Raised questions in relation to NTM and NAV update

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NAV Dairy cattle webinar 19 January 2022

NTM - Genetic response check

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Background for decision 2018

- Expected response 2018 based on bulls born in 2015 and 2016 (GEBVs from NOV 2017)

Situation today

- Expected response 2022 based on bulls born in 2020 and 2021 (GEBVs from JAN 2022)

Note

- *Saved feed has been introduced in NTM in 2020*

Batch of bull calves

	Genotyped bull calves born
2022	2020-2021
2020	2017-2018
2018	2015-2016

Changes in genetic evaluation

2018 Females included in reference population for calving, birth, fertility, claw health, general health, and longevity and the standardization was updated – largest impact for fertility HOL

2019 General health

2020 Mastitis and Saved feed

2021 Fertility, and Metabolic efficiency

Genetic response check

What can we expect:

- Changes in NTM – Saved feed (some effect)
- Differences caused by changes in genetic evaluation e.g. females included in reference population for more traits, update general health (some effect)
- Another batch of bull calves (minor effect)

Expected response

Jersey genotyped DFS bull calves

Minor effect of bull batch

	2022	2020	2018
Yield	0.64	0.65	0.63
Growth	0.01	0.14	0.02
Fertility	0.12	0.06	0.31
Birth	-0.02	0.05	0.09
Calving	0.17	0.14	0.16
Udder health	0.41	0.42	0.57
General health	0.30	0.24	0.33
Frame	0.00	0.01	0.11
Feet & legs	0.23	0.17	0.20
Udder	0.22	0.16	0.30
Milkability	0.20	0.15	0.08
Temperament	0.05	0.05	-0.01
Longevity	0.47	0.39	0.52
Claw health	0.07	0.02	(0.16)
Young stock surv.	-	-	-
Saved Feed	0.06	0.06	-

Expected response

RDC genotyped DFS bull calves

Effect of bull batch limited

	2022	2020	2018
Yield	0.69	0.70	0.69
Growth	-0.05	-0.05	0.02
Fertility	0.21	0.20	0.25
Birth	0.21	0.26	0.16
Calving	0.19	0.18	0.18
Udder health	0.28	0.30	0.29
General health	0.24	0.21	0.19
Frame	-0.13	-0.13	0.04
Feet & legs	0.27	0.27	0.23
Udder	0.21	0.18	0.27
Milkability	0.15	0.12	0.20
Temperament	0.04	0.07	0.07
Longevity	0.43	0.47	0.45
Claw health	0.22	0.23	0.15
Young stock surv.	0.28	0.28	0.28
Saved Feed	0.14	0.17	-

Expected response

Holstein genotyped DFS bull calves

Effect of bull batch limited

	2022	2020
Yield	0.72	0.69
Growth	0.08	0.07
Fertility	0.30	0.24
Birth	0.21	0.18
Calving	0.21	0.20
Udder health	0.26	0.30
General health	0.29	0.26
Frame	-0.08	0.02
Feet & legs	0.14	0.20
Udder	0.17	0.19
Milkability	0.07	0.05
Temperament	0.14	0.08
Longevity	0.40	0.37
Claw health	0.26	0.16
Young stock surv.	0.19	0.20
Saved Feed	0.06	-0.01

Expected response

Holstein genotyped DFS bull calves

Effect of changes in evaluation

	2022	2020	2018
Yield	0.72	0.69	0.58
Growth	0.08	0.07	0.08
Fertility	0.30	0.24	0.45
Birth	0.21	0.18	0.25
Calving	0.21	0.20	0.33
Udder health	0.26	0.30	0.39
General health	0.29	0.26	0.35
Frame	-0.08	0.02	0.02
Feet & legs	0.14	0.20	0.19
Udder	0.17	0.19	0.28
Milkability	0.07	0.05	0.08
Temperament	0.14	0.08	0.09
Longevity	0.40	0.37	0.52
Claw health	0.26	0.16	0.24
Young stock surv.	0.19	0.20	0.23
Saved Feed	0.06	-0.01	-

Summary – genetic response

- Bull batch has limited effect on expected response, same response expected in 2022 and 2020
- Changes in methods in 2018 had a significant effect on expectations for Holstein (yield versus fertility/health), hardly any effect for RDC and Jersey

