Implementation of a Single-Step genomic evaluation system for dairy cattle in Wallonia, Belgium

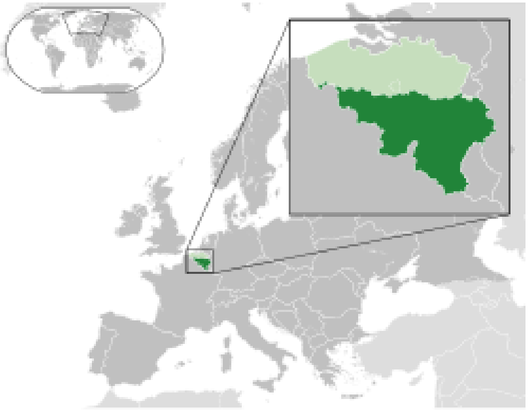
Sylvie Vanderick[1], **Katrien Wijnrocx[1]**, Jeremie Vandenplas[2], Alain Gillon[3] & Nicolas Gengler[1]

[1] *Animal Sciences, Terra Teaching and Research Centre, University of Liège-Gembloux Agro-Bio Tech, 5030 Gembloux, Belgium*
[2] *Animal Breeding & Genomics, Wageningen University abd Research, 6708PB Wageningen, the Netherlands*
[3] *Elevéo asbl, AWE Groupe, 5590 Ciney, Belgium*

www.uliege.be
www.gembloux.uliege.be

Introduction

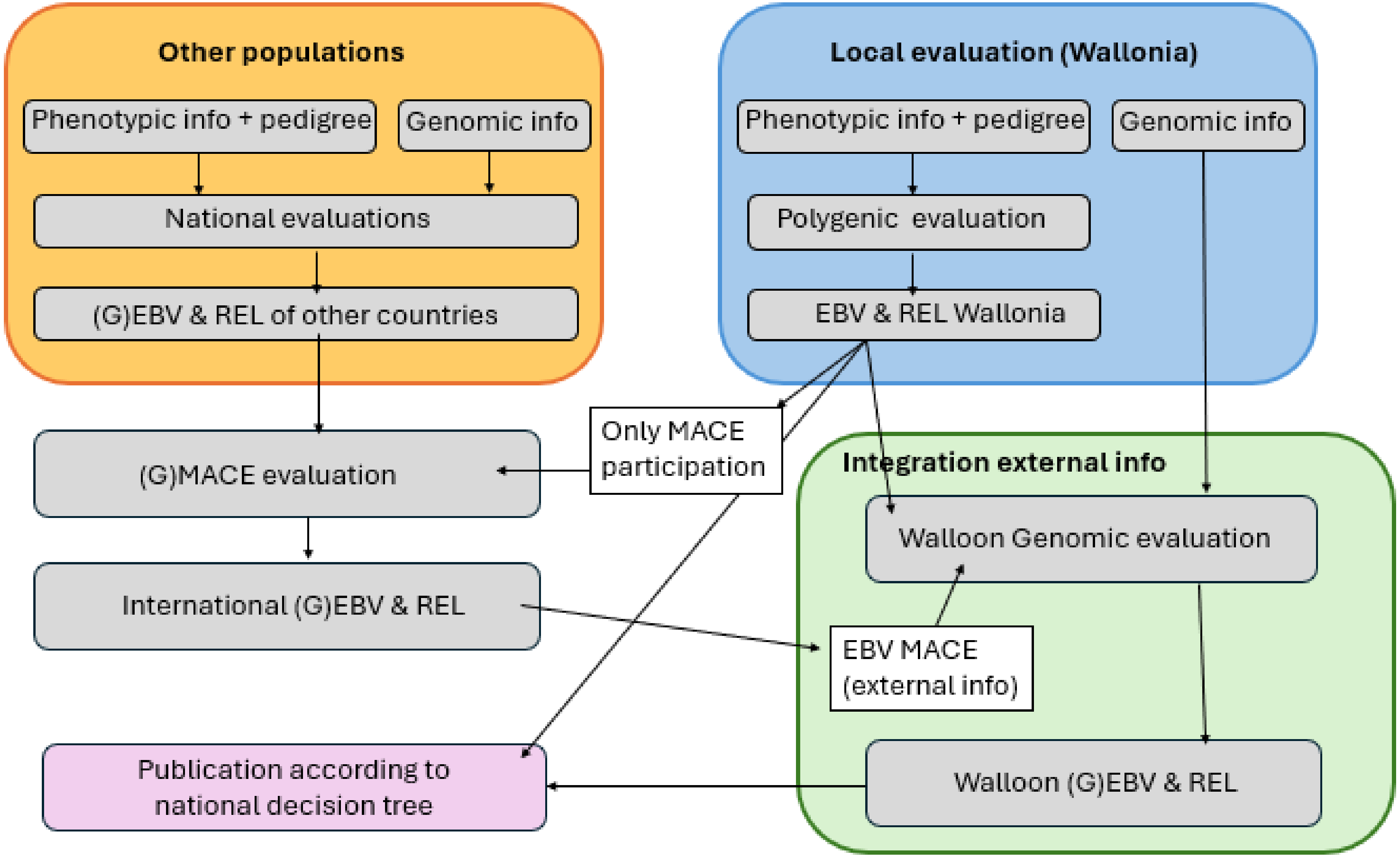
- Since several years → dairy cattle breeders in the Walloon Region of Belgium have access to locally estimated breeding values
  - Production, conformation, udder health and functional traits
- Participation in MACE evaluation
- Ongoing effort to implement a single-step strategy



