VikingGenetics

Breeding for what truly matters

Presented by

Hans Stålhammar

VIKINGGENETICS®

VikingGenetics locations

- 3 main offices – Denmark (HQ), Sweden & Finland
- Daughter companies in Australia and UK

Cooperative owned by 20,000 dairy and beef producers

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VÄXA SVERIGE

www.vikinggenetics.com

Genomic selection
-experiences from dairy cattle
-possibilities in beef cattle

World Charolais Conference

July 4 2018

Tylösand. Sweden

VIKINGGENETICS

How is Hans Stålhammar?

Outline

- Factors influencing the reliabilities of GEBV in dairy cattle
- Changes of breeding programs due to introduction of GEBV
- Other implications of genomic selection

- Availability of Charolais phenotypes and genotypes
- Update of current situation in Australia. Canada. Ireland. France and USA
- Summary and future expectations

Key factors for genomic selection

- Size of the reference population
- Quality and quantity of data registrations
- Efficiency of the methodology, chip technology and calculation methods

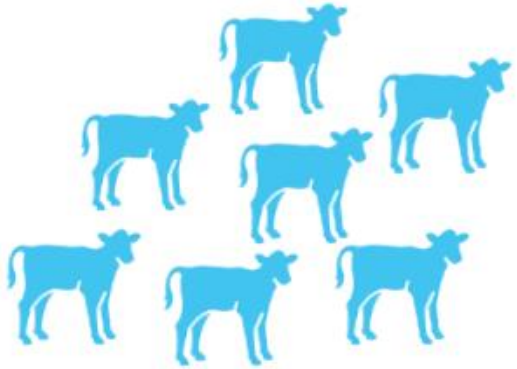
Genomic selection - how does it work?

Reference population

Old daughter proven sires are typed with 54,000 markers

Genomic model

Each marker gets a value for each trait



DNA-typed heifer- and bull calves get a genomic proof

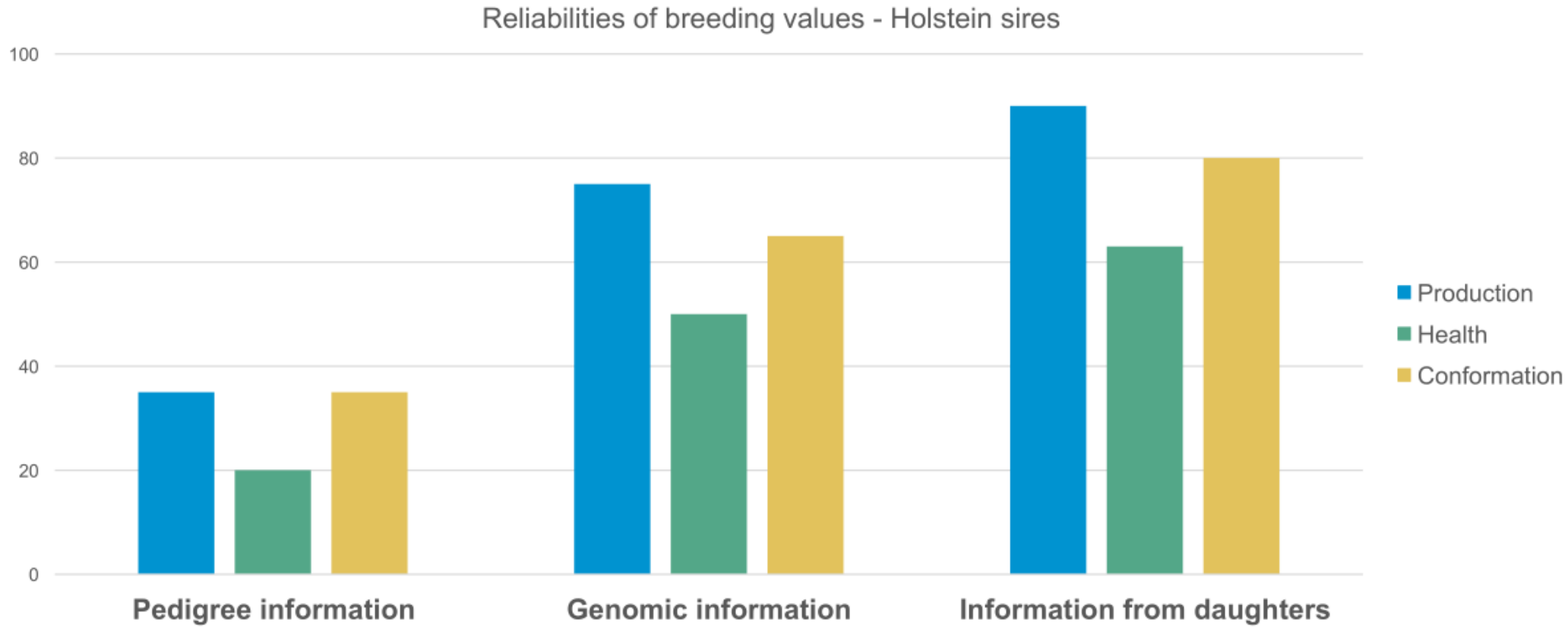
Size of reference population

	No. of sires	No. of cows	Source	LD project**
VikingHolstein	34,535	30,103	VG + Eurogenomics*	15,000
VikingRed	8,212	32,318	VG + Norway	10,000
VikingJersey	2,609	17,788	VG + USA/Canada	7,000