Temperament

Temperament

- Conclusions NAV webinar 14.10.2021
- Status – January 2022

Conclusions from webinar 14.10.2021:

Short term – current definition of the temperament trait is used

- NAV harmonization group will within each country investigate possibilities to get more temperament registration than today
- Jakob Lykke Voergaard, VG will take action to get Danish RDC breeders to register temperament for a larger proportion of the classified cows than today to remedy country differences

Status 19.1.2022

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Conclusions from webinar 14.10.2021:

Long term – possibilities for alternative/improved definition of temperament

- NAV harmonization group will investigate possibilities to get data relevant for developing future improved definition of cow temperament on the national data bases eg splitting in milking and handling temperament.
  - All data with relevance for temperament, which is available at farm level from milk equipment from all brands including AMS data but not only AMS data eg interrupted milkings
  - Data potential available from Tru test meters about interrupted milkings
  - Activity data e.g., Sensehub
  - Position data

Status 19.1.2022

Long term – possibilities for alternative/improved definition of temperament

- Delaval VMS data might be available in near future (S)
- SenseHUB data available in large scale in future (S)

Research

- A Swedish project had got funding looking at cow behavior based on automatically registered data as well as interview of farmers about desired temperament

Persistency

NAV-persistency definition

Breeding values are calculated as:

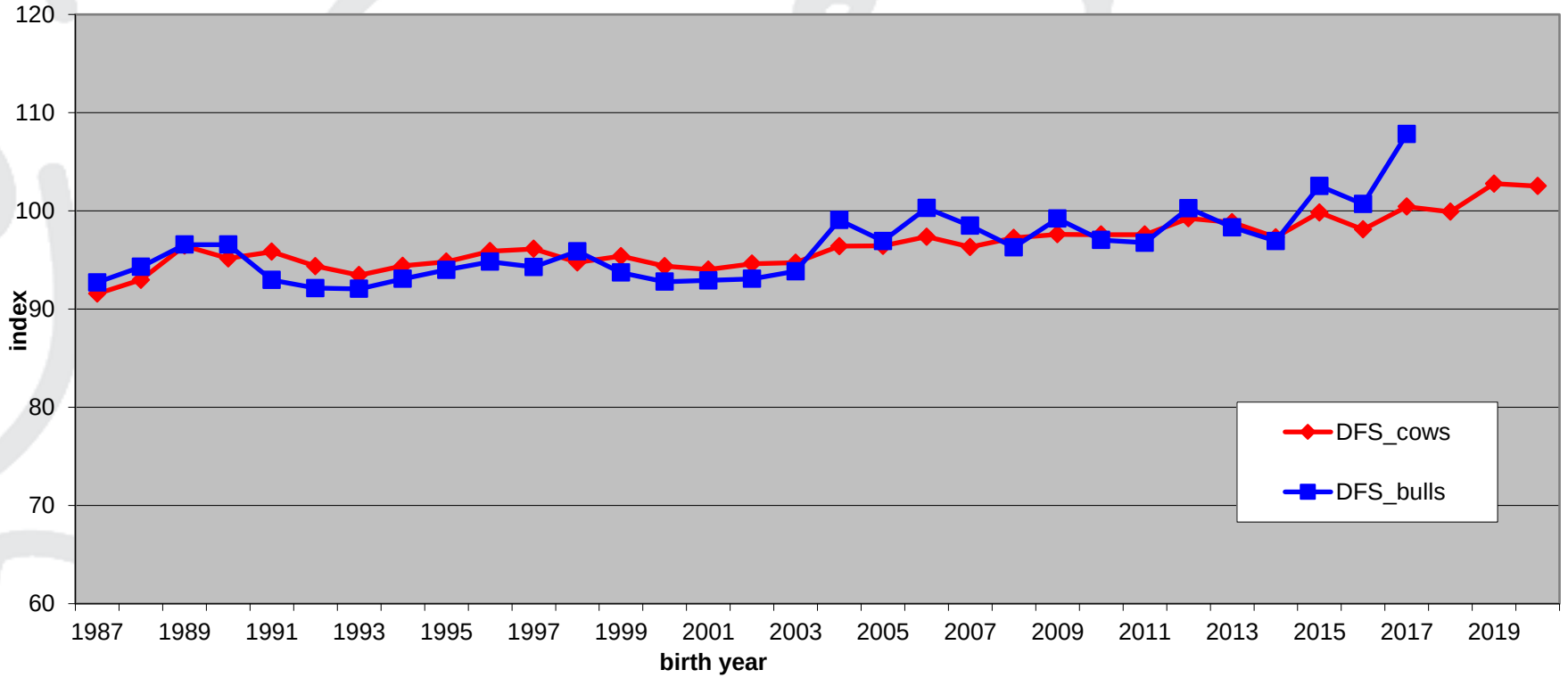
$$EBVpersistency = EBVday101 \times 200 - EBVd101\text{-}d300$$