- Objectives:

To test and validate a single-step analysis that simultaneously incorporates all available national data alongside MACE information

The current Walloon evaluation system … with its particularities



Other populations

Phenotypic info + pedigree

Genomic info

National evaluations

(G)EBV & REL of other countries

Local evaluation (Wallonia)

Phenotypic info + pedigree

Genomic info

Polygenic evaluation

EBV & REL Wallonia

Only MACE participation

(G)MACE evaluation

International (G)EBV & REL

Integration external info

Walloon Genomic evaluation

EBV MACE (external info)

Walloon (G)EBV & REL

Publication according to national decision tree

Polygenic evaluation

- Multilactation (1-3), multitrait random regression test-day model (RRTDM) for milk, fat and protein yield
- Calculation of average lactation EBV
  - Sum of genetic random regression solutions for 305 days and over 3 lactations
- Sent to Interbull for MACE evaluation
- We get back the international EBV from MACE

Auvray & Gengler (2002); Croquet et al. (2006)

Genomic system

- This international info (MACE) combined with the estimated EBV and genomic information → local GEBV
- Bayesian integration
  - Accounting for double counting (discounted for EBV sent to MACE)
  - Propagation of external info across all animals
  - Replacing $\mathbf{A}^{-1}$ by $\mathbf{H}^{-1}$

- But: not perfect:
  - Still relies on the first polygenic step (BLUP)
  - Potential biases → biased contemporary group solutions (HTD solutions)

Vandenplas et al. (2016)

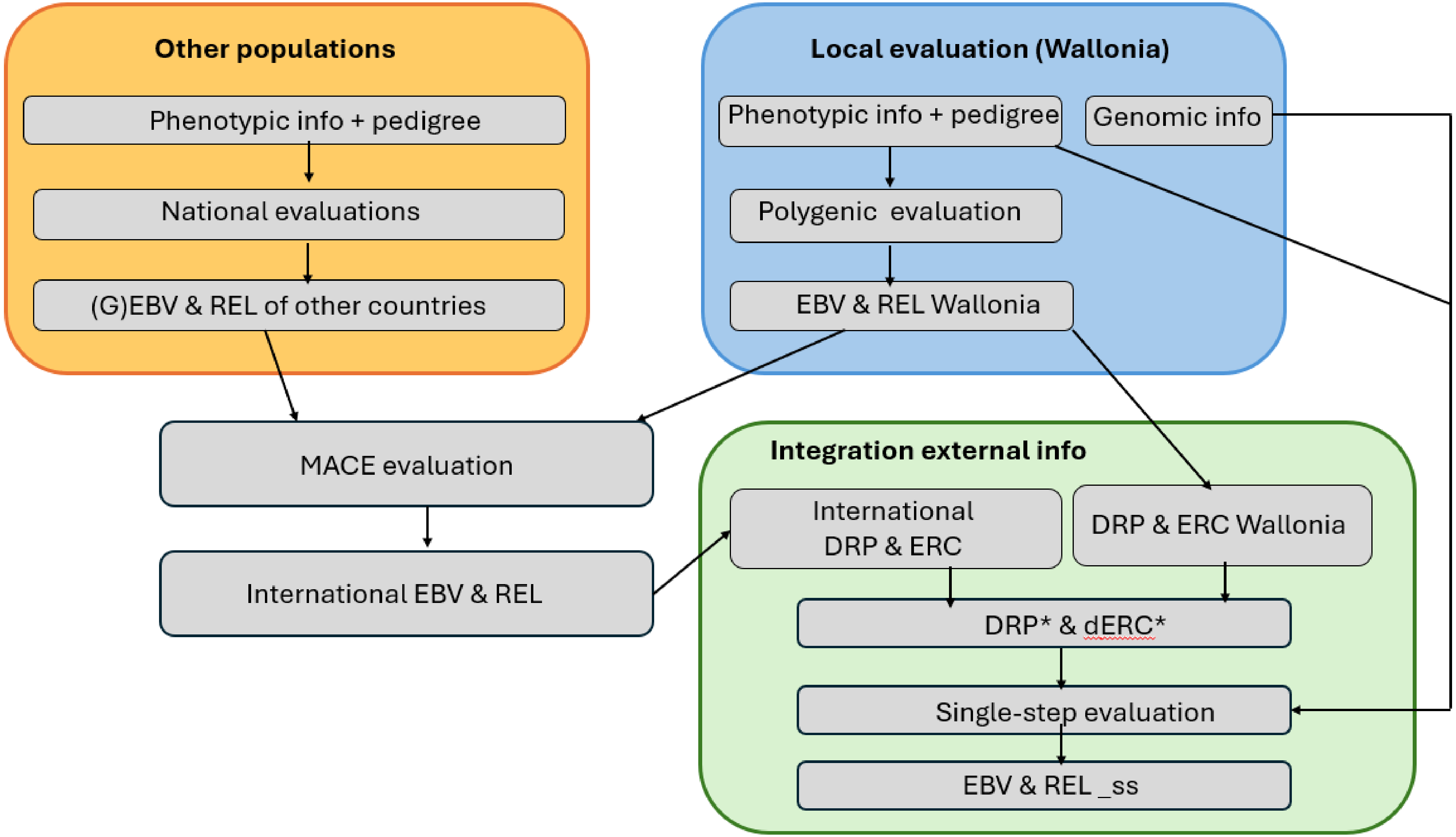
Single-step is the way to go!

