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IT-Solutions for
Animal Production

How to Consider Genetic Characteristics in Dairy Cattle Breeding?

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Background

- VanRaden et al. (2011) showed that some **H**olstein **H**aplotypes (HH1,HH2,HH3) may cause embryonic loss in the homozygote state
  - HH1 BTA 5 : 62 Mb - 64 Mb, *APAF1*
  - HH2 BTA 1 : 93 Mb – 98 Mb
  - HH3 BTA 8 : 95 Mb – 96 Mb, *SMC2*

- Fritz et al. (2013) and Cooper et al. (2013) identified additional haplotypes
  - HH4 BTA 1 : 2.1 Mb – 2.9 Mb, *GART*
  - HH5 BTA 9 : 92 Mb – 94 Mb

- Carriers of these haplotypes have a reduced non return rate, because bb embryos die

mating carrier (Bb) with non-carrier (BB)

	B	**B**
B	BB	BB
b	Bb	Bb

→ 50% carrier (Bb)

mating two carrier (Bb)

	B	**b**
B	BB	Bb
b	Bb	bb

→ 50% carrier (Bb)

→ **25% death (bb)**

Background
Economics of fertility defect HH1

- Pawnee Farm Arlinda Chief (born 1962) (VanRaden, 2014)
  - Carrier HH1
  - Contributed 14% of genes to the current Holstein population
  - $25 billion value of increased milk yield
  - $0.4 billion cost of HH1 mid-term abortions

- How many more fertility defects are there?
  - Average 0.2 / animal based on inbreeding depression
    (VanRaden and Miller, 2006 JDS)

Background
Identification of genetic disorders

- **Each animal of every breed carries genetic disorders**

- **Number of known genetic disorders will drastically increase**
  - Large scale genotyping of the population
  - Next generation sequencing

- **E.g.: VSD – vertebral and spinal dysplasia** (Kromik et al., Genetics 2015)
  - Variable number of vertebrae & neurological deficits
  - T gene
  - Easy to eliminate
  - Young dominate mutation
  - Very low allele frequency

Background
Publication & handling of genetic disorders

- It's not intended to „destroy" the Holstein breed, or single bulls

- Important to find the right handling of genetic disorders
  - How to use bulls with good and bad genetic characteristics?
  - →Find the appropriate mating partner

- Comprehensive investigations are needed before publication of genetic defects/disorders
  - Allele frequency
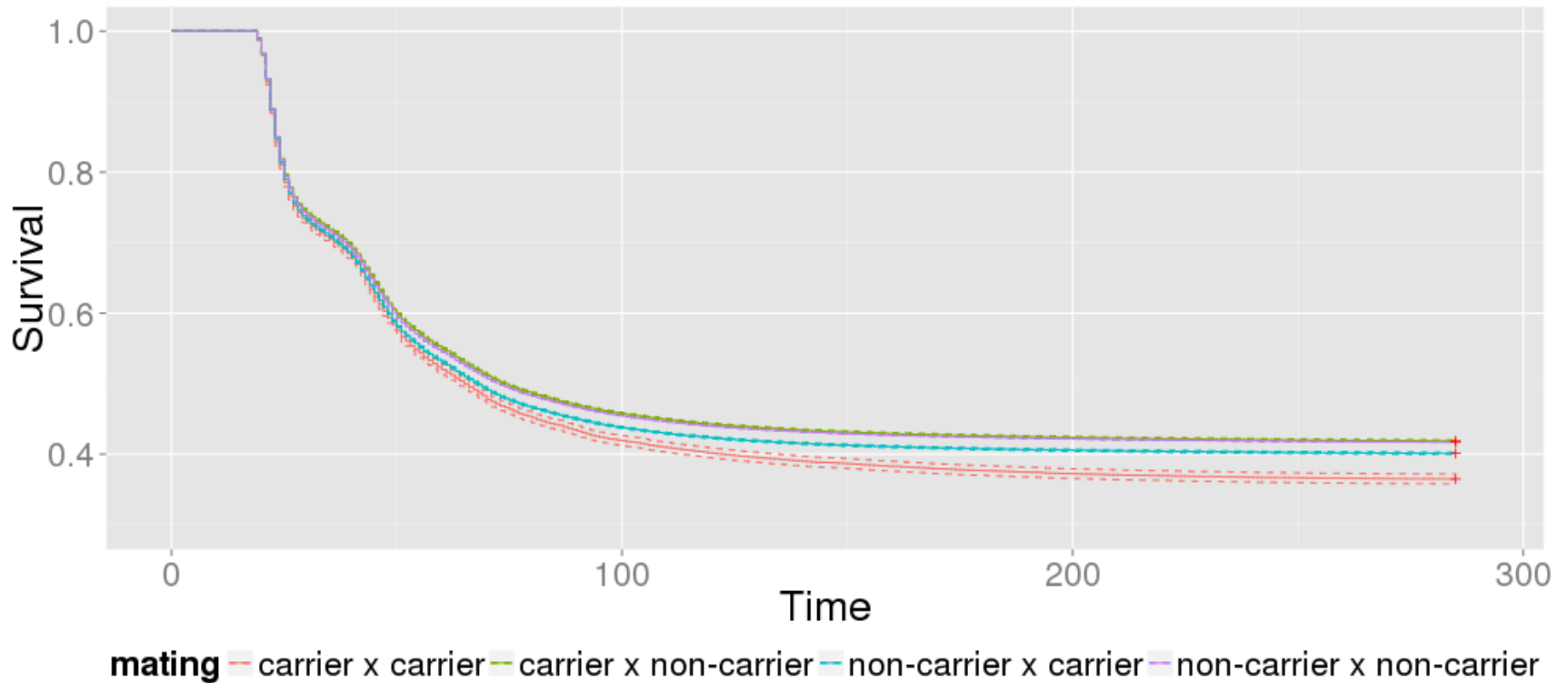 - Inheritance
  - Economic value
  - Causal mutation
  - …

