What could the pig sector learn from the cattle sector. Nordic breeding evaluation in dairy cattle

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Nordic Cattle Genetic Evaluation

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Seminar/Workshop on Genomic selection in pigs

Copenhagen

NAV

STØTTET AF
mælkeafgiftsfonden

Cattle and pigs are different species

What is equal in breeding structure and what is different?

What is equal when using genomic selection prediction and what is differnet

Cattle and pigs are different species

Major reason for the different breeding structure is number of offspring per female and male

A sow get 20 piglets - A cow get one calf

Majority of breeding goal traits expressed in both sexes in pigs but only in one sex in cattle

Pigs versus cattle - 2016

Pigs	Cattle
3 major pure breeds	3 major pure breeds
Small purebred nucleus with intense phenotyping	Large purebred production population with relatively intense phenotyping Few cross bred cows with relatively intense phenotyping
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Pigs versus cattle – genetic evaluation 2016

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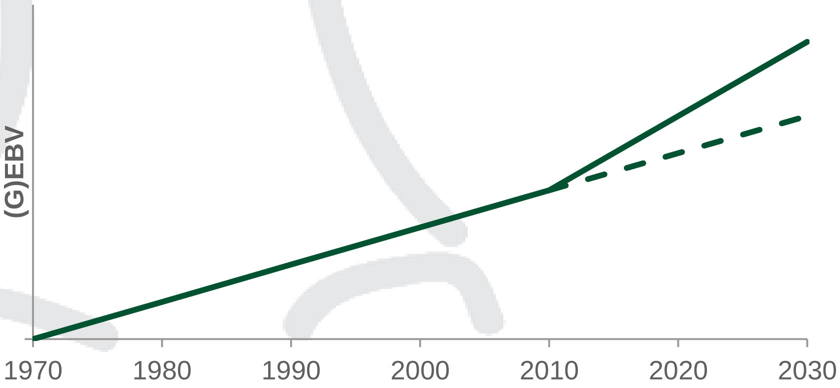
Cattle breeding plan, % semen from different AI-bull categories

	2009	2016
1-2 years old AI bulls	30% (pedigree selected)	95% (genomic selected)
5+ years old AI bulls	70% (have milking daughters)	5%(have milking daughters)

Genomic selection has created a revolution in cattle breeding

Genomic selection – new opportunities

- Accurate selection of young animals
  - 50 to 100 % increase in genetic progress
  - 75 to 150 DKK extra per cow



Use of genomic prediction in dairy cattle

- Today – tool in breeding plan for the whole population
- Future – mamagement tool within herds – used in combination with sexed semen and crossbreeding

