Experiences with the GMACE evaluations and Walloon single-step genomic evaluation system

F.G. Colinet[1], J. Vandenplas[2], S. Vanderick[1], C. Bertozzi[3], H. Hubin[3], A. Gillon[3], and N. Gengler[1]
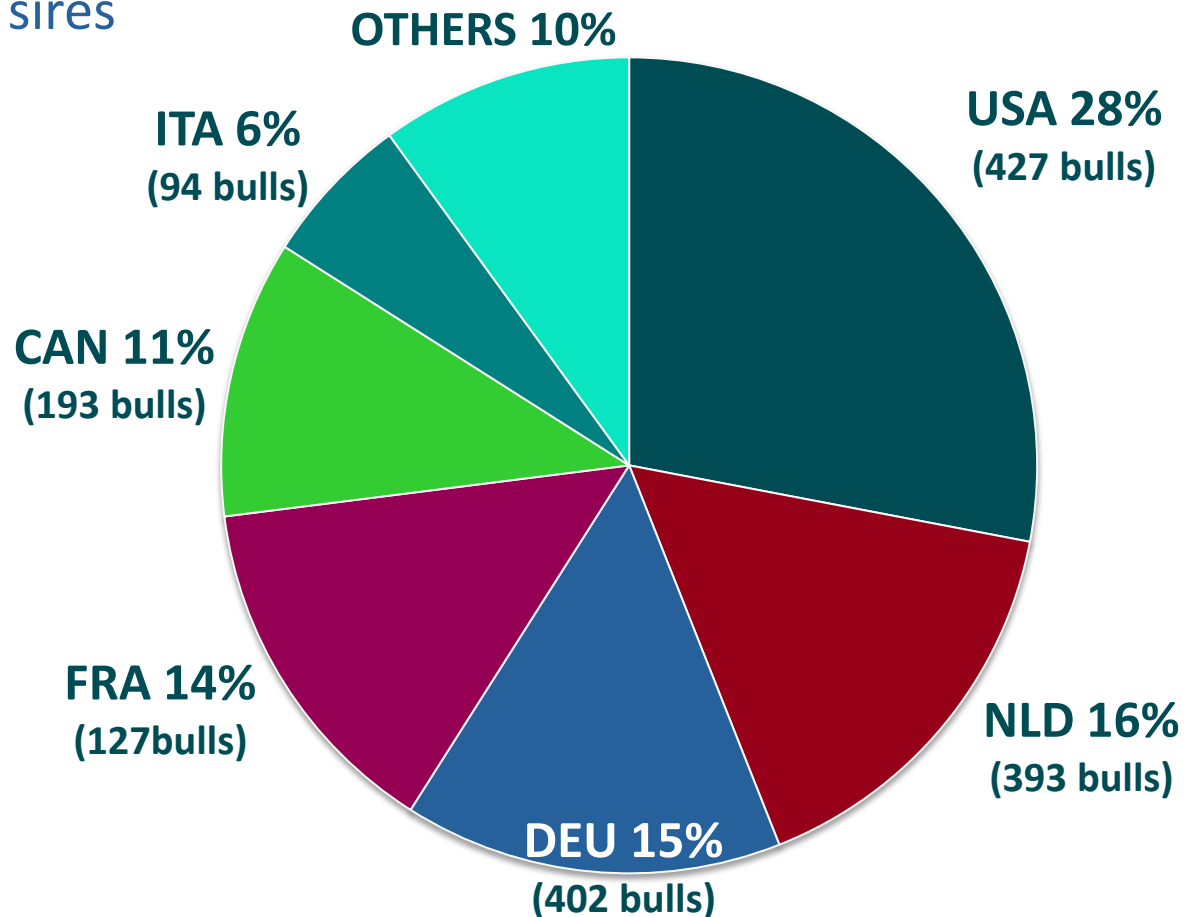
[1] University of Liège, Gembloux Agro-Bio Tech, Belgium
[2] Wageningen UR Livestock Research, Animal Breeding and Genomics Centre, Netherlands
[3] Walloon Breeding Association, Belgium

Walloon dairy cattle

- Small population size
- **82%** of cows (in 1st to 3rd lactation in 2014 and milk recorded) sired by foreign AI sires
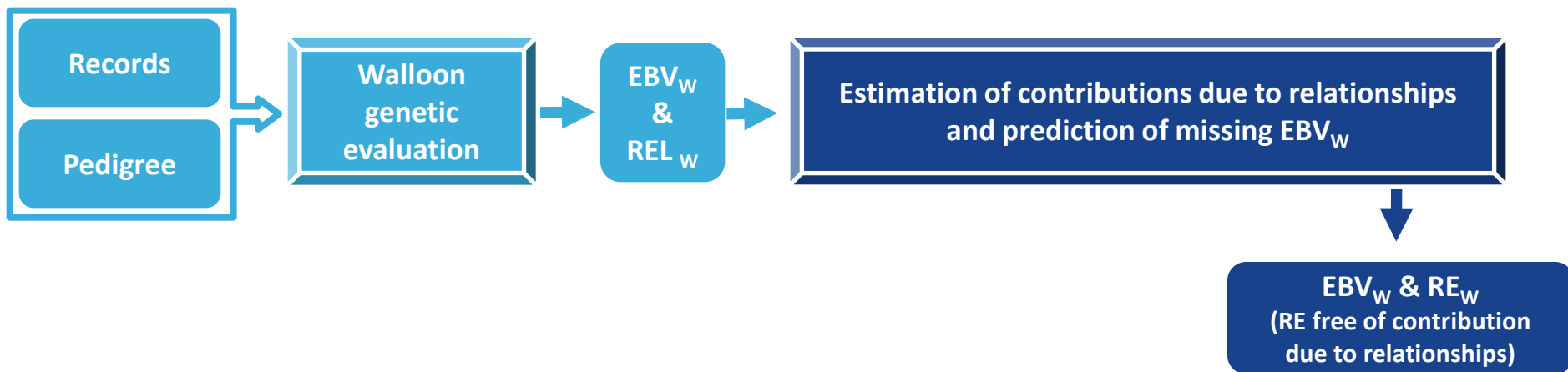

Pie chart:
- USA 28% (427 bulls)
- NLD 16% (393 bulls)
- DEU 15% (402 bulls)
- FRA 14% (127 bulls)
- CAN 11% (193 bulls)
- ITA 6% (94 bulls)
- OTHERS 10%

Walloon genomic evaluation system

❑ Adapted to Walloon dairy cattle

❑ Combine simultaneously:

