

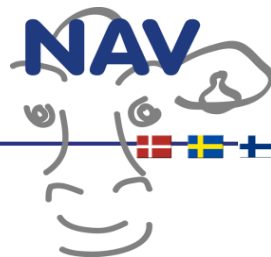
Status on routine evaluation in NAV and Interbull

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NAV routine

- **What are we doing today from DNA tissue to GEBV?**
- **Which steps have room for improvement in the short and longer run?**

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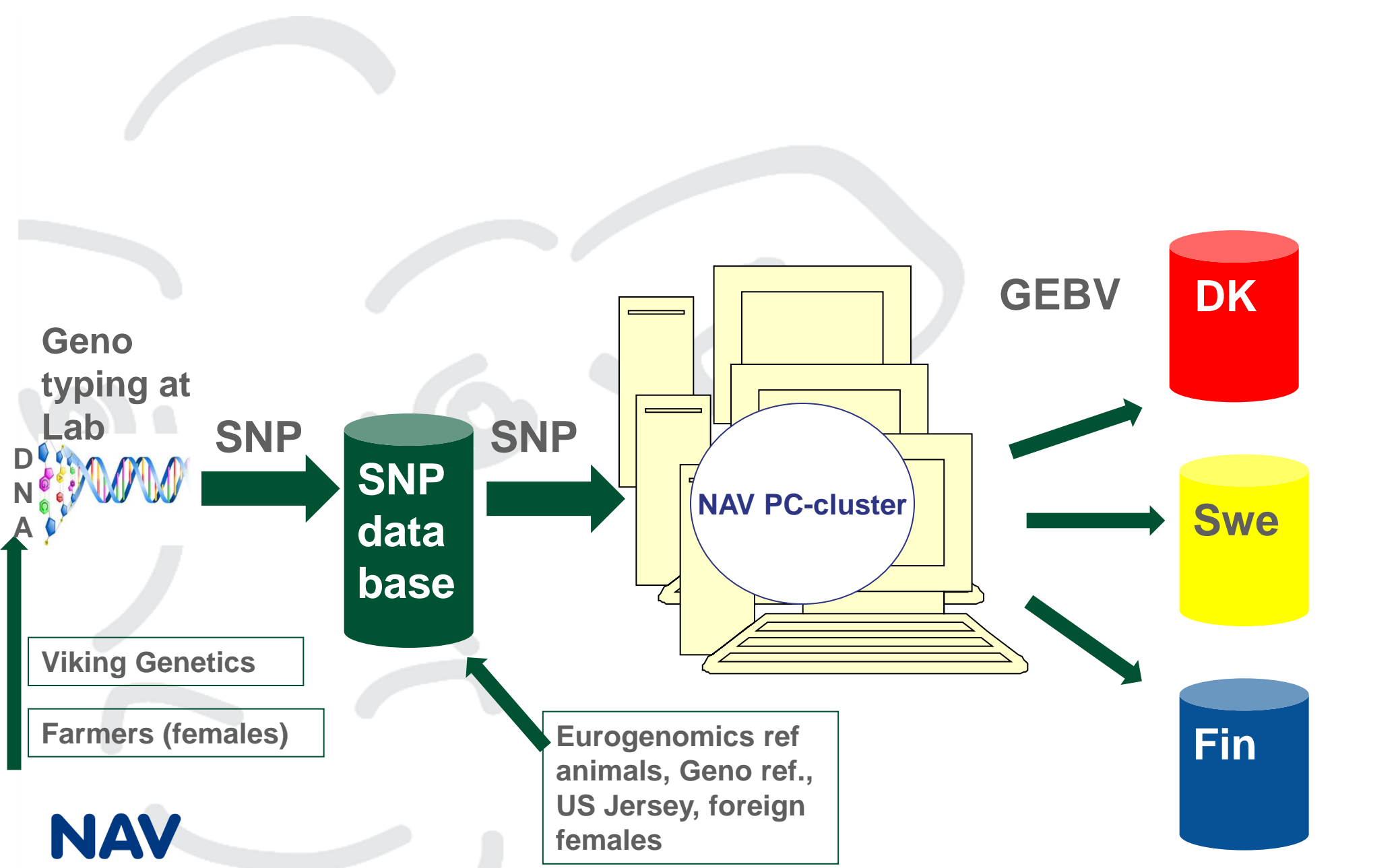
Outline