where

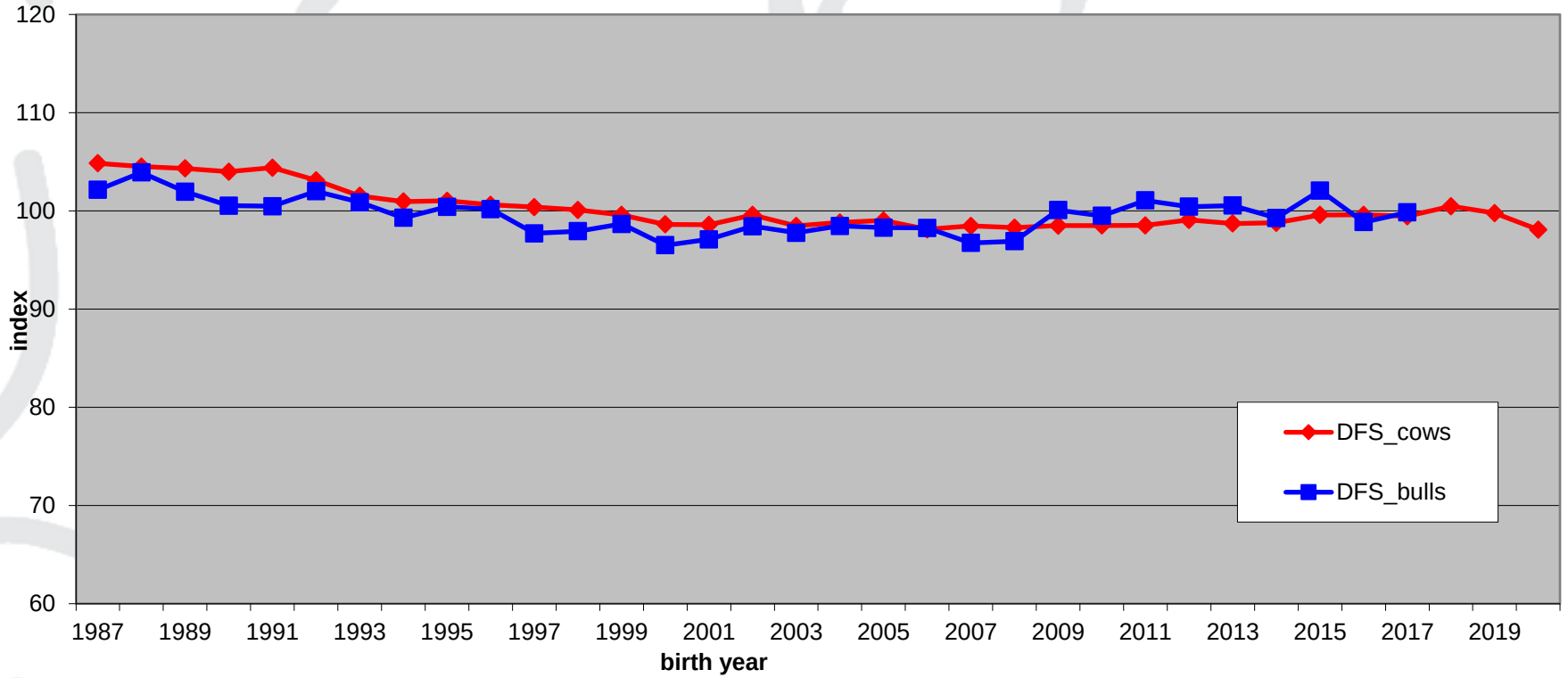
- EBVday101 is the breeding value for milk on day 101
- EBVd101-d300 is the sum of breeding values for milk in the period 101 - 300 days

