Multibreed single-step genomic evaluation model for Finnish beef cattle

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Starting point of the project

- Existing **Single breed (SB)** evaluation models for
  Angus, Charolais, Hereford, Limousin, and **Simmental.**

- Separate evaluations for
  slaughter, growth, and calving -trait groups within breed.

- Same **model effects** in all **breeds.**

- **Breed specific variance components.**

- **No genomic information were used in the existing evaluation**

- **No observations from F1 crosses can be used**

- **Evaluation of breed crosses not optimal**

Traits and evaluations, three trait groups:

Breed specific heritabilities

Trait
Calving ease
Birth weight
Weaning weight (day 200)
Yearling weight
Slaughter weight
EUROP quality class
EUROP fat class

1) Calving ease evaluation

2) Growth evaluation

3) Slaughter evaluation

Source
Herd
Slaughter house

Multibreed Single-Step Model was built in two steps

Multibreed pedigree BLUP (PBLUP) evaluation model[1]

- Single breed models used as base.
- Unknown parent groups (**UPG**) in the pedigree.

Multibreed ssGBLUP Metafounder (MF) evaluation model

- Multibreed PBLUP model as base.
- Genomic relationships within and across breeds were included.
- UPG groups replaced by metafounders (Matti Taskinen's presentation)
- Residual polygenic proportion 30 %.

[1] Pitkänen T, et al. 2021. Towards genomics in Finnish beef cattle . Interbull Bulletin 56.

Development goals for MB evaluation model

- All animals included, also pedigree, genotypes, and observations of the F1 crosses.

- Logical differences between **breeds** in **breeding values**.

- **High correlation** within breed on EBVs between
Multi- and **Single Breed** evaluations for **purebred** animals.

- Breed proportions of **main breeds** estimated for each animal

- For each animal, specific variance components based on individual's **breed proportions** were applied .

Changes compared to SB model

- Observations from F1 animals were included.

- Model of heterosis effects.

- Full Finnish pedigree instead of limited "beef pedigree" from routine evaluation.
  - Breed proportions of 5 main breeds and "other breeds" estimated from pedigree and rounded to closest quarter (25%).
    - SB model used sire's breed as a breed of offspring.
  - More accurate inbreeding coefficients, UPG (and MF) definitions include breed.

- Breed interaction in fixed effects.

Heterosis and recombination in the models

Heterosis

- **Total heterosis** (of the 7 breeds in the evaluation) and **heterosis coefficients** for the most common 10 breed crosses included in the model, 11 parameters for each trait.

Recombination

- After examining different alternatives we decided to include only the **total recombination loss** in to the model, i.e., 1 effect for each trait.

For all three evaluations, heterosis and recombination is modelled in the same way.