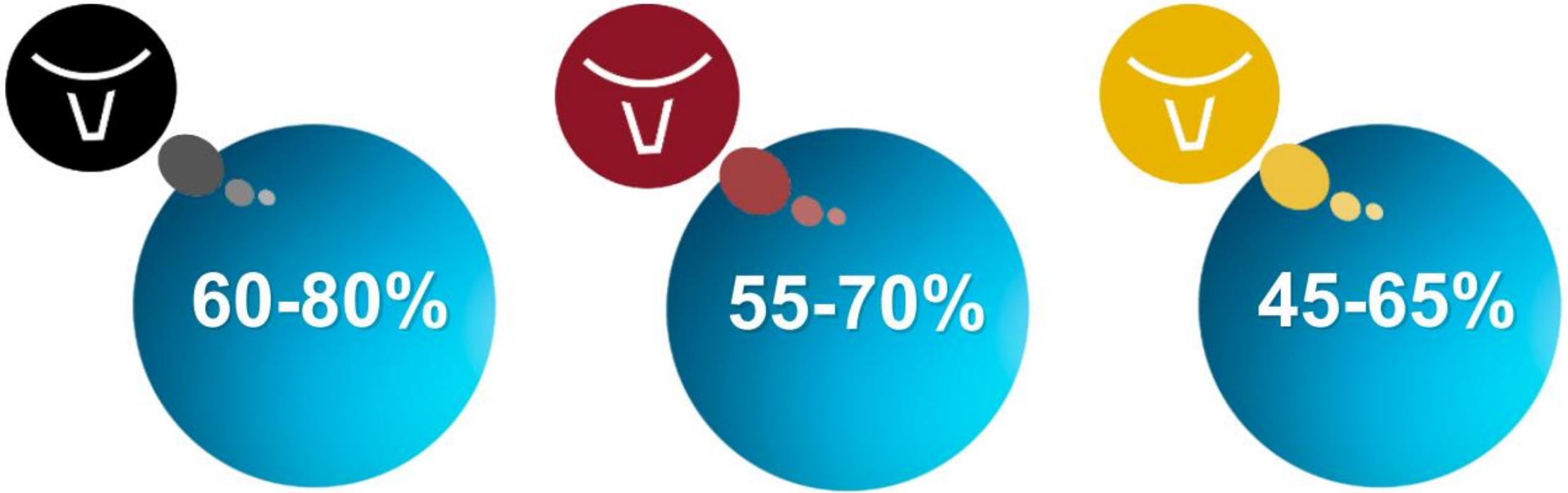
Updated: 2018-02-07

* EuroGenomics includes proven bulls from the Netherlands, France, Germany, Spain and Poland
** No. of females financially supported by VikingGenetics to maintain/improve strong reference group