    ➢ **Genotypes**

    ➢ **Pedigree**

    ➢ **Local information**
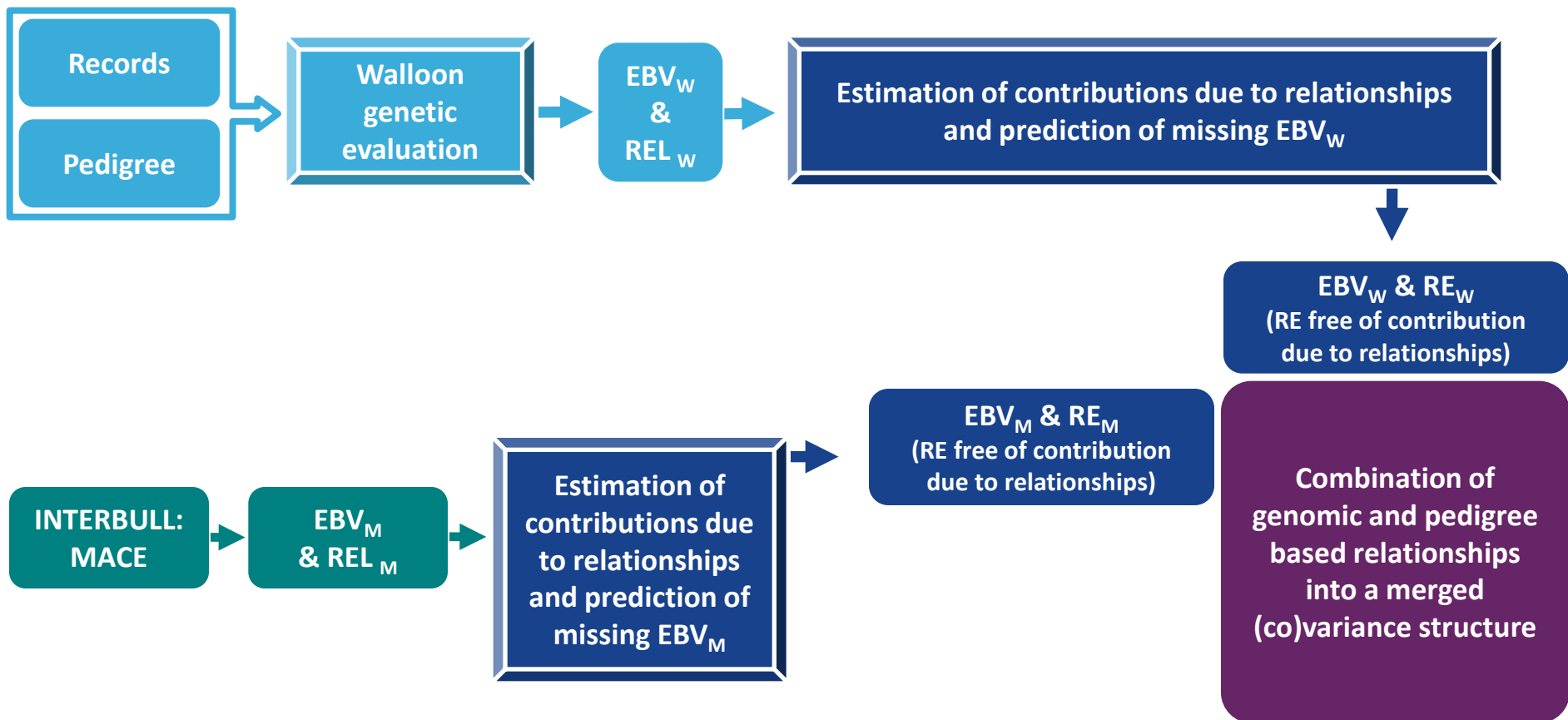
    ➢ **Foreign information (MACE EBV and REL)**

Walloon genomic evaluation system

❑ Local and foreign information:

➢ **Considered as a priori known external information**

➢ **Incorporated using a Bayesian approach**

➢ **Correct propagation of all this information without multiple considerations of contributions due to relationships and due to records**

