

EAAP 2009 - Barcelona

INCORPORATING GENOMIC INFORMATION INTO DAIRY INTERNATIONAL GENETIC EVALUATIONS

João Walter Dürr
Interbull Centre, SLU, Sweden



Presentation Outline

- Introduction
- Major issues
- Interbull action plan
- Developments



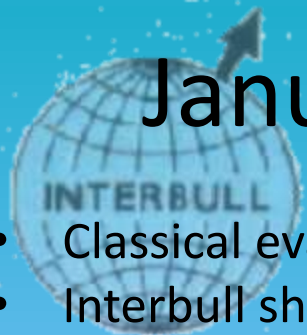
Incorporating genomic information

- Genome-wide dense marker maps (Meuwissen et al., 2001)
- Improves young bulls reliability
- SNP arrays very affordable
- Speeds up genetic progress
- Needs a sufficiently large reference population to predict SNP effects
 - **PHENOTYPES ARE STILL NEEDED!**



Interbull - Genomics

- Interbull Scientific Advisory Committee report (2008)
- Interbull-ICAR joint session on genomic selection (Niagara Falls, June 2008)
- Task Force on the role of genomic information on genetic evaluations (September 2008 to **June 2010**)
 - Set the scientific framework for the use of genomic data in national and international genetic evaluations
 - Promote the idea and benefits of international collaboration, under the auspices of Interbull, with regards to genomic evaluation and selection
- Survey on the use of Genomic Information (Dec. 2008)
- Technical Workshop (Uppsala, January 2009)
- 2009 Interbull Meeting in Barcelona
- Follow-up Workshop on Genomics (Paris, March 2010)



January 2009 Workshop Conclusions

- Classical evaluation of EBV is base of SNP effect estimation and GEBV calculation
- Interbull should continue providing MACE-EBVs that contain no genomic information
- Investigation and consideration of selection bias in national evaluation systems is needed
- Good definition of reference population with progeny test is crucial
- Collaboration between countries is highly desirable
 - Small populations: improve the size of reference population
 - Large populations: compare animals in different scales
- Interbull should progressively account for genomic information:
 - Validation procedures
 - Conversion equations for young bulls without progeny once validation procedures are in place
 - developing and implementing GMACE
 - applying different countries prediction equations for the same genotyped animals
- Interbull should provide a variety of different services for different countries, depending on the status of national genomic evaluation programs, the needs and the priorities of each member



Task Force Critical Issues

- Data accessibility
- Technical and process issues
 - Genomic selection bias
 - Validation
 - Data combination (EBV / DGV / GEBV)
 - Data (in)dependence
 - Weighting factors
 - Reliability
 - De-regression
 - SNP array consistency



Interbull Task Force: possible scenarios

Requirement	Scenario				
	I	II	III	IV	V
Genotypes	X	X			
National prediction equations		X			
National DGVs			X		
National GEBVs				X	X
National EBVs	X	X	X	X	
Developing, validating, testing and implementing proper methodology	X	X	X	X	X
Changing current sire models used by Interbull into animal models (account for dam genomic information)	X	X			
New framework of analysis on top of current in a very short period	X	X			
Estimating SNP effects several times per year	X	X			
Same SNP array to genotype the animals	X	X			