Number of animals with observations and genotyped animals by breed

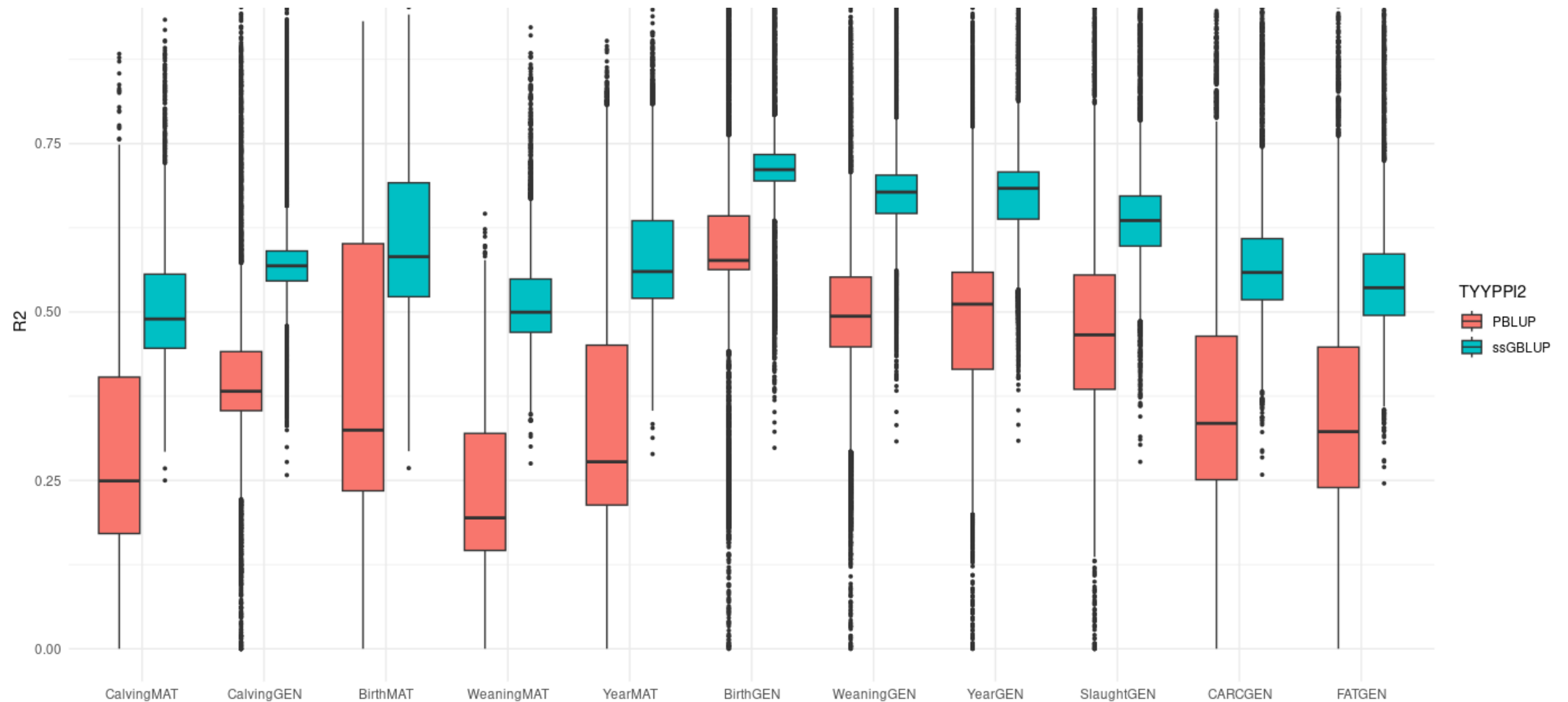| Breed	Animals with at least one observation	Genotyped, n
Aberdeen Angus	59 973	3 796
Charolais	70 601	3 212
Hereford	108 865	3 917
Limousin	63 876	2 061
Simmental	37 227	2 363
OTHER/CROSS	206 019	2 145
TOTAL	546 561	17 494

Results

- **GEBV**s and standardised **indices** compared between breeds.

- **Reliabilities** (R^2) of GEBVs[2] and EBVs compared between PBLUP and ssGBLUP for genotyped and non-genotyped animals

- Validation results of MB PBLUP model and MB ssGBLUP model

[2]Gao, Hongding,et al. 2023. A computationally efficient method for approximating reliabilities in large-scale single-step genomic prediction. Genetics Selection Evolution 55 1: 14 p.