Reliabilities of breeding values

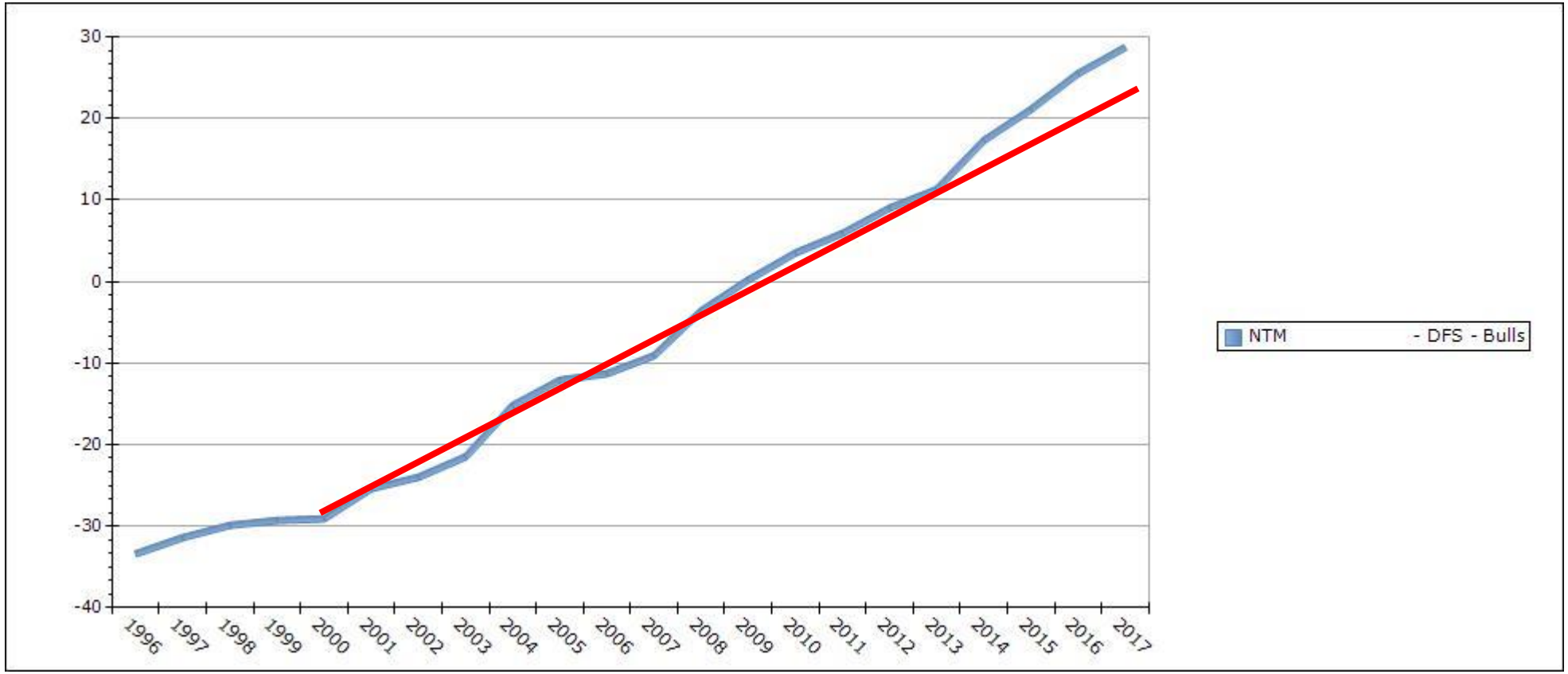


Reliabilities on GEBV's

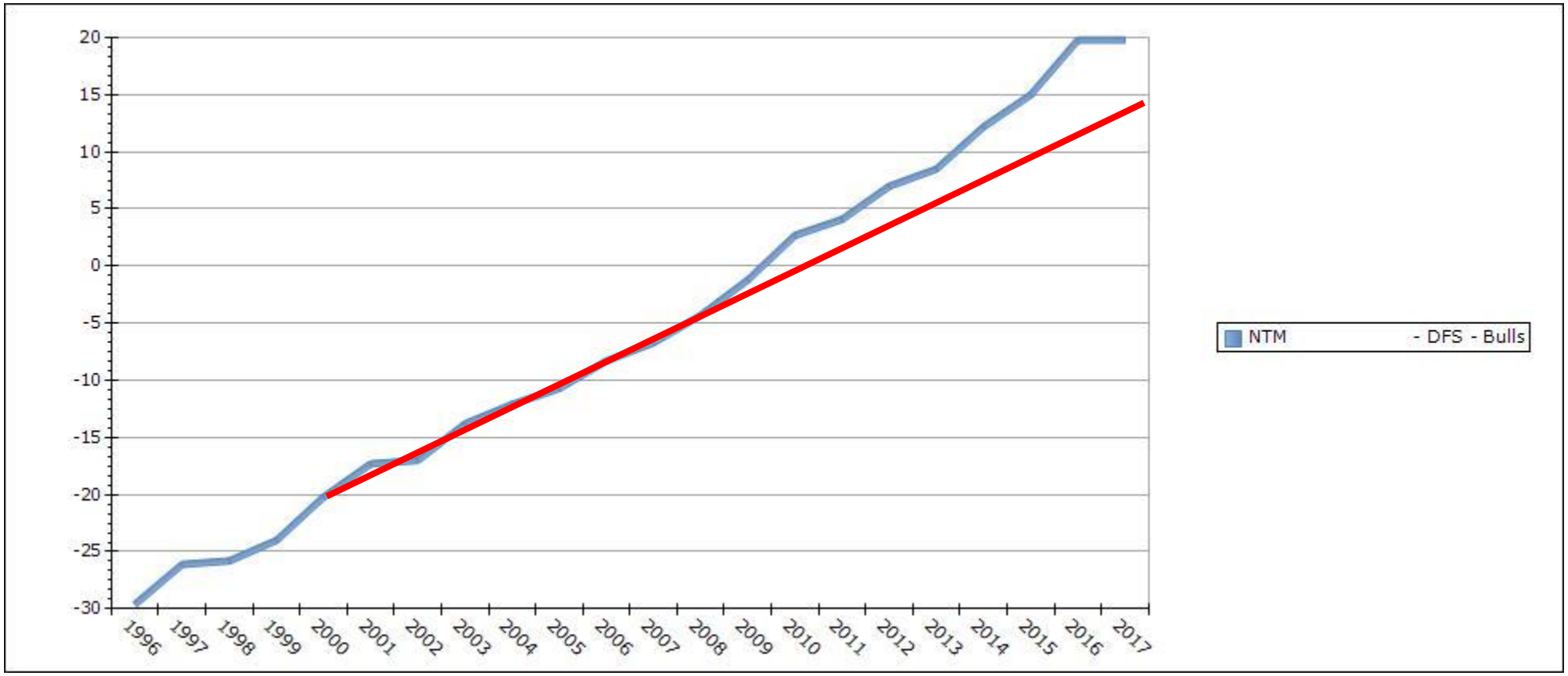


Updated: April 2018

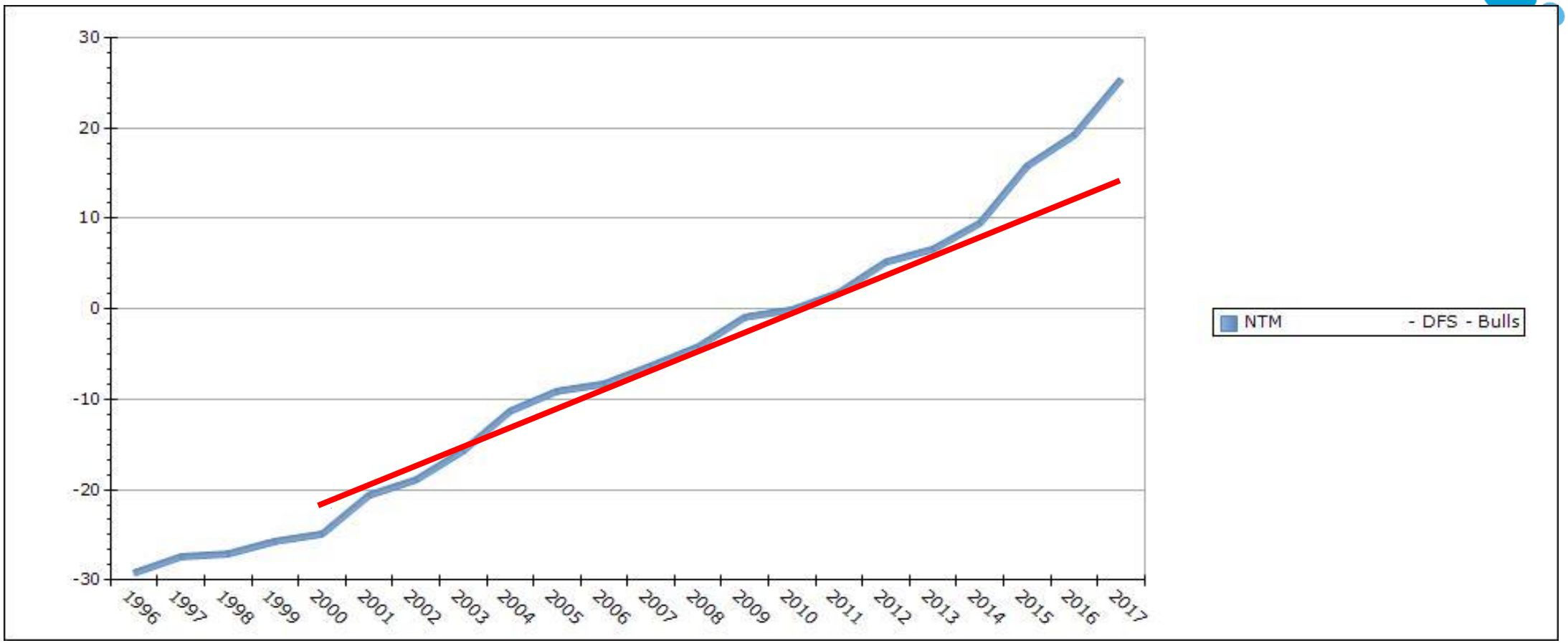
Trends NTM. VikingHolstein bulls



Trends NTM. VikingRed bulls



Trends NTM. VikingJersey bulls



Annual genetic trend per year. females

Period	Annual genetic trend per year		
	2000-2008	2009-2012	2013-2017
Holstein	1.85	2.61	2.82
Red	1.88	2.34	2.11
Jersey	1.75	2.24	2.57