Background
Positive genetic traits

- Other genetic characteristics are desirable (Polled, Casein),
  and should be spread into the population

- Question: How to combine positive and negative characteristics for publications and mating decisions?

- *Aim:*

  → Index of genetic properties which summarize the genetic characteristics and their economic values
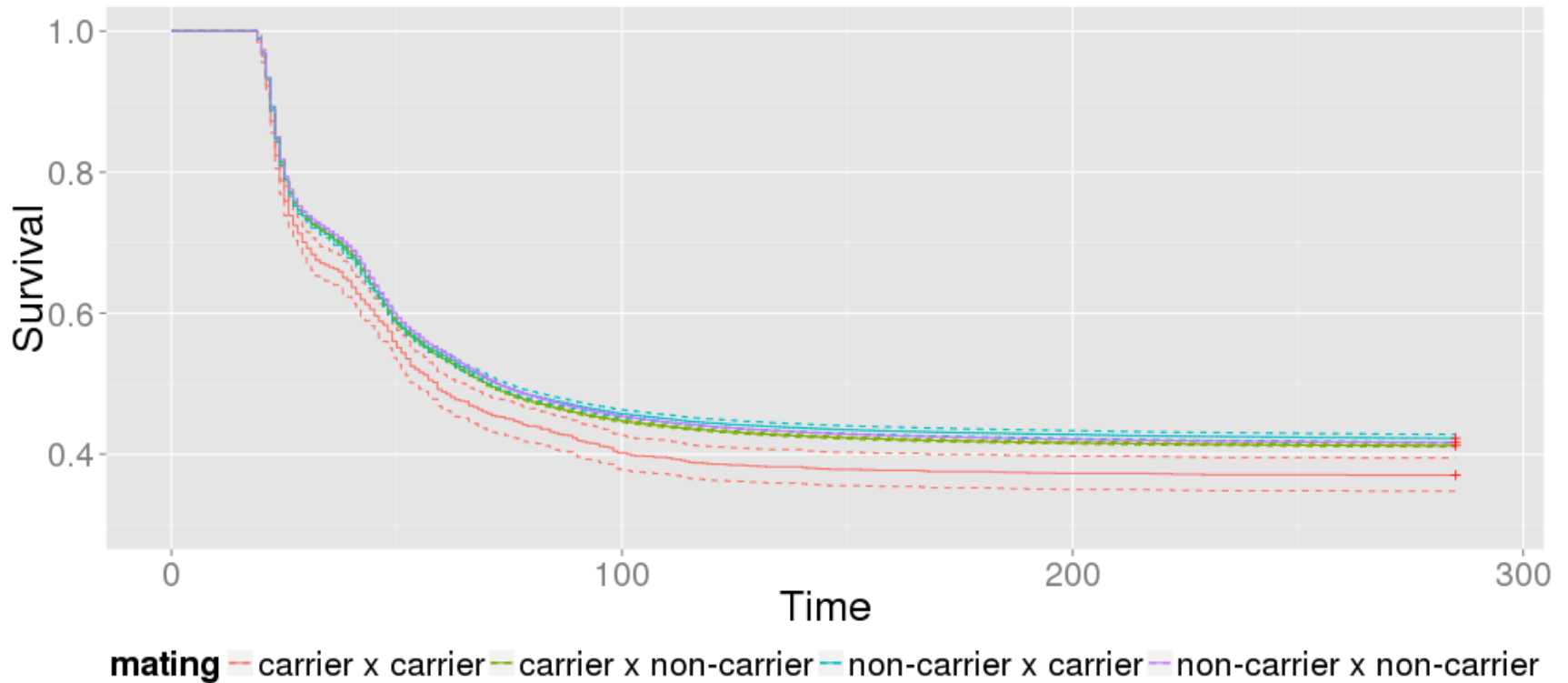
maternal grandsire   maternal granddam   maternal grandsire   maternal granddam