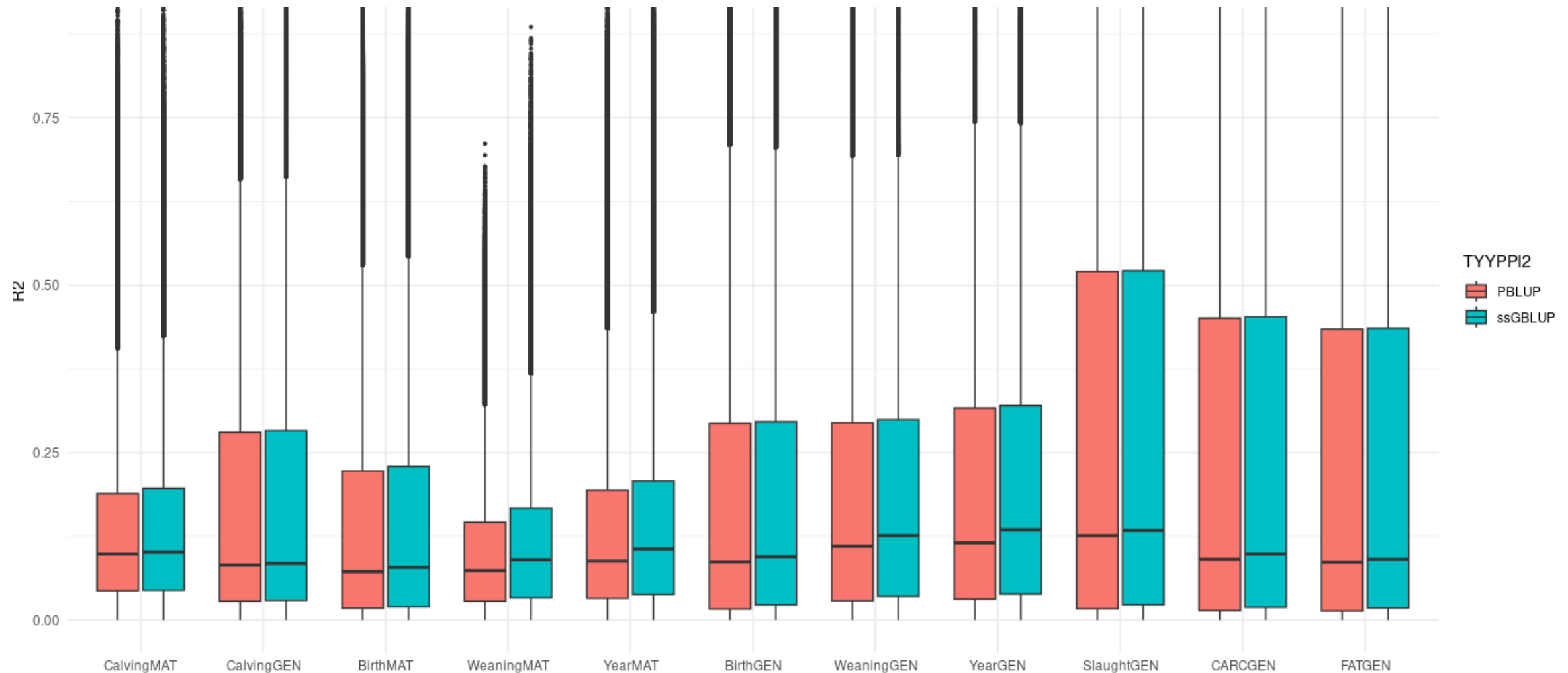# Trends of GEBVs and indices for weight traits
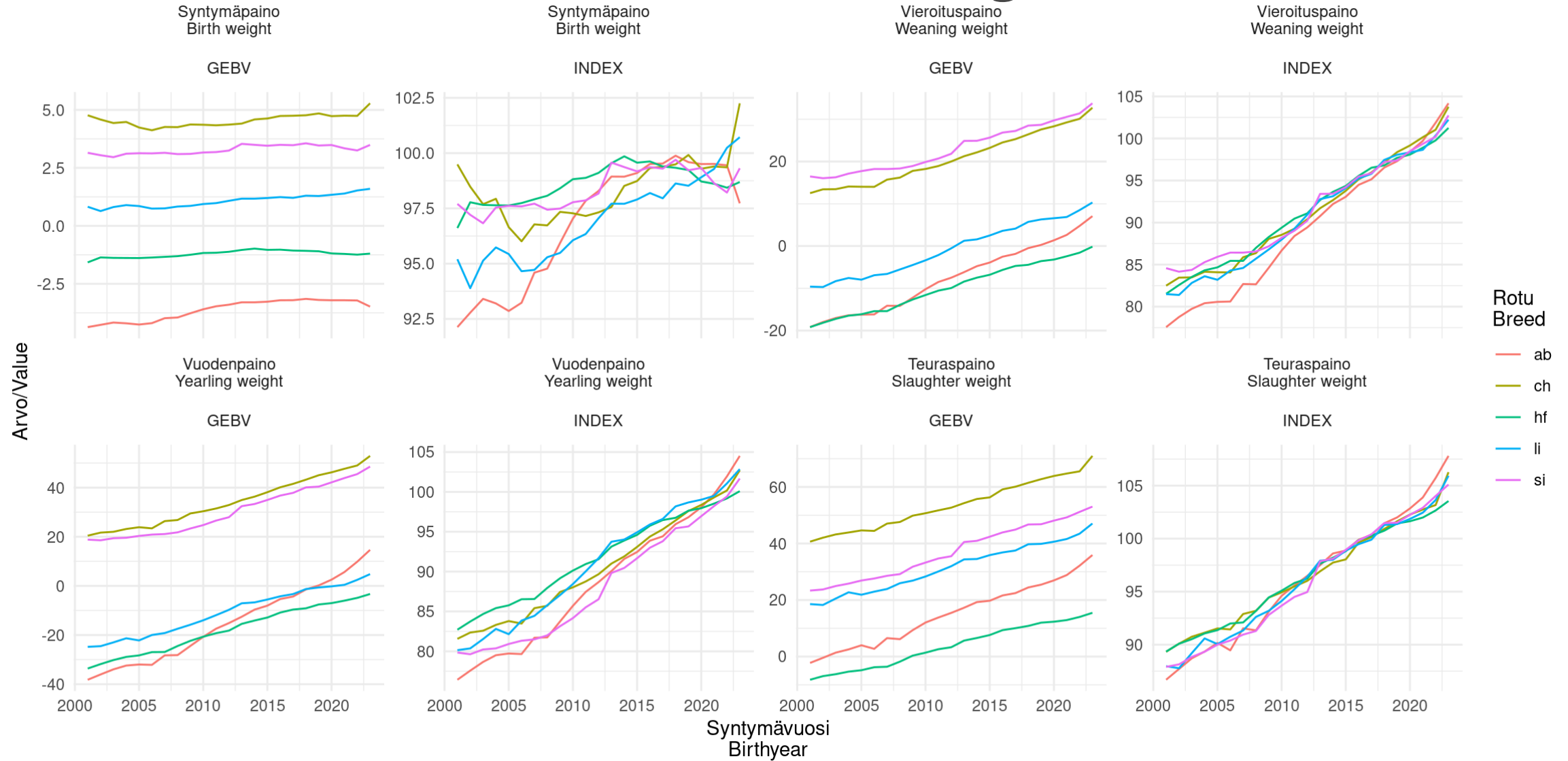
Model R² for genotyped animals in PBLUP and ssGBLUP