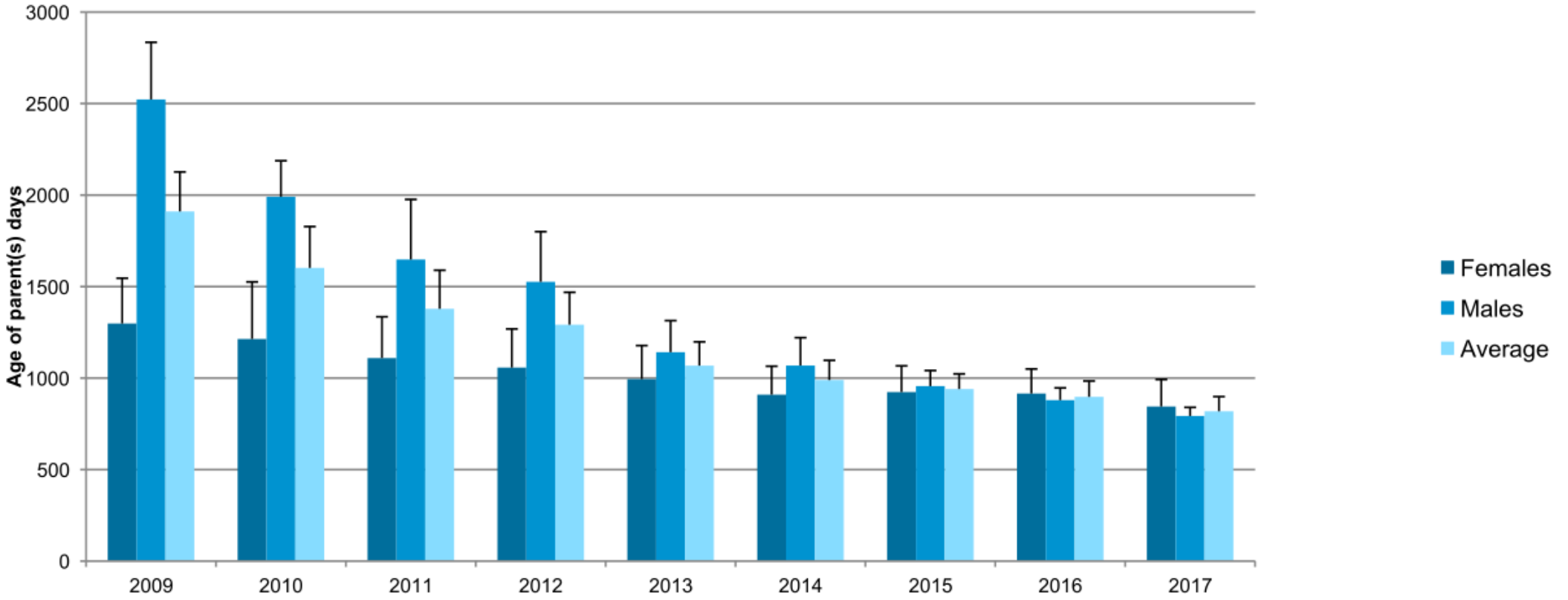
Effect of female test

No. of animals: 107

	Average sub index (Reliability)				
	Before GS	After GS	Diff.	Increase	Decrease
NTM	8	8	0	15	-15
Production index	106 (29)	106 (67)	0	15	-22
Fertility	104 (17)	103 (42)	-1	11	-12
Udder Health	102 (23)	103 (56)	1	15	-10
Udder	102 (25)	102 (60)	0	14	-19

Updated: April 2018

Change of generation interval, Holstein



Use of different sire/semen category

	2016	2017	Actual 2018
Daughter proven	8	3	6
Genomic	91	96	93
Sexed semen	20	30	37

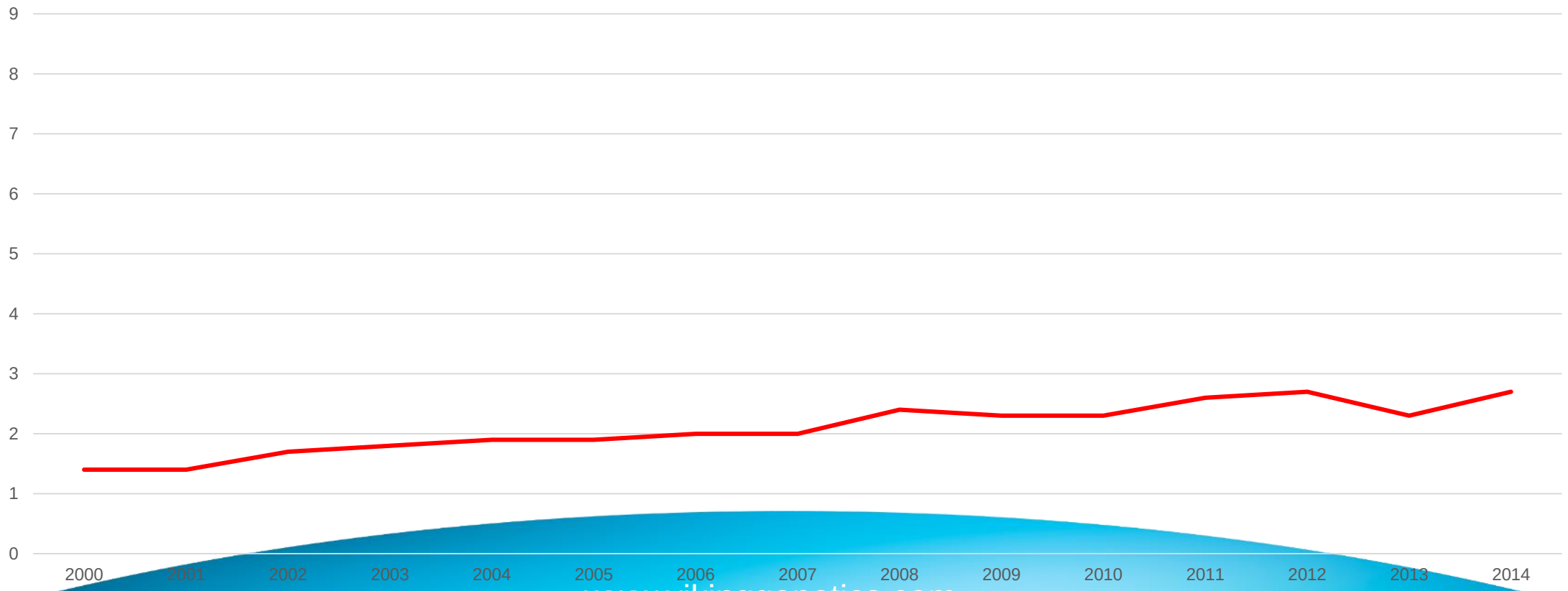
Updated: April 2018

Other implications of GS

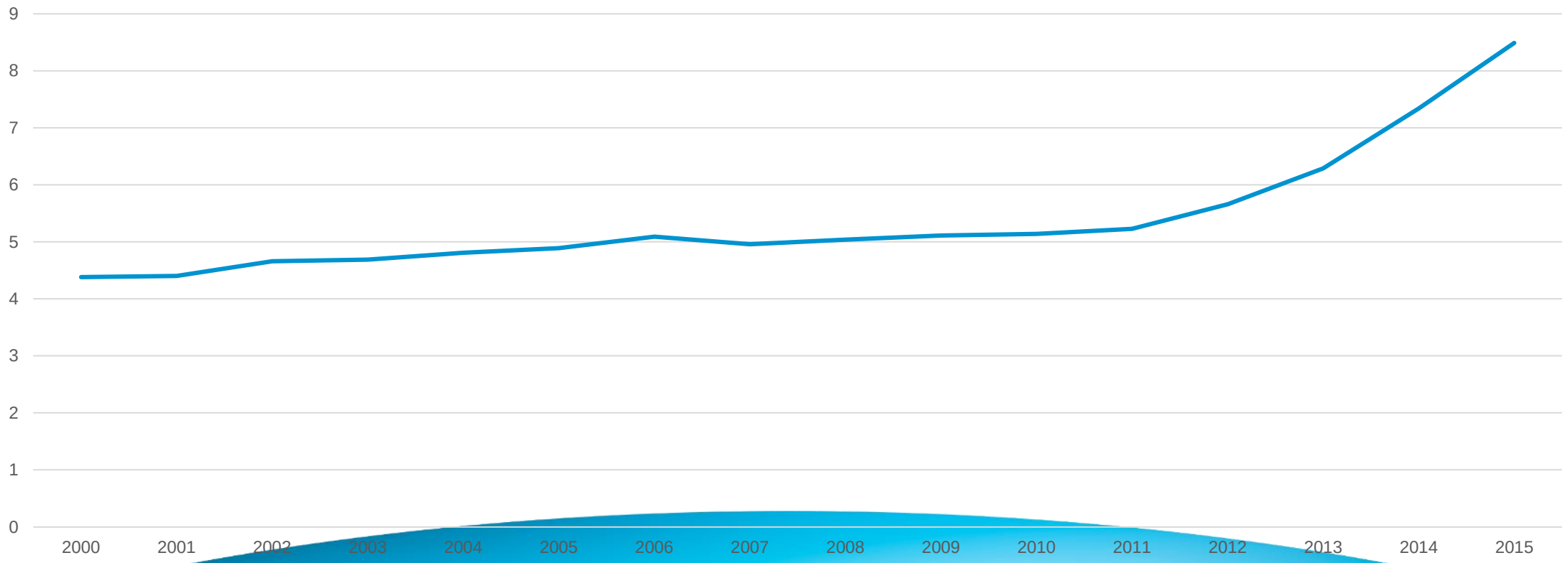
- Shorter generation interval higher risk for increased inbreeding

