Interbull Survey on the Use of Genomic Information

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Introduction

In December 2008 Interbull Centre sent out a survey about genomic selection to all member organizations participating in the international genetic evaluations. The questions in the survey were extensive and covered many aspects of genomic selection. The answer rate of the survey was 100%.

The purpose of the survey was to paint a picture of the situation today in the world of genetic evaluations of dairy cattle when it comes to genomic selection. Asking questions like, which countries have started, which plan to start, are there any co-operations between countries, which animals are being genotyped and evaluated and what methodology is being used.

Summary results from questionnaire

Table 1a. Does your country include genomic information in genetic evaluation of dairy cattle?

Yes	0	
planning to start in	11	NZL, ISR, FRA[1], IRL, CAN, DEU(HOL), USA[2], AUT, POL, ESP, AUS
not defined yet	14	
prefer not answering	0	
No	6	

[1] YES, 2009 for some official results; and 2011 planned for all official results. Notice: Genomic information has been included in unofficial genetic evaluation since 2001 (with microsatellite markers) and 2008 (with SNPs).
[2] YES, Official in January 2009, preliminary PTAs distributed since April 2008.

Table 1b. Year of planned start of genomic selection.

Planning to start in	
2009	NZL, ISR, FRA, IRL, CAN, DEU(HOL), USA, ESP[1]
2010	AUT, POL, AUS

[1] depending on genotypes availability. Combined genomic + traditional evaluations in 2010.

Table 2a. Who owns the cattle genomic data in your country?

Breeding companies	4	ITA(HOL), JPN, NLD, NZL
Farmers	3	NOR, ITA(BSW), AUT
More than one body	7	FRA, ITA(SIM), ISR, CAN, GBR, DEU(SIM), USA
Other	5	DNK, FIN, SWE, CHE, AUS
Not defined yet	12	
prefer not answering	0	

ESP. Not defined yet, It will be defined in next months, it seems ownership will be breeder assoc + AI units.

Table 2b. If more than one body.

More than one body	
Breeding companies, INRA (50%), likely with the increase of genotyped animals	FRA
Farmers, Israel Cattle Breeders Associal	ISR
Breeding companies, and AI Stations	ITA(SIM)
Research institutes, breeding companies, farmers	DEU(SIM)
Farmers, The owner of the animal in question (AI for bulls & Farmers for females)	CAN
Farmers, those who own DNA (i.e. semen), maybe farmers may start taking DNA from their cows	GBR
Breeding companies, male genotypes controlled by CDDR and NAAB. Female genotypes paid for by farmers or breeding companies and controlled by breed associations.	USA

Table 2c. If body is other.

Other	
Project	DNK, FIN, SWE
Department of Primary Industries	AUS
Herd book organizations	CHE

Table 3. Where is the animal genotyping carried out in your country?

Commercial labs	12	AUT, ITA(HOL), FRA, JPN, GBR, ITA(SIM), IRL, ITA(BSW), CHE, DEU(SIM), CAN, USA[1]
University labs	8	NOR, DNK, EST, FIN, SWE, ISR, NLD, LVA
Publicly funded labs	1	AUS
Other	0	
Not defined yet	8	
Prefer not answering	1	

[1] Commercial lab, much of the initial genotyping was publicly funded at USDA and universities.

Table 4a. Who in your country performs genomic evaluation of cattle?

National evaluation center	15	AUT, NOR, DEU(HOL), IRL, CHE, DEU(SIM), CAN, ITA(HOL), NLD, USA, ISR, FRA, ITA(BSW), NZL[1], ESP[2]
Breeding company	0	
Other	4	AUS, DNK, FIN, SWE
Not defined yet	10	
Prefer not answering	1	

[1] National evaluation center, LIC and CRV acting independently from each other

[2] It will be run by National evaluation center, however a project with research institute will work on development and application of methods.

Table 4b. If owner is other.

Other	
Project	DNK, FIN, SWE
Research Departments in Associations with National evaluation centre	AUS

Table 5. What type of genomic evaluations are (will be) officially published in your country?

