Genomic selection of latent variables related to the milk fatty acid profile, milk composition, and udder health in dairy cattle

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Novel phenotypes in animal breeding

- ✓ Fine quality of products, production efficiency and sustainablity
- ✓ Often difficult to measure routinely
- ✓ Big data
- ✓ Difficult to interpret

Milk fat composition

- ✓ Key point for improving nutritional and dietary properties of milk
- ✓ Genetic basis
- ✓ Routine determination by MIR spectra
- ✓ Large number of variables
- ✓ Complex correlation pattern

Multivariate factor analysis

The (co)variance matrix of a system could be decomposed

$$S = BB' + \Psi$$

S = (Co)variance matrix of original data

B = (Co)variance between original data and latent factors

Ψ = Specific variance matrix

Use of MFA on FA profile

✓ Relevant reduction of the dimension of the system (<77%)

✓ Twelve new variables with biological meaning explaining about 75% of the variance (Mele et al., 2016)

✓ Grouping of original variables with similar metabolic origin and meaning

✓ Low to moderate values of heritability

Genetic parameters (Cecchinato et al., 2019)

Item	h^2_{AH}
F1: De novo FA	**0.14** **(0.05)**
F2: MY - Branched FA	**0.21** **(0.04)**
F3: Biohydrogenation	**0.19** **(0.03)**
F4: Long chain FA	**0.05** **(0.01)**
F5: Desaturation	**0.31** **(0.07)**
F6: Short chain FA	**0.16** **(0.03)**
F7: Milk fat protein	**0.27** **(0.06)**
F8: Odd FA	**0.13** **(0.04)**
F9: CLA	**0.06** **(0.01)**
F10: Linolenic	**0.20** **(0.04)**
F11: Udder health	**0.14** **(0.06)**
F12: C18:2*t*11*c*15	**0.05** **(0.02)**

Use of MFA on FA profile

- ✓ FA could be used as a reduced set of variables for improving milk nutritional quality
- ✓ They stress the attention on metablic pathways
- ✓ GS could be an interesting option for implementing a breeding programme

Aim of the work

- ✓ Evaluation of GEBV accuracy for Factor scores
- ✓ Comparison between two different models GBLUP and Single-step GBLUP

Data

- ✓ Fatty acid composition (GC), milk composition of 1,099 Italian Brown cattle
- ✓ 965 were genotyped with the 50K Illumina beadchip , 918 gen+phen
- ✓ 12 latent factor (FAF) scores
- ✓Animal model that included the fixed effects of herd, lactation stage, parity, and the random additive genetic effect