NAV/national

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

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Collection of DNA

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Collection of DNA - today

- **Eartags**
- **Noose swap**
- **Blood**
- **Weak points**
 - **An extra operation**
 - **Correct link between tissue and animal id**
 - **An increasing challenge when number genotypes increase**

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Danish
study

Future

Sample with minimal effort and maximal reliability!

Sampling - part of
normal work flow



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



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Learnings from Dansih pilot study 2012/13

- Tags are easy to use
- Important to do tagging systematically
- Bit more time consuming than ordinary tags
correct top/bottom important



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Status!



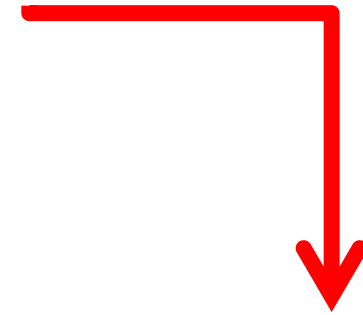
- Allflex has develop a new part to existing applicator that fixate liquid container
- Tested in 3 herds in September/October 2013
- Tissue seems to have good quality no matter how it is conserved
- BUT we recommend that tissues is stored in deep freezer or refrigerator

Ready for use in large scale!

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Procedure for large-scale collection



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Evaluation of procedure

- Use in 2 - 3 months (**start December 2013**)
- 5 - 10 herds (**presently 8 herds**)
- Feedback from Farmers and Genoskan

Positiv respons – more herds

Negativ respons – revision of procedure

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Parentage verification

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Routine evaluation

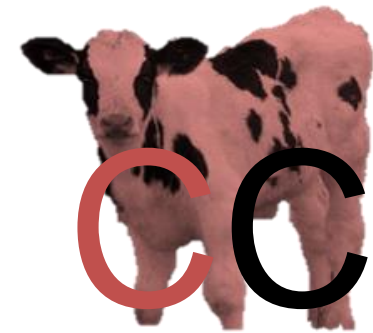
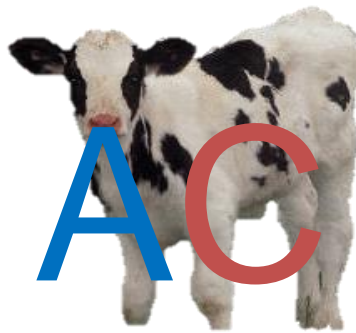
- For most candidates we have a genotype of the sire, but not the dam
- Check for mendel errors
- Mendel errors indicate a disagreement between official pedigree and genotype

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Principle behind Mendel Error Check



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Mendel Error Check - Failed



- Rejected pedigree or sire is unknown / not genotyped
 - search for potential parents
- Technique similar as for ME-Check
 - Counting opposite homozygous loci
- Result is returned to VG or Växa
 - When errors are corrected genotype can be included again – farmers responsibility

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How many genotypes are accepted?