- More genetic defects have been identified

Inbreeding level VikingRed



Inbreeding level European Holstein



More haplotypes are found

Bulls' status for haplotypes impacting fertility on the records of Holstein Association USA, Inc. as of 04/11/2016 (Blank=Tested-Free, C=Carrier) Use CTRL-F to search.

Stud Code	Name	Registration	HH1	HH2	HH3	HH4	HH5	HCD
29HO09061	208 D G DANO-ET	USA 17395753	C					
	2ND-LOOK ALEXANDER 9990	840003004418274						1
7HO11511	2ND-LOOK FREDDIE 9997	840003004418281						1
29HO16289	2ND-LOOK FREDDIE PRIDE-ET	840003004418282					C	
	2ND-LOOK LEIF LUCAS-ET	840003004418271						1
7HO09546	2ND-LOOK MALLOY	USA 60882194						1
14HO06571	2ND-LOOK MILLENNIUM-ET	840003004418265		C				1
	2ND-LOOK MILLION 9980-ET	840003004418264						1
	2ND-LOOK OBSERVER 11014-ET	840003008562090					C	
204HO00219	528 NEW-WORLD EMPIRE-ET	USA 17190309	C		C			
7HO09021	A L H DUKE-ET	NLD 418232477			C			
	A-DOUBLESTAR ALAMO	USA 143144636						3

Genomic selection
-a possibility for Charolais breeding programs

- In the genomic era, phenotype still is the KING
- We need to continue to register traits of interest
- Phenotypes are more expensive than DNA profiles

Trends in dairy cattle with impact on the use of beef bull semen

- More and more dairy heifers are DNA-tested
- The use of sexed semen is increasing

- Increased interest to use beef bull semen in dairy herds

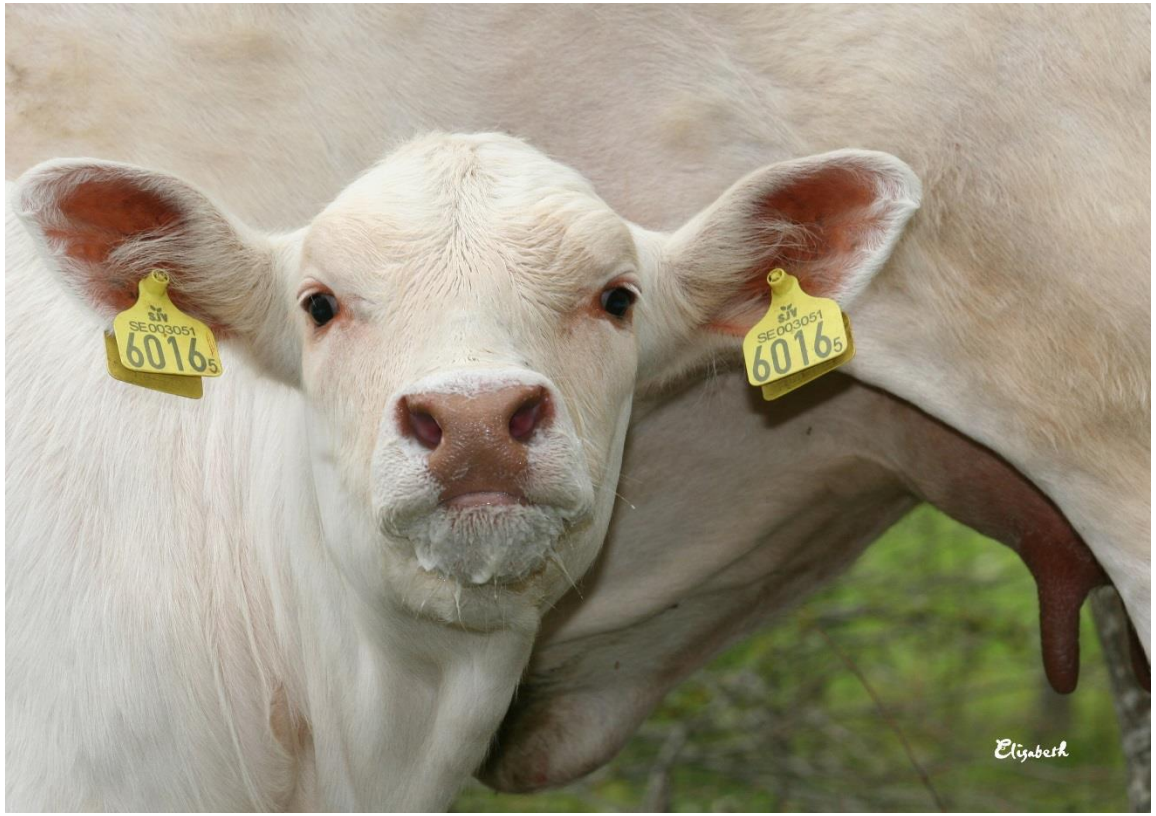
Traits of interest for dairymen

- Direct calving traits
- Calving ease
- Calf survival

- Different trait when recorded on beef and dairy cattle?
- Different traits when recorded on heifers and cows?

