



Genomic “Postcard” from Dairy Cattle Breeding – GUDP Project

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VikingGenetics**

• VikingGenetics owned by more than 30.000 farmers



Assentoft – head office



Skara – Office in Sweden



Hollola – Office in Finland

- Bull stud and semen production
- Bull stud with waiting bulls/quarantine facilities



VikingDanmark, Faba and the Swedish livestock coops are responsible for advising and insemination on farms

• A complete breeding program – number of cows

	Denmark	Sweden	Finland	In total
Holstein	371,000	141,000	81,000	593,000
Jersey	65,000	2,000	-	67,000
VikingRed	37,000	113,500	143,000	293,000
Red Holstein	5,500	-	-	5,500
SKB/Finncattle	-	1,100	2,700	3,800
Total	478,500	257,100	226,700	961,900



Holstein



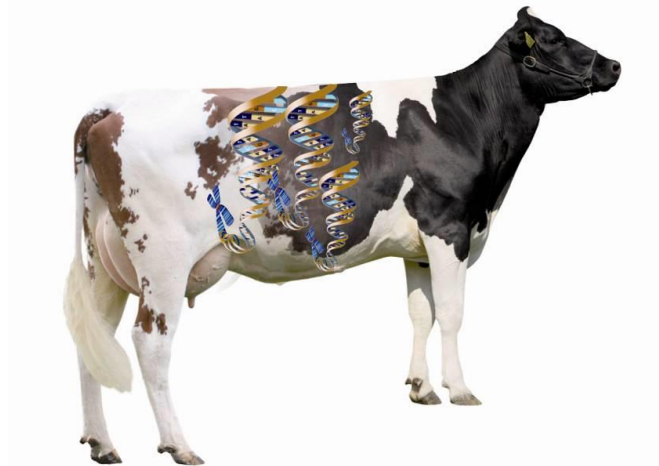
Viking Red



Jersey

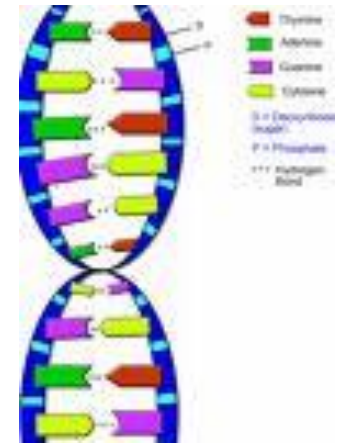
• Genomic Selection – Keys to improvement

- **Genomic Prediction:**
 - Increased selection accuracy of young breeding candidates compared to only use of Parent Average
- **Genomic Breeding Scheme**
 - Focus on use of young breeding candidates
- **Structure**
 - Change in conducting breeding in practice



• Genomic Prediction – key factors

- Quality and quantity of data-registration
- Size reference population
 - Sire reference
 - Cow reference
- Efficiency of the methodology
 - Chip technology
 - Model and Calculation methods