- As it combines phenotypic data, pedigree information and genomic information simultaneously
- Replacement of pedigree-based relationship matrix ($\mathbf{A}^{-1}$) by $\mathbf{H}^{-1}$
- Resulting GEBV more accurate and less biased

- Our new system should be as close to the current system as possible!

- We need a single-step system with external info coming from MACE

Strategy to develop single-step



Other populations

Phenotypic info + pedigree

National evaluations

(G)EBV & REL of other countries

Local evaluation (Wallonia)

Phenotypic info + pedigree

Genomic info

Polygenic evaluation

EBV & REL Wallonia

MACE evaluation

International EBV & REL

Integration external info

International DRP & ERC

DRP & ERC Wallonia

DRP* & dERC*

Single-step evaluation

EBV & REL _ss

So… what did we do?
The strategy to include external info from MACE

- Transform MACE EBV in deregressed proofs (DRP) for MACE bulls
  - Excluding local information!
  - Associated to weights called effective record contributions (ERC)

- Strategy by Bonifazi (2023): deregression where EBV are adjusted by their reliability to produce DRP
  - Correction for Mendelian Sampling deviation by transforming REL to ERC, and subtract ERC associated with PA REL from total ERC → **dERC**
  - Elimination of double-counting by subtracting local info sent to Interbull → **DRP* and dERC***

Vandenplas et al. (2016), Bonifazi et al. (2023)

So… what did we do?
The strategy to include external info from MACE

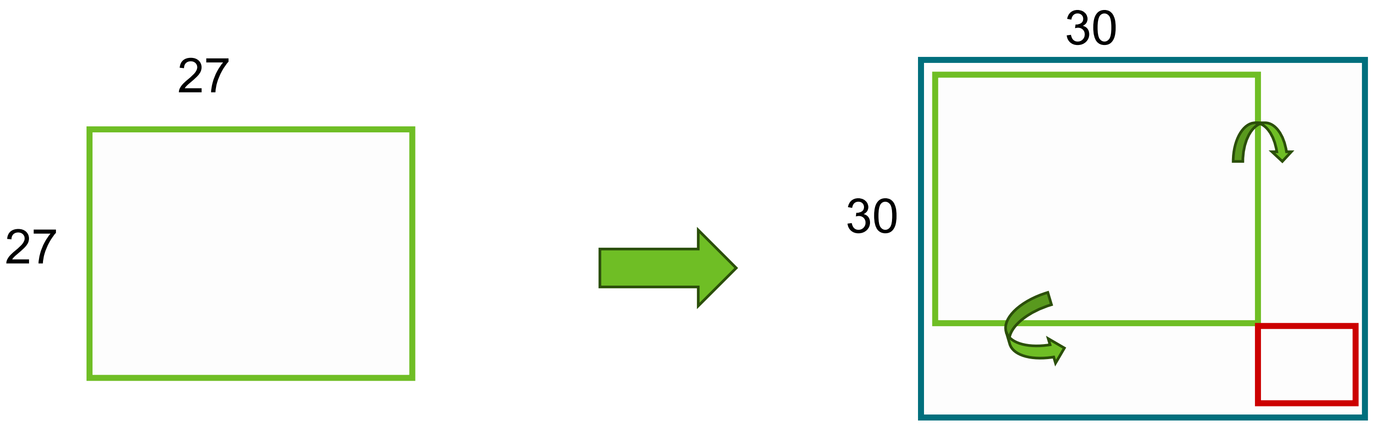
- Selection of MACE bulls in our analysis
  - Cows in production + their descendants + genotyped animals