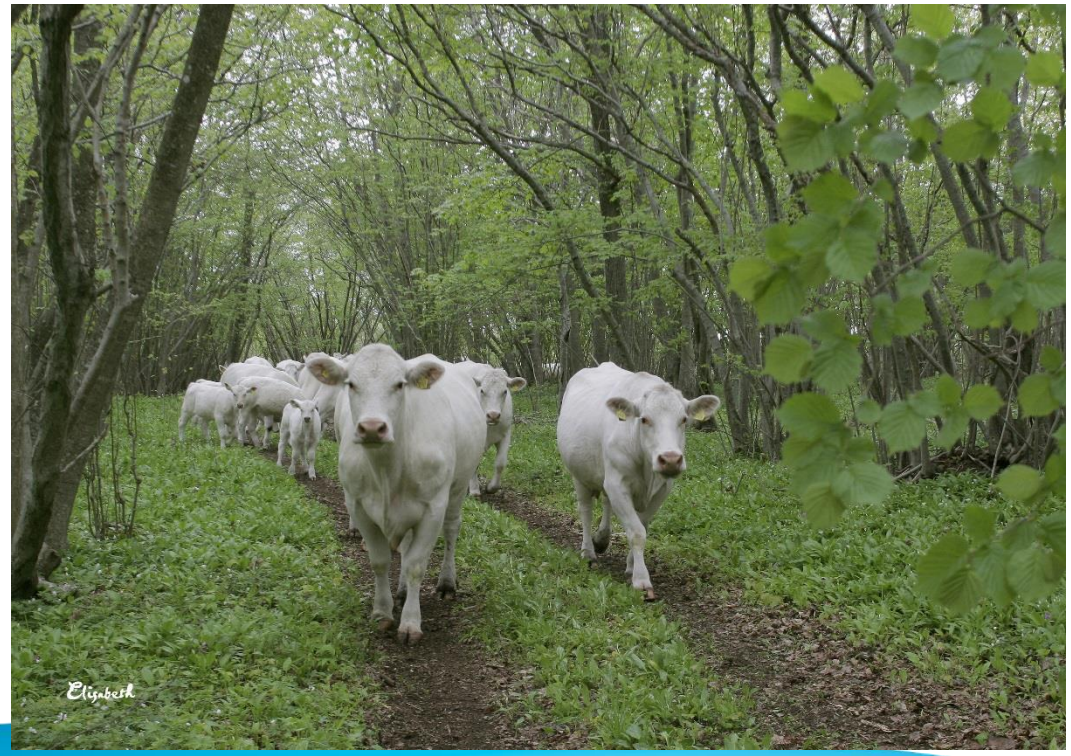
Traits of interest for rearing units

- Growth
- Carcass traits
- Feed efficiency
- Survival



Survey mid June 2018

- I contacted persons in the following countries
  - France
  - USA
  - Canada
  - Ireland
  - Australia



The questions

- Is genomic selection used in estimation of breeding values for Charolais in your country?
- What is the number of purebred Charolais bulls in the reference population?
- Are also purebred Charolais females included in the reference population?
- For what traits do you have breeding values including genomic information?
- What is the improvement in reliability for young and proven bulls due to use of genomic information?
- Are you involved in international cooperation regarding estimation of GEBV for Charolais cattle?
- What changes, in the national breeding evaluations, can you foreseen the coming 2-3 years?

Is genomic selection used in estimation of breeding values for Charolais in your country?

Country	Comment
France	Yes, multi step method, DGV blended with national pedigree EBV. Developing a single step method.
USA	Yes, use a single step genetic evaluation since December 2017
Canada	Yes, starting in July 2018 with a single step method
Australia	Not yet, single step method will be introduced in late 2018
Ireland	Yes, genomics since 2015, multi-breed evaluations with use of cross-bred animals

What is the number of purebred Charolais bulls in the reference population?

Country	Comment
France	dBW, dCE, dWW210, dMTS, dSTS and dBT. 20'-22' (total) / 1.800-2.000 (high accuracy) mCE and mWW210. 5.900-6.700 / 1.100 SA, CC and CW. 3.100-3.600 / 1.000
USA	N.a.
Canada	1365 bulls in a test run
Australia	1339 LD and 60 HD (+National BREEDPLAN evaluation 22' bulls and 153' dams)
Ireland	See following slide

Number of genotyped animals in Ireland

Category	Total	CH
Animals genotyped	1.163.748	257.624
Pedigree animals genotyped	173.343	39.774
Pure-bred, non registered animals genotyped	81.058	21.940
AI Bulls	5.382	470
Stock (breeding) bulls	60.795	16.888
Cows (pure-bred & multi-breed)	612.169	112.869

Are also purebred Charolais females included in the reference population?

Country	Comment
France	Yes
USA	Yes
Canada	Yes some
Australia	Yes some
Ireland	Yes

For what traits do you have breeding values including genomic information?

Country	Comment
France	dBW, dCE, mCE, dWW210, mWW210, dMTS, dSTS,dBT, SA, CC and CW
USA	dCE, mCE, BW, WW, YW, MILK, total maternal, scrotal, CW, REA, fat and marbling
Canada	CE, BW, WW, YW, MILK, CWT, REA, fat and marbling
Australia	Not yet
Ireland	All traditional calving, growth and carcass traits (?)

What is the improvement in reliability for young and proven bulls due to use of genomic information?

Country	Comment
France	See following slide
USA	N.a.
Canada	See following slides
Australia	Not yet determined
Ireland	N.a.

What is the improvement in reliability for young and proven bulls due to use of genomic information? France, accuracy

Traits	IFNAIS dBW + dCE	mWW210
Reliability of pedigree based EBV	Improvement of reliability	Improvement of reliability
0.10	+0.27	+0.10
0.30	+0.18	+0.06
0.50	+0.10	+0.03
0.70	+0.04	+0.01

What is the improvement in reliability for young and proven bulls due to use of genomic information? Canada, accuracy of WW

# of progeny	EPD	GEPD	Difference
0	0.19	0.38	+0.19
20	0.43	0.53	+0.10
30	0.47	0.55	+0.08
277	0.78	0.78	+0.00

What is the improvement in reliability for young and proven bulls due to use of genomic information? Canada, accuracy

Trait	# animals	Accuracy GEPD	Accuracy EPD	Difference
CE	1081	0.36	0.22	+0.14
BW	1365	0.65	0.40	+0.25
WW	1365	0.42	0.25	+0.17
YW	1365	0.33	0.18	+0.15
MILK	1365	0.25	0.14	+0.11
CWT	1365	0.16	0.10	+0.06
REA	1365	0.17	0.08	+0.09
Fat	1365	0.16	0.10	+0.06
Marbeling	1365	0.15	0.07	+0.08

Animals with high genetic merit perform better! Ireland

Do the indexes work?

	Dam – 1 Star	Dam – 3 Star	Dam – 5 Star
Sire - 1 Star on Terminal Index	378 kg	393 kg	400 kg
	863 days	847 days	825 days
	R= 3=	R+ 3=	R+ 3=
Sire - 3 Star on Terminal Index	382 kg	395 kg	
	854 days	838 days	
	R= 3=	R+ 3=	
Sire – 5 Star on Terminal Index	388 kg		405 kg
	845 days		798 days
	R= 3=		R+ 3=

** Based on 83,944 ¾ bred beef steers slaughtered in 2017, where sire and dam were both genotyped*

A cross breed evaluation for carcass weight, Ireland

Resultant Genetic Evaluations.

