Genomic prediction of Finnish beef cattle breeds

Anna-Maria Leino, **Timo Pitkänen**, Matti Taskinen and Esa Mäntysaari
Genomics and breeding, Production systems,
Natural Resources Institute Finland

Maa- ja metsätalousministeriö
Jord- och skogsbruksministeriet
Ministry of Agriculture and Forestry

ATRIA TUOTTAJAT

HKSCAN

Snellman

NAV Nordic Cattle Genetic Evaluation

faba

VIKINGGENETICS
breeding for what truly matters

Luke
LUONNONVARAKESKUS

Finnish Beefgeno project

MAKERA foundation (Finnish Ministry of Agriculture and Forestry) financing 2019 - 2021

Extension year 2022

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

Finnish beef producers

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 comes from production herds

- Breeds: Hereford, Charolais, Angus, Limousine, Simmental

Building genomic evaluations

- What is needed (for Finland having small pure-breed populations):
  1. Multi-breed models
  2. Genomic information
  3. Well defined base for evaluation: metafounders

  → Single-step genomic evaluations → GEBV for all breeds

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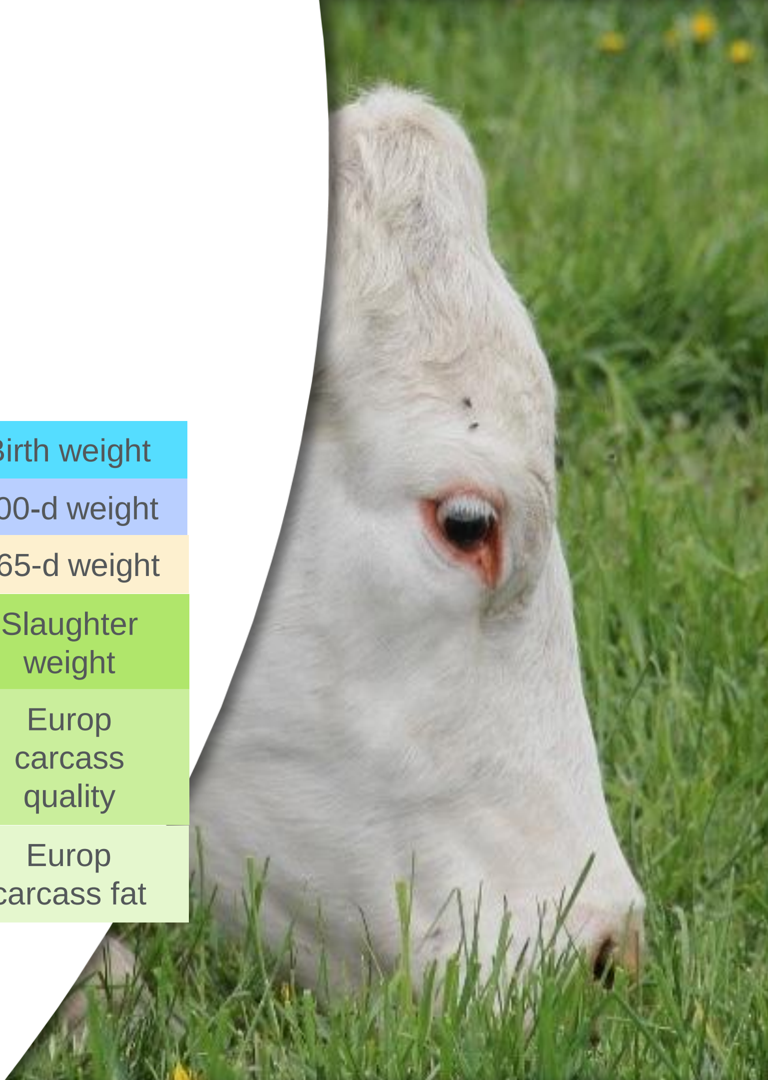
Current national evaluations

- Birth, weaning and yearling weights
- Carcass weight, EUROP quality and fat classifications
- Direct and indirect calving ease
- Maternal traits
- Each breed evaluated separately in 3 trait groups

		Birth weight
		200-d weight
		365-d weight
	Birth weight	Slaughter weight
	200-d weight	Europ carcass quality
Calving ease	365-d weight	Europ carcass fat
Birth weight	Slaughter weight	