MACE EBVs blended w. genomics	3	NZL, GBR, USA
Nat' EBVs blended w. genomic	4	AUS, FRA, IRL, CAN[1]
Direct genomic value	1	POL
Other	0	
Not defined yet	21	
Prefer not answering	1	

[1] CAN, DGVs as well as MACE and national EBVs blended with DGVs will be publicly available

Table 6. Will conventional EBVs (without genomic information) continue to be calculated in your country?

Not at all	0	
Yes, not published	3	FRA, NZL, CAN
Yes, published	8	NOR, EST, POL, DEU(SIM), ZAF, SVN, USA, ITA(HOL)
Not defined yet	18	
Prefer not answering	1	

Table 7. Which breeds and traits are currently evaluated with genomic information?

Production traits	HOL	10	DNK, FIN, SWE, NZL, USA, AUS, CAN, FRA, DEU, NLD
	JER	3	NZL, USA, AUS
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Conformation traits	HOL	10	DNK, FIN, SWE, NZL, USA, AUS, CAN, FRA, DEU, NLD
	JER	3	NZL, USA, AUS
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Udder health traits	HOL	9	DNK, FIN, SWE, NZL, USA, CAN, FRA, DEU, NLD
	JER	2	NZL, USA
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Longevity traits	HOL	8	DNK, FIN, SWE, NZL, USA, CAN, DEU, NLD
	JER	2	NZL, USA
Calving traits	HOL	8	DNK, FIN, SWE, NZL, USA, CAN, DEU, NLD
	JER	2	NZL, USA
Female fertility traits	HOL	10	DNK, FIN, SWE, NZL, USA, AUS, CAN, FRA, DEU, NLD
	JER	3	NZL, USA, AUS
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Workability traits	HOL	8	DNK, FIN, SWE, NZL, CAN, DEU, NLD, FRA
	JER	1	NZL
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)

NZL. Note that these current evaluations are NOT conducted by the national centre
DNK. All traits in NTM (TOTAL Merit index) - Jersey, Holstein and Rdc considered

Table 8. Which breeds and traits are going to be evaluated with genomic information within the next three years?

Production traits			
	BSW	5	DEU, CHE, AUT, USA, ITA
	HOL	15	DNK, AUS, FIN, SWE, NZL, IRL, ITA, ISR, FRA, POL, NLD, AUT, CHE, USA, ESP
	JER	7	DNK, FIN, SWE, NZL, USA, AUS, CAN
	RDC	6	DNK, FIN, SWE, NZL, CAN, NOR
	SIM	4	ITA, AUT, CHE, DEU
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Conformation traits			
	BSW	4	CHE, AUT, USA, ITA
	HOL	14	DNK, AUS, FIN, SWE, NZL, IRL, ITA, FRA, POL, NLD, AUT, CHE, USA, ESP
	JER	7	DNK, FIN, SWE, NZL, USA, AUS, CAN
	RDC	6	DNK, FIN, SWE, NZL, CAN, NOR
	SIM	3	ITA, AUT, CHE
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Udder health traits			
	BSW	5	DEU, CHE, AUT, USA, ITA
	HOL	13	DNK, AUS, FIN, SWE, NZL, IRL, ITA, ISR, FRA, POL, NLD, CHE, USA
	JER	7	DNK, FIN, SWE, NZL, USA, AUS, CAN
	RDC	6	DNK, FIN, SWE, NZL, CAN, NOR
	SIM	4	ITA, AUT, CHE, DEU
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Longevity traits			
	BSW	5	DEU, CHE, AUT, USA, ITA
	HOL	15	DNK, AUS, FIN, SWE, NZL, IRL, ITA, ISR, FRA, POL, NLD, AUT, CHE, USA, ESP
	JER	7	DNK, FIN, SWE, NZL, USA, AUS, CAN
	RDC	6	DNK, FIN, SWE, NZL, CAN, NOR
	SIM	3	AUT, CHE, DEU
Calving traits			
	BSW	3	CHE, AUT, USA
	HOL	14	DNK, AUS, FIN, SWE, NZL