Breed	1pc	50 pc	99pc
All Breeds	-6.07	15.99	33.88
- Angus	-8.25	5.00	20.00
- Charolais	16.50	32.88	47.50
- Hereford	-7.50	4.37	15.50
- Limousine	9.75	22.75	38.50
- Simmental	7.96	21.25	36.50

- Resultant evaluations presented as PTA's (i.e., what the sire/dam will pass on to progeny).
- Range of 25kg within breed & 40 kg across breeds
- Considerable overlap between breeds.

A cross breed evaluation for heifer performance, Ireland

Average heifer performance (2017).

Sire	Dam	Number	Cwt kg	Conf (1-15)	Fat (1-15)	Price/kg	Overall	Age Slau	Cwt/day*
Main beef breeds.									
CH	CH	39,147	348.5	8.8	8.7	€4.08	€1,422	811.1	0.43
LM	LM	43,802	336.0	9.0	8.5	€4.07	€1,368	816.0	0.41
SI	SI	3,107	320.2	7.6	8.9	€3.95	€1,265	827.5	0.39
AA	AA	8,684	285.1	6.5	10.0	€3.85	€1,097	761.4	0.37
HE	HE	3,669	282.8	6.1	10.2	€3.88	€1,097	795.6	0.36
Main dairy cross									
HE	FR	42,669	277.5	5.3	9.9	€3.99	€1,107	748.0	0.37
AA	FR	70,470	273.5	5.5	9.6	€4.00	€1,094	741.3	0.37
Dairy									
HO	HO	25,092	274.1	3.5	8.2	€3.57	€978	887.4	0.31
** Expressed as carcass weight/age at slaughter.*									

- Charolais is best breed based on overall carcass weight, carcass value and carcass gain/day.
- This does ***NOT*** consider "cost of feed" (either feed intake during finishing period or system of finish) => Profit.

Animals with high genetic merit perform better!

Accuracy of carcass weight evaluations

Genomic Eval Cwt	Number	Actual Cwt kg	EBV Cwt (pred)	Price/kg	Overall	Age Slau	Cwt/day
5 stars - Top 20%	10,953	365.3	52.1	€4.29	€1,582	751	0.49
4 stars	8,160	348.3	38.9	€4.23	€1,497	760	0.46
3 stars - Ave	8,150	339.3	31.1	€4.19	€1,450	766	0.44
2 stars	7,417	326.1	22.4	€4.13	€1,384	774	0.42
1 star - Btm 20%	6,013	301.7	7.3	€3.94	€1,266	775	0.39
No Stars	21,342	326.6		€4.22	€1,383	779	0.42

- Genomic Evaluations for carcass weight accurately predicted actual performance.
  - Top 20% predicted at +52.1 kg compared to +7.3 for bottom 20%. Difference of 44.8. Actual difference => 63.6
  - Significant additional gains on age at slaughter.
- Moving industry from 3 stars to 5 stars=>+€200 per animal slaughtered (~€200m for Irish beef industry).

Different breed origin of animals with high performance, owerlapping

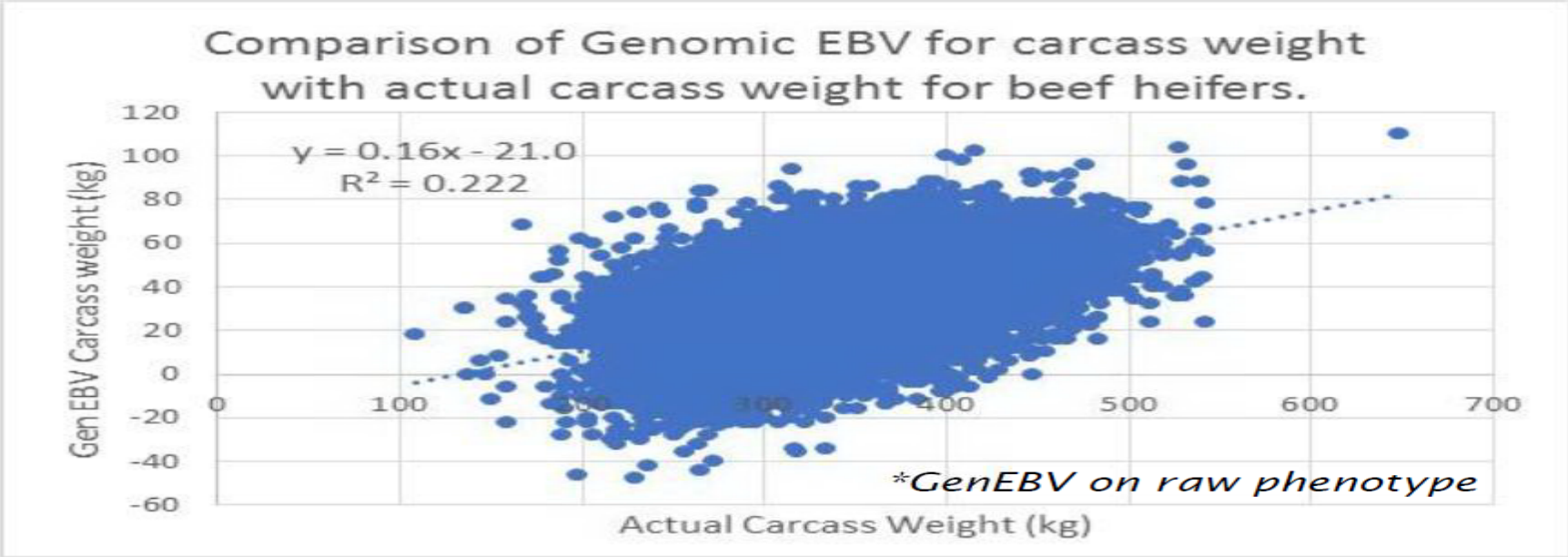
5 Stars versus CH breed?

Comparison	Number	Actual Cwt kg	EBV Cwt (pred)	Price/kg	Overall	Age Slau	Cwt/day
5 stars - Top 20%	10,953	365.3	52.1	€4.29	€1,582	751	0.49
Breed							
CH*CH	45,200	350.0	40.0	€4.27	€1,499	767	0.46

- 5 star animals significantly outperformed the CH breed. Similar trends for other breeds.
- 5 star animals are made up of animals from all of the individual breeds.
- The key reason why ICBF invests so much effort into our within breed improvement programs (i.e., G€N€ IR€LAND)=> *genetic gain for beef industry.*

Benefit of GS in the evaluation of carcass weight?

Genomic vs Traditional evaluation.



