Approximating genomic reliabilities for genotyped Walloon Holstein cattle using the SNP-BLUP software

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First experiences

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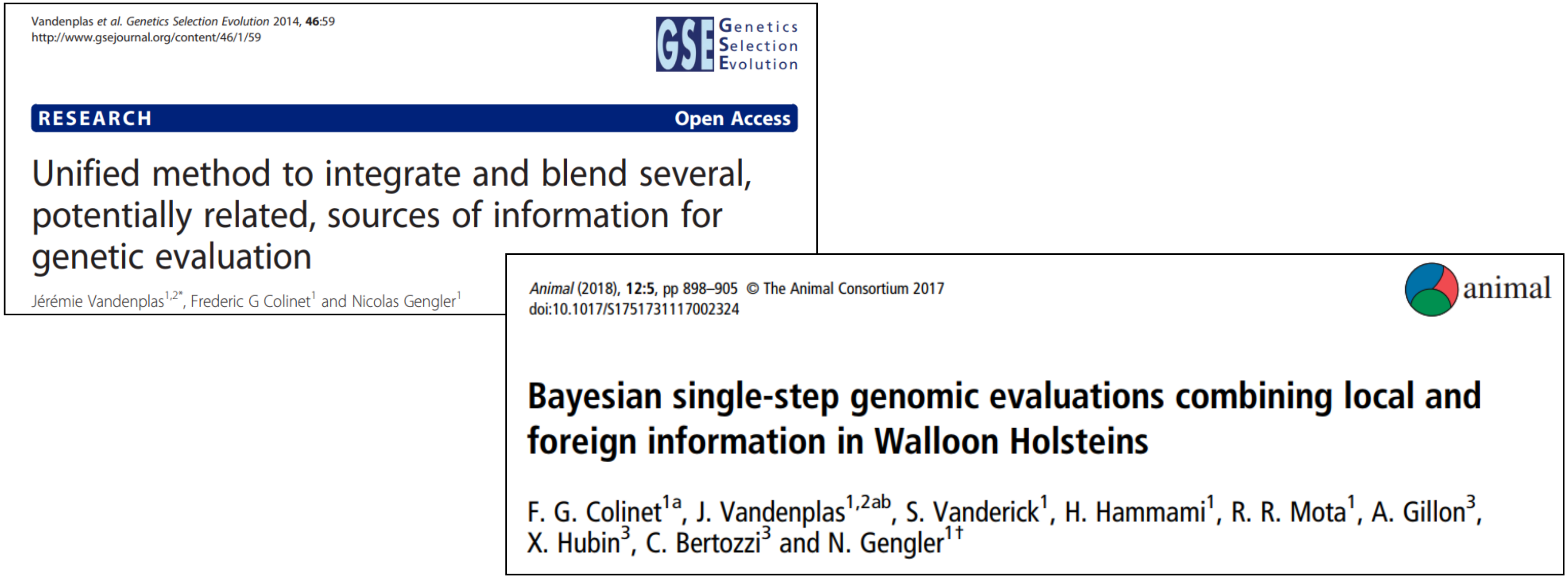
Walloon Genomic System

- ➢ Current Walloon Holstein genomic evaluation system: Single-step genomic “Bayesian” procedure (ssGBayes)
  - ➢ Blending genomic, local and MACE information using EBV and REL
  - ➢ Subtract Walloon information contributing to MACE



Vandenplas *et al. Genetics Selection Evolution* 2014, **46**:59
http://www.gsejournal.org/content/46/1/59

GSE Genetics Selection Evolution

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Unified method to integrate and blend several, potentially related, sources of information for genetic evaluation

Jérémie Vandenplas[1,2*], Frederic G Colinet[1] and Nicolas Gengler[1]

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animal

Bayesian single-step genomic evaluations combining local and foreign information in Walloon Holsteins

F. G. Colinet[1a], J. Vandenplas[1,2ab], S. Vanderick[1], H. Hammami[1], R. R. Mota[1], A. Gillon[3], X. Hubin[3], C. Bertozzi[3] and N. Gengler[1†]

Larger Project

- Current Walloon Holstein genomic evaluation system: Single-step genomic “Bayesian” procedure (ssGBayes)
  - Blending genomic, local and MACE information using EBV and REL
  - Subtract Walloon information contributing to MACE

- However needed:
  - “Continuous” generation of GEBV ← flow of genotypes
  - Generating also associated GREL → SNP-BLUP software

- Context of this presentation

Objectives

- Reported here:
  - First experiences with INTERBULL method
  - For genotyped Walloon Holstein cattle and improve its efficiency

- Comparison facilitated because routine GREL in our evaluation based on diag($\mathbf{C}^{-1}$)

How was the method used?

