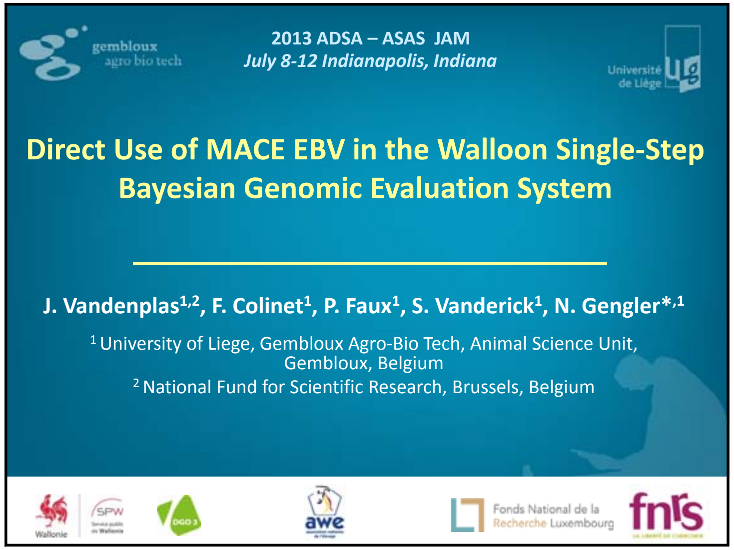
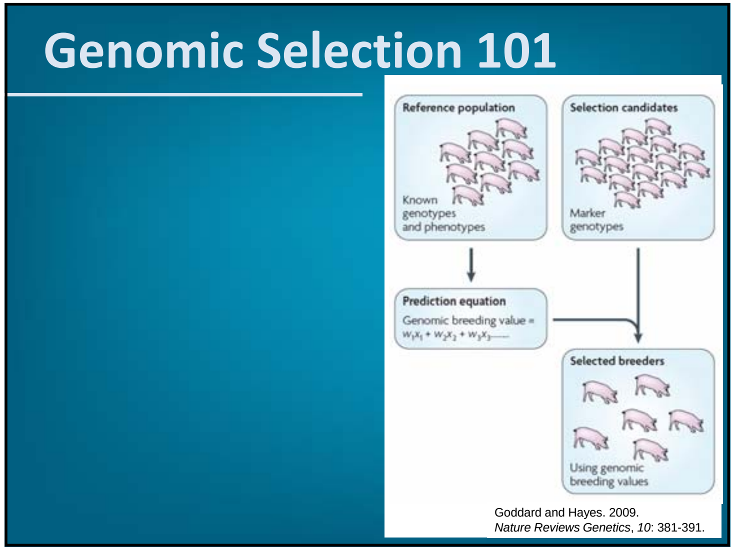


2013 ADSA – ASAS JAM
July 8-12 Indianapolis, Indiana

Direct Use of MACE EBV in the Walloon Single-Step Bayesian Genomic Evaluation System

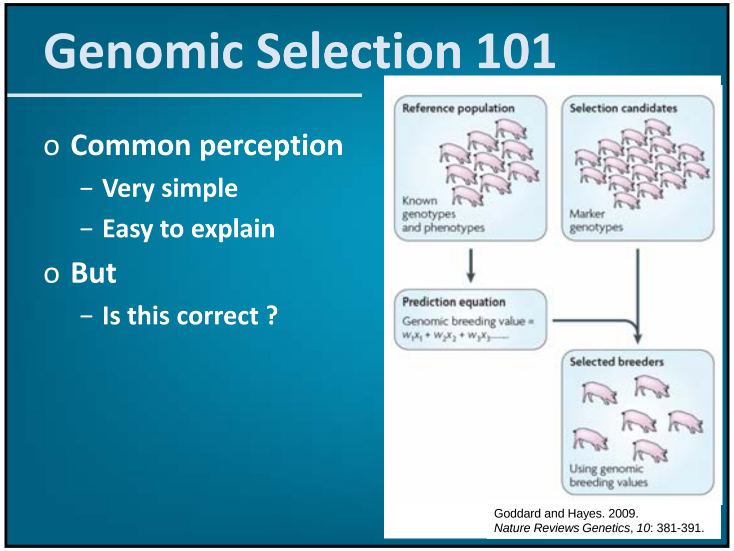
J. Vandenplas[1,2], F. Colinet[1], P. Faux[1], S. Vanderick[1], N. Gengler*[,1]

[1] University of Liege, Gembloux Agro-Bio Tech, Animal Science Unit, Gembloux, Belgium
[2] National Fund for Scientific Research, Brussels, Belgium



Genomic Selection 101

Goddard and Hayes. 2009.
Nature Reviews Genetics, *10*: 381-391.