  → extracted from our pedigree
  - For all bulls in this extracted pedigree: MACE values if available
- DRP* are included directly in our model as 3 pseudo-phenotypes
  - Only for bulls having a MACE (whether we sent in local info or not)
  - For cows ➔ pseudo-phenotype missing 🡄 external info in the future
- dERC* become weights
  - Also only for bulls
  - For cows also missing

Vandenplas et al. (2016), Bonifazi et al. (2023)

So… what did we do?
The problem of the different scale between MACE / local data …

- MACE proofs (cumulative EBV over time) scale differs from scale of the national evaluations (RR coefficients)
- Modification of the variance-covariance matrices of the RRTDM to include the MACE pseudo-traits as correlated traits
  - Avoid singularity by multiplying the covariance between RR and MACE by 0.999
  - This system also generates natively EBV to be sent to Interbull



So… what did we do?
Calculation of approximate reliabilities

- Approach adapted from Gao et al. (2023):
  - Calculation of polygenic REL (PEV of solutions)
  - Updating of REL based on REL of MACE bulls
  - This REL will serve as a prior for GREL
  - Removing double-counting due to pedigree information (Zaabza, 2022)
  - Compute GREL for non-genotyped animals using weighted pedigree BLUP with ssERC as weights

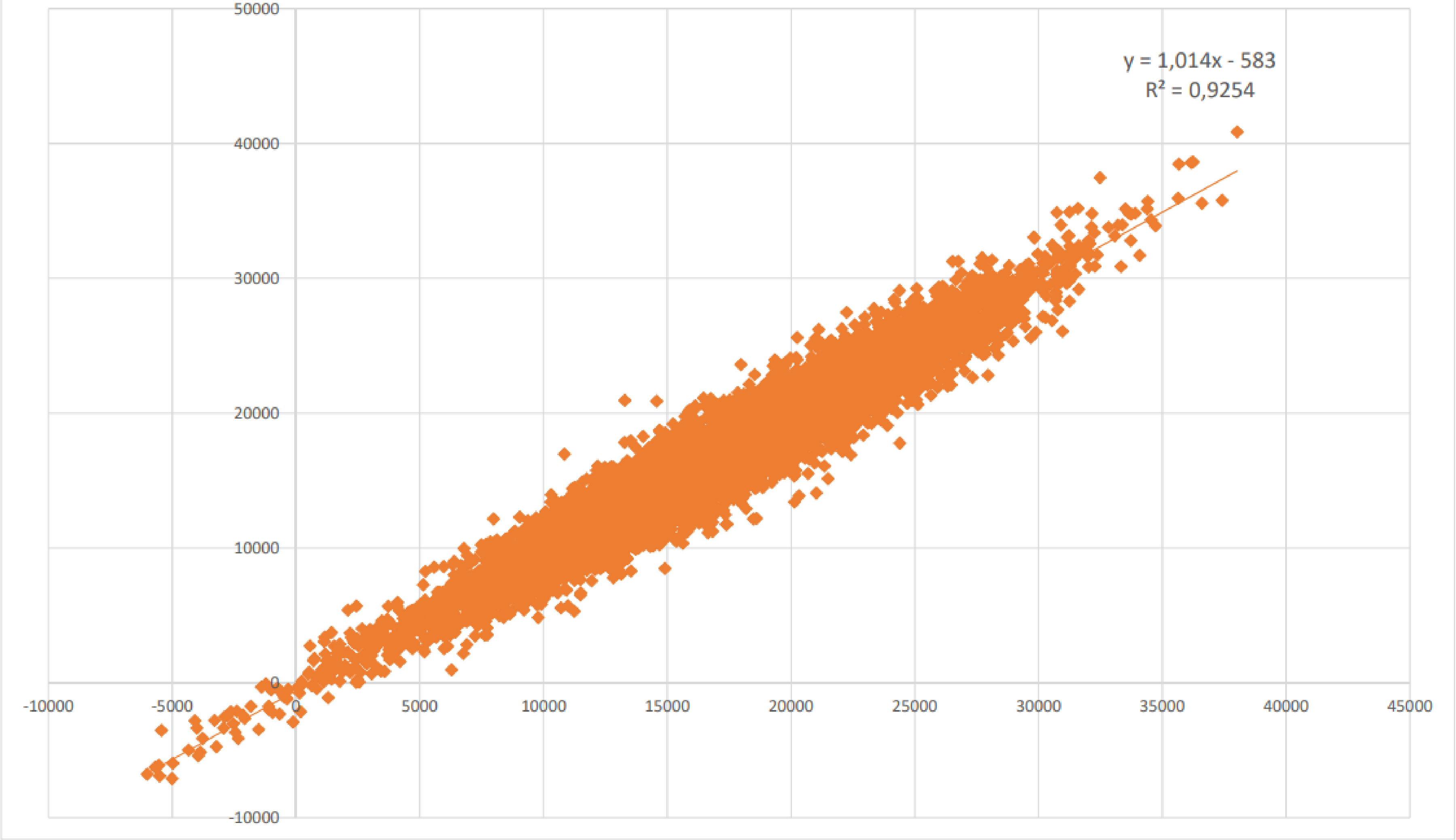
Vandenplas (2023) – genomicrel program

Validation on Walloon data

- Testing of the ssGBLUP
  - Data:
    - 4 851 501 test-day records for 305-day milk-, fat-, and protein yields across 3 lactations
    - 2 230 bulls which were sent to Interbull for MACE evaluation
    - Genotypes for 13 604 animals
    - Inclusion of 12 547 MACE bulls as DRP info
  - ssGBLUP was performed with/without genomic information included (for testing)
  - Comparing of different scenarios in following slides (displayed only for milk yield)