➢ **Based on Vandenplas *et al.*, 2014. GSE 46, 59**

❑ Miming hypothetical mixed model equations and replacing pedigree information by combined pedigree and genomic information
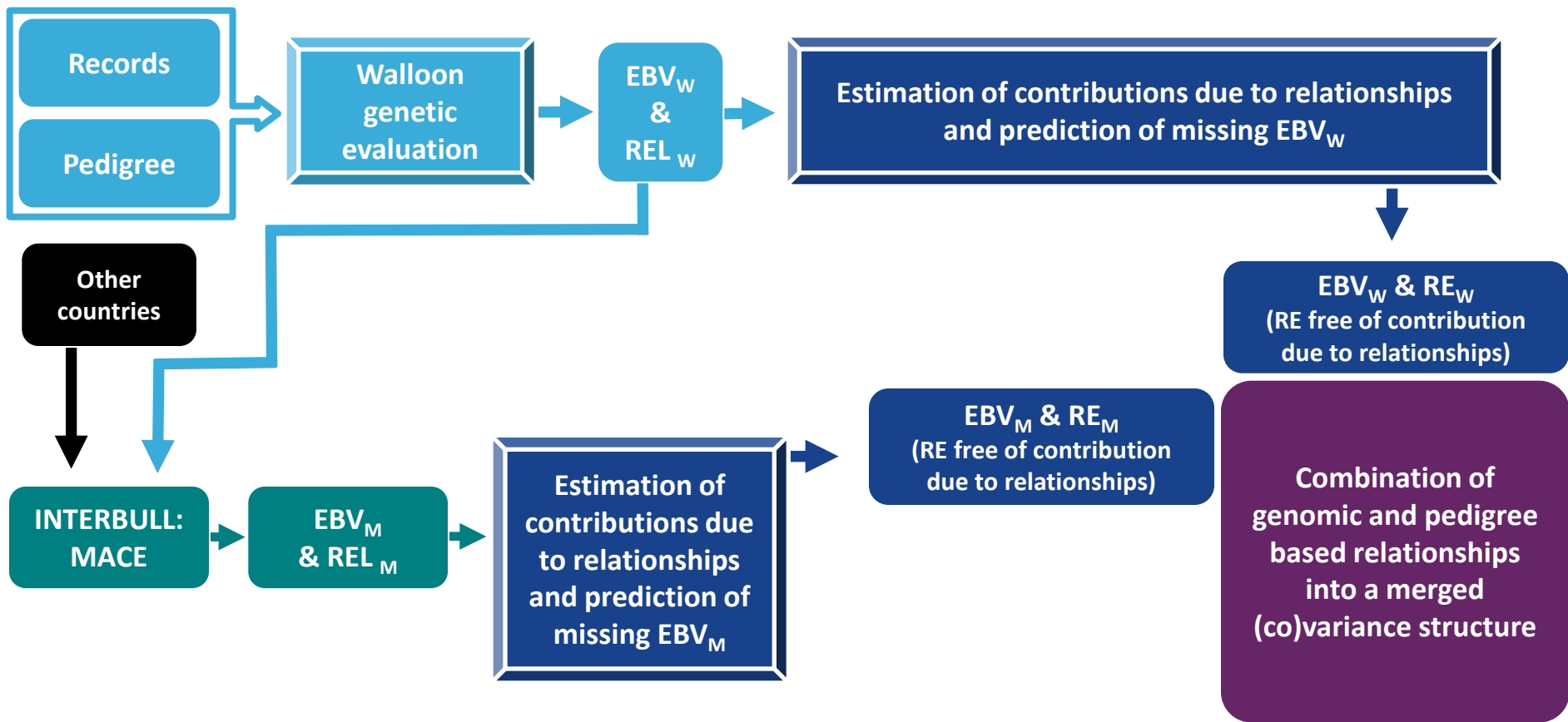➡ **Bayesian single step Genomic Evaluation: ssGBayes**
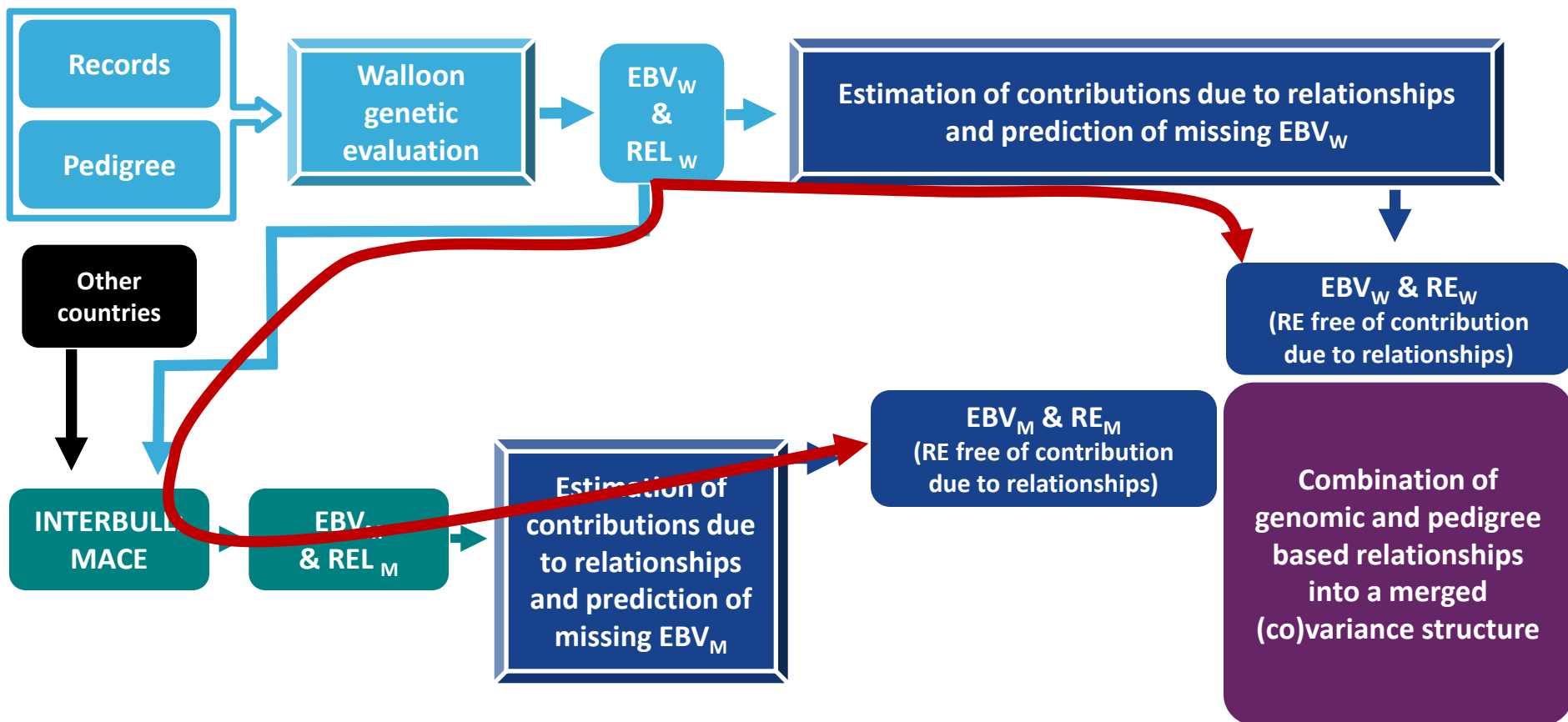
Walloon genomic evaluation system

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┌─────────────┐      ┌──────────────┐      ┌────────┐      ┌──────────────────────────────────────────────┐
│   Records   │      │   Walloon    │      │ EBV_W  │      │ Estimation of contributions due to relationships │
├─────────────┤ ──►  │   genetic    │ ──►  │   &    │ ──►  │     and prediction of missing EBV_W             │
│  Pedigree   │      │  evaluation  │      │ REL_W  │      │                                                 │
└─────────────┘      └──────────────┘      └────────┘      └──────────────────────────────────────────────┘
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EBV_W & RE_W
(RE free of contribution
due to relationships)