Genomic Selection 101

- Common perception
  - Very simple
  - Easy to explain
- But
  - Is this correct ?

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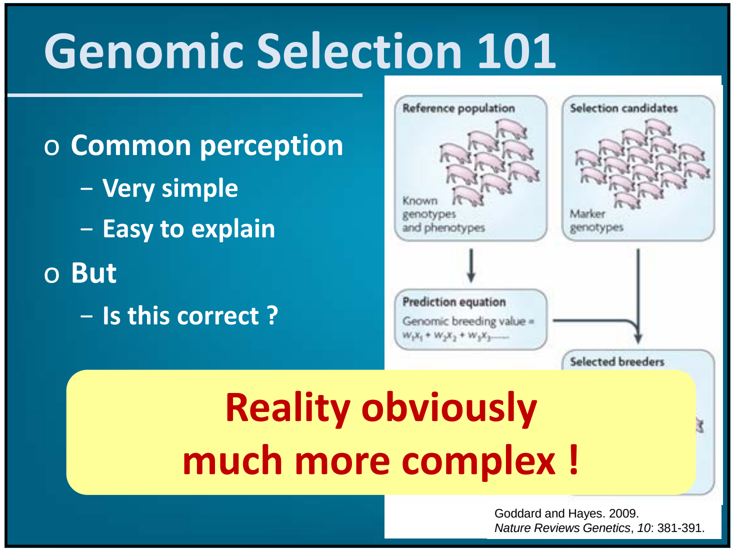

Genomic Selection 101

- Common perception
  - Very simple
  - Easy to explain
- But
  - Is this correct ?

Reality obviously much more complex !

Goddard and Hayes. 2009.
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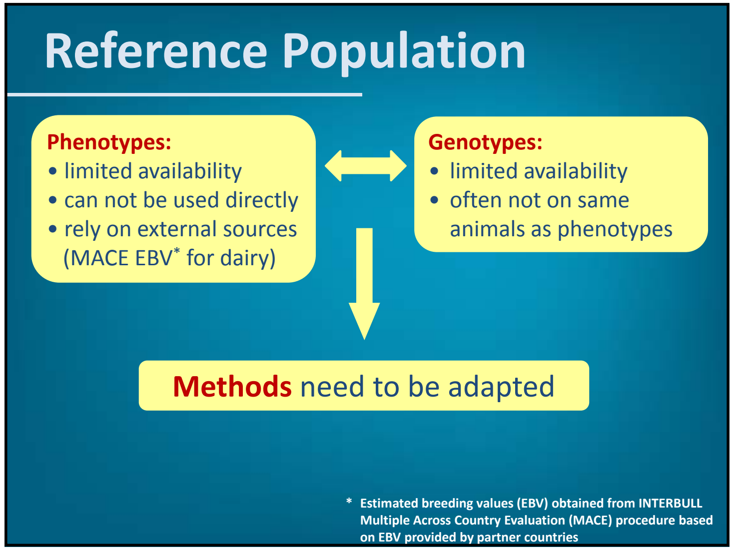


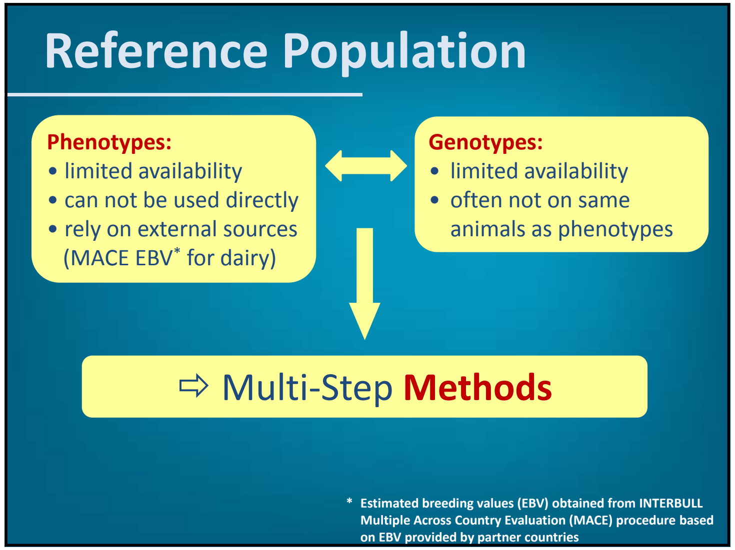
Reference Population

Phenotypes:
- limited availability
- can not be used directly
- rely on external sources (MACE EBV* for dairy)