carrier   unknown   non-carrier   unknown

sire   dam   sire   dam

carrier   unknown   non-carrier   unknown

12,5 % of all embryos die   0 % of all embryos die

Survival of embryos (HH1)

Materials and Methods
Genetic effects

	NRR56 decrease heifer (%)	NRR90 decrease heifer (%)	NRR56 decrease cow (%)	NRR90 decrease cow (%)	Stillbirth increase (%)	Economic loss per embryo (€)
BY	-0,2 ± 0,3	-1,6 ± 0,3 ***	0,5 ± 0,5	-0,7 ± 0,6	1,8 ± 0,3***	95
HH1	-0,5 ± 0,3	-2,1 ± 0,3 ***	1,5 ± 0,8	0,8 ± 0,8	1,3 ± 0,2***	95
HH2	-0,6 ± 0,1	-2,8 ± 0,1	-0,3 ± 0,3	-0,2 ± 2,8	2,7 ± 0,9 **	95
HH3	-3,5 ± 0,7***	-4,4 ± 0,7 ***	-2,8 ± 1,5	-3,2 ±1,5 *	-0,3 ± 0,5	52
HH4	-4,0 ± 0,4***	-4,2 ± 0,4 ***	-2,3 ± 0,9 *	-3,1 ± 0,9 **	-0,7 ± 0,2**	52
HH5	-3,0 ± 0,3 **	-1,0 ± 1,2	2,3 ± 0,2	-1,1 ± 0,3	2,1 ± 0,8*	52

Materials and Methods
Carrier frequency & economic weights

- Birth years 2011 - 2013 were used to determine the allele frequency in the German population
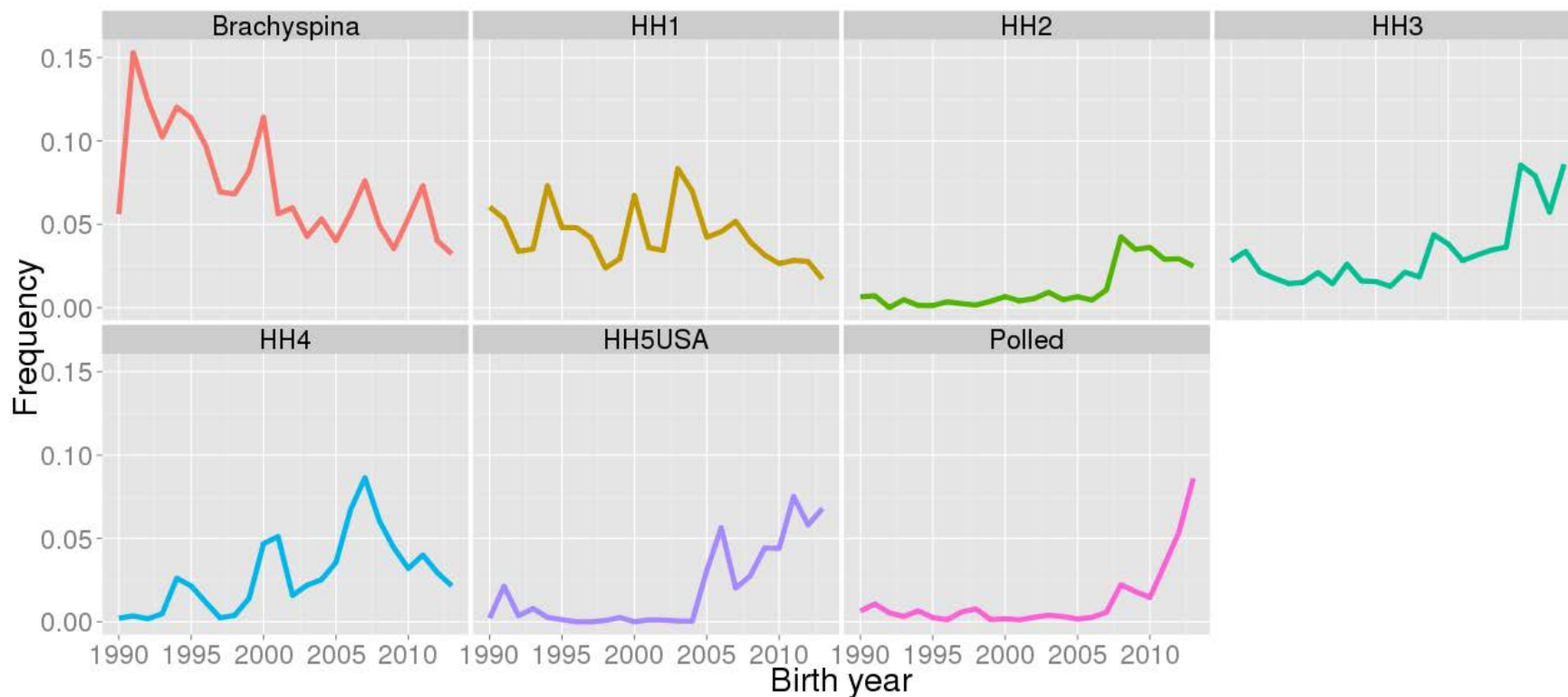
- Polled:
  - Economic value: 7 €/calf (5 € salary, 2 € drugs)
  - Social policy value not considered