Towards genomic evaluations: changes in evaluation models

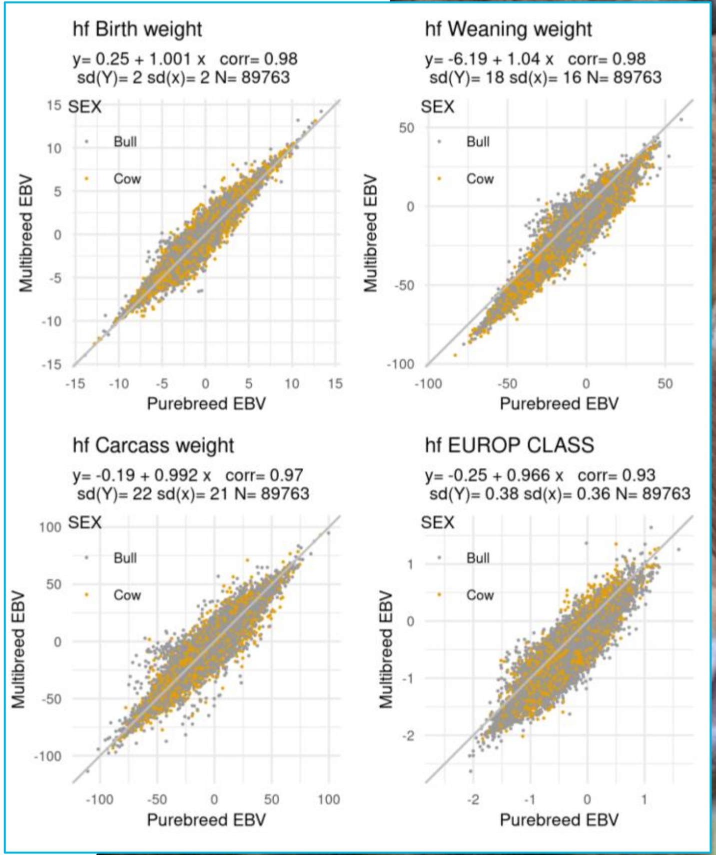
- From single-breed models into multi-breed

- Multi-breed models consider:
    - Breed-specific features such as:
        - Different effects for age and sex
        - Different heritabilities within breeds
    - F1 crossess included → **NEW: Breeding values for F1 animals**
        - Heterosis and recombination loss effects
    - Estimate breed proportions of main breeds for each animal
    - Variance components based on animal's breed proportions
    - Larger herd-year groups if more than one breed

Towards genomic evaluations: changes in evaluation models

Comparison of EBVs between single- 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 & breeds on correct level relative to each other
- Some of the changes due to improved modeling:
    - More accurate breed definition
    - Larger pedigree
    - Increased information from other breeds



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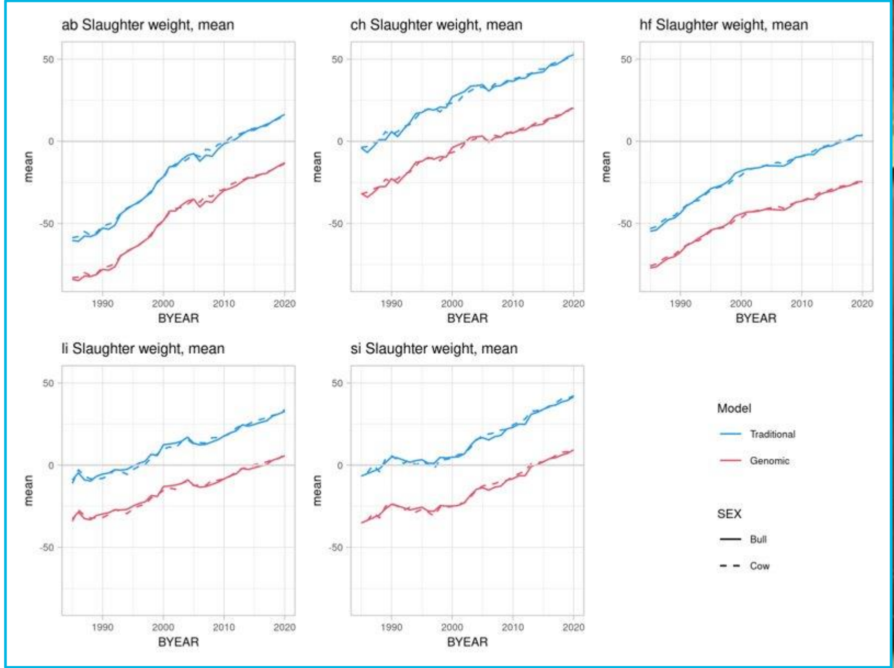