Genotypes:
- limited availability
- often not on same animals as phenotypes

Methods need to be adapted

* Estimated breeding values (EBV) obtained from INTERBULL Multiple Across Country Evaluation (MACE) procedure based on EBV provided by partner countries



Reference Population

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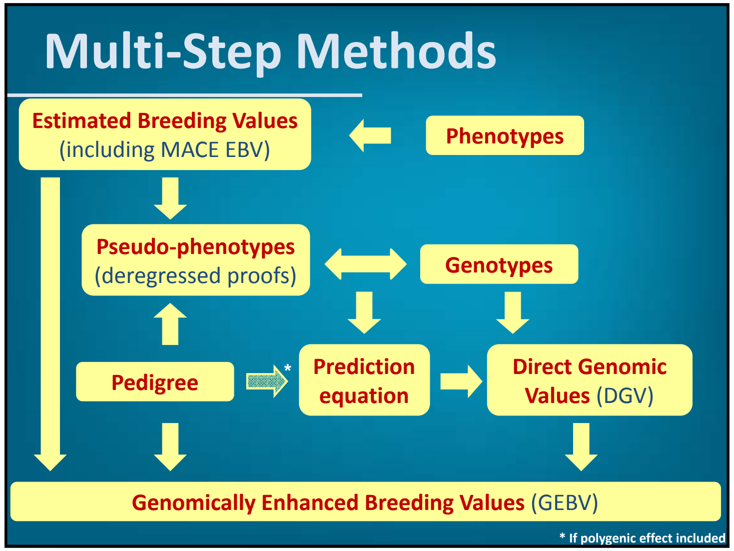
⇨ Multi-Step **Methods**

* Estimated breeding values (EBV) obtained from INTERBULL Multiple Across Country Evaluation (MACE) procedure based on EBV provided by partner countries



Multi-Step Methods

Estimated Breeding Values (including MACE EBV)

Phenotypes

Pseudo-phenotypes (deregressed proofs)

Genotypes

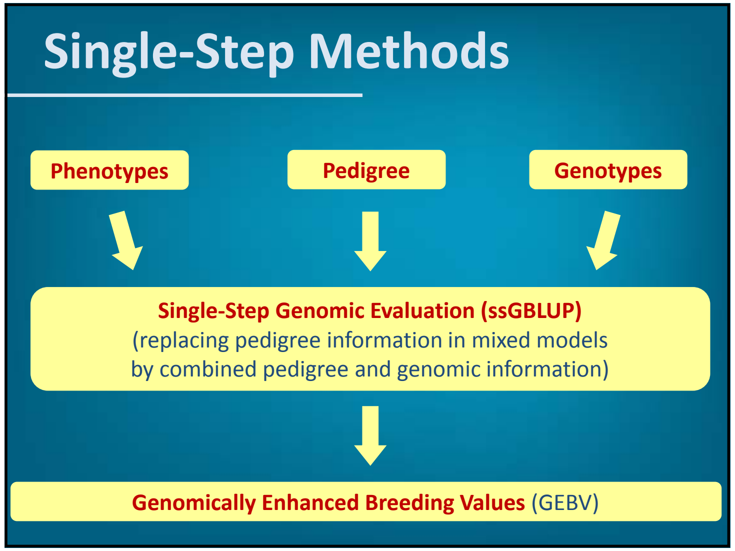
Pedigree

Prediction equation

Direct Genomic Values (DGV)

Genomically Enhanced Breeding Values (GEBV)

* If polygenic effect included



Single-Step Methods

Phenotypes

Pedigree

Genotypes

Single-Step Genomic Evaluation (ssGBLUP)
(replacing pedigree information in mixed models by combined pedigree and genomic information)

Genomically Enhanced Breeding Values (GEBV)

Innovations Needed !