Price
is key
factor

NAV routine

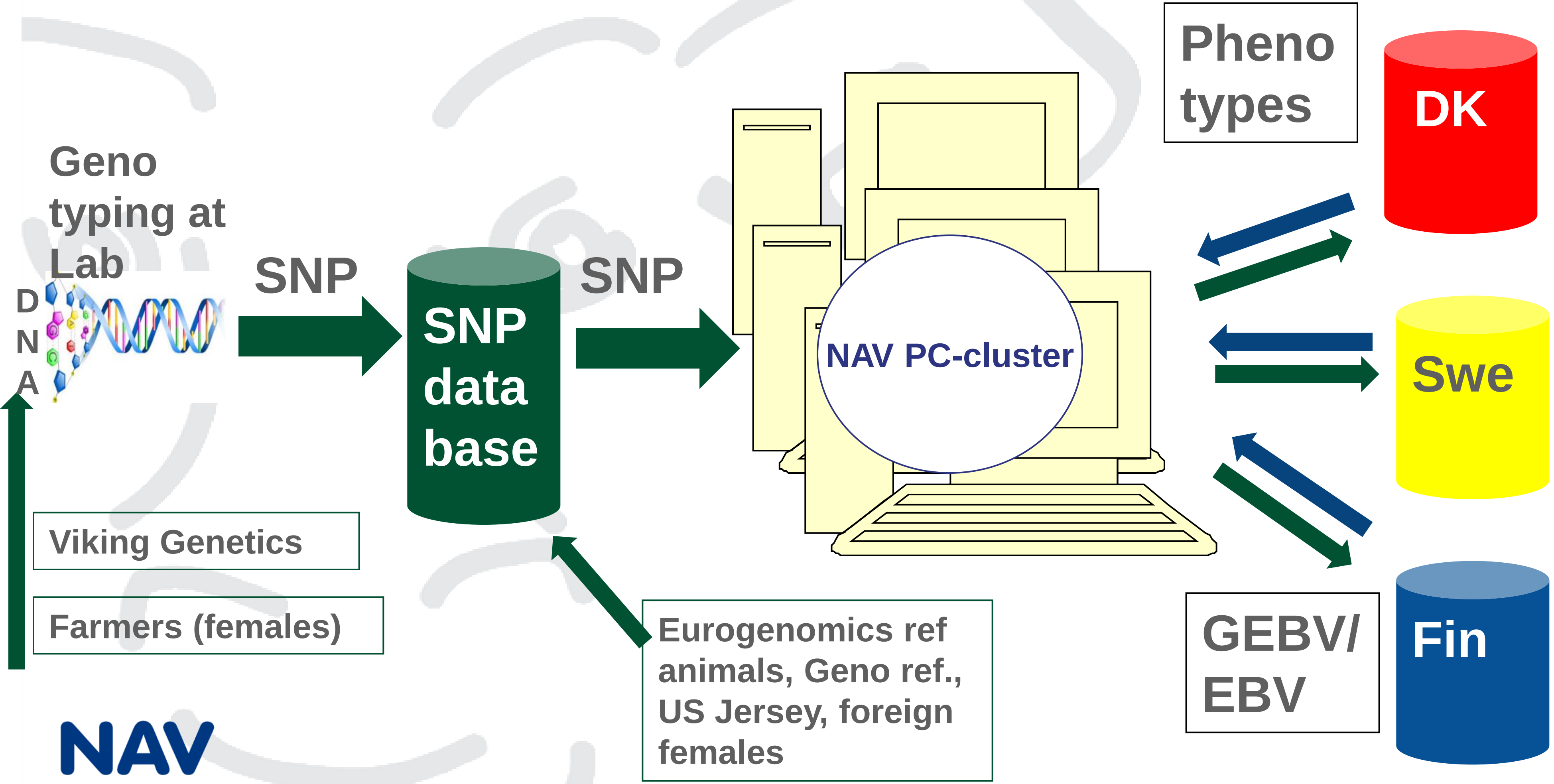
- What are we doing today from DNA tissue to GEBV?

- Which steps have room for improvement in the short and longer run?

Outline

NAV/national

1. Collection of DNA Tissue
2. Parentage verification
3. Exchange of genotypes
4. Imputation
5. DRP
6. Genomic prediction



Geno typing at Lab

DNA

SNP

SNP data base

SNP

NAV PC-cluster

Pheno types

DK

Swe

Fin

GEBV/ EBV

Viking Genetics

Farmers (females)

Eurogenomics ref animals, Geno ref., US Jersey, foreign females

Tested females per country and birth year

Year	Holstein			RDC			Jersey		
	DNK	FIN	SWE	DNK	FIN	SWE	DNK	FIN	SWE
2009	871	138	138	96	295	108	151	1	5
2010	1,104	353	150	506	1,848	1,257	2,176	1	43
2011	1,637	1,137	358	897	3,605	1,783	4,038	6	89
2012	2,408	1,799	570	1,304	3,731	1,930	4,442	16	111
2013	3,746	2,575	1,602	1,630	3,427	2,226	3,194	12	84
2014	3,985	2,693	2,154	1,762	3,475	2,651	3,668	26	82
2015	3,080	1,820	1,360	1,408	2,697	2,140	2,546	20	53
Total	**18,408**	**10,643**	**6,564**	**7,738**	**19,394**	**12,201**	**20,506**	**82**	**480**
	HOL total : 35,615 **Last year: 13,978**			**RDC total : 39,333** **13,645**			**Jersey total : 21,068** **6,910**		

Level of genomic tested Holstein

November 2015

	AI -Bulls		Culled bulls		Females	
Born	**Number**	**NTM**	**Number**	**NTM**	**Number**	**NTM**
2009	296	5.8	844	1.4	1,147	0.4
2010	248	9.2	903	2.7	1,607	3.9
2011	200	15.3	1,532	7.2	3,132	5.8
2012	222	19.7	1,958	10.8	4,777	8.1
2013	186	23.7	2,210	13.9	7,923	10.7
2014	133	30.7	3,033	18.3	8,832	14.8
2015	32	35.1	2,073	23.0	6,260	18.3