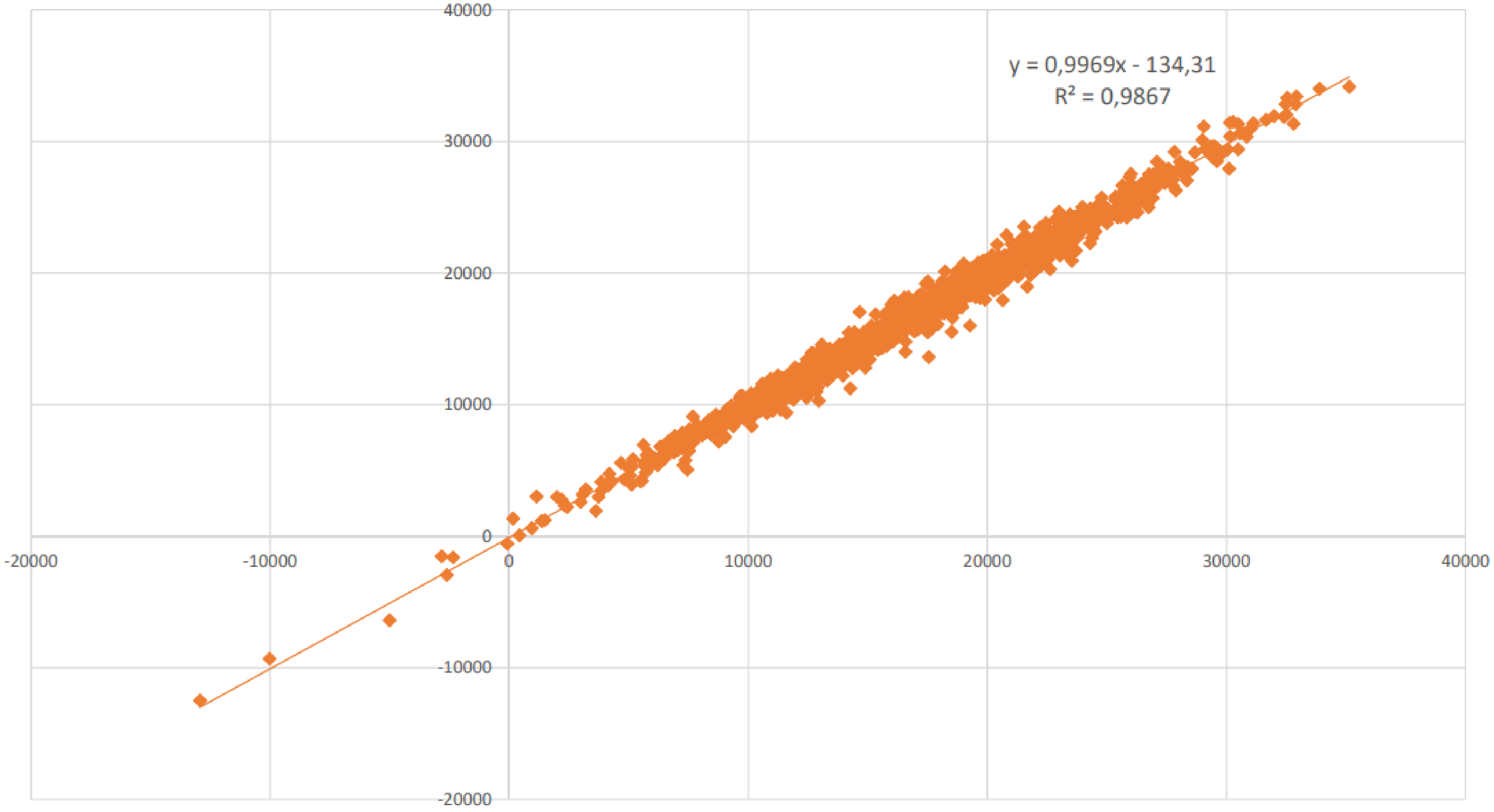
Validation on Walloon data

Results ssGBLUP without genomic info versus MACE values
For bulls with at least a MACE value