- **% approved, routine: 96-97 %**

Percent approved per breed, LD-project

- JER: 94.5 %
- RDC: 97.9 %

Errors are
mainly ME

Percent approved per country, LD-project

- DNK: 94.9 %
- SWE: 97.6 %
- FIN: 98.0 %

% of errors
correlated to
herd size

Genotypes

Today

- In most cases we have a genotype of the sire, but not the dam – we do mendel error check
- Herds with many errors have to improve ear tagging/registration procedures

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Genotypes

Near Future

- MGS genotypes can be used to verify pedigree in some cases,

BUT

- It might create a puzzle (lots of manual work)
- Avoid an economic problem for a farmer if a calf suddenly has no dam (EU-support)

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Genotypes

Future

- **Also a lot of (all) females genotyped**
- **Possible to assign parents automatically instead of traditional manual parentage verification**
- **Get everything running more smoothly, as automatic as possible, avoid bottlenecks**

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Reference group in routine evaluation Jan 2014

	HOL	RDC	JER
Bulls	25600	7800	1240+(1150 US)
Origin of ref animals	NLD, FRA, DEU, ESP	NOR	USA+CDN

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Future reference group including cows?

	HOL	RDC	JER
Bulls	25600	7800	1240+(1150 US)
Cows jan 2014 LD	0	3050	2300
Cows jan 2014 not LD project	5100	2350	760
Females total	11412	11938	5712

During 2014 amount of potential ref cows will increase significantly

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Imputation

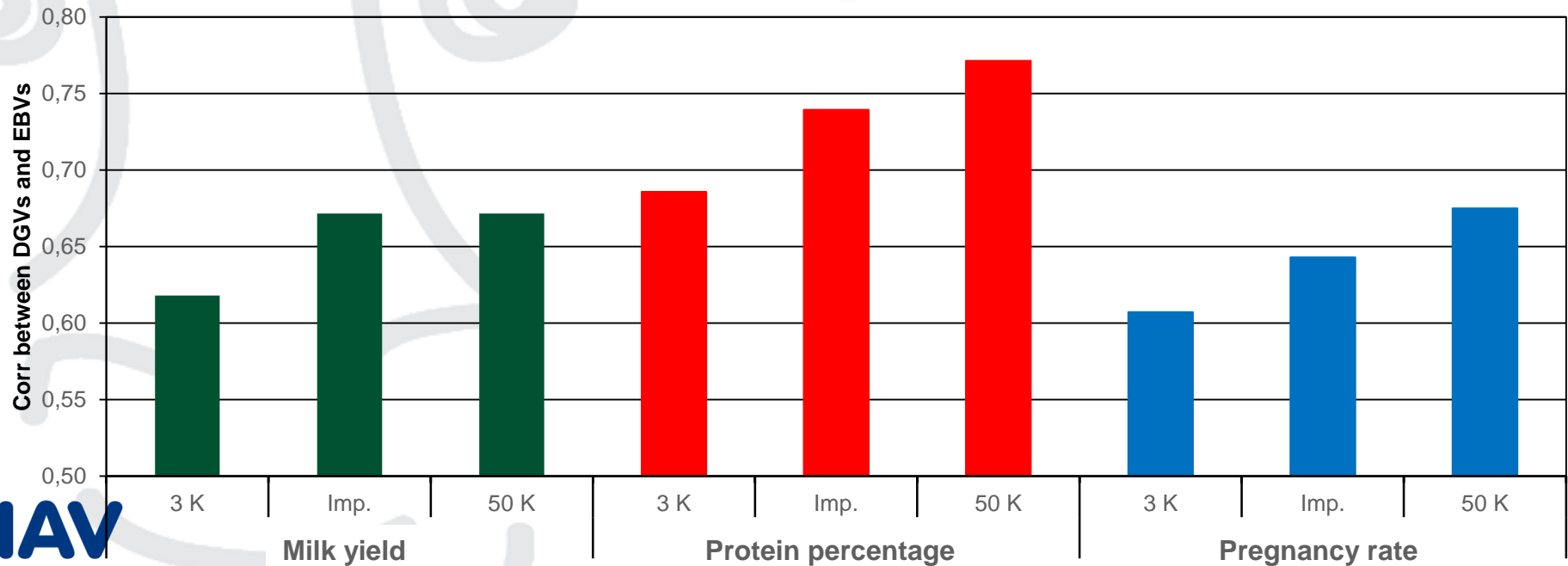
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Why do we impute?