Walloon genomic evaluation system

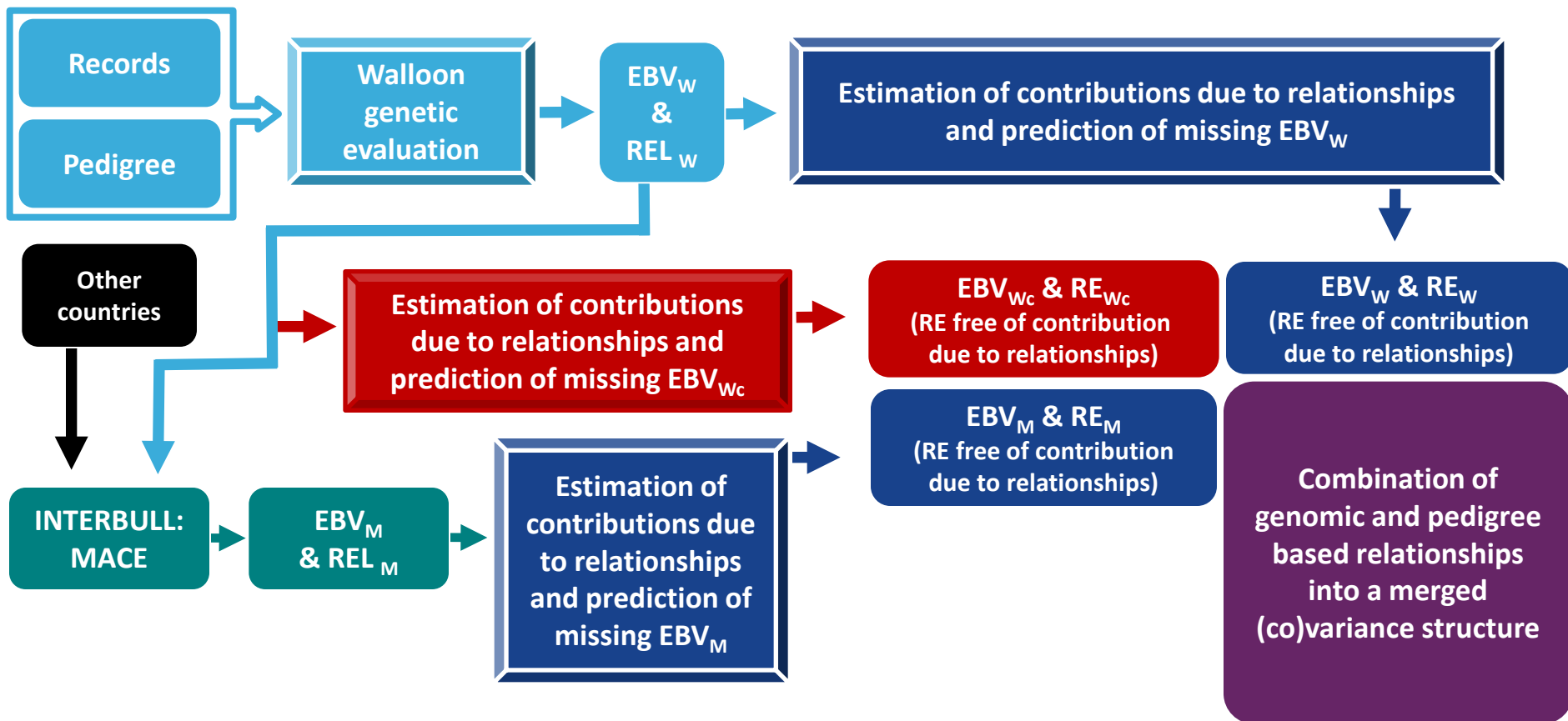# Walloon genomic evaluation system

Walloon genomic evaluation system

Records

Pedigree

Other countries

Walloon genetic evaluation

EBV_W & REL_W

Estimation of contributions due to relationships and prediction of missing EBV_W

EBV_W & RE_W (RE free of contribution due to relationships)

INTERBULL MACE

EBV_M & REL_M

Estimation of contributions due to relationships and prediction of missing EBV_M

EBV_M & RE_M (RE free of contribution due to relationships)

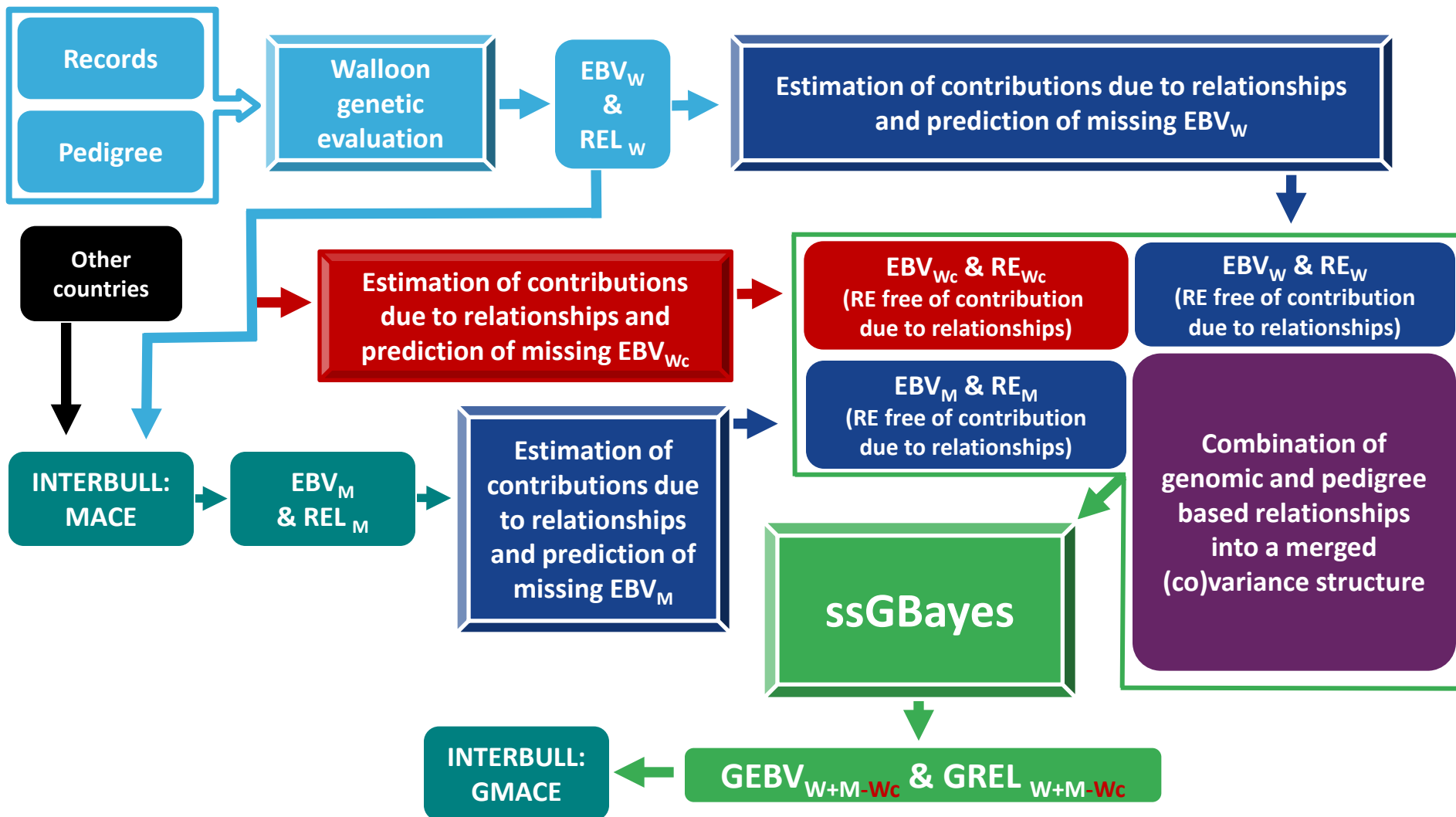Combination of genomic and pedigree based relationships into a merged (co)variance structure

Double counting of information!!