A high EBV indicates a more flat lactation curve

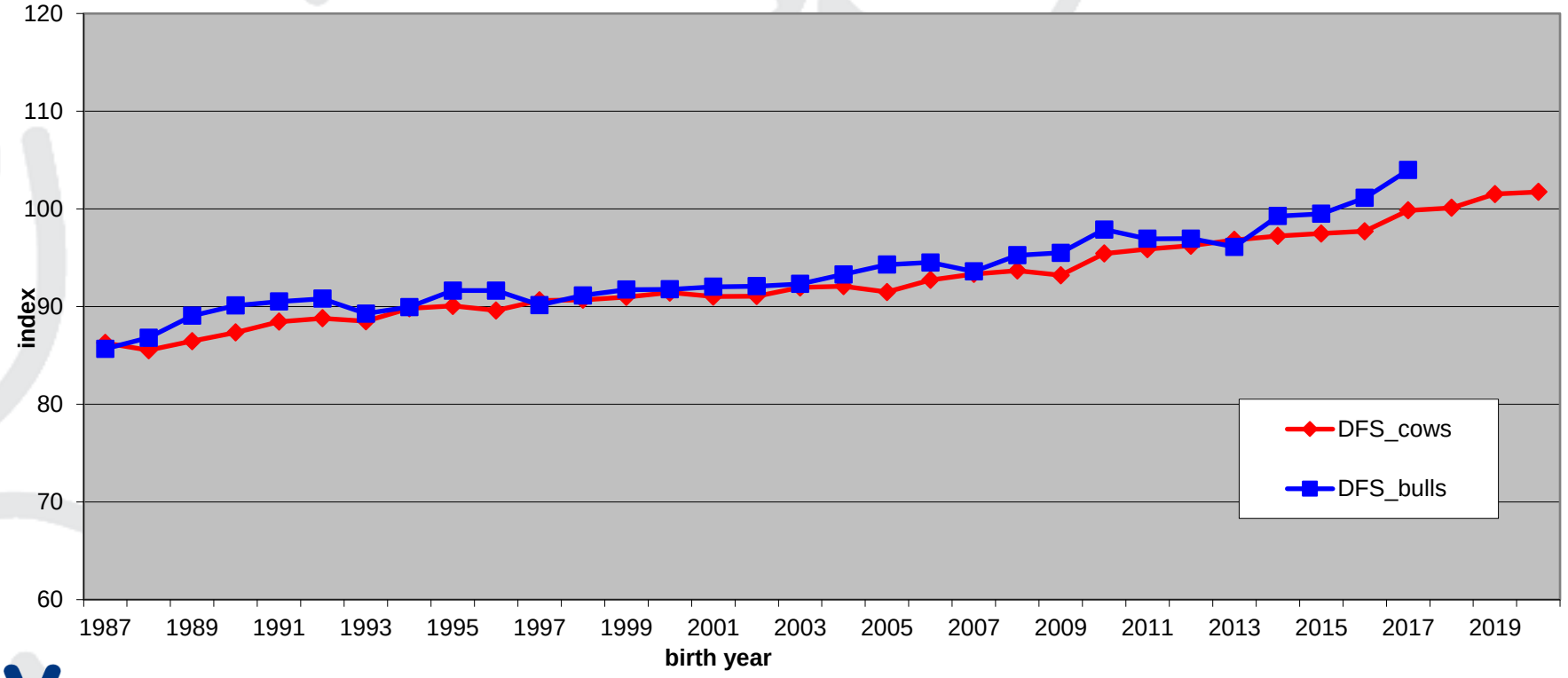
Genetic trend: persistency index of DFS JER bulls and cows



Genetic trend: persistency index of DFS RDC bulls and cows



Genetic trend: persistency index of DFS HOL bulls and cows



How to deal with persistency in the breeding goal/NTM?

RDC question

Why interest in persistency?