- Accuracy of GEBV
 - 54K > imputed LD > LD



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American Jersey; modified after Weigel et al., 2010

Why do we impute?

- Cows (in referencegroup - RDC and Jersey) and heifers
 - **Low density chip**
- Illumina Bovine 54K chip
 - Version 1 and 2
- Eurogenomics (Holstein) og GENO (RDC)
 - NLD (HOL) and Geno (RDC) has previously used another chip

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Imputation

- When pedigree, sex, and ID is verified the genotype can be imputed
- HOL - **FImpute**
 - **Quick & accurate in homogeneous populations**
- RDC & JER - **Beagle**
 - **Slow** but **accurate and robust**

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How accurate can we impute Genotype error rates

Animals genotyped in 2013

	00	01	10	11
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)
RDC* Beagle LD Male/No Geno	3.0 (9)	3.7 (3)**	1.4 (1147)	1.1 (234)**
JER FImp LD	3.0 (5)	2.0 (3)	1.5 (110)	0.5 (75)
Jer Beagle LD	Not investigated, but we expect Beagle will perform better than Fimpute			

00 = No parents genotyped/parents unknown in pedigree

01 = Only dam genotyped

10 = Only sire genotyped

11 = Sire and dam genotyped

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Imputation future

- **Impute all SNPs**
 - **Today 6K SNPs from LD is imputed to 54 K**
 - **4K from LD chip not available at 54K is not used**

Additional gain limited

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Deregressed proofs

Used for Estimating direct genomic breeding values and Blending

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Routine DRP

Sire MGS pedigree used

For reference animals

- DRP for DFS bulls (NAV EBVs) and foreign ref bulls (Interbull EBVs)
- DRP for genotyped bulls having official EBVs based on a progeny test

For blending:

- All reference animals plus genotyped cows

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DRP - future reference

- **Single cows are only informative if EBV's are calculated by an Animal model, not a Sire model (Today SM for other disease, Calving traits and fertility)**
- **Apply AM pedigree instead of Sire-MGS pedigree in deregression**
- **Include all animals in degression**

DGV prediction

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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**

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DGV prediction

Observed:

- Underprediction of genetic trend for candidates of Jersey and RDC – research focus

Near future:

- Get rid of underprediction
- Polygenetic effect might be considered again (but research have shown minimal effect) and substitute current scaling

Future:

- One step – all information simultaneously, selection (but today still bias problems)

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Preliminary results of inclusion of females in reference group

	RDC	JER
Production	X	XXX
Udder health	XX(X)	XXX
Body	XX	XXX
Feet and legs	-	X
Mammary	XXX	XXX
Milking speed	XXX	XXX
Temperament	-	-

XXX ≈ 5 pct. units

Note validation include daughters of proven sires only

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Blending

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Blending – routine (GEBV) (Mantysaari, 2010)

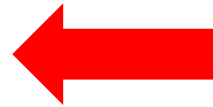
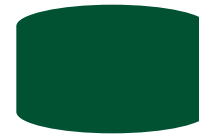
Inputs:
DRPs genotyped
animals

Phenotypic
information



Inputs:
Scaled DGV +
DGV reliabilities

Genomic
information



Observation: Challenge to avoid double
counting of information

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Blending – future (GEBV)? (Taskinen & Mantysaari 2013)

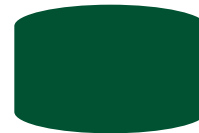
Inputs:
DRPs genotyped
animals

Inputs:
Scaled DGV +
DGV reliabilities

Phenotypic
information



Genomic
information



Can we better avoid double counting of
information?

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One step (research focus)

Phenotypic
information

Genomic
information

But test runs
so far still
show
inflations in
candidates
GEBV

All information utilised in the same step:

- No risk of double counting
- Optimal use of information
- Handling selection

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Frequency and publication

Prediction

- 4 times a year based on "new" phenotypic data and "new" genotypes
- 8 times a year "old" phenotypes and "new" genotypes

Publication

- Monthly – females
- 4 times a year bull > 17 month (10 month in 2014?)