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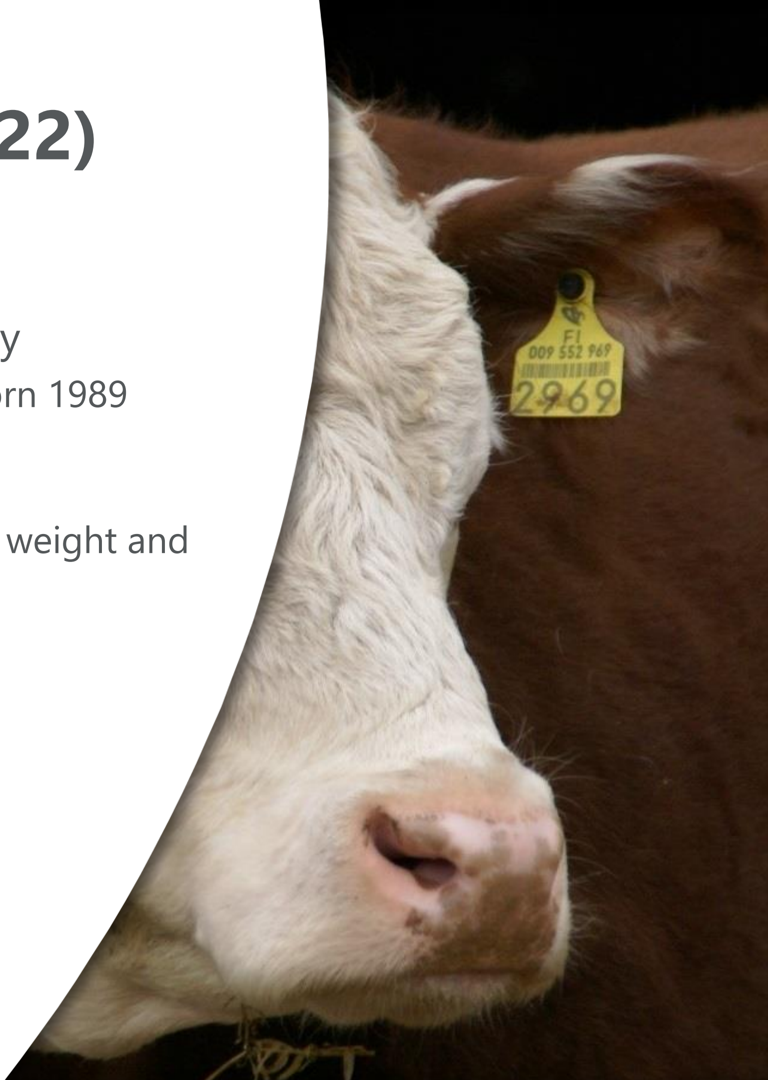
Current status of genotyping

Breed	Genotyped, n	Goal	% out of goal
AAN	4132	2000	207
CHA	3294	2000	165
HER	4086	2000	204
LIM	2112	2000	106
SIM	2478	2000	124
TOTAL	16102	10000	161

Updated: 6.9.2022

Genotyped animals (data Feb 2022)

- N=12 224, of which 71 % cows, 29 % bulls
- Genotypings mainly from animals born in 21st century
    - Some older AI bulls with many offspring, oldest born 1989
- The frequency of own observations:
    - 90 % birth weight, 83 % 200-d weight, 65 % 365-d weight and 14 % slaughter weight
    - 63 % with ≥ 3 observations
- The frequency of having offspring:
    - 70 % females: average 4.2 (min 1, max 17)
    - 20 % bulls: average 4.2 (min 1, max 1016)
- Around 6 % cross-breeds