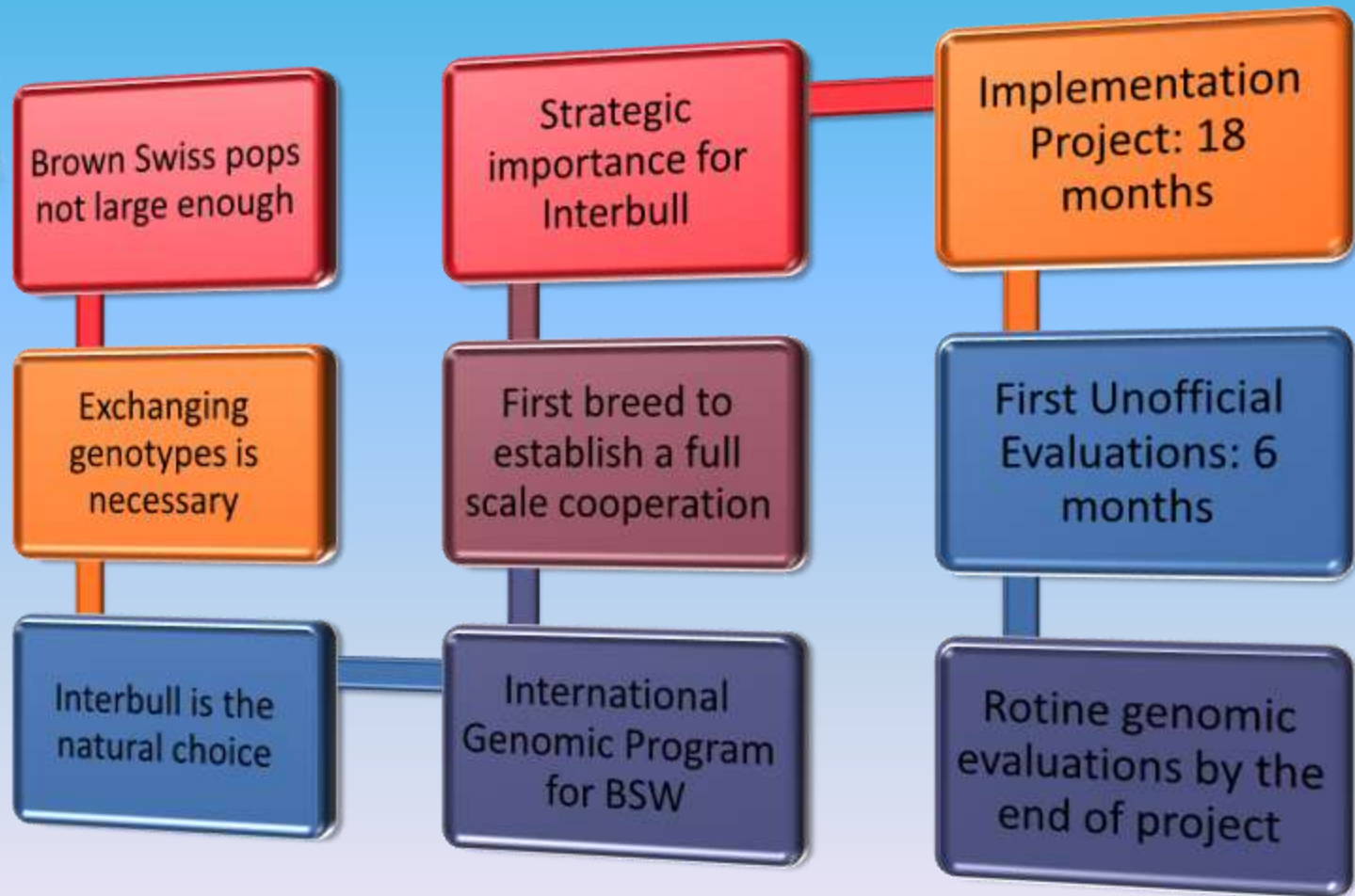


Benefits of GENOMIC Data Exchange

- Improves reference population
- Avoids that same individuals are genotyped several times
- SNP effects differ between countries (G x E)
- EU trade regulations
- Traits difficult to record
- Low heritability traits
- Young bulls can be simultaneously evaluated in several country scales
- Facilitates accounting for biases due to pre-selection
- Validation of methods and results
- Standardization of procedures and quality control
- Integrating genomic information from different SNP arrays
- Monitoring genetic variability and inbreeding worldwide
- Confidentiality



Brown Swiss Proposal





Cooperative software

- Coffey & Mrode, 2009
- Collaborative software development and testing for genomic evaluation is a reality
- Basic framework has been established
- Some modules are already available
- Needs continuing committed activity (people)
- Seek funding



Post-Workshop Developments

- USA, New Zealand, Ireland, France and Canada have published official GEBVs to date
 - Expected soon: the Netherlands, Germany-Austria, Australia, Nordic countries, Poland, Italy,...?
- International genotype database for Brown Swiss to be implemented at Interbull Centre with data from members of the European BSW Federation, which is to be used as a common reference population
- Ireland, UK, Spain, Belgium, Poland and Switzerland are starting to share genotyped bull IDs and possibly will evolve to exchange genotypes through Interbull
- Interbull Centre hired a post-doctoral scientist to work on genomic evaluations



Developments

- GMACE (VanRaden & Sullivan, 2009; Sullivan & VanRaden, 2009)
- Selection bias (Clotilde & Ducrocq, 2009; Liu et al., 2009)
- Combining DGV & EBV (Ducrocq & Liu, 2009)
- Reliabilities (Calus et al., 2009)
- Validation (Kistemaker & Sullivan, 2009)
- Single step genomic evaluation (Miszta et al., 2009)
- Multi-trait genomic prediction (Calus & Veerkamp, 2009)



Interbull short-term plans

- Conversion equations (Loberg et al., 2009)
- Research run for validation procedures (October 2009)
- GMACE research run (December 2009)
- Multicountry genotype database – BSW project (Next 18 months)
- GMACE test run (May 2010)
- GMACE implementation (August 2010)



Conclusions

- Interbull still has a major contribution
 - Future existence of conventional EBV is essential
 - Exchange between countries allows improving reference population
 - Importing countries still need a fair comparison
 - Genotype by Environment Interaction still exists!
- Challenges
 - Bias
 - Inbreeding
 - Keep and improve quality of phenotypic data collection



Acknowledgements

- G. Banos
- M. Calus
- V. Ducrocq
- H. Jorjani
- Z. Liu
- E. Mäntysaari
- P. Sullivan
- P. VanRaden



Joao.Durr@Hgen.SLU.se

THANK YOU!