

Genomic selection in Finnish beef cattle

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Genomics and breeding, Production systems,
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Finnish Beefgeno project

MAKERA foundation (Finnish Ministry of Agriculture and Forestry) financing 2019- March 2022

Partners:
Luke, Faba, VG, NAV, Finnish Slaughter industry
(Atria, HK Scan, Snellman)



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Finnish Beefgeno project

- First development step towards large scale Nordic genomic evaluations for beef
- Aim: whole population is the breeding population
 - Recording and production herds, pure- and cross-breeds
 - F1-crosses will be included
 - 41% of slaughter trait evaluation data from production herds
- Breeds: Hereford, Charolais, Angus, Limousine, Simmental

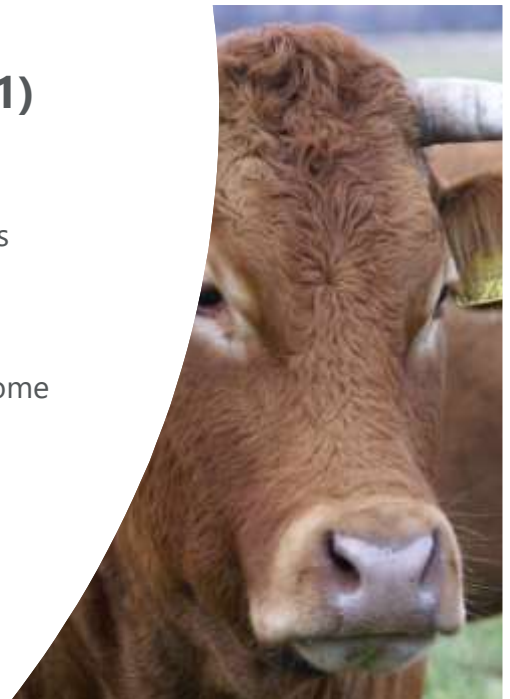


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Why is beef breeding needed? (1)

- Beef bulls used more and more to the dairy cows
 - FIN 25 %, SWE 11.5 %, DNK 21 % of all inseminations
- Beef bulls used for beef x dairy program must come from pure-bred beef breeding stock



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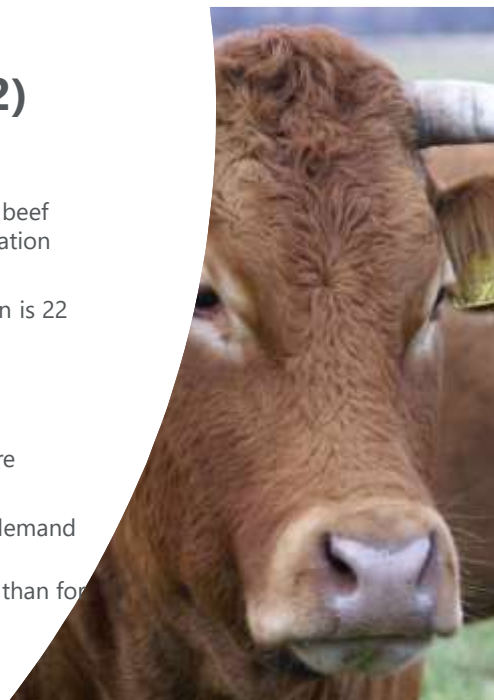
Why is beef breeding needed? (2)

- Country-specific needs in Finland:
 1. Annual domestic consumption of beef is higher than beef produced as a side-product from Finnish dairy population
 2. Dairy population size is still expected to decrease
 3. Current gap of consumption and domestic production is 22 %
- Global needs and responsibility:
 1. Shift of food production towards northern hemisphere
 2. Global demand of food increases
 3. Economic growth in developing countries increases demand for animal proteins
 4. Finnish fields more suitable for grassland production than for cultivation of cereals

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Genotypings by breed

Breed	Genotyped, n	Goal	% out of goal	Expected until end of 2021
AAN	2512	2000	126	2867
CHA	2099	2000	105	2394
HER	2487	2000	124	3256
LIM	1466	2000	73	2057
SIM	1595	2000	80	2061
TOTAL	10159	10000	102	12635

Updated:

30.4.2021

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Genotyped animals

- 72 % cows, 28 % bulls
- Genotypings mainly from animals born in 2000 or later
 - Some older AI bulls with many offspring, oldest born 1989
- Most commonly, cows have observations of their own + offspring
 - Oldest cows more than 10 offspring on average
 - Most have both birth, 200-d, and 365-d weights
- Cross-breeds 8.6 %
 - Main breed prop < 87.5 %
 - E.g. F1 that will be included in the new eval.