Genotypings by birth year & breed

Syntvuosi	AAN	CHA	HER	LIM	SIM
1989	0	0	0	1	0
1990	0	1	0	0	1
1994	0	1	0	0	0
1997	0	1	0	0	0
1999	0	0	1	0	0
2000	0	4	3	1	1
2001	2	0	1	1	1
2002	1	0	0	2	1
2003	1	3	2	7	0
2004	1	4	2	4	1
2005	10	4	0	15	11
2006	30	7	14	22	18
2007	19	19	7	19	11
2008	24	18	21	28	14
2009	33	28	25	33	15
2010	48	42	35	50	21
2011	58	49	54	66	35
2012	72	82	100	103	36
2013	70	112	114	75	48
2014	113	114	164	92	62
2015	138	137	170	121	86
2016	158	225	224	145	93
2017	213	279	321	201	150
2018	376	294	459	234	222
2019	519	399	547	126	254
2020	582	424	529	165	365
2021	676	342	352	93	295
Yhteensä	3144	2589	3145	1604	1741

Building genomic evaluations

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Genomic model

- Both genotyped and non-genotyped animals are included in single-step genomic model
- Relationships are based in pedigree and genomic information coming from genotyped animals and their genotyped relatives
- Breed relations and unknown base population animals within breeds are built through metafounders
  - Parameters estimated from genomic data
- It was assumed that genomic information explains 70 % of genetic variation

Results from genomic evaluations

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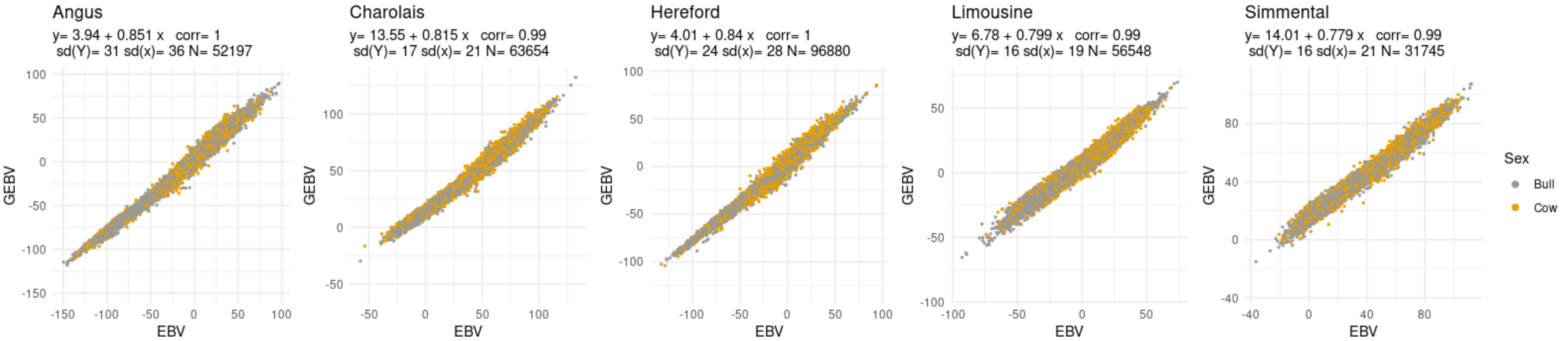
Multi-breed EBV vs. GEBV model

All animals



Angus
y= 3.94 + 0.851 x   corr= 1
sd(Y)= 31 sd(x)= 36 N= 52197

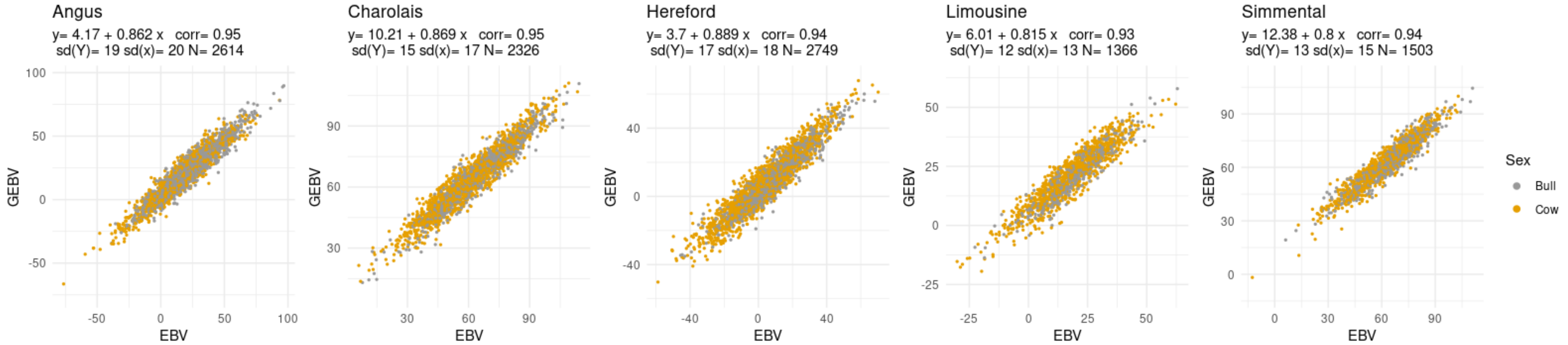
Charolais
y= 13.55 + 0.815 x   corr= 0.99
sd(Y)= 17 sd(x)= 21 N= 63654