- Irish experience; Genomic evaluation is only marginally better than traditional evaluation (R^2=0.20).

- Benefits of genomics=> more from lower h^2 traits.
- Work on single step ongoing but size & complexity of data remains a challenge! (Garrick, Veerkamp, Stranden)

Are you involved in international cooperation regarding estimation of GEBV for Charolais cattle?

Country	Comment
France	No
USA	AICA staff continues to stay abreast of activities related to international genomic applications
Canada	Not yet
Australia	Yes, through ABRI, BREEDPLAN is a cross country evaluation
Ireland	No. open for collaboration in data sharing

What changes, in the national breeding evaluations, can you foreseen the coming 2-3 years?

Country	Comment
France	Replace multi step genomic evaluations by a single step GBLUP
USA	A continued rapid growth of genetic testing in cattle populations and a better use and understanding of selection tools by seedstock and commercial breeders
Canada	Expect greater use of genomics in both male and female evaluations. Encouraging breeders to produce more carcass data
Australia	Single step BREEDPLAN at end of 2018, Pedigree confirmation with a SNP-DNA panel
Ireland	No major changes of the indices, incentive programs focused on data quality

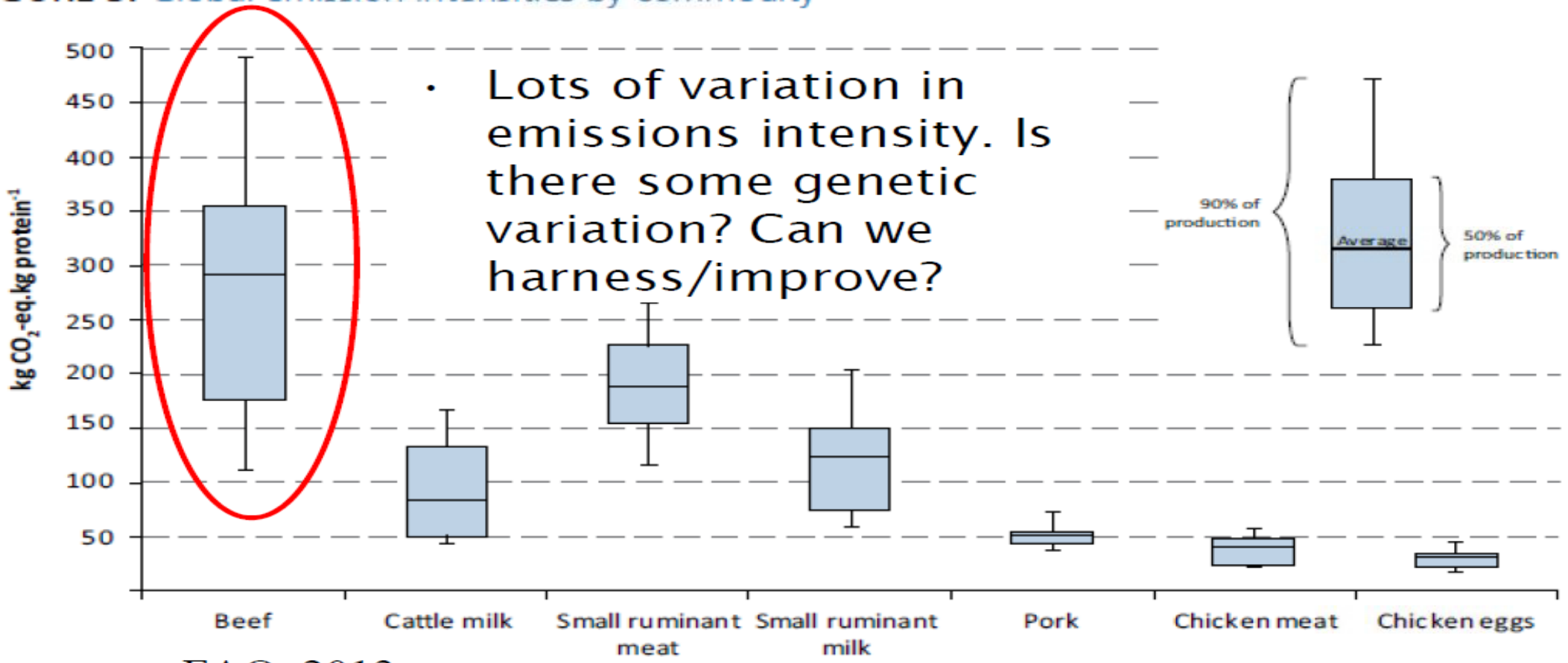
Irish priorities

Current Priority Projects.

- DNA Calf Registration.
- Carcass cut and meat eating quality.
- App's for collection of data on farm.
  - Particular focus on health & disease traits (including animal treatments etc).
- GHG => cow size/live-weight (cow efficiency).
- Dairy beef => increasing value of beef from dairy herd (sexed semen, calving, carcass, quality....).
- G€N€ IR€LAND => increase rate genetic gain in beef.
- International collaboration => to ensure Irish beef farmers have access to best genetics globally.

1. Opportunity; Genomics Programs.

FIGURE 3. Global emission intensities by commodity



- Lots of variation in emissions intensity. Is there some genetic variation? Can we harness/improve?

Source: GLEAM. FAO, 2013

Additional slide not presented at the World Congress

- In the estimations of GEBV in US 1,018 genotyped sires with progeny that also have phenotypic observations are included. Other genotyped animals would be nonparents or dams.
- The mean accuracy for a genotyped animal with no progeny or contemporary group phenotypes in the NCE single step estimations are:
  - BW 0.30
  - WW 0.27
  - YW 0.23
  - MILK 0.20

11th World Congress on Genetics Applied to Livestock production

Individual cow identification in a commercial herd using 3D camera technology

1:30 PM–1:45 PM Feb 16, 2018

NZI 2 & 3, Aotea Centre

Dr Jorn Thomasen Project Manager at VikingGenetics

Individual measure of feed intake on in-house commercial dairy cattle using 3D camera technology

1:45 PM–2:00 PM Feb 16, 2018

NZI 2 & 3, Aotea Centre

Mr Jan Lassen Projectleader at VikingGenetics

Feed efficiency

- VikingGenetics is developing a new method for registration of feed intake based on 3D camera technology
- This is a possible game changer regarding feed intake registrations
- Easier to register and evaluate growing compared with lactating animals

Summary

- Genomic selection has totally change the dairy cattle breeding
- In the genomic era, we still need relevant phenotypes
- Increasing interest to use beef bull semen in dairy herds
- In the future, pedigree verification will be made by DNA SNP panels and it will give a large number of genotyped animals
- In the future, genomic selection will be the standard evaluation method also in beef cattle breeding
- In the future, we have to option to include feed intake and feed efficiency recorded on a large number of animals

Thank you for your attention