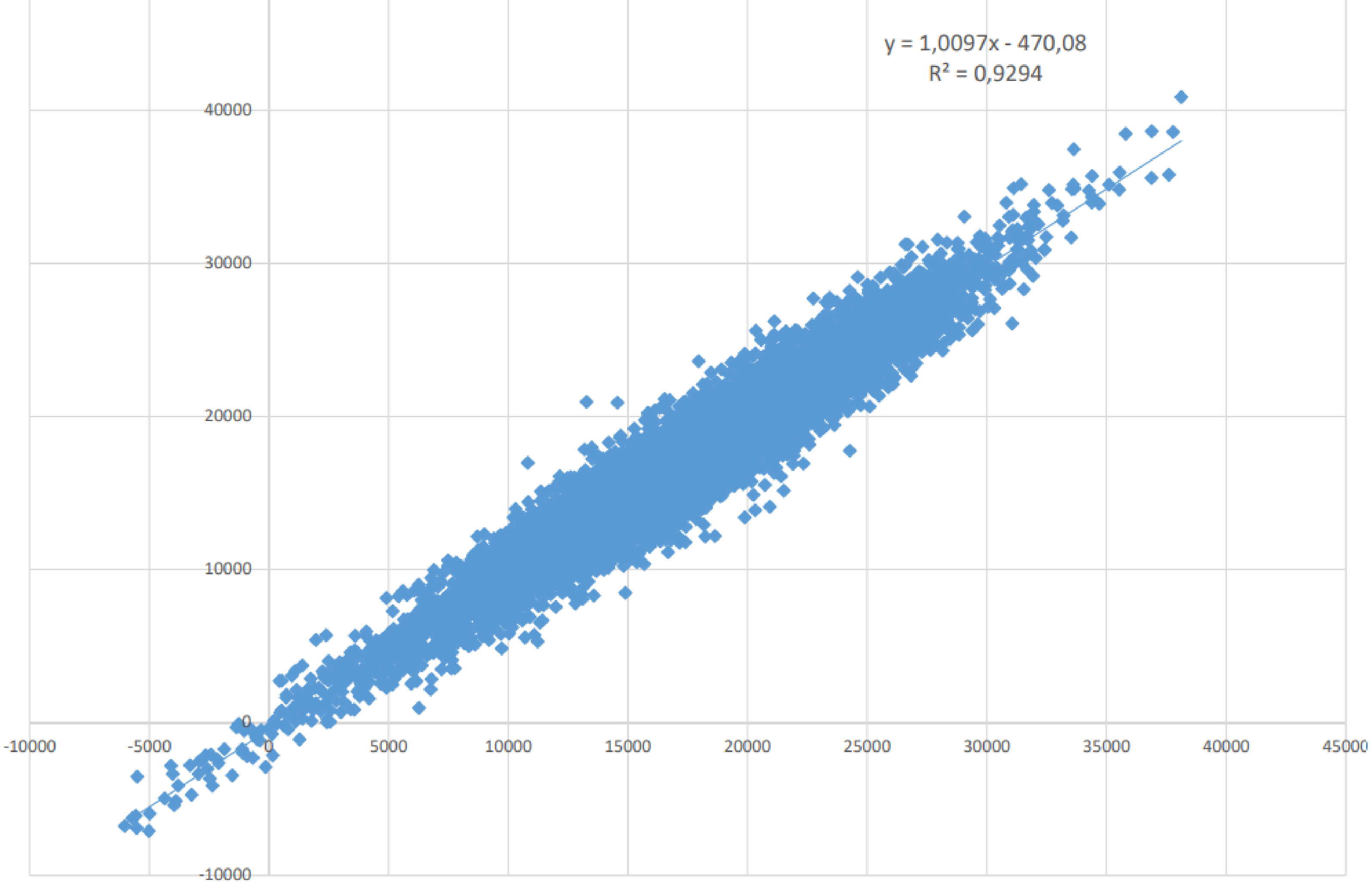
Validation on Walloon data

Results ssGBLUP without genomic info versus MACE values
For Walloon bulls with a value sent to Interbull