Breeding value prediction

- Pedigree based BLUP (A_BLUP)
- GBLUP

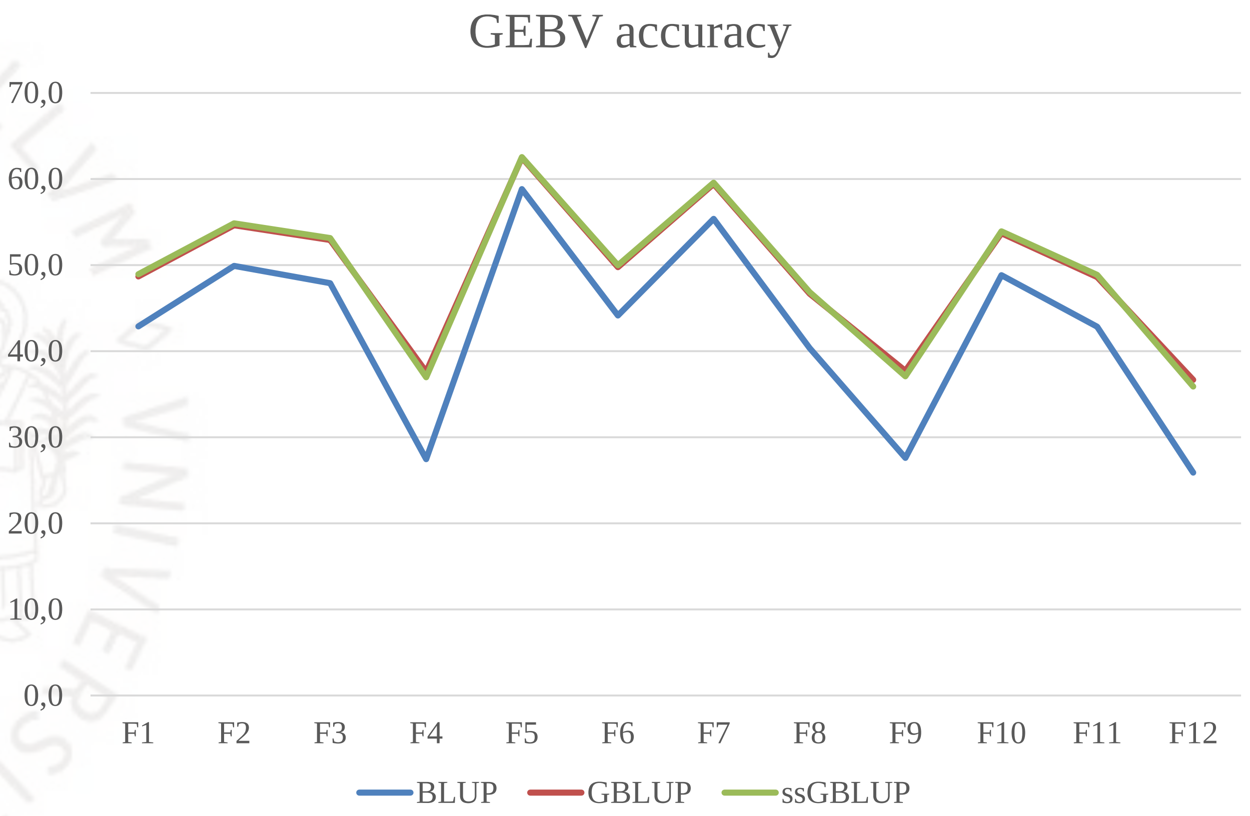
$$G = \frac{Z'Z}{2\sum p_i(1-p_i)}$$

- Single Step GBLUP (SS_GBLUP)

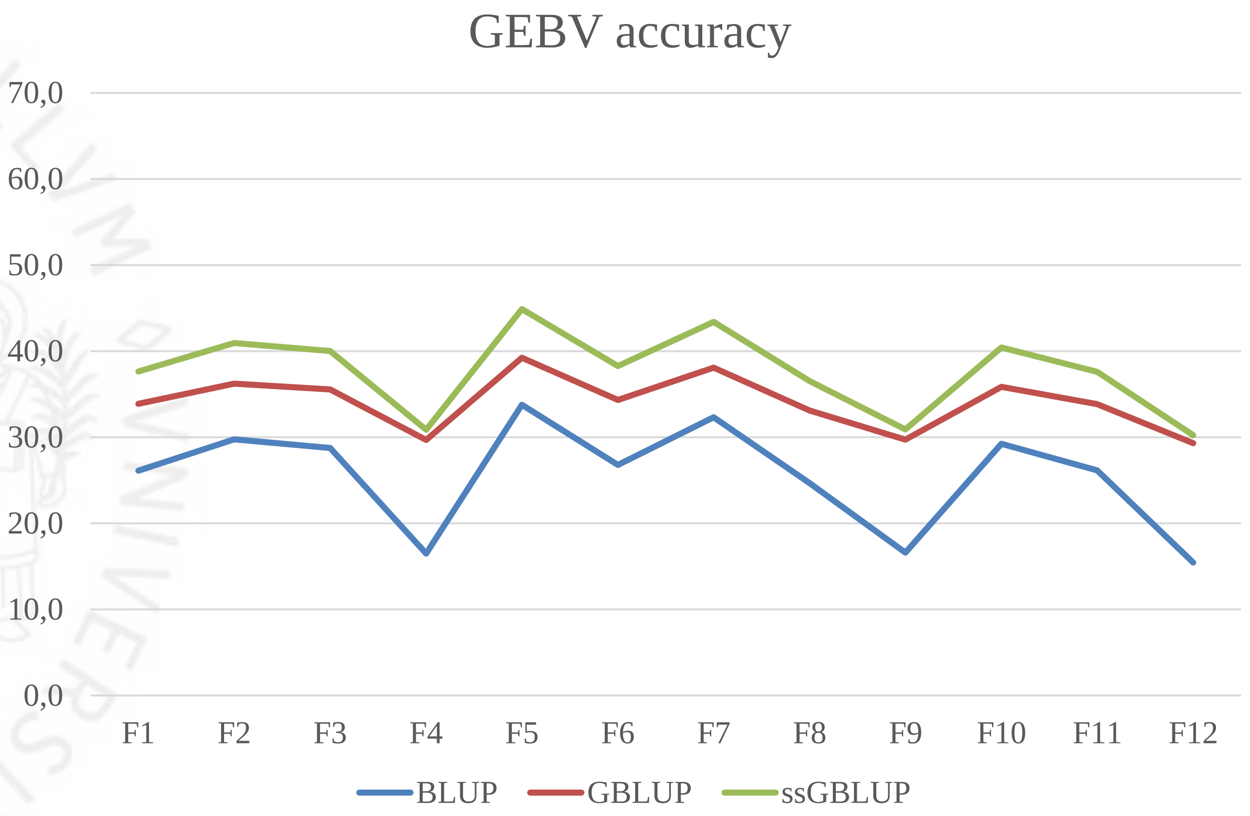
$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A_{22}}^{-1} \end{bmatrix}$$