Hereford
y= 4.01 + 0.84 x   corr= 1
sd(Y)= 24 sd(x)= 28 N= 96880

Limousine
y= 6.78 + 0.799 x   corr= 0.99
sd(Y)= 16 sd(x)= 19 N= 56548

Simmental
y= 14.01 + 0.779 x   corr= 0.99
sd(Y)= 16 sd(x)= 21 N= 31745

Genotyped animals



Angus
y= 4.17 + 0.862 x   corr= 0.95
sd(Y)= 19 sd(x)= 20 N= 2614

Charolais
y= 10.21 + 0.869 x   corr= 0.95
sd(Y)= 15 sd(x)= 17 N= 2326

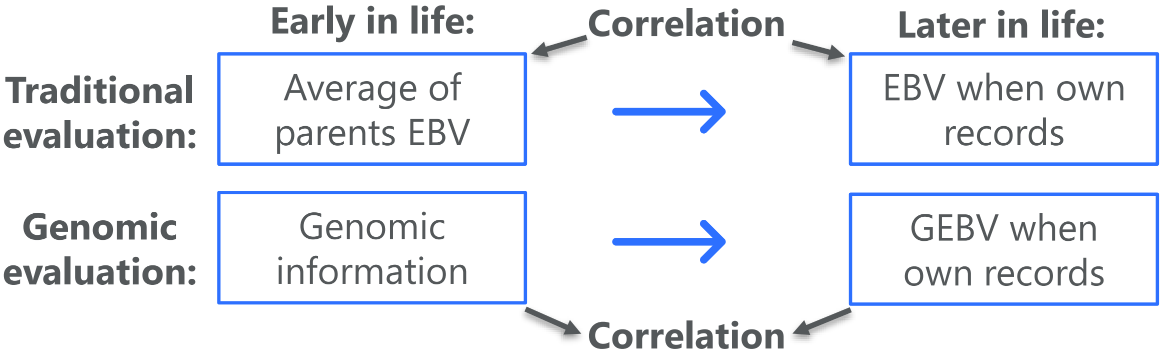
Hereford
y= 3.7 + 0.889 x   corr= 0.94
sd(Y)= 17 sd(x)= 18 N= 2749

Limousine
y= 6.01 + 0.815 x   corr= 0.93
sd(Y)= 12 sd(x)= 13 N= 1366

Simmental
y= 12.38 + 0.8 x   corr= 0.94
sd(Y)= 13 sd(x)= 15 N= 1503

Validation of models

- Aims to evaluate how well estimated breeding value (EBV) of young animal explains its future EBV when animal has more observations