- Correlated to other important traits:
  - Yield
  - Fertility
  - Diseases
  - Longevity
- Indirect economic importance
  "Less expensive feed needed with flat lactation curve"

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  - Longevity
- Indirect economic importance
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Economic value in direct traits

Limited economic value

Correlations GEBV Persistency and NTM traits

	Holstein	RDC	Jersey
NTM	0.08	0.17	0.25
Yield	0.08	0.12	0.07
Fertility	-0.04	0.00	0.08
Mastitis	0.08	0.16	0.19
General health	-0.05	0.05	0.09
Longevity	0.18	0.11	0.25

Genotyped bull calves born 2020 and 2021: Holstein 5694; RDC 5005; Jersey 848

All correlations are low to moderate!

Effect weighting persistency in NTM

- Persistency has an (limited) economic value assuming if less expensive feed is needed with flat lactation curve – how much cheaper is the feed in practice?
- Weighting persistency in NTM
  - Based on economics the weight should be low

  and
  - Only minor effect on genetic trend in persistency compared to current NTM

Monogenetic traits

Monogenetic traits in NTM?

- Lethal:
  - The unfavorable allele is recessive e.g., CVM
- Polled:
  - The allele for polled is dominant

Economic value of monogenetic traits

- The economic value is nonlinear
- The value of traits measured in an offspring depends on the status of the mate (which often is unknown)

Lethals

- Studies show that a lethal can efficiently be managed by mating plans without losses in NTM

  (Bengtsson et al)
- Do not consider to include them in NTM

Example the phenotype of offspring with different genotype of dam and sire

	Genotype of the dam		
Genotype of the sire	**Homozygotic Horned**	**Heterozygotic Polled**	**Homozygotic Polled**
Homozygotic Polled	100% Polled	100% Polled	100% Polled
Heterozygotic Polled	50% Polled 50% Horned	75% Polled 25% Horned	100% Polled
Homozygotic Horned	100% Horned	50% Polled 50% Horned	100% Polled

Examples assuming the economic value of an animal being polled is 10 euro more than a horned animal

	Genotype of the dam		
Genotype of the sire	**Homozygotic horned**	**Heterozygotic polled**	**Homozygotic polled**
Homozygotic polled	10 euro	10 euro	10 euro
Heterozygotic polled	5 euro	7.5 euro (on average)	10 euro
Homozygotic horned	0 euro	5 euro (on average)	10 euro

The value of a bull's genetic status for polled depends on the dam's genetic status.

% polled genotyped calves in DFS

Birth year	RDC	HOL	Jersey
2019	5.5	4.3	0.8
2020	6.7	6.2	1.5
2021	8.1	10.3	2.1

% polled increases for all breeds

The NAV technical group views:

Lethals can be handled most efficient in mating plans

The NAV technical group views:

Polled has an economic value, but nonlinear

Inclusion in NTM:

- Economic value is approximative and need to be updated regularly when population frequency changes
- Probability of Polled need to be considered for all animals not only for bulls and females having a known status
- Normal rules for e.g., parentage average of NTM will not hold anymore

Genomic prediction of dairyxdairy crosses

Genomic prediction of dairyxdairy crosses implemented DEC21

Requirement for crosses to be included:

- The sire of the crossbred animals must be HOL, JER or RDC
- The maternal grandsire of the crossbred animals must be HOL, JER or RDC.

GEBV dairy*dairy (JER,HOL,RDC) DEC 2021

- Principles
  - For each genotype detect which SNPs originate from which breed
  - SNP solutions from pure breeds used to predict GEBVs for crossbreeds
  - Breed means considered
  - All traits considered in NTM, but with approximation since breed means can not be directly estimated for combined traits e.g., fertility based on IFL

GEBV dairy*dairy (JER,HOL,RDC) DEC 2021

- Overall principle
  - GEBVs expressed on a crossbreed base – females 1-7 years old
  - Holstein STD factors and NTM weights applied
  - GEBV for crossbreeds can not be compared with any pure breeds!!