- Considering simultaneously
  - Genotypes
  - Pedigree
  - Phenotypes
  - ⇨ but all local and foreign information simultaneously
- Avoiding
  - Deregression
  - Multiple considerations of contributions
- Maximum flexibility
  - Allowing to add and to subtract contributions from different information sources (e.g., local, MACE)
  - Avoiding double counting (e.g., local information already contributing to MACE EBV)

Innovations

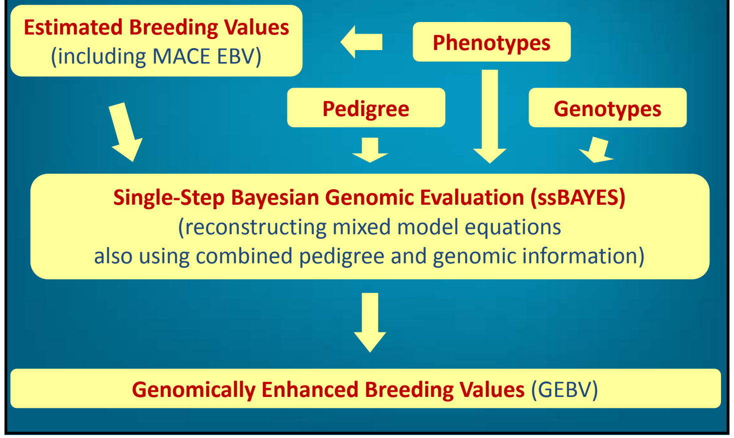
Bayesian Integration

- Preliminary work outlined by Vandenplas and Gengler (2012) J. Dairy Sci., 95: 1513-1526
- Creating system equivalent to mixed model equations
  - Integration of external information
  - Avoids deregression
- Adaptation to include multiple sources of information
  - E.g., adding MACE EBV, subtract local EBV included in MACE EBV

Context of Single-Step Genomic Prediction

- Replacing pedigree information in mixed models by combined pedigree and genomic
- Can therefore be applied to Bayesian models

Single-Step Bayesian Method



Estimated Breeding Values (including MACE EBV)

Phenotypes

Pedigree

Genotypes

Single-Step Bayesian Genomic Evaluation (ssBAYES)
(reconstructing mixed model equations
also using combined pedigree and genomic information)

Genomically Enhanced Breeding Values (GEBV)

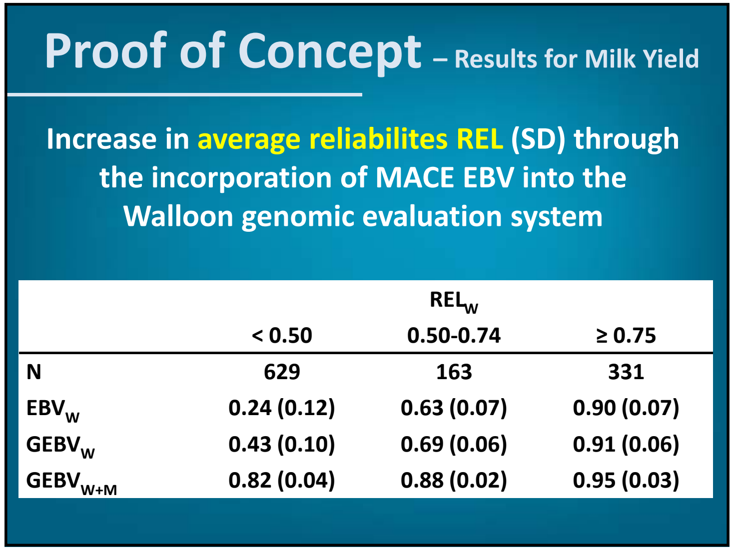
Proof of Concept

Walloon Genomic Evaluation System

- Small population (southern part of Belgium)
- Few genotypes
- Phenotypes ⇦ use of MACE EBV + local EBV
- ⇨ ssBAYES: optimal use of available data (including MACE EBV)