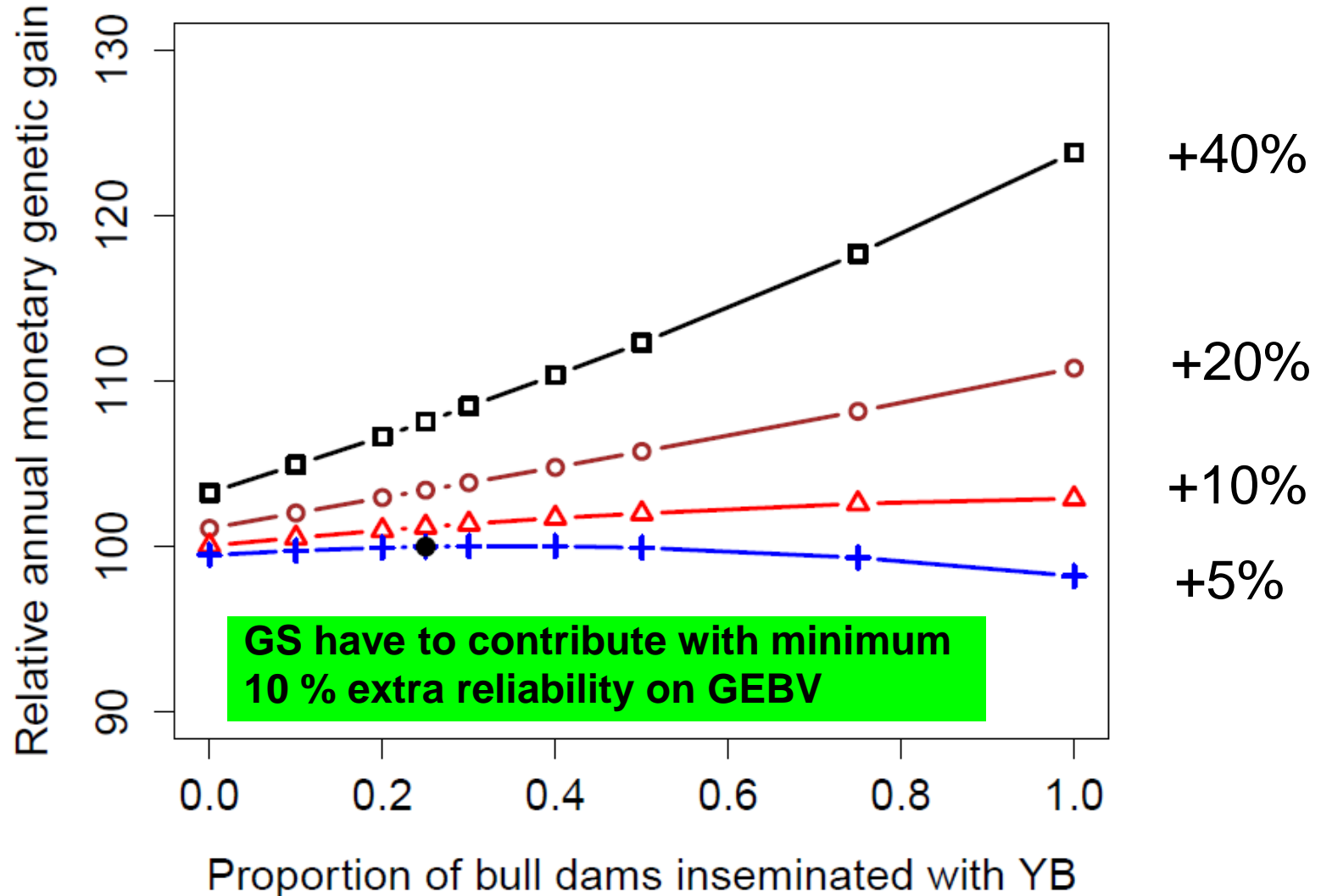
Challenge: Low reliability specially small breed

• Genomic Selection - Development

- First results for Holstein August 2008 – Start use in Selection
- First results for Jersey June 2009
- First results for Red Breeds October 2009
- First results with EuroGenomics – Reference HF March 2010
- Official Breeding Values Autumn 2010
- Collaboration common reference with GENO, Norway, 2011
- Cooperation with US Jersey, December 2013
- Exchange semen on Young bulls with Geno, 2013/14
- Cows in reference July 2014
- Collaboration with NOG, HF on selection candidates – September 2014



