



Plans for joint Nordic genomic prediction of beef cattle

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Today genetic gain is limited in the beef breeds

- **Beef breeds for B×B:**
 - Decentralized decisions
 - Less systematic collection of phenotypes and pedigree
 - Multiple breeding goals
- **Beef breeds for B×D:**
 - *Limited pure breeding of beef breeds for crossbred performance*

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Wishes for a breeding scheme for beef cattle



High genetic gain

- Reliable breeding values
- High selection intensity
- Short generation interval

Phenotypes are the  to achieve reliable GEBVs

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Genetic evaluation - methods



Current NAV evaluation – traditional model



- Pedigree
- Phenotypes

Official Nordic breeding values for beef cattle today

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Genetic evaluation - methods

Genomic evaluation – single step



- Pedigree
- Phenotypes
- Genotypes

Development projects for beef cattle in Sweden and Finland

Future Nordic breeding values for beef cattle

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Genetic evaluation - methods

Genomic evaluation – single step

- Pedigree
- Phenotypes
- Genotypes



Genotypes can improve the pedigree – verification!

Future Nordic breeding values for beef cattle

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Genetic evaluation - methods

Genomic evaluation – single step

- Pedigree
- Phenotypes
- Genotypes

Animals having both phenotypes and genotypes are called reference animals

Future Nordic breeding values for beef cattle

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Nordic Genetic evaluation

- **Current - EBVs**
 - Late in life
 - Low to moderate reliabilities except a few bulls having lots of many progeny
- **Future - GEBVs**
 - Early in life
 - Both sexes get information for all traits
 - Reliabilities of breeding values increase – depends on ref. population?

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Genomic prediction of beef cattle in general

- Largest value for traits expressed late in life
 - Dam traits
 - Traits measured at the slaughtered animal
- Smaller effect for traits measured early in life
 - Note a part of the effect by genomic prediction can also be achieved by improved phenotyping of the animals itself

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Genotypes Sept 2023

	Total	DK	FIN	SWE
Angus	8048	1446	4524	1927
Charolais	8800	167	3613	4698
Hereford	10531	1384	4504	4564
Limousine	5818	2228	1138	2295
Simmental	6030	702	2858	1785
Blond Aquitaine	694	293	165	171
High Land	437	350	10	52


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Genomic prediction of beef cattle based on purebred performance




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Growth, carcass conformation, birth and calving




NAV genomic prediction of purebred beef development is initiated – first results in 2024


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NAV official genetic evaluation for beef cattle 2024+

Breedwise genomic evaluation – single step

- Pedigree
- Phenotypes 
- Genotypes - also very important

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Finnish beefgeno-project

- Genotype testing subvented heavily by slaughter industry
 - Need for GEBVs for pure breed beef animals and BxB crosses
- Outcome of the project:
 - Finnish national single step genomic evaluation for beef cattle, started in May 2023
 - Only Finnish data, BxB crosses included
 - Trait definitions based on old Finnish national evaluation -> not 100% harmonised with NAV traits
 - National genomic evaluation will be replaced by NAV genomic evaluation for pure breed animals
 - For BxB crosses FIN will continue calculation of GEBVs nationally

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NAV genomic prediction Breed wise versus multibreed model

Pros breed wise

- Well documented – it works
- Easiest to implement in the Nordic model
- SNP markers not the same across breeds – other breeds will add "noise"

Pros multibreed

- Few results with limited data sets – validation?
- More data – larger reference
- GEBVs more reliable if same SNP markers have an effect in all breeds
- BxB crosses can be included

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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 improvements for Nordic beef cattle

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Take home messages



- Nordic genomic breeding values is coming
- Essential to phenotype and genotype thousands of beef animals to benefit from genomic evaluation

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