Local test-run ⇨ GMACE test-run

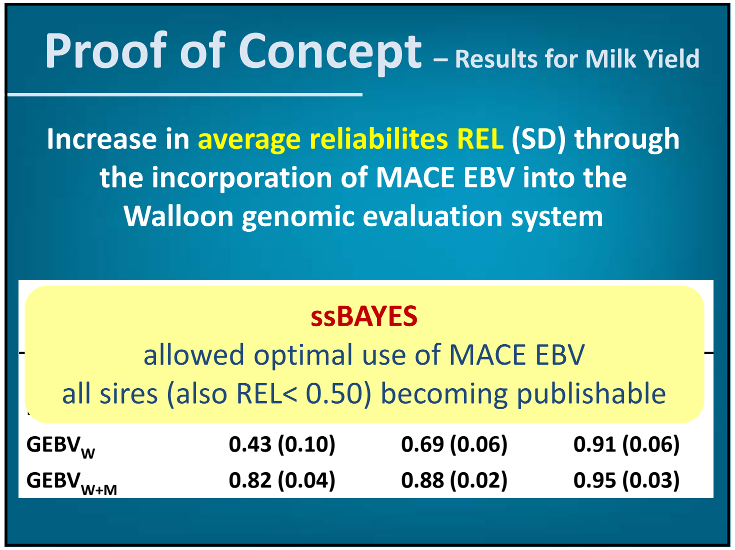
- 02/2013: passed the GEBV tests for yields + most type traits
- Results using data for 06/2013:
  - 16 234 animals
  - 12 046 Walloon EBV added
  - 1981 MACE EBV added (601 bulls sent, EBV subtracted)
  - 1909 cows and bulls with genotypes



Proof of Concept – Results for Milk Yield

Increase in average reliabilites REL (SD) through the incorporation of MACE EBV into the Walloon genomic evaluation system

	REL_W < 0.50	0.50-0.74	≥ 0.75
N	629	163	331
EBV_W	0.24 (0.12)	0.63 (0.07)	0.90 (0.07)
GEBV_W	0.43 (0.10)	0.69 (0.06)	0.91 (0.06)
GEBV_{W+M}	0.82 (0.04)	0.88 (0.02)	0.95 (0.03)



Proof of Concept – Results for Milk Yield

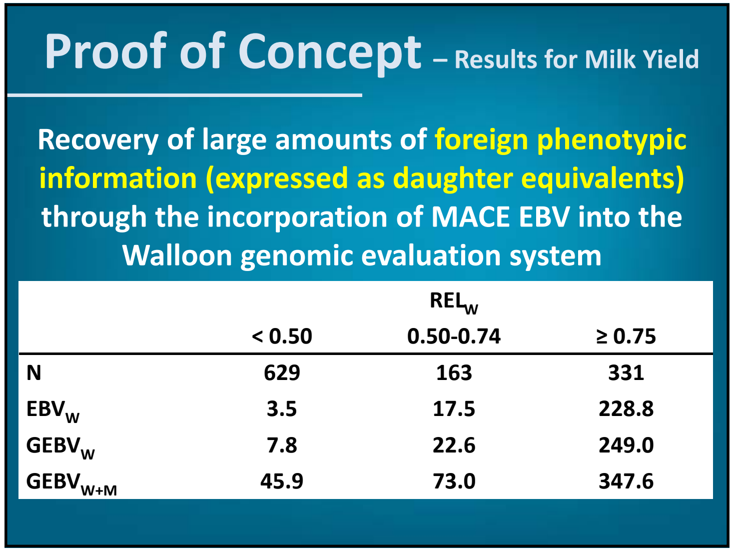
Increase in average reliabilites REL (SD) through the incorporation of MACE EBV into the Walloon genomic evaluation system