- No other positive traits, because no economic benefit for an average farmer

Materials and Methods

Carrier frequency of the analyzed traits

Materials and Methods
Index for genetic characteristics (Falconer,1980)

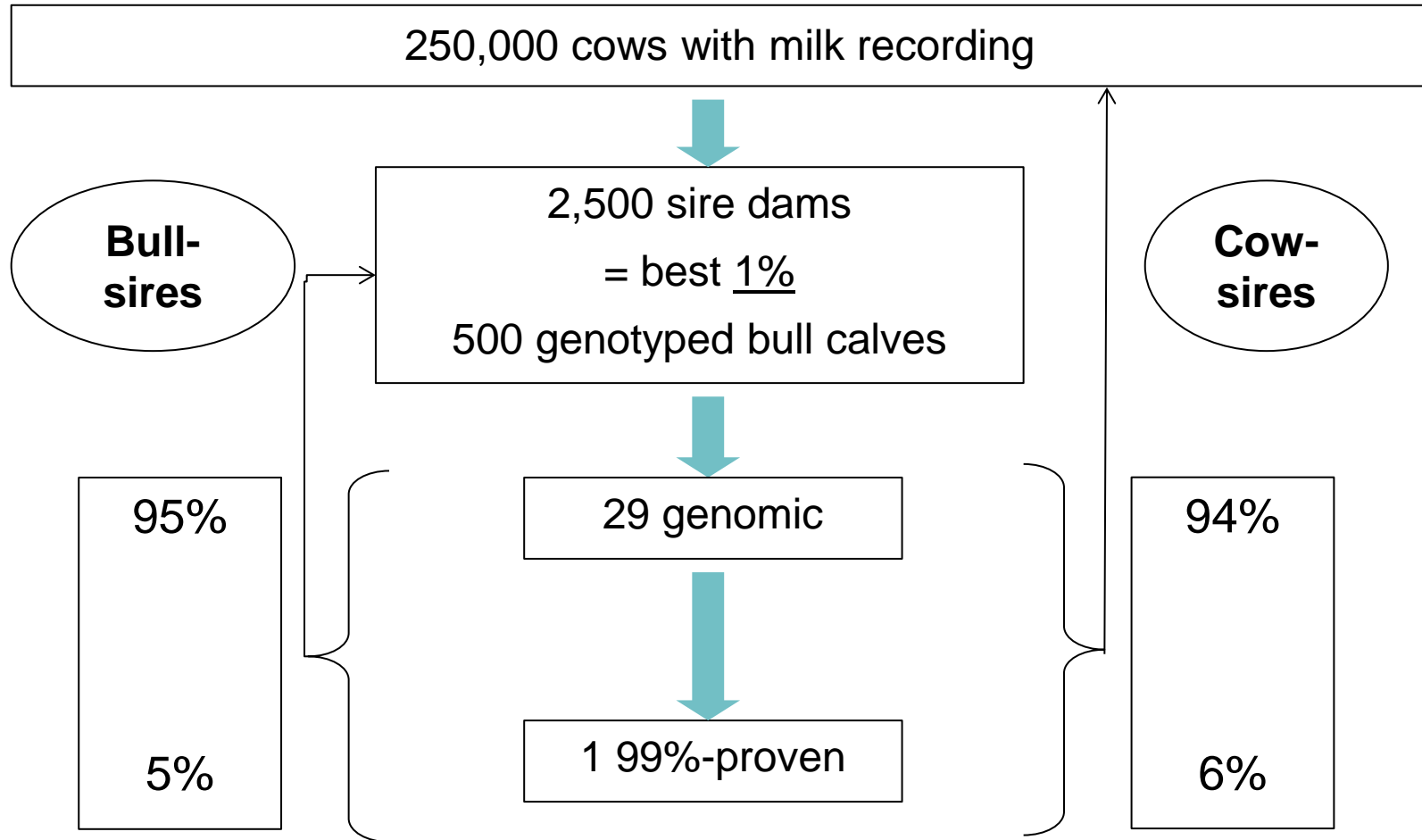| Genotype	Average effect (AV)
AA	2q α
AB	(q-p) α
BB	-2p α