Model R² for NON -genotyped animals in PBLUP and ssGBLUP

Validation

- For the validation results for **1 year** data cut is presented.

- **All observations** of **a validation animal were removed** from the reduced data, if animal had at least one observation in data cut window.

  - I.e. if a slaughter weight was to be removed, also birth, weaning, and yearling weights were removed, even they were observed outside of the cut window.

  - => No own observations in reduced data.

- Validations separately for traditional EBV and single step models:

  - **Full (G)EBV** vs **reduced (G)EBV**, (Legarra-Reverter)

  - **Full data YD** vs **reduced data (G)EBV.** (cross validation)

- Results for **bulls and cows together**

Validations: correlations and accuracy, 1 year data cut, genotyped animals, PBLUP and ssGBLUP compared

Breed	Birth weight				200-d weight				365-d weight				Slaughter weight				Europ carcass quality			Europ carcass fat		

Legarra-Reverter correlation of BV between full and reduced data, 1-year cut

Breed	n	ebv	gebv	change, %	n	ebv	gebv	change, %	n	ebv	gebv	change, %	n	ebv	gebv	change, %	ebv	gebv	change, %	ebv	gebv	change, %
AAN	1103	0,70	0,82	**17**	1133	0,69	0,80	**16**	1133	0,74	0,83	**12**	1152	0,62	0,78	26	0,64	0,8	25	0,63	0,83	32
CHA	687	0,63	0,77	**22**	700	0,78	0,84	**8**	700	0,77	0,85	**10**	714	0,74	0,86	16	0,79	0,91	15	0,77	0,90	17
HER	937	0,74	0,88	**19**	844	0,66	0,83	**26**	844	0,68	0,84	**24**	865	0,62	0,81	31	0,70	0,87	24	0,71	0,89	25
LIM	297	0,70	0,80	**14**	297	0,54	0,65	**20**	297	0,59	0,70	**19**	306	0,42	0,65	55	0,63	0,85	35	0,68	0,84	24
SIM	647	0,83	0,89	**7**	647	0,78	0,83	**6**	647	0,83	0,87	**5**	692	0,71	0,84	18	0,76	0,89	17	0,69	0,83	20

Cross-validation correlation between full data YD and reduced data BV, 1-year cut

Breed	n	ebv	gebv	change, %	n	ebv	gebv	change, %	n	ebv	gebv	change, %	n	ebv	gebv	change, %	ebv	gebv	change, %	ebv	gebv	change, %
AAN	1103	0,35	0,39	**11**	633	0,38	0,43	**13**	1070	0,23	0,29	**26**	345	0,35	0,35	0	0,2	0,2	0	0,09	0,09	0
CHA	687	0,26	0,32	**23**	389	0,32	0,36	**13**	583	0,31	0,31	**0**	197	0,38	0,38	0	0,36	0,37	3	0,3	0,31	3
HER	937	0,39	0,51	**31**	646	0,27	0,35	**30**	919	0,2	0,26	**30**	209	0,48	0,48	0	0,15	0,16	7	0,32	0,33	3
LIM	292	0,28	0,33	**18**	142	0,1	0,12	**20**	271	0	0	**0**	73	0,16	0,16	0	0,36	0,37	3	0,62	0,62	0
SIM	643	0,47	0,49	**4**	304	0,35	0,37	**6**	595	0,31	0,31	**0**	193	0,22	0,22	0	0,13	0,13	0	0,19	0,20	5

Conclusions and implementation

Reliabilities for genotyped animals clearly **higher** compared to non-genotyped.

- ssGBLUP model **gave mainly the same or better validation** results than PBLUP model.

- Also **MF ssGBLUP** slightly **better** than **UPG ssGBLUP** .

First official multi-breed ssGBLUP evaluations were published March 2023

- Published indices were standardized **within breed.**

References

1. Pitkänen T, et al. 2021. Towards genomics in Finnish beef cattle . Interbull Bulletin 56.

2. Gao, Hongding,et al. 2023. A computationally efficient method for approximating reliabilities in large-scale single-step genomic prediction. Genetics Selection Evolution 55 1: 14 p.