ssBAYES

allowed optimal use of MACE EBV

all sires (also REL< 0.50) becoming publishable

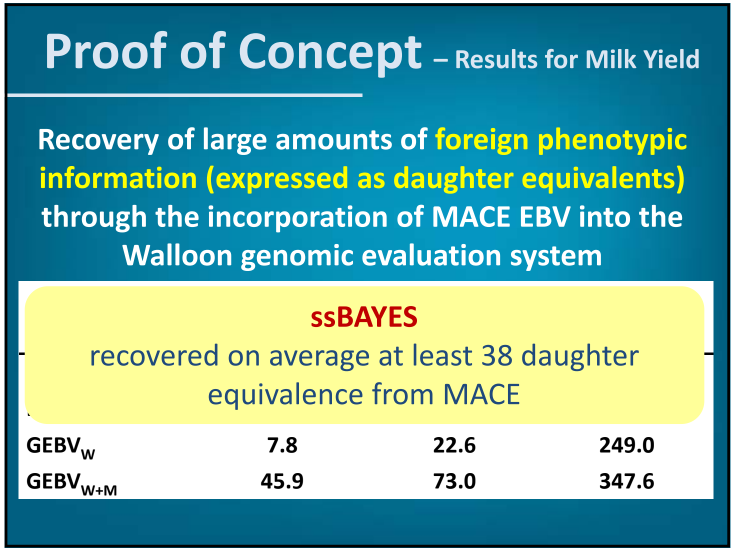
GEBV_W	0.43 (0.10)	0.69 (0.06)	0.91 (0.06)
GEBV_{W+M}	0.82 (0.04)	0.88 (0.02)	0.95 (0.03)



Proof of Concept – Results for Milk Yield

Recovery of large amounts of foreign phenotypic information (expressed as daughter equivalents) through the incorporation of MACE EBV into the Walloon genomic evaluation system

	REL_W < 0.50	0.50-0.74	≥ 0.75
N	629	163	331
EBV_W	3.5	17.5	228.8
GEBV_W	7.8	22.6	249.0
GEBV_{W+M}	45.9	73.0	347.6



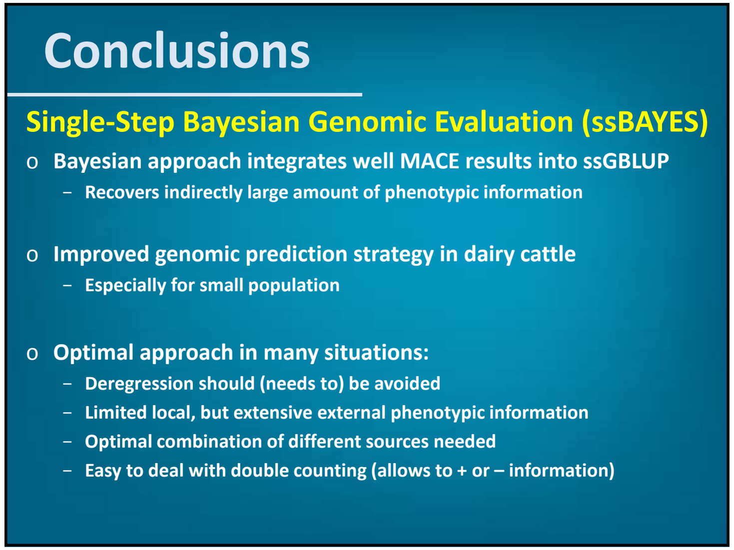
Proof of Concept – Results for Milk Yield

Recovery of large amounts of foreign phenotypic information (expressed as daughter equivalents) through the incorporation of MACE EBV into the Walloon genomic evaluation system

ssBAYES

recovered on average at least 38 daughter equivalence from MACE

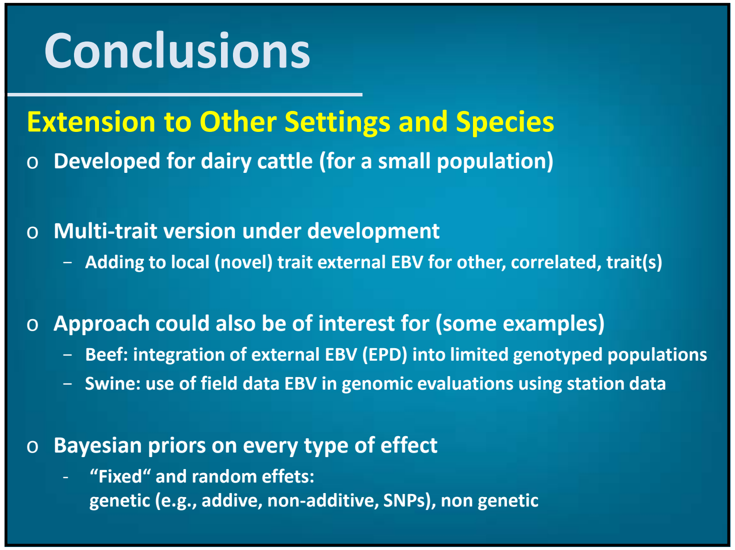
GEBV_W	7.8	22.6	249.0
GEBV_{W+M}	45.9	73.0	347.6