Walloon genomic evaluation system

Walloon genomic evaluation system

ssGBayes

□ Combination of genotype, pedigree, local and foreign information

$$\left(H^{-1} + \Lambda_W + \Lambda_M - \Lambda_{Wc}\right)\hat{a} = D_W^{-1}\,\hat{u}_W + D_M^{-1}\,\hat{u}_M - D_{Wc}^{-1}\,\hat{u}_{Wc}$$

➢ H : Combined genomic and pedigree based relationships into a merged (co)variance structure

➢ $\hat{a}$: $GEBV_{W+M-Wc}$

➢ $\hat{u}_W, \hat{u}_M$ and $\hat{u}_{Wc}$: Available and predicted EBV_W, EBV_M and EBV_{Wc}

➢ D_W, D_M and D_{Wc} : Prediction error (co)variance matrix of $\hat{u}_W, \hat{u}_M$ and $\hat{u}_{Wc}$

ssGBayes

❑ Combination of genotype, pedigree, local and foreign information

$$\left(H^{-1} + \Lambda_W + \Lambda_M - \Lambda_{Wc} \right) \hat{a} = D_W^{-1} \hat{u}_W + D_M^{-1} \hat{u}_M - D_{Wc}^{-1} \hat{u}_{Wc}$$

Least square part of LHS of hypothetical BLUP of Walloon information

Least square part of LHS of hypothetical BLUP of foreign information free of Walloon information

RHS of hypothetical BLUP of Walloon information

RHS of hypothetical BLUP of foreign information free of Walloon information

❑ Modification of BLUPF90 (Misztal, 2013) by J. Vandenplas

H^{-1}

- Single step GBLUP

- Combined genomic and pedigree based relationships into a merged (co)variance structure

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \tau\left(\alpha\mathbf{G} + \beta\mathbf{A}_{22}\right)^{-1} - \omega\mathbf{A}_{22}^{-1} \end{bmatrix}$$

- α + β = 1

➔ **How to choose α ?**

How to choose α ?

❑ Test of predictability of the system

➢ **Reference: actual conventional evaluation (201412) ➔ DRP**

➢ **200 evaluation systems tested**

✓ EBV and REL from reduced conventional evaluation (**P**)

✓ P + Genotypes: α ranged from 0.01 to 0.99 (**P + G**)

✓ P + MACE EBV and REL delivered in 201012 (**P + M**)

✓ P + M + Genotypes: α ranged from 0.01 to 0.99 (**P + G + M**)

➢ **Bulls with   EDC = 20 in actual conventional evaluation**
EDCr = 0 in reduced conventional evaluation

➢ **Regression of DRP on (G)EBV with EDC as a weight**
➔ Minimization of RMSE

Data

- ❏ 4,255 genotyped animals
  - ➢ **3,589 bulls and 666 cows**
  - ➢ **38,374 SNP after editing**
- ❏ 6-generations extracted pedigree: 26,260 animals

- ❏ Traits: milk, fat and protein yields, SCS, conformation traits

- ❏ Walloon EBV (EBV_W)
- ❏ MACE EBV (EBV_M)
- ❏ Bulls with Walloon EBV contributing to MACE (EBV_{Wc})

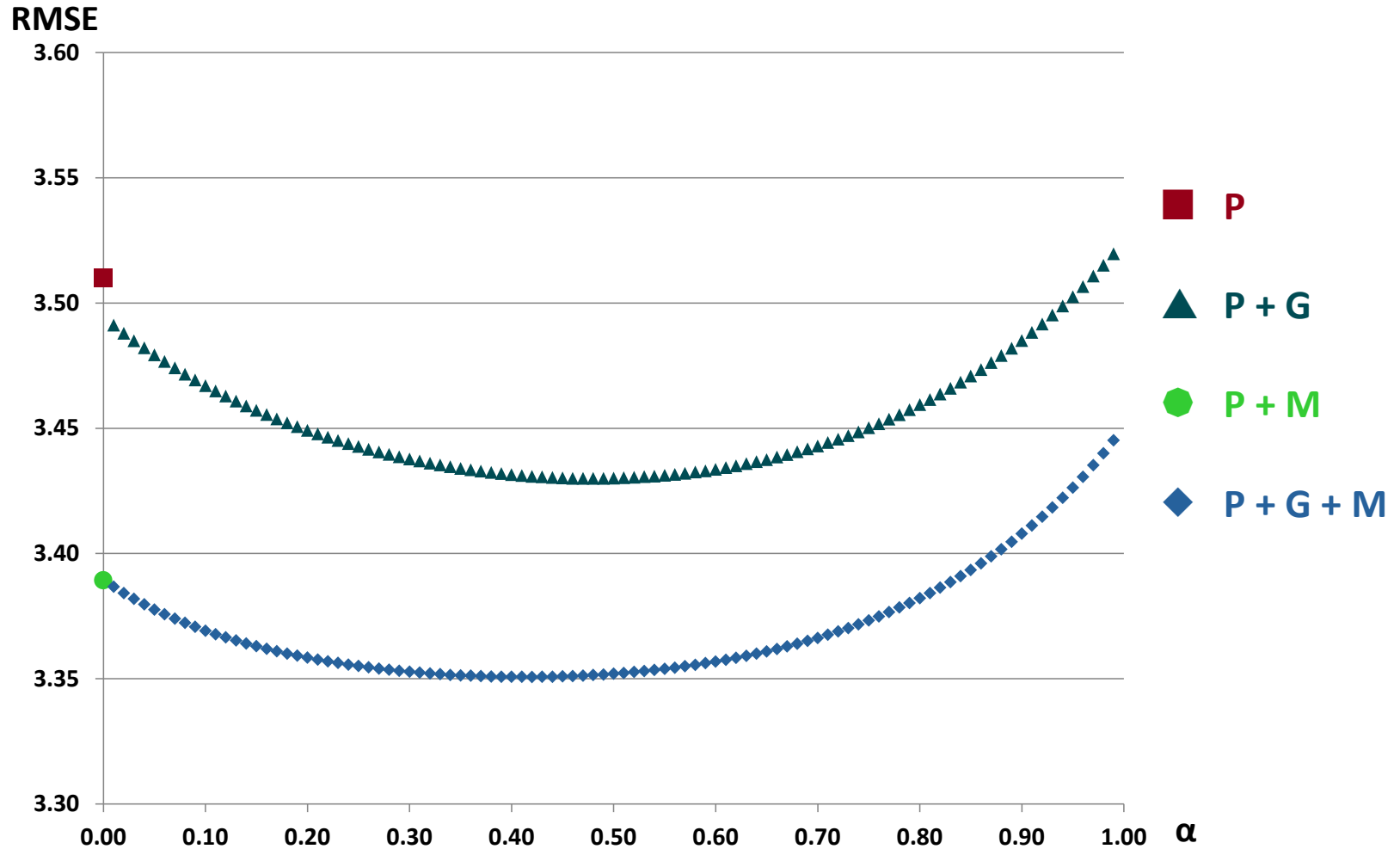- ❏ REL obtained through inversion of left-hand side