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Summary

1. Collection of DNA Tissue (**ear tagging**)
2. Parentage verification (**assigning of parents**)
3. Exchange of genotypes (**US jersey, candidates**)
4. Imputation (**limit gain in near future**)
5. DRP (**AM-pedigree in DRP step, all traditional models AM**)
6. Genomic prediction (**solve JER, RDC problem, polygenetic effect?, onestep solve bias**)
7. Blending (**new method?**)
8. Publication (**lower publication age bulls**)

Summary

1. Collection of DNA Tissue (**ear tagging**)
 2. Parentage verification (**assigning of parents**)
 3. Exchange of genotypes (**US jersey, candidates**)
 4. Imputation (**limit gain in near future**)
 5. DRP
 6. Genomic prediction
 7. Blending
 8. Publication (**lower publication age bulls**)
- One step

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Outline

Interbull

1. GMACE
2. International reliabilities

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Work flow MACE

National
EBVs

DRP

MACE

Interbull
EBV

National EBVs are subtracted the pedigree information and degressed – national reliabilities/EDCs used
Little variation in national EDCs

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Work flow GMACE

National
GEBVs

DRP

GMACE

Interbull
GEBV

National EBVs are subtracted the pedigree information and degressed – national reliabilities/EDCs used

National reliabilities have relatively large variation

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GMACE status and plans

- February 2013 test run
- August 2013 (Implementation run = countries allowed to but not forced to publish)
- September 2013 test run
- December 2013 Implementation run
- End December 2013 – two new pilot runs (January 2104 national inspections ongoing)
- End January and early February IB ITC and SC meetings (decisions about routine)

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GMACE status and plans

- **End January and early February IB ITC and SC meetings (decisions about routine)**
- **February 2014 Test run**
- **April 2014 Routine or implementation run**
- **August 2014 Routine or implementation run**

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Interbull ongoing activities

- **International working group formed in August 2013 has to come up with a standard for calculating reliabilities before May 2014 (Martin Lidauer. MTT is in the group)**

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General picture from GMACE results from test and implementation runs

- NAV finds unexpected high STD of IB GEBV on NAV scale for more traits
- The most extreme case is clinical mastitis
- NAV has communicated the findings to IB

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Simple statistics. Young bulls birth year 2010 or later. Udder health (CM)

	Number	CM DFS	SD CM	REL CM
CAN	3017	97.2	7.7	56.8
DEU	6547	98.6	7.9	55.8
DFS	1601	101.2	7.6	57.6
FRA	7541	97.5	7.1	53.0
GBR	1004	98.2	7.8	56.1
ITA	1456	98.0	7.8	58.0
NLD	5093	98.8	6.9	51.2
US	28408	101.9	7.7	54.9

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Very unexpected results in RED



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Ratio MACE or GMACE results

STD (G)EBV national/STD (G)EBV DFS scale

Country	MACE EBV birth year 2006	GMACE GEBV birth year 2010
CAN	0,45	0,51
DEU	0.55	0.56
DFS	1.00	1.00
FRA	0.54	0.53
ITA	0.51	0.60
NLD	0.57	0.58
USA	0.49	0.58

We hope the IB pilot runs have solved the problems

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Expected to be the same given progeny group size and reference group are about the same DFS versus foreign countries



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Interbull ongoing activities

- Investigate effect on national assumption about GEBV reliabilities on GMACE results
- International working group has to come up with a standard for calculating reliabilities before May 2014

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From country comparisons involving DFS, FRA, NLD, DEU

- Ranking of animals: NAV-DEU, NAV-NLD and DEU-NLD have same size of correlations
- NAV rank animals as efficient as other countries - IB validation reliabilities the same.

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GMACE

- **Hope Interbull are able to estimate routine international genomic breeding values during 2014**

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