- 200 youngest animals with masked phenotype
- GEBV accuracy calculated from the LHS of MME
- Variance components by Cecchinato et al. 2019

Results: training



Results: Validation



Overall GEBV accuracy

	A_BLUP	G_BLUP	ssG_BLUP
Training	**0.43 ± 0.11**	**0.49 ± 0.08**	**0.49 ± 0.09**
Prediction	**0.26 ± 0.06**	**0.34 ± 0.03**	**0.38 ± 0.05**

Results

GEBV accuracy: training

Factor	A_BLUP	G_BLUP	ssG_BLUP
De novo	**0.43 ± 0.04**	**0.49 ± 0.07**	**0.49 ± 0.05**
MY - Branched FA	**0.50 ± 0.04**	**0.55 ± 0.06**	**0.55 ± 0.04**
Biohydrogenation	**0.48 ± 0.04**	**0.53 ± 0.06**	**0.53 ± 0.05**
Long chain FA	**0.28 ± 0.05**	**0.38 ± 0.09**	**0.37 ± 0.06**
Desaturation	**0.59 ± 0.03**	**0.62 ± 0.05**	**0.62 ± 0.03**
Short chain FA	**0.44 ± 0.04**	**0.50 ± 0.07**	**0.50 ± 0.05**

Results

GEBV accuracy: validation

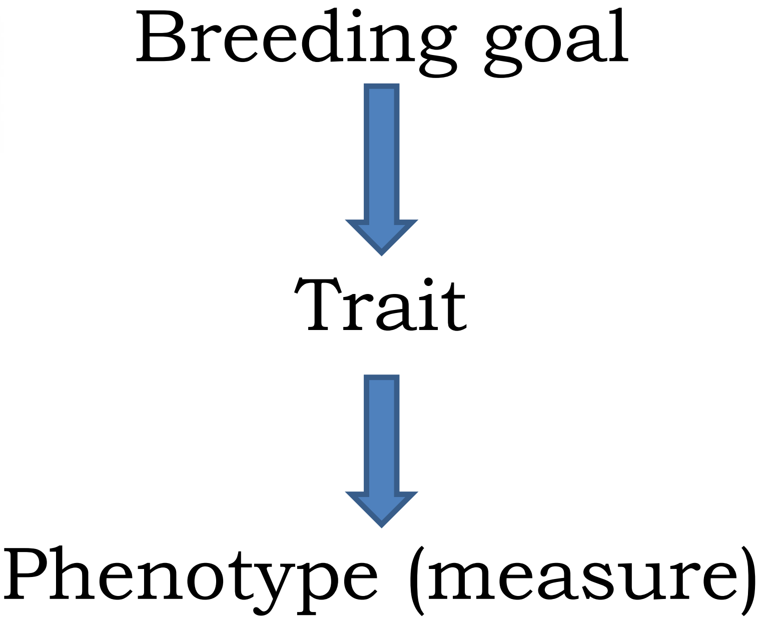
Factor	A_BLUP	G_BLUP	ssG_BLUP
De novo	**0.26 ± 0.10**	**0.34 ± 0.16**	**0.38 ± 0.09**
MY - Branched FA	**0.30 ± 0.10**	**0.36 ± 0.17**	**0.41 ± 0.09**
Biohydrogenation	**0.29 ± 0.10**	**0.36 ± 0.17**	**0.40 ± 0.09**
Long chain FA	**0.17 ± 0.08**	**0.30 ± 0.15**	**0.31 ± 0.09**
Desaturation	**0.34 ± 0.10**	**0.39 ± 0.18**	**0.45 ± 0.10**
Short chain FA	**0.27 ± 0.10**	**0.34 ± 0.17**	**0.38 ± 0.09**

Some considerations

- ✓ Accuracies small to moderate
- ✓ Sample size and structure
- ✓ Accuracies from ssGBLUP slightly larger than GBLUP for the validation animals
- ✓ Genomic methods with equal performances on training individual
- ✓ Related to the genetic basis of the latent variables

Some considerations

- ✓ Factor scores could be proposed as an alternative phenotype for improving milk nutritional quality



Breeding goal

Trait

Phenotype (measure)

Implications

- ✓ Small accuracies → increase sample size
- ✓ On large scale MIR predictions have to be used
- ✓ Genotyping strategies
- ✓ Phenotyping strategies