Results for α
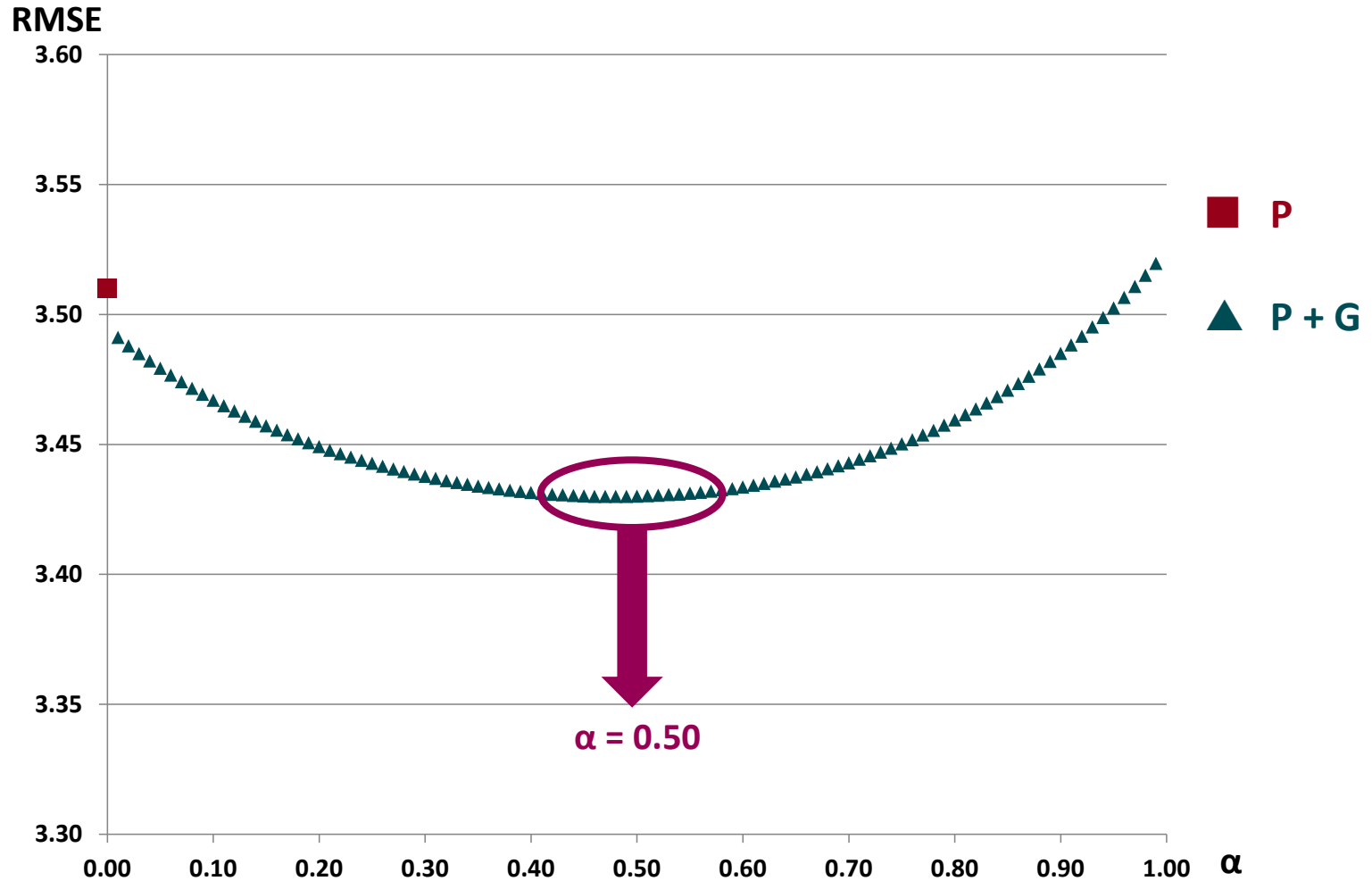
❑ Example for SCS

Results for α

□ Example for SCS

Results for α

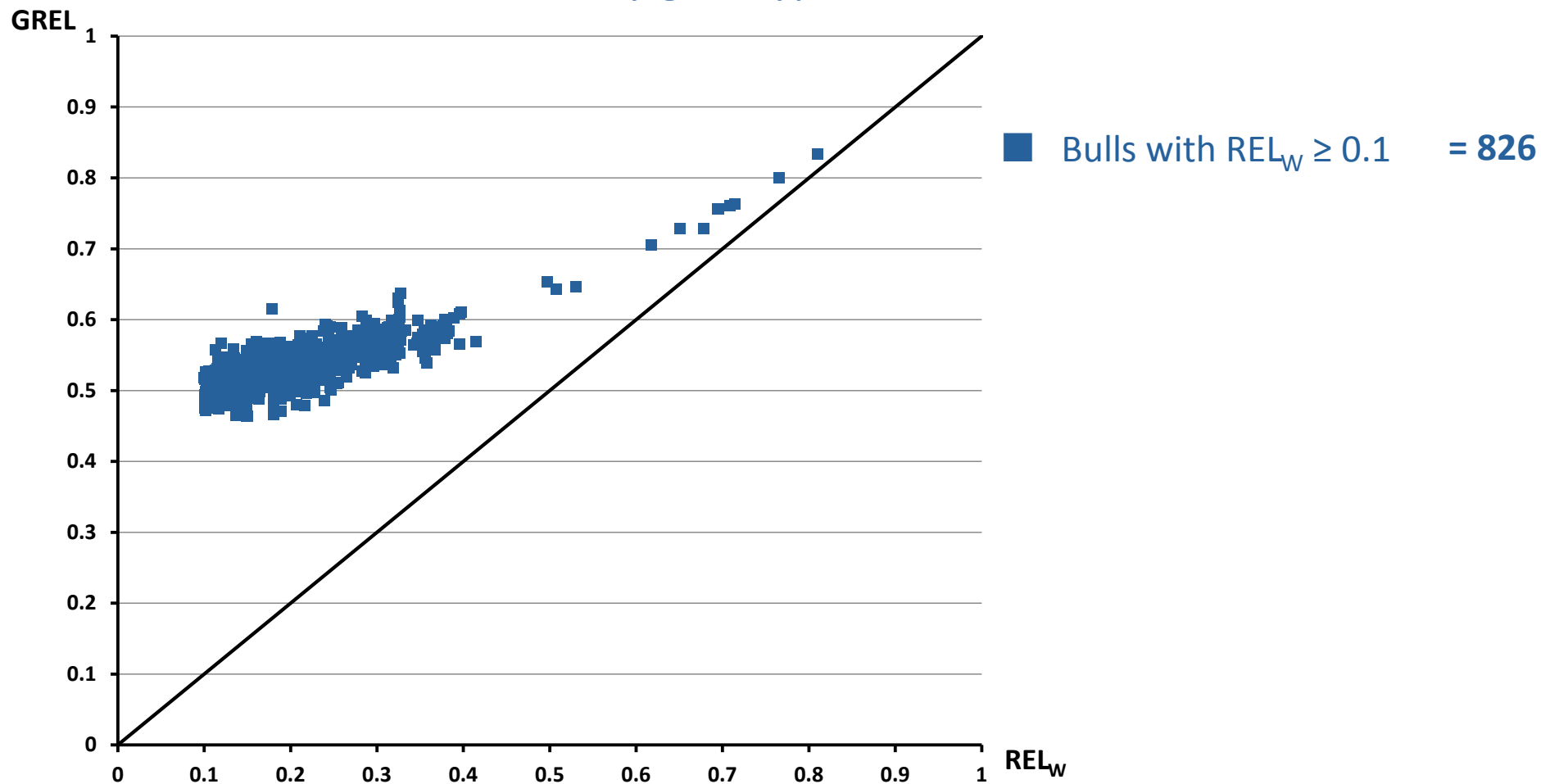|	α
Milk, Fat, Protein yields	0.60
SCS	0.50
Conformation traits	0.65