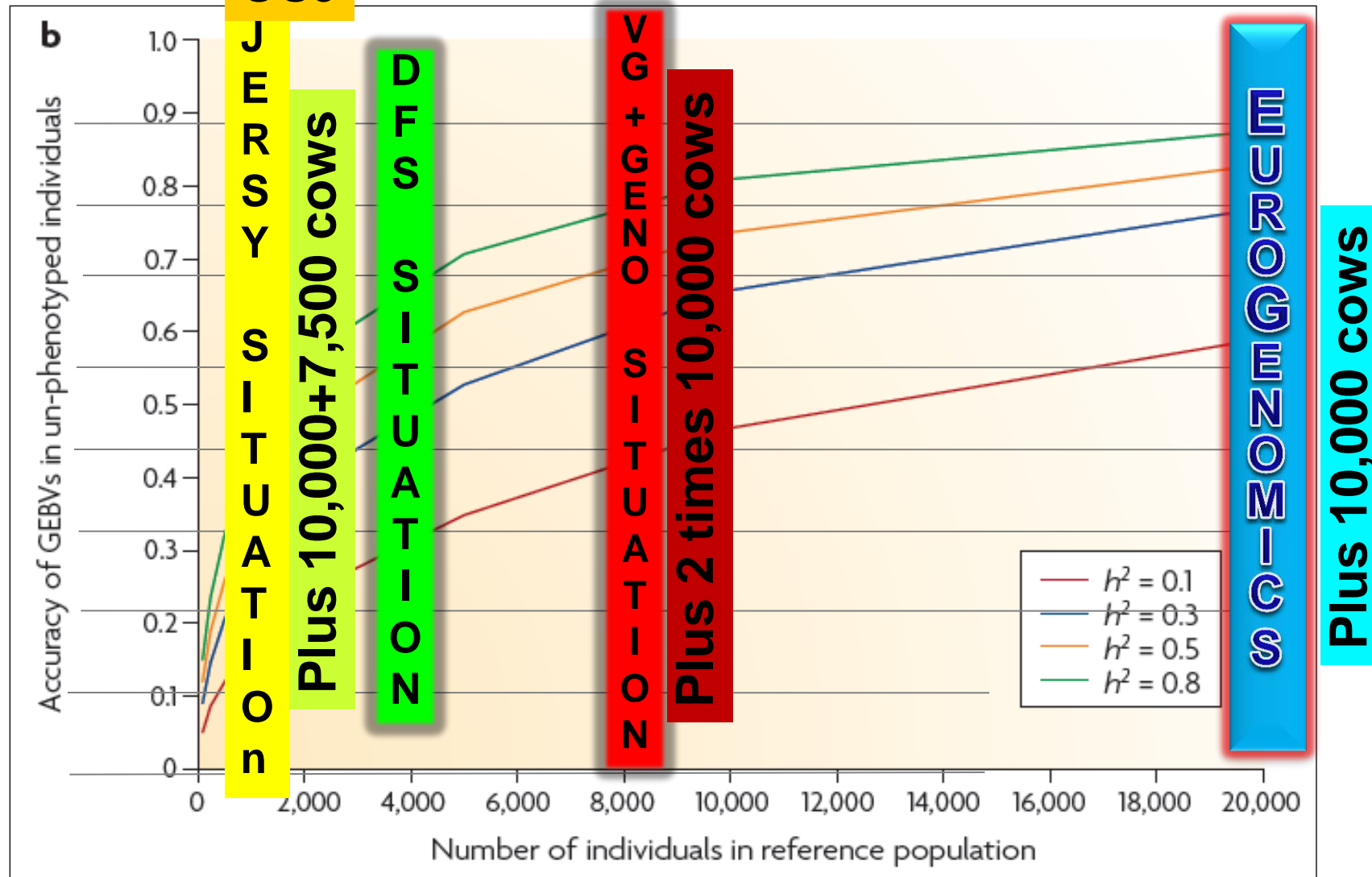
Low reliability GEBV reduce genetic progress



• **Results Genomic Selection due to prediction**

- **Higher reliabilities (5-10%) due to International collaboration “Bull reference” ➡ Increase in Genetic progress**
- **Better methodology due to collaboration with Scientific partners ➡ reliable use of GS**
- **Higher reliabilities (5-10%) due to females in reference ➡ increase in Genetic progress**
- **Chip technologies – development of customized chip ➡ Higher reliabilities and increase in Genetic progress**