Std 10

Level of genomic tested RDC

November 2015

	AI-bulls		Culled bulls		Females	
Born	Number	NTM	Number	NTM	Number	NTM
2009	247	1.4	344	-0.8	499	2.1
2010	256	6.4	738	2.5	3,611	0.9
2011	294	9.3	1,518	6.2	6,284	3.0
2012	267	14.2	2,071	8.2	6,965	8.2
2013	249	16.7	2,103	10.2	7,281	8.5
2014	148	23.4	2,177	14.2	7,884	12.0
2015	48	29.0	1,746	19.2	6,240	15.9

Std 10

Level of genomic tested Jersey

November 2015

	AI-Bulls		Culled bulls		Females	
Born	**Number**	**NTM**	**Number**	**NTM**	**Number**	**NTM**
2010	72	5.7	179	0.7	2,896	1.1
2011	73	8.1	325	2.8	4,806	2.2
2012	58	10.0	369	5.3	4,713	3.0
2013	67	12.1	386	7.3	3,291	5.6
2014	67	16.1	412	9.4	3,776	7.6
2015	7	21.7	400	14.5	2,619	10.5

Std 10

Reference population

January 2016

	Reference population	
	Bulls	Cows
Holstein	31,800[a)]	14,900
RDC	7,600[b)]	19,600
Jersey	2,500[c)]	13,500

a) Includes proven bulls from NLD, FRA, DEU, ESP, POL
b) Includes proven bulls from NOR
c) Includes proven bulls from USA

Model based GEBV reliabilities, average young bulls born 2014 (validation r^2_{IA} are lower)

Traits	Holstein	RDC	Jersey
Yield	74	67	67
Growth	60	49	28
Fertility	65	47	42
Birth	70	57	44
Calving	64	43	
Udder health	68	57	56
Other disease	45	38	26
Claw health	43	33	-
Longevity	61	38	37
Frame	73	58	63
Feet & Legs	68	54	53
Udder	73	55	60
Milking speed	69	66	60
Temperament	62	53	27

Extra reliability
– in addition to pedigree information for HOL

	Extra reliability based on validation reliabilities
Yield	**0,35**
Growth	0,24
Fertility	0,32
Birth	0,31
Calving	0,22
Udder health	**0,41**
Other diseases	0,06
Frame	**0,36**
Feet&Legs	**-**
Udder	**0,52**
Milking speed	**0.46**
Temperament	0.14
Longevity	0.21
Claw health	(0,00)

Collection of DNA

Collection of DNA – so far

- Eartags
- Noose swap
- Blood
- Weak points
  - An extra operation (in most cases)
  - Correct link between tissue and animal id
  - An increasing challenge when number genotypes increase

Future
Sample with minimal effort and maximal reliability!

Sampling - part of normal work flow

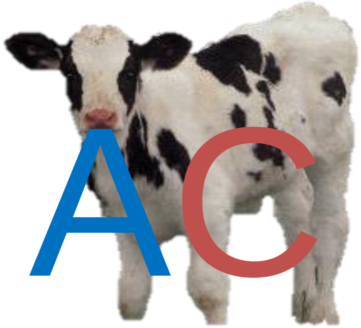
Unique connection between tag and sample (also checked at lab)

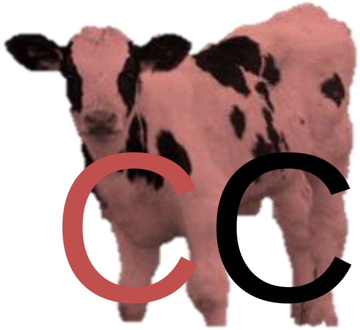
Parentage verification

Routine evaluation

- For most candidates we have a genotype of the sire, but not the dam
- Check for mendel errors
- Mendel errors indicate a disagreement between official pedigree and genotype

Principle behind Mendel Error Check





Imputation

Why do we impute?

Accuracy of GEBV: 54K > imputed LD > LD

Golden standard so far Illumina Bovine 54K - in which cases do we impute?

- Illumina Bovine 54K chip - different versions
  - AI bulls are all tested with 54K
- Low density chip
  - Females and candidate bulls genotyped with
- Other chips
  - Some foreign animals
- Missing calls

Imputation

- When pedigree, sex, and ID is verified the genotype can be imputed
- Fimpute – used today in all breeds
  - Quick & accurate in homogeneous populations, but pedigree has to be correct
- Beagle – used earlier in RDC and Jersey
  - Slow but accurate and robust

How accurate can we impute?