Results for *GEBV test*

❑ Passed test for:

➢ **Milk, fat and protein yields**

➢ **SCS**

➢ **Conformation traits**

❑ Difficulties:

➢ **Not always enough genotyped bulls to perform the *GEBV test***

➢ **Not always enough genotyped bulls to participate to GMACE evaluation**

➔ **Small population size**

Results for GEBV: e.g. Milk yield

❑ Increase of REL for genotyped animals born after 2007, without MACE results and sired by genotyped bulls with MACE results

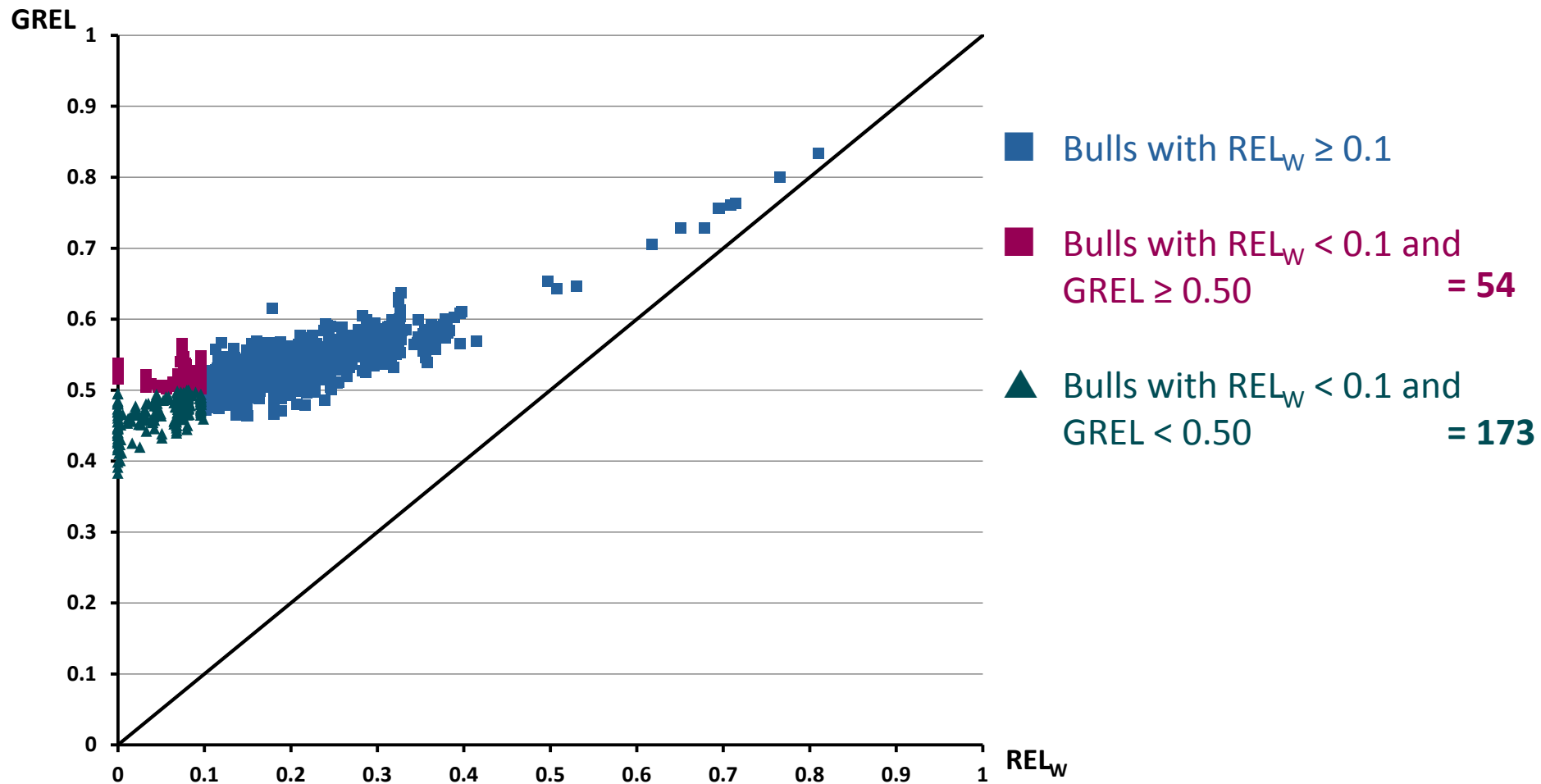Bulls with $REL_W \geq 0.1$ = 826

Results for GEBV: e.g. Milk yield

❑ Increase of REL for genotyped animals born after 2007, without MACE results and sired by genotyped bulls with MACE results