GEBV dairy*dairy (JER,HOL,RDC) DEC 2021

- Validation
  - Proved that GEBVs for cross breeds are more reliable than pedigree
  - No reliabilities are published

Next step

- To be able to include Montbeliarde(MON)
  - Genotypes needed on all used MON bulls or 500-1000 pure breed MON
  - Use traditional MON EBVs - no SNP solution available and not straight forward to use

NAV development projects in 2022 related to dairy cattle

Genetic evaluation of young genomic bulls and proven bulls

Genetic evaluation - what we aim for

- Highest possible reliability (precise ranking within birth year)
- No bias (= correct genetic trend – ranking across birth years)

Methods

Two step – current

I. Traditional genetic evaluation based on pedigree and phenotypes only

II. Genomic prediction using degressed EBV for combined indices from traditional evaluation and genotypes as input

One step – future (single step)

I. Simultaneous evaluation based on all phenotypes and genotypes

GEBV – challenges JAN 2022

Genomic prediction highest possible reliability (precise ranking within birth year)

- Works well for Holstein and Jersey
- Results seems to be less reliable than expected for RDC especially for production

No bias (= correct genetic trend – ranking across birth years)

- Current methods give too large level changes for bulls breeding values going from genomic information only to including daughter information

What can cause the observed weakness in NAV genetic evaluation?

- Weakness in current methods
  - Genomic prediction (input is combined traits across lact, 2 step, post processing etc)
  - Traditional models (preselection bias and/or not optimal models) (= we do not know if the traditional model is the “answer book”)
  - Transition from genomic only to GEBV based on daughter performance
  - Postprocessing needed to handle inflation (too large variation) of GEBVs – a well know phenomena in genomic prediction

What can single step handle?

- Genomic prediction (combined traits across lact, 2 step, post processing etc) YES
- Traditional models (preselection bias) YES
- Transition from genomic only to GEBV based on daughter performance YES

BUT

- In Single Step there might also be a need to do postprocessing of GEBVs to handle inflation of GEBVs
- The traditional model should be optimal

Please note that ranking among genomic bulls within same birth year will be nearly the same with SS as today

Focus - ongoing work

- Single step :
  - Conformation traits – looks very promising
  - Yield – Currently focus is on effect of discarding genotypes from the oldest animals. Results indicate that it:
    - Improves across year comparison
    - Might improve reliability for RDC
  - Discussion, knowledge exchange ongoing with other countries – they face similar problems
- Traditional model for yield
  - Inspect RDC TD model for potential weaknesses

NAV will inform asap new results occur

Eurogenomic harmonisation

Eurogenomic harmonisation

Harmonize to golden standards:

- Registration
- Data editing
- Trait definition
- Genetic model including genomic prediction

Goal:

- Higher correlation across countries and more benefit from exchange of Holstein reference bulls
- Make closer cooperation easier

Calving evaluation upgrade to EG golden standard

Things to be updated in NAV model:

- Heterogeneous variance adjustment - Snell score should be applied for binary traits: calving ease, stillbirth and calf size
- Variance component estimation
- Inbreeding

Status majority of work done in 2021 – finalise and implement in 2022

Mastitis evaluation upgrade to EG golden standard

Things to be updated in NAV model:

- Data editing from raw data to evaluation data
- Trait definitions – somewhat diiferent from current ones
- Heterogeneous variance adjustment
- Variance component estimation
- Inbreeding

Saved feed – model improvements

- Metabolic efficiency
  - Better correction for energy sinks (milk production and maintenance)
  - Estimate genetic parameters
  - Split in first and later lactations
- Maintenance efficiency
  - Include slaughter weight as indicator trait

Beef bulls used in dairy herds

2018 First release of breeding values

- Calving traits
- Carcass traits

2019 Nordic beef × dairy index (NBDI)

2022 Breeding values for Gestation length and Young stock survival (inclusion in NDBI)

NAV webinar and workshop 2022

NAV plans to have:

- A NAV workshop in Copenhagen 19 May 2022 including group work about the NTM check up
- Webinar(s) during the year based on actual topics

NAV

Nordisk Avlsværdi Vurdering • Nordic Cattle Genetic Evaluation

NAV strategy 2022-2024

- Approved by NAV board in November 2021
- Will be presented at webinar for NAV co-workers 20.1.2022

Strategy Map NAV – 2022-2024

Guiding Stars

Financial

Customers

Processes

Learning & growth

Future genetic evaluation of cattle?

- Increased international cooperation within cattle breeding has raised the question how future genetic evaluation should look like in Europe:
  - Discussion across Eurogenomic countries has started in 2021
  - A group established with two participants per organization that will further lead the investigation of and needs for a more efficient evaluation
  - Chairman and manager will represent NAV