



# Toward a standardized Genomic reliability method

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# The G\_REL INTERBULL WG

Formed in 2014

Chair: Zengting Liu  
(*Bevin Harris 2014-2016*)

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Haifa Benhajali  
(*M. Nilforooshan 2014-2015*)



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# Why this group?

Currently:

- Genomic reliabilities are not comparable between countries
  - Different methods used
  - Lack of standard calculation procedure
- Consistency across evaluation?
  - Between conventional and genomic evaluations
  - Consistency across time: candidates → getting own phenotypes,  
→ entering reference population



# Why this group?

Similar situation in the past with conventional EDC

In 2011:

Interbull developed standardized procedures for calculating conventional EDC  
([https://wiki.interbull.org/public/CoP\\_AppendixIV](https://wiki.interbull.org/public/CoP_AppendixIV))

**An Interbull standard method for approximating Genomic reliabilities ?**



# Mission

To develop standard procedures for approximating GREL for national genomic evaluation

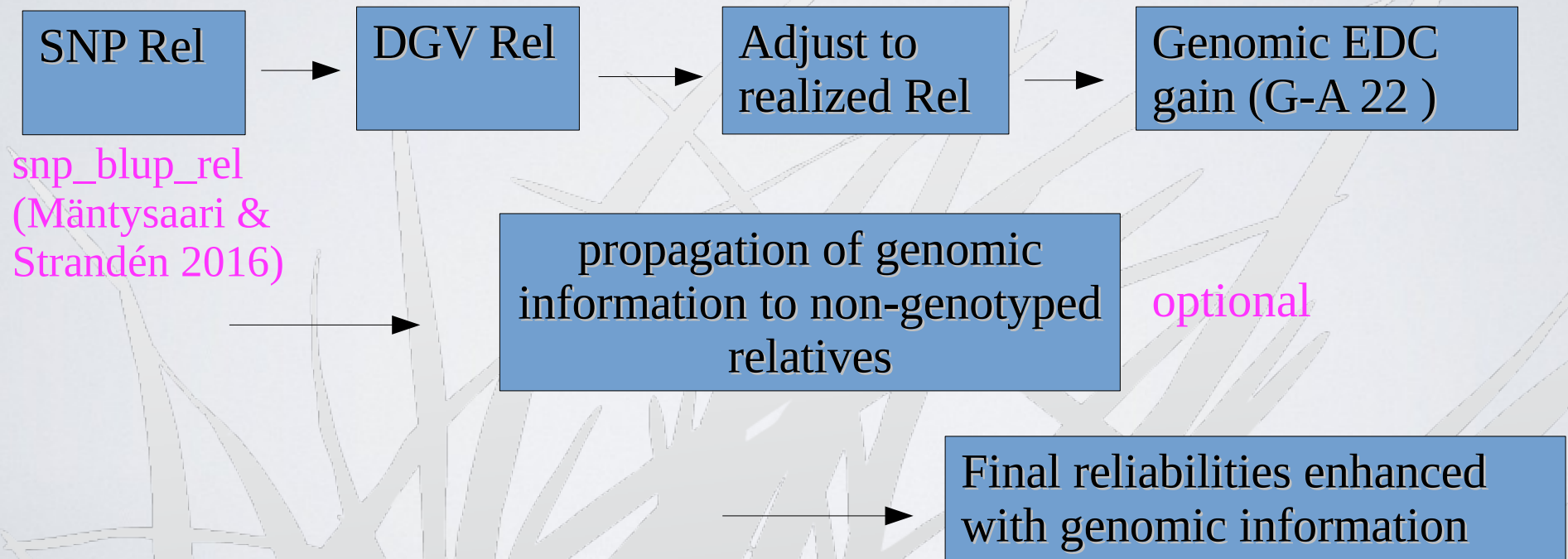
- ✓ Comparable GREL between countries
- ✓ Consistent with conventional reliabilities
- ✓ Feasible for any number of genotyped animals
- ✓ Applicable to single-step genomic models
- ✓ Efficient for frequent genomic evaluation
- ✓ Consistent with the genomic validation  $R^2$



# The method in short

Based on a SNP BLUP model  
*without a residual polygenic effect (at this stage)*  
(Liu et al., 2017, Interbull Bulletin: 51:75-85.)

Six steps





# The method in short

The method:

- Was presented at the Interbull open meeting in Tallin, 2017  
[http://www.interbull.org/static/web/09\\_00\\_Liu.pdf](http://www.interbull.org/static/web/09_00_Liu.pdf)
- is fully described in Liu et al. 2017. Interbull Bulletin: 51:75-85  
<https://journal.interbull.org/index.php/ib/article/view/1433>
- An additional document providing recommendation on how to avoid double counting of performance data contribution of cows, in case of a mixed reference population  
<http://www.interbull.org/static/web/A%20supplementary%20document%20to%20the%20Interbull%20genomic%20reliability%20method-1.pdf>



# Still things to be done

- Effect of allele frequency of SNP markers
  - Base population, current population, 0.5 for all
- How to get quick and frequent estimates of GREL
  - REL SNP most time-consuming
  - NGS: need for weekly genomic evaluations
- Verification and validation in different national evaluations systems
  - **Purpose of today's session**





# Today

- Snp\_blup\_rel - A tool to calculate reliabilities of individual genomic evaluations. *Esa A Mäntysaari, Martin Lidauer and Ismo Strandén*
- Experiences with the Interbull genomic reliability method applied to a mixed reference population. *Zengting Liu, H. Alkhoder and F. Reinhardt*
- Approximation of reliability in Single Step Models using the Interbull Standardized Genomic Reliability Method. *M. Erbe, J. Doderhoff, C. Edel*
- Reliabilities for genomic evaluation: Test of the SNPBLUP software with Spanish Holsteins data. *N. Charfeddine*
- Experiences with the implementation of the Interbull genomic reliability protocol. *H. Eding, J. Vanderplas, G de Jong*
- Using the snp-blup-rel software for prediction reliability of DGV in Poland. *Tomasz Suchocki, M. Mielczarek, A. Zarnecki, and J. Szyda*
- Approximating genomic reliabilities for genotyped Walloon Holstein cattle using the SNP-BLUP software. First experiences. *S. N. Darbaghshahi, S. Vanderick, R. Reis Mota, Nicolas Gengler.*



# Your feedback is still welcome

All documents cited in this presentation can be downloaded from  
[www.interbull.org](http://www.interbull.org)

If you need help

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# Acknowledgments

Esa Mäntysaari and Ismo Strandén, LUKE, Finland



*snp\_blup\_rel is developed and owned by Natural Resources Institute Finland (Luke). With the permission of Luke, the evaluation centers of the Interbull members can use snp\_blup\_rel program to estimate reliabilities for the snp BLUP genomic evaluations. You are not allowed to distribute the program to third parties. For other than above specified use, please contact Luke.*

All our colleagues who helped testing snp\_blup\_rel or the new Interbull Grel method, in particular today's speakers

Thanks to all of you for attending the GREL session