Conclusions

Single-Step Bayesian Genomic Evaluation (ssBAYES)

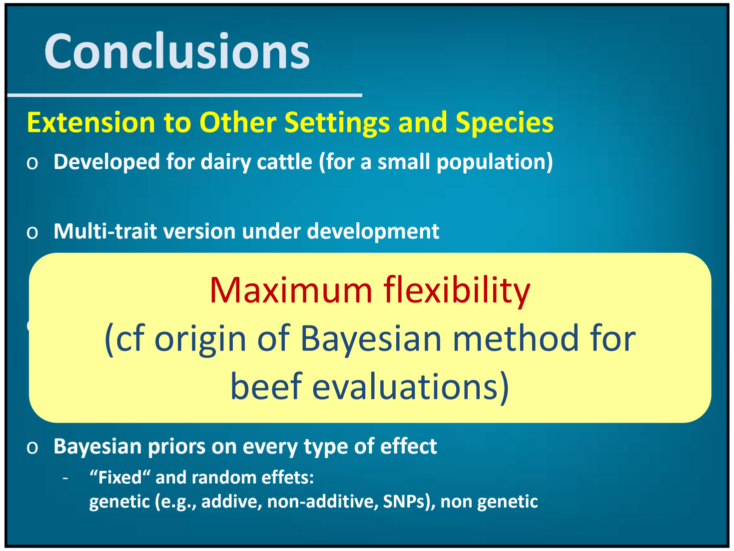
- Bayesian approach integrates well MACE results into ssGBLUP
  - Recovers indirectly large amount of phenotypic information
- Improved genomic prediction strategy in dairy cattle
  - Especially for small population
- Optimal approach in many situations:
  - Deregression should (needs to) be avoided
  - Limited local, but extensive external phenotypic information
  - Optimal combination of different sources needed
  - Easy to deal with double counting (allows to + or – information)



Conclusions

Extension to Other Settings and Species

- Developed for dairy cattle (for a small population)
- Multi-trait version under development
  - Adding to local (novel) trait external EBV for other, correlated, trait(s)
- Approach could also be of interest for (some examples)
  - Beef: integration of external EBV (EPD) into limited genotyped populations
  - Swine: use of field data EBV in genomic evaluations using station data
- Bayesian priors on every type of effect
  - “Fixed“ and random effets:
    genetic (e.g., addive, non-additive, SNPs), non genetic



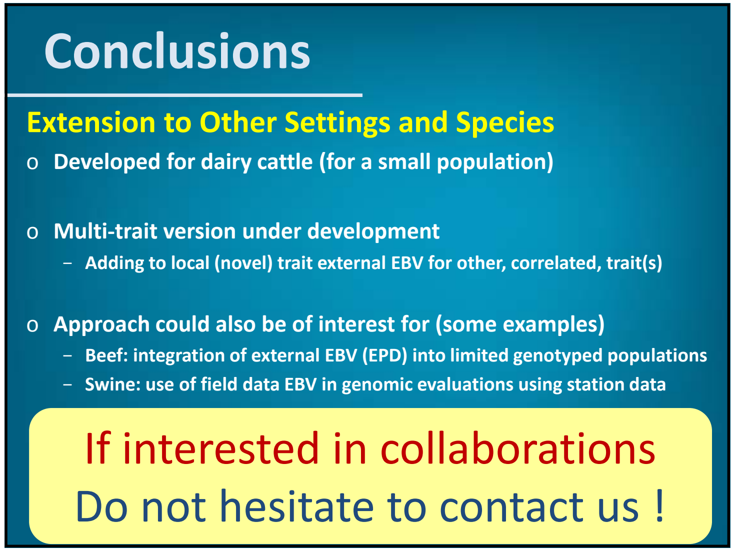
Conclusions

Extension to Other Settings and Species

- Developed for dairy cattle (for a small population)
- Multi-trait version under development

Maximum flexibility
(cf origin of Bayesian method for
beef evaluations)

- Bayesian priors on every type of effect
  - “Fixed“ and random effets:
    genetic (e.g., addive, non-additive, SNPs), non genetic



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If interested in collaborations
Do not hesitate to contact us !

Acknowledgements

E-mail of presenting author:
nicolas.gengler@ulg.ac.be