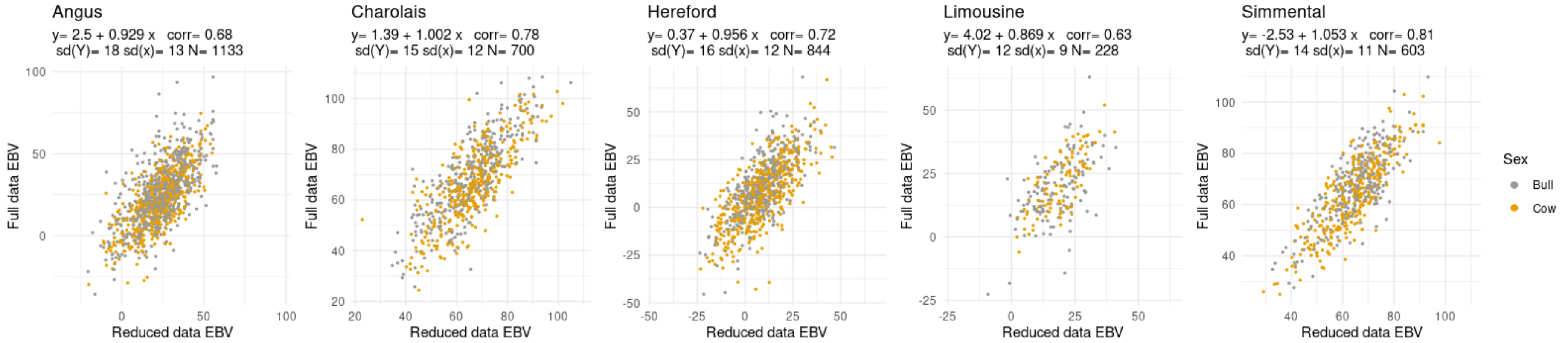
	Early in life:		Later in life:
Traditional evaluation:	Average of parents EBV	→	EBV when own records
Genomic evaluation:	Genomic information	→	GEBV when own records

Correlation (top: between Average of parents EBV and EBV when own records)

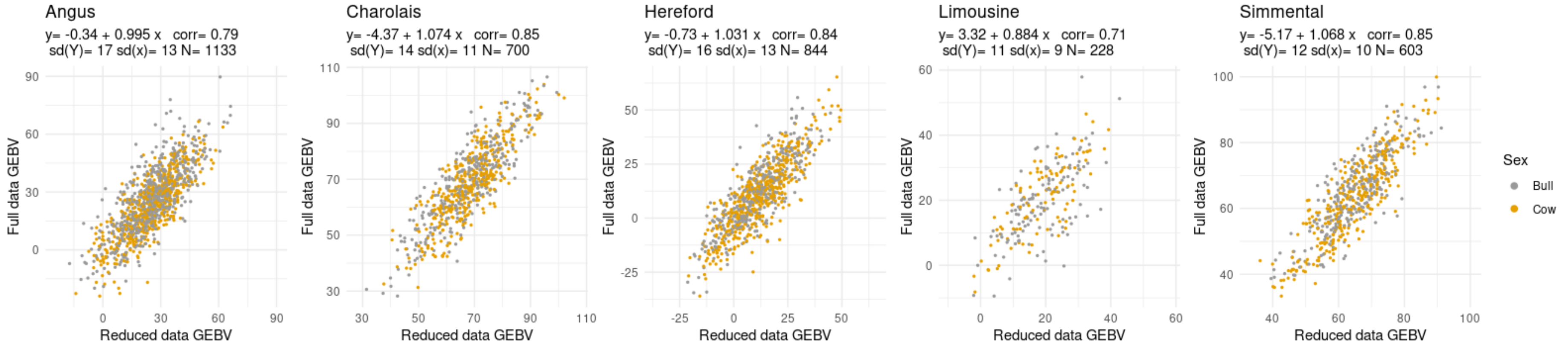
Correlation (bottom: between Genomic information and GEBV when own records)

Validating genomic models, example: 365-d weight

EBV



GEBV



Summary of model validations for weight & slaughter evaluations

- AAN, HER and CHA that have highest number of genotypings clearly benefit from genomic information
    - Based on correlations between full and reduced data EBV/GEBV, correlations between full data YD and reduced data EBV/GEBV, and Legarra-Reverter model validation accuracies

- Results for LIM and SIM are more difficult to validate since number of genotyped (validation) animals lower
    - In places, results controversary among traits, sexes, and validation data sets

→ Important to increase the reference groups for them too!

Next steps

- Finalizing validation of maternal & calving traits
- Changing current evaluations to genomic
    - Pre- and post-processing steps of the evaluations

Genomic testing benefits you through:

1. Parentage verifications → less errors in pedigree, more accurate breeding values
2. Genomic breeding values → more accurate breeding decisions earlier
3. Testing for genetic defects and diseases

How to benefit from for genomic era:

1. Take care your herd genetics is in the reference group: genotype breeding bulls and at least some dams (most influential in your herd)
2. Buy genotyped animals for breeding
3. Select best candidate heifers as usually (growth, conformation, temperament, pedigree & PA…), genotype candidates, select according to GEBV

Thank you!