Step 1: Reliabilities of SNP genotypes using the SNP_BLUP software using ~9000 genotyped animals (${R_i}^{SNP}$)

Step 2: Reliabilities of DGV

$$\boxed{{R_i}^{DGV} = {R_i}^{SNP}}$$

How was the method used?

Step 3: Adjusting the theoretical reliabilities

$$EDC_i^{DGV} = \lambda \; Ri^{DGV} / (1 - Ri^{DGV})$$

$$EDC_{real-i}^{DGV} = f \; * EDC_i^{DGV}$$

$$\lambda = \frac{4 - h^2}{h^2}$$

$f = 1$

f = regression expected – observed

How was the method used and tested?

- **Step 4: Calculating the genomic EDC gain**

$$\boxed{EDC_i^{Gain} = EDC_{real-i}^{DGV} - EDC_i^{A22}}$$

EDC_i^{A22} ➔EDC based on conventional and local parent average

- **Step 5:Final reliabilities enhanced with genomic information**

$$\boxed{EDC_i^{Final} = EDC_i^{CONV} + EDC_i^{Gain}}$$

$$\boxed{R_i^{Final} = EDC_i^{Final} / EDC_i^{Final} + \lambda}$$

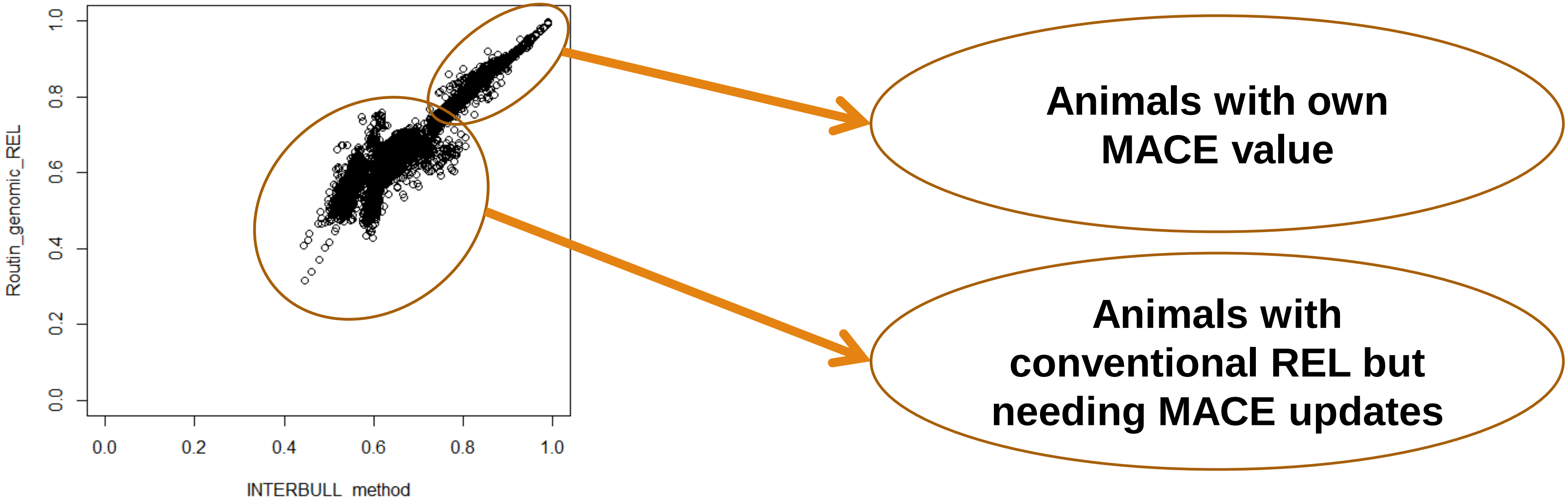
EDC_i^{CONV}

MACE: EDC based on MACE value (2411 animal)

W_MACE: EDC based on conventional EBV (updated with MACE) (6600 animal)

How was the method tested?

Information	Cor(R_REL, IB_REL)	Mean_R_REL	Mean_IB_REL
MACE	0.99	0.828	0.827
Sire and/or maternal grand sire with MACE	0.76	0.630	0.626
Total	0.96	0.684	0.680



Animals with own MACE value

Animals with conventional REL but needing MACE updates

Conclusions

- ➢ First results – promising
- ➢ Depend clearly on group of animals
- ➢ To emulate our system where MACE information flows in ➔ update of conventional REL also needed
- ➢ Currently our published conventional EBV and REL are also updated (other method) ➔ to be continued

➔ SNP-REL method entering well current efforts