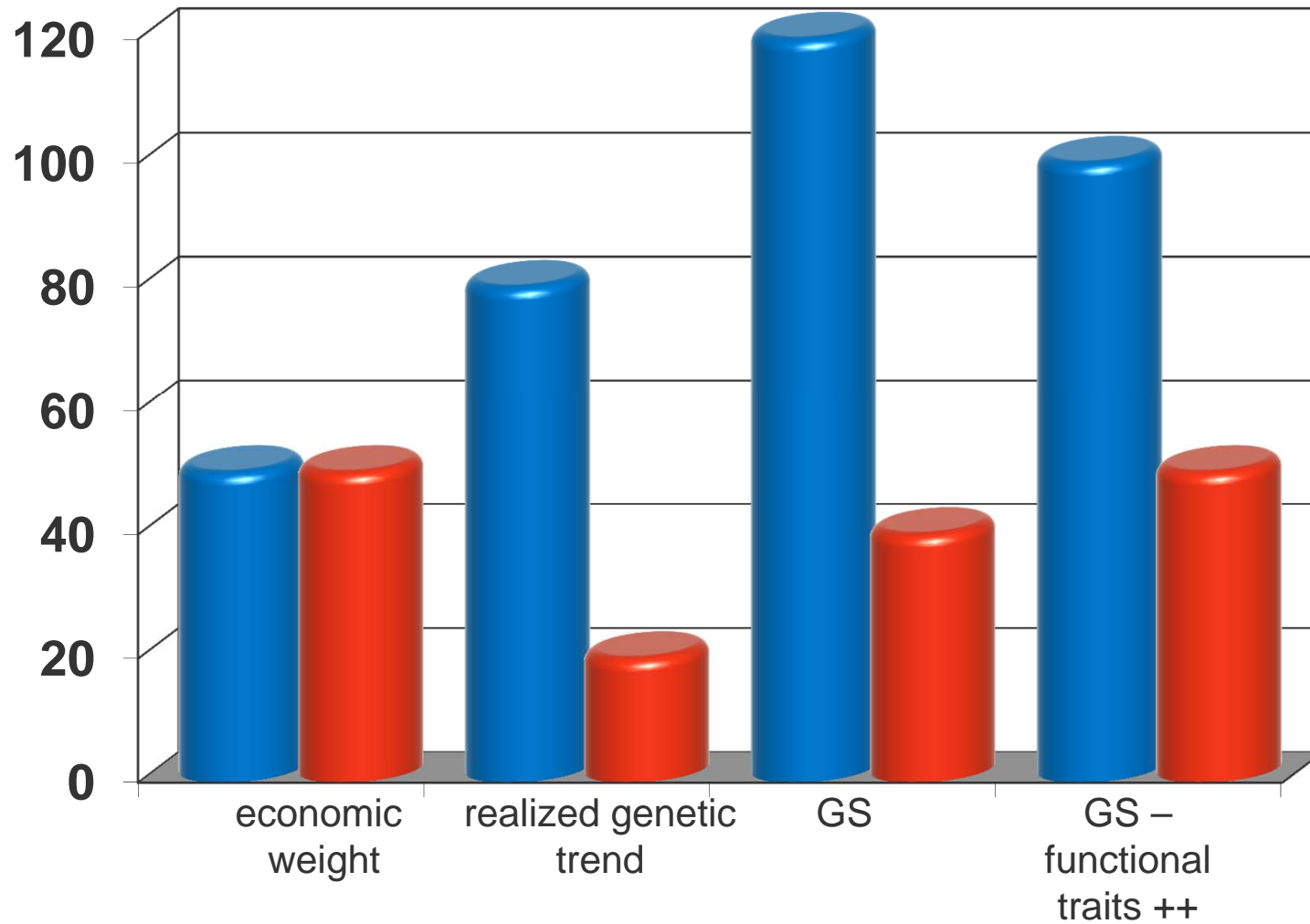
+100 kg → +150 kg milk/year

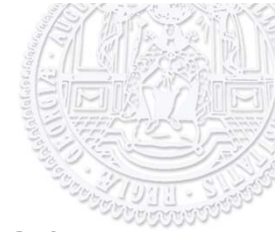
- will **production technology** (especially w.r.t. feeding, energy metabolism) keep up with this development?
- will the **management skills of farmers** keep pace?
- will **society** accept, especially if the gap between productivity and welfare-related traits widens?
- AND we need to select actively to solve/reduce problems caused by **inbreeding depression**.

Breeding goals with genomic selection



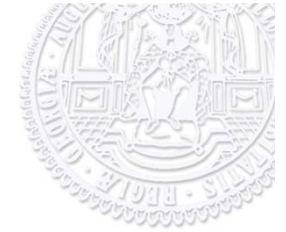
Production traits vs. functional traits – options for genomic selection





Summary and Conclusions

- Genomic selection will put genetic progress on a **wider genetic basis** regarding the pedigree of selected bulls
- Rate of inbreeding **per generation** will decrease
- However, rate of **inbreeding per unit genetic progress** and **per year** will increase
- Although functional traits will benefit relatively more from genomic selection than production traits, **the gap will widen** between genetic trend in production vs. functional traits
- A **relocation of selection weight** from production to functional traits might help
 - to maintain **fitness and health** of the animals
 - to allow production technology to **keep pace** with genetic trend
 - to ensure **societal acceptance** of dairy industry



Thank you

This talk is based on research in the projects **Fugato+ brain** and **Fugato plus GenoTrack**, the financial support by the BMBF and the following organisations is gratefully acknowledged