α : economic value

p & q: allele frequency of the population

AV: Average economic effect in a given population

→Genetic index: $GI = \sum_{k=1}^{n} AV_k$

Simulation of a genomic breeding program

250,000 cows with milk recording

Bull-sires

2,500 sire dams
= best 1%
500 genotyped bull calves

Cow-sires

95%

29 genomic

94%

5%

1 99%-proven

6%

Täubert et al., 2012

Materials and Methods
Simulation of a genomic breeding program

- EBV = true breeding value + mendelian sampling + residual

- Breeding values for the base cow population:
  - Mean: 100
  - Standard deviation: 20
  - Reliability: 50%

- Breeding values for the AI bulls:
  - 500 bulls with mean 130
  - Selection of the top 30
  - Reliability 67% genomic bulls 99 % proven bulls

- No mating of close related animals
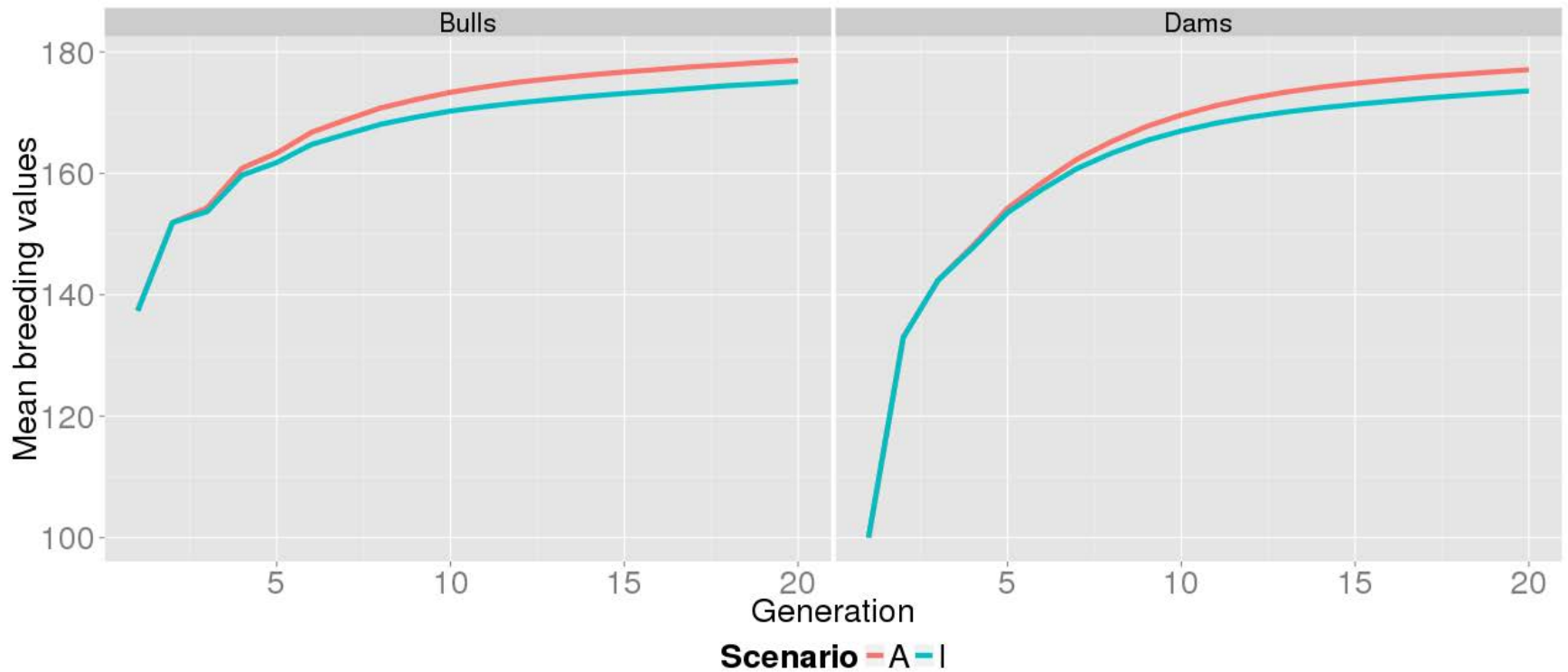
- 100 repeats of the simulation