Reliability and Size of Reference Population



Goddard & Hayes, 2008

• International collaboration - Scoop EuroGenomics



- Farmer owned Coop's
- Partnership between European A.I. organizations
- Joined forces to improve results with Genomic Selection within Holstein breed
- Improvement of reliable and innovative cattle breeding since 2009 together with scientific partners:

- INIA, Spain
- INRA, France
- Liege University, Belgium
- Aarhus University, Denmark
- Nordic Genetic Cattle Evaluation, NAV, DFS
- Institute Animal Production, Poland



- Exchange of Genotypes



Genomika Polska



• Reliabilities Breeding values

Holstein

Trait	Proven bull, 5 years (Traditional Breeding Scheme)	Genomically tested bull calves (Gain compared to PA)
Yield	91	55 (+32)
Udder Health	68	45 (+31)
Fertility	60	46 (+28)

Validation reliabilities,
Nav 2013

GS favoring reliabilities for functional traits

• Test of females – Focus area

- Implementation of cows in reference population
- Benefit from test of females:
 - Higher reliability (5-10%) VikingRed and VikingJersey
 - Diversity in our three dairy breeds
 - Fast implementation of new traits and functional traits ex. Feed Efficiency and Claw Health and increase of reliabilities



Use of Genomic Selection in VikingGenetics

• Genomic Selection - Use on herd level

- **Test of all females in herd:**
 - **Higher reliability for Genomically Enhanced Breeding Values, GEBV**
 - * Same level for females as for young A.I. Bulls
 - * Specific advantage for functional traits
- **Optimal selection of animals with low and high breeding values**
 - **Use of sexed semen on females with high Genomically Enhanced Breeding Values, GEBV**
 - **Use of semen from beef bulls on females with low Genomically Enhanced Breeding Values, GEBV**
- **Genomic selection generates need for implementation of new herd selection strategy – and new possibilities in using new mating plans on herd level**



Results Genomic Selection due to breeding scheme

- Efficient use of Genomic Selection in practice ➡ decrease in number of test bulls
- More use of “young” genetic ➡ lowering generation interval and higher genetic progress due to higher ➡ selection intensity among young bull calves
- Higher genetic progress due to use of reproduction technology ➡ Select donors more accurate and select among full sibs
- Higher genetic progress at lower costs ➡ more profit to farmers
- Relative higher genetic progress for functional traits more sustainable breeding

• Breeding plan example Holstein VG

1. Screening all born calves in population
2. 3,000 selected based on NTM, and genomic tested + second choice NOG candidates
3. 150 calves bought based on GEBV's
4. 100 approved as young genomic bulls – Sire of Sons



5. Registration of daughters for 4 years
= breeding values for the bulls



• Use of bulls on categories in VG 2013-2014


Percent	Before GS	VikingRed	Holstein	Jersey
Proven	70	25	10	50
GenVikPlus	0	51	67	25
Young bulls	30	24	23	25
Young GS bulls	0	75	90	50

Young bulls is dominating with Genomic Selection

GS 100 percent within 1-2 year

Genomic Selection effect in VG

- Number of tested young bulls today and before GS



	Before GS	Today	Tomorrow
Holstein	350	175	100
VikingRed	225	175	100
Jersey	55	55	40
Total	620	440	240

Reliability
level GS:

High

Medium

Low

“High change in Breeding Plans with highest reliability on GEBV”

Challenge is to optimize number of GS Young bulls and females in reference

Farms participating in registrations

Milk recording	90 %
Use of AI	88 %
Health registrations	92 %
Insemination plan	88 %

"Phenotyping is King"

Focus R&D together with scientific partners

- Harmonization of registration and key traits
- Implementation of new traits like Claw Health, Feed Efficiency, Para tuberculosis
- Development of methodology and comparison of calculation methods
- Expand reference population with females
- Implement output from sequence data
- Breeding plans and long term consequences
 - Implementation and development of new chip
 - Inbreeding – managed at SNP Level
- ...



• **Thank you for your attention!**



• The Database - effective breeding programme