Genotype error rates (results from 2013)

	Parents genotyped			
Breed/method	NONE	DAM	**SIRE**	**DAM and SIRE**
HOL FImp LD	3.4 (67)	1.7 (14)	**3.2 (1213)**	**0.7 (432)**
RDC* Fimp LD	10.3 (9)	3.7 (3)	**4.3 (1147)**	**0.7 (234)**
RDC* Beagle LD	2.3 (9)	1.0 (3)	**1.3 (1147)**	**1.0 (234)**
JER FImp LD	3.0 (5)	2.0 (3)	**1.5 (110)**	**0.5 (75)**

Routine model – two step model

1. **Traditional evaluation within breed**
    - **EBVs based on phenotypic data**
2. **DRPs**
    - **Backward transformation of EBVs for genotyped animals**
3. **GEBV estimated by SNP BLUP**
    - **Input DRP and 54K imputed genotypes**

DGV prediction

- GBLUP
  - Same genetic parameters as in traditional model
  - No polygenetic effect
  - DGV's scaled according to validation results to get rid of inflation

Dependent variable

	2009	2015	Future
All breeds	NAV EBVs (genotyped animals)	DRPs (genotyped animals) from NAV EBVs and MACE EBVs	One step phenotypes and genotypes simultanously

As long foreign reference bulls are important dependent variable has to be DRP or foreign information has to be blended in the one step model

Traits

	2009	2015	Future
All breeds	Combined NTM traits used as single traits	Single traits combined across lactations – Interbull traits	Near future - follow Interbull

Trait definitions have to follow Interbull traits e.g. combined across lactation - as long as foreign reference bulls are important.

Method

	2009	2016	Future
All breeds	Bayesian without polygenetic effect	SNPBLUP without polygenetic effect	Reconsider polygenetic effect One step Take SNPs carrying ”additional information into account”

Validation

	2009	2016	Future
All breeds	Cross validation applied	Validation based om last birth years – Interbull standard	Continue to apply international standards

Interbull has set up standards for validation a requirement to fulfill the standard to have an international recognized evaluation system - Interbull standard check genetic trend

Validation reliabilities (increase in reliability next to pedigree)

	2009	Exchange ref bulls	Cows in ref	Future
HOL	+20-30%	+12%	+2%	+?
RDC	+10-20%	+1-2%	+3-7%	+?
Jer	+0-10%	+3-4%	+5-10%	+?

Further increased reliabilities require more cows in reference and/or improved methods

Handling of inflation of DGVs

	2009	2016	Future
All breeds	Not handled	DGVs standardised to fulfill validation	Reconsider adding polygenetic effect

General picture GEBVs are inflated – without some kind of restandardisation animals in youngest birth year classes will be overevaluated – no effect on within birth year selection, but cattle select across birth year and make across country comparisons

Ongoing development work

- Improve current 2 step model
  - Include cows in reference more traits – fertility, claw health, calving traits (require change from SM to AM - ongoing), Other diseases (require change SM to AM)
  - Reconsider polygenetic effect
- Improve traditional models – still relevant

Further improvement - GEBVs

- One step (Luke)
  - Simultaneously use of phenotypes and genotypes in evaluation
- Handling more informative SNPs (AU)
  - Give additional weight to SNPs carrying more information

Requirements/challenges for the next generation genomic breeding tool

- Scale to a huge number of individuals with genotypes and phenotypes
    - Millions ungenotyped and hundereds of thousands genotyped individuals
- Use information from advanced models
    - Bayesian mixture models, haplotypes, QTL etc.
- Information from WGS data across several breeds

Traditional genetic evaluation

- EBVs from traditional genetic evaluation based on pedigree and phenotypes only is the basis for genomic prediction and it is still important to:
  - Improve models
  - Include new phenotypes

Summary

1. Collection of DNA Tissue (ear tagging)
2. Parentage verification (assigning of parents)
3. Exchange of genotypes (less important – more cows genotyped)
4. Imputation (limit gain in near future)
5. DRP
6. Genomic prediction

} One step, informative SNPs

What can pig and cattle learn from each other in relation to genomic prediction

- Crossbreed animals
- Model experiences
  - One step
  - Single informative SNPs
- Validation/reliabilities
- …..

Pigs versus cattle - 2016

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Cattle and pigs are different species, but how different in 2030

Major reason for the different breeding structure is number of offspring per female and male, but will that remain – maybe in vitro techniques be very common, cattle get more closed breeding companies, and crossbreeding be more common?

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Cattle and pigs are different species, but how different in 2030?

The aim is to breed for pigs and cattle producing efficient under future production circumstances – use of lots of phenotypes from production herds is important to ensure we get the genetic progress we expect in practice