- **A**: Selection of all animals due to breeding values – assortative mating
  - No consideration of genetic index

- **I**: Selection dam-dam due to the genetic index
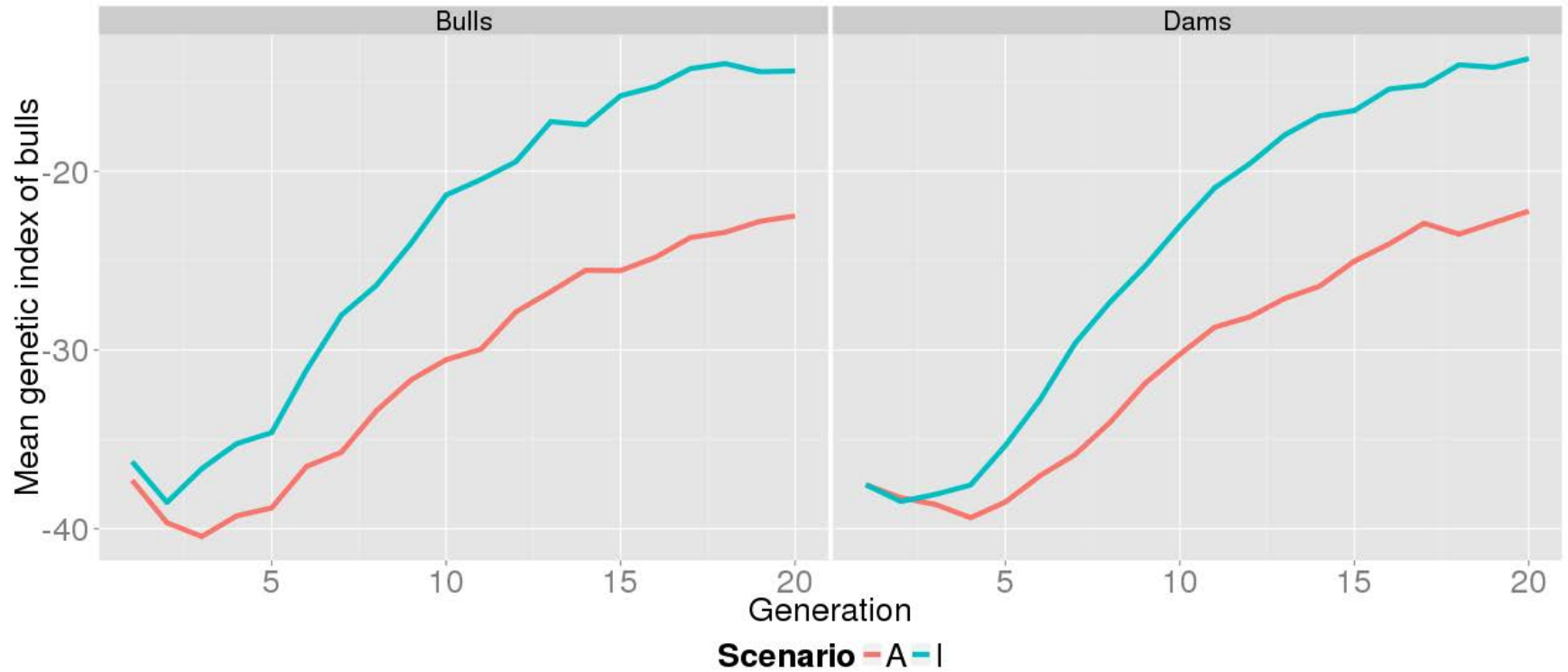
- Selection of the AI bulls always due to EBVs