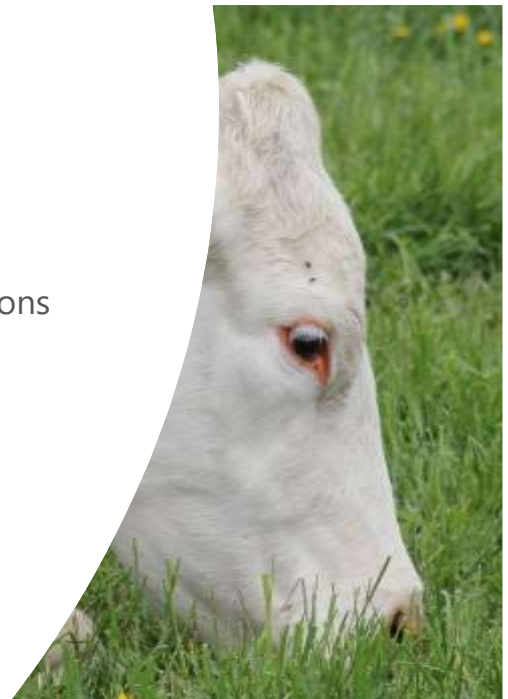


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Current evaluations

- Birth, weaning and yearling weights
- Carcass weight, EUROP and fat classifications
- Direct and indirect calving ease
- Maternal traits
- In 3 trait groups



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Towards genomic evaluations: changes in evaluation models

From single-breed pure-bred models into multi-breed

- Single-breed models: the same model effects but breed specific data, pedigree and variance components
- Multi-breed models:
 - Also F1 crosses included
 - Estimate breed proportions of main breeds for each animal
 - Variance components based on animal's breed proportions
 - Fixed effects that do not include breed means but model differences between bulls and cows
 - Heterosis and recombination effects



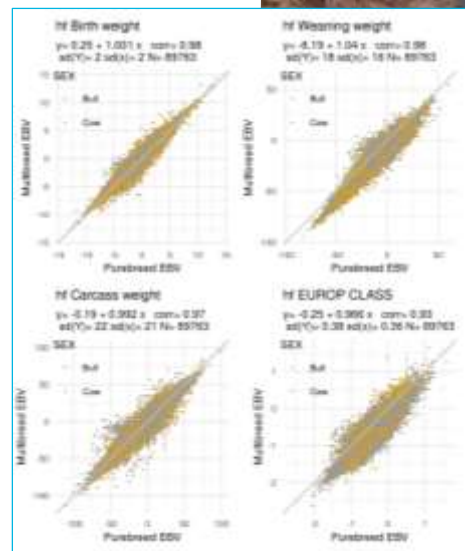
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Towards genomic evaluations: changes in evaluation models

Comparison of EBVs between pure- and multi-breed evaluations for purebred animals:

- Correlations high for bulls and cows in all weight traits, but little bit lower for classifications
- Genetic trends did not change
- Some of the changes due to more accurate breed definition, larger pedigree, increased information from other breeds

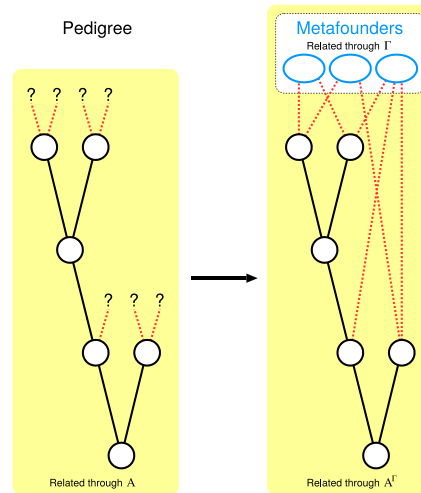


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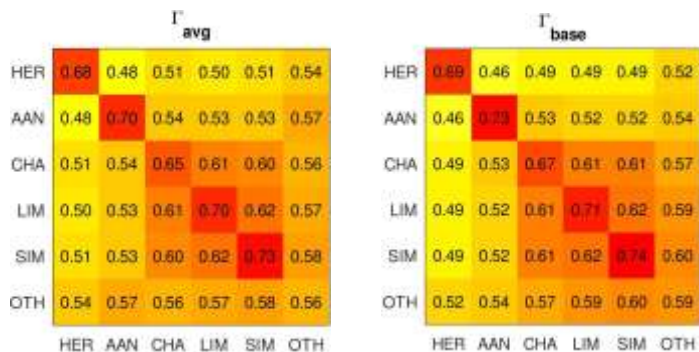
Metafounders: supplementing pedigree with unknown parent group relations Γ

- Unknown parents replaced with "metafounder" ancestor groups.
- Pedigree relationships in A^Γ will build up from the metafounder relations (Γ matrix).
- Tasks:
 - Choosing suitable grouping, e.g. breeds and/or year-groups.
 - Estimating Γ , e.g. from genomic data.



First estimates of metafounder groups

- 6 metafounder groups: 5 largest breeds + others.
- Estimating Γ matrix from genomic information using:
 - averages of genotyped pure-breeds: Γ_{avg}
 - group base population allele frequencies: Γ_{base}



Thank you!