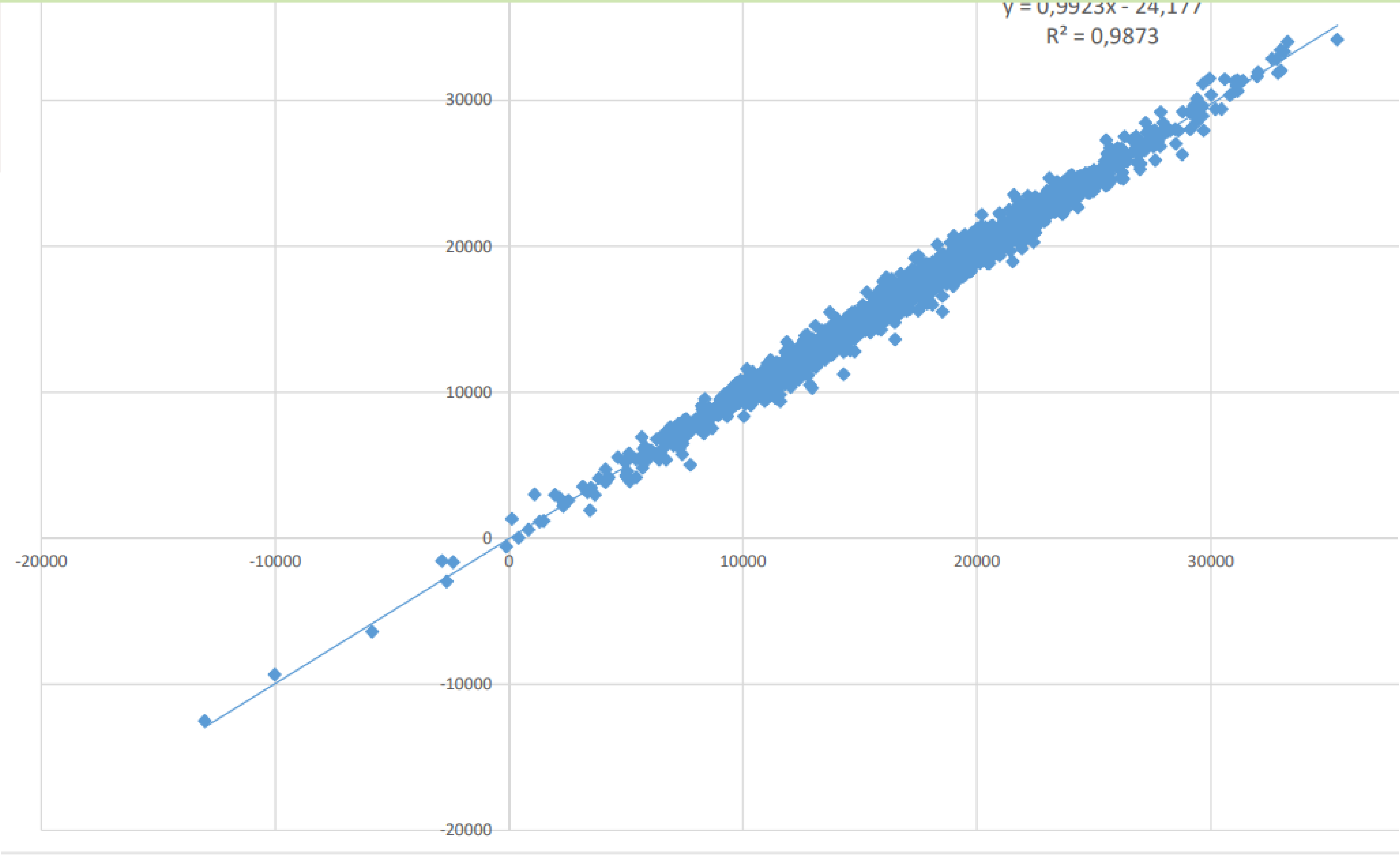
Validation on Walloon data

Results ssGBLUP with genomic info versus MACE values
For bulls with at least a MACE value