Legend:
- ■ Bulls with $REL_W \geq 0.1$
- ■ Bulls with $REL_W < 0.1$ and $GREL \geq 0.50$ **= 54**
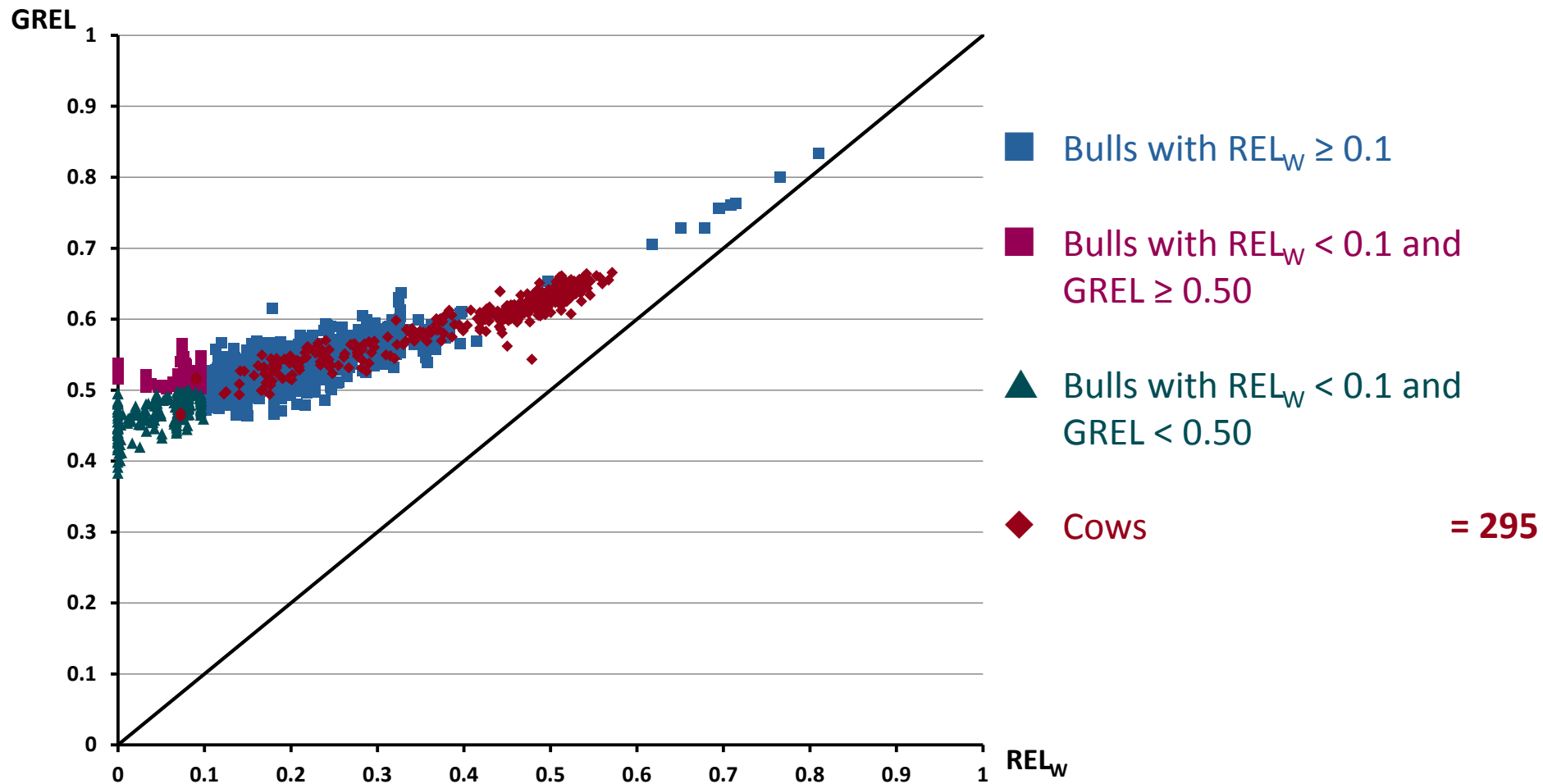- ▲ Bulls with $REL_W < 0.1$ and $GREL < 0.50$ **= 173**

Results for GEBV: e.g. Milk yield

❑ Increase of REL for genotyped animals born after 2007, without MACE results and sired by genotyped bulls with MACE results

■ Bulls with $REL_W \geq 0.1$

■ Bulls with $REL_W < 0.1$ and $GREL \geq 0.50$

▲ Bulls with $REL_W < 0.1$ and $GREL < 0.50$

◆ Cows   = 295

GMACE

- ❑ ± 800 – 1.000 GEBV with GREL ≥ 0.50 for bulls born after 2007
- ❑ GMACE delivered in decembre 2014

GMACE

❑ ± 800 – 1.000 GEBV with GREL ≥ 0.50 for bulls born after 2007

❑ GMACE delivered in decembre 2014

❑ Bulls:

More than 8.500-9.000 'new' bulls with GMACE value

Few bulls in common between GEBV and GMACE

	Bulls
Milk	231
Fat	231
Protein	231
SCS	230
Stature	242
Udder support	242

❖ Some bulls enter in MACE evaluation

❖ 70-80 bulls through file734

❖ GEBV sended but no GMACE return ?!

GMACE

- ± 800 – 1.000 GEBV with GREL ≥ 0.50 for bulls born after 2007
- GMACE delivered in decembre 2014
- Bulls
- High correlation between GEBV and GMACE

	Bulls	Correlation GEBV & GMACE
Milk	231	0.936
Fat	231	0.936
Protein	231	0.954
SCS	230	0.865
Stature	242	0.926
Udder support	242	0.957

GMACE

- ❏ ± 800 – 1.000 GEBV with GREL ≥ 0.50 for bulls born after 2007
- ❏ GMACE delivered in decembre 2014
- ❏ Bulls
- ❏ High correlation between GEBV and GMACE
- ❏ Increase of reliability through GMACE evaluation system

|	Bulls	Correlation GEBV & GMACE	$REL_{MACE} - REL_{GEBV}$			
			Mean	STD	Min.	Max.
Milk	231	0.936	0.09	0.07	0.00	0.19
Fat	231	0.936	0.09	0.07	0.00	0.20
Protein	231	0.954	0.09	0.06	0.00	0.19
SCS	230	0.865	0.13	0.09	0.00	0.25
Stature	242	0.926	0.12	0.08	0.00	0.26
Udder support	242	0.957	0.07	0.06	0.00	0.16

Conclusion

❑ Walloon genomic evaluation system

➢ **Bayesian approach integrates well MACE results into ssBLUP**
  ➔ **Recovers indirectly large amount of phenotypic information**

➢ **Highly adapted for our small population size**

➢ **Optimal use of cow and bull genotypes**
  ➔ **Accurate prediction for genotyped animals**

➢ **Easily adaptable (e.g., use of correlated traits from MACE),
  also therefore useful for novel traits as fatty acids or methane**

Conclusion

❑ GMACE evaluation system

➢ **New bulls (unfortunately some important missing)**

➢ **Increase of reliability up to 0.25 for bulls with Walloon GEBV**

➢ **GMACE highly correlated with GEBV**
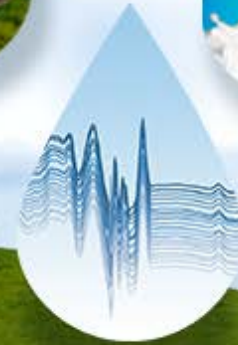
"From milk analysis to advisory tools"

www.namur2015.be

❑ Acknowledgments for financial support

➢ **Service Public de Wallonie (SPW – DGO3, Belgium) through project D31-1274 DairySNP**

➢ **National Fund for Scientific Research**

❑ Are also acknowledged

➢ **Animal and Dairy Science Department, University of Georgia, Athens, USA for collaboration in the development of evaluation software**

➢ **CECI for computational resources**

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