






Future development in Nordic genetic evaluation for beef cattle, and state of art about genomic evaluation

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Implementation, and time schedule

- 2nd November 2021 (implementation)
 - NAV EBVs calculated for all single calving and carcass traits for HER, AAN, LIM, SIM and CHA
 - Combined traits calculated nationally based on single NAV traits
 - NAV EBVs are published on NAV search page for relevant animals
 - 4 NAV evaluation takes place per year (March, April, June and November)

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**Future plans sub-indices
Carcass traits and calving traits**



Outline for joint Nordic beef evaluation to benefit from cooperation:

- Joint single EBVs ✓
- Joint sub-indices – hopefully closer after today webinar ✓
- (Joint TMI – not a short-term goal)

Outcome: Animals rank the same in all three countries for all single EBVs and sub-indices




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Future plans – more breeds

- Establish NAV evaluation for calving and carcass traits for remaining beef breeds (e.g., BBL, BAQ, HLA) by using:
 - The developed NAV models
 - The estimated genetic parameters
 - The same definitions of genetic base, sd etc

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Future plans – more traits

Establish NAV evaluation for remaining trait groups:


- Fertility (calving interval)
- Young stock survival?

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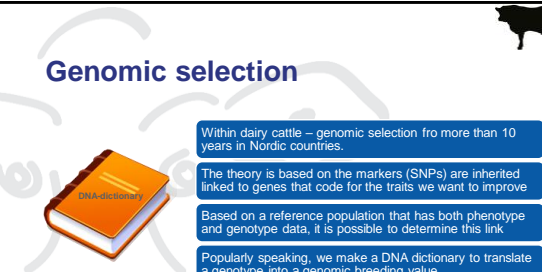
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State of art genomic prediction for beef cattle

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Genomic selection


Within dairy cattle – genomic selection for more than 10 years in Nordic countries.

The theory is based on the markers (SNPs) are inherited linked to genes that code for the traits we want to improve


Based on a reference population that has both phenotype and genotype data, it is possible to determine this link

Popularly speaking, we make a DNA dictionary to translate a genotype into a genomic breeding value

• The quality of the dictionary determines the quality of the estimated genomic breeding value


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Reference population


- Thousands of animals with phenotypes and genotypes required to be able to make reliable genomic predictions

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Challenges genomic selection in beef cattle


- Nordic populations are quite small
- Populations are only expected to give each other a limited "help"
- Genomic selection still require lots of valid phenotypes – room for improvement for Nordic beef cattle


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Beef cattle genomic prediction worldwide (might not be complete)

- Limousine – France
- Charolais – France
- Blonde AQ – France
- Simmental – Germany
- Blue Cattle – Belgium
- Angus/Hereford – USA/CAN/AUS
- Across beef breeds – Ireland



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Current Nordic project


Sweden – 2019-2021

- Charolais & Hereford
- Aim: about 2000 reference animals per breeds

Finland - BeefGeno 2019-2021

- Hereford, Charolais, Angus, Limousine and Simmental

Breed	N	Aim	% Aim	Expected until end of 2022
AAN	3236	2000	162	3556
CHA	2545	2000	127	2825
HER	3252	2000	163	3717
LIM	1677	2000	84	2276
SIM	1829	2000	91	2361
Total	12589	10000	125	14735


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Current Nordic project

Denmark – 2019-2023

- Charolais, Angus and Belgian Blue
- 12.000 reference calves with Holstein dams
- Registration of Feed intake and methane emission
- Registration of eating quality (image technology)

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The genomic prediction "pot"

- Interbeef
incl FRA,
IRL, DFS
- DFS all
breeds
- DFS
single
breeds
- D/F/S
single
breeds

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Future plans – genomic prediction and Interbeef

Nordic countries should aim for:

- Make use of joint Nordic phenotypes, traits definitions and model from the joint Nordic beef cattle genetic evaluation and combine with as many beef cattle genotypes as possible - the biggest genomic "pot"
- Active search for possibilities via Interbeef – discussion to be initiated
- Make best use of Nordic research activities
- Genomic prediction of Nordic beef cattle will be a possibility in the future ... but too early to say how and when

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Summary

- Joint Nordic genetic evaluation for beef cattle opens the door for:
 - Closer Nordic cooperation
 - Participation in international evaluation
 - Possibilities for taking part in genomic prediction
- Joint Nordic genetic evaluation for beef cattle requires joint decisions and compromises

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