Results

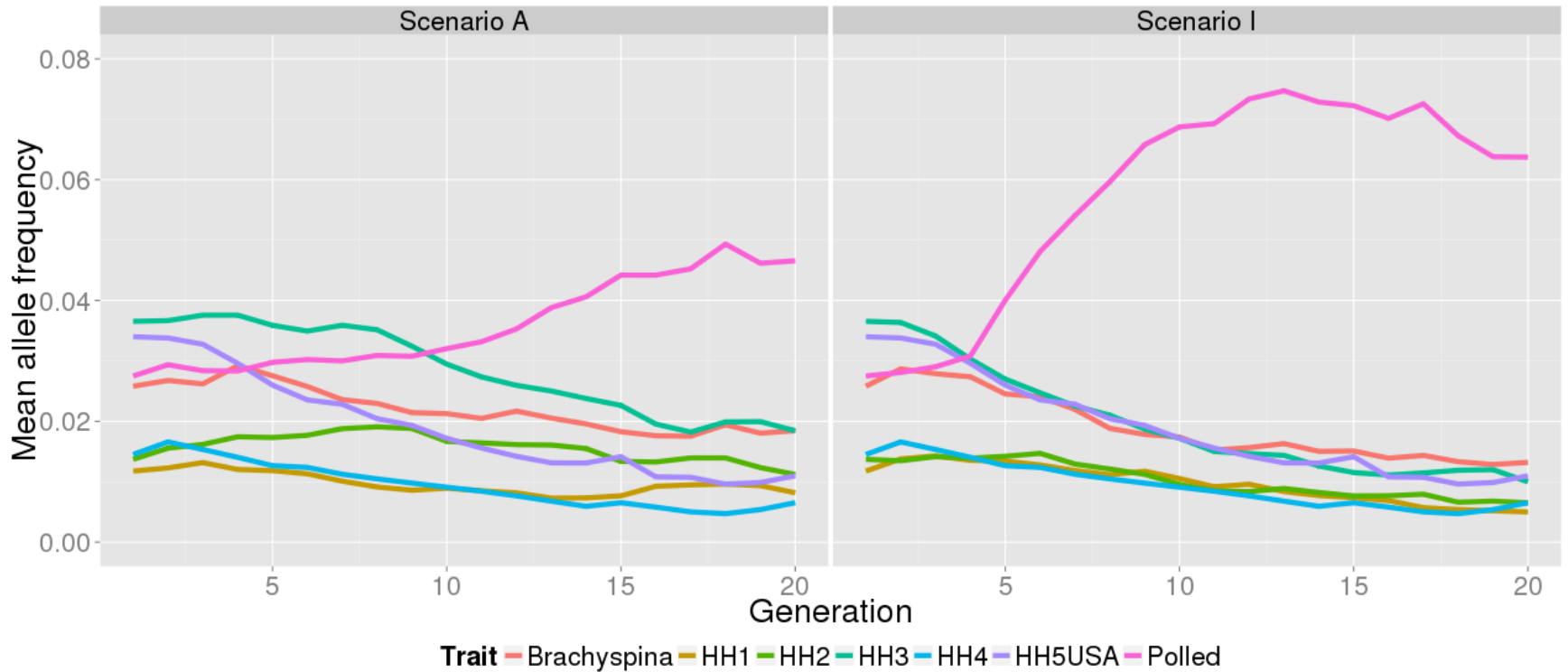Development of the breeding values over 20 generations

Results

Development of the genetic index over 20 generations

Development of the allele frequencies over 20 generations

Conclusion

- Genetic index method to combine different genetic characteristic with different economic values

- Further investigation is needed to determine the correct phenotype (time of embryo loss) and the economic value

- Breeding programs: The index should be used for the female path, bulls should be selected due to breeding values

Practical Application - Prospective
## gBAP+ next generation mating software

- ■ gBAP+ considers all genomic information:
    - ▪ Genomic breeding values
    - ▪ Inbreeding
    - ▪ Genetic characteristics
    - ▪ Prediction of genetic variation in potential offspring
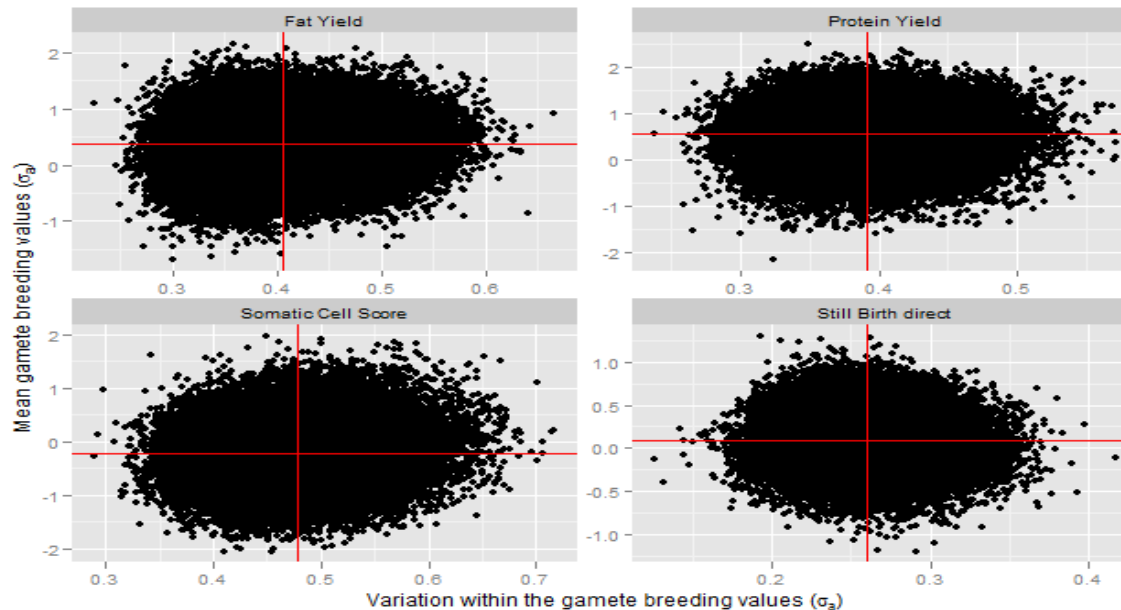
Genomic mating software gBAP+

Sperm (σ_a)		Ovar (σ_a)		Offspring (σ_a)		>1σ_a		> 2σ_a		>3σ_a		> 4σ_a	
MGBV	VGBV	MGBV	VGBV	E(mBV)	E(vBV)	p(%)	N	p(%)	N	p(%)	N	p(%)	N
1.81	0.29			2.36	0.68	98	2	70	6	17	36	1	860
1.68	0.52	0.55	0.39	2.23	0.91	91	3	60	8	20	31	3	262
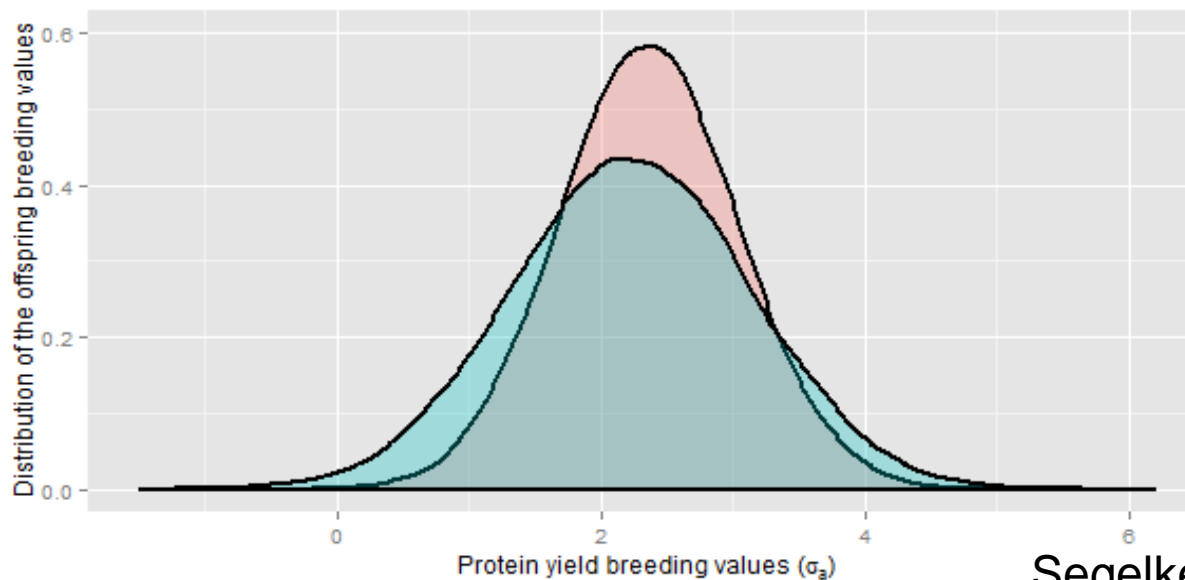
Segelke et al., GSE 2014

Acknowledgements

Thank you for attendance!