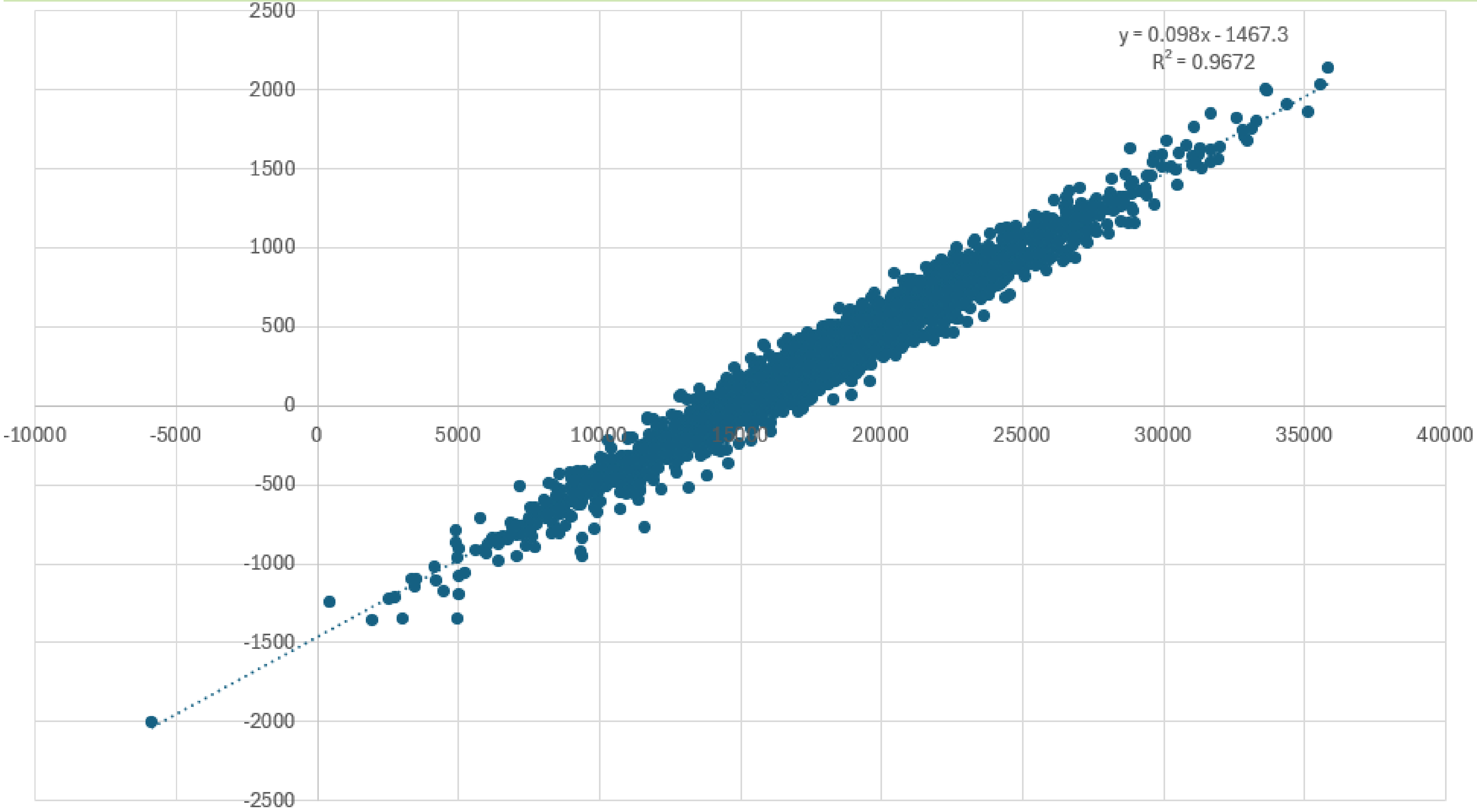
Validation on Walloon data

Results ssGBLUP with genomic info versus MACE values
For Walloon bulls with a value sent to Interbull



Validation on Walloon data

Results ssGBLUP with genomic info versus published GEBV values
For bulls with a genotype



Discussion

- The proposed method is accurate and efficient

- Some small remarks:
  - Deregression phase of MACE is based on parent-averages of Interbull based on a sire-grand-sire model

  - Reliability estimates strategy without integration has been validated in our methane study (see presentation of Nicolas Gengler tomorrow ☺) and in pigs

Thank you for your attention!

katrien.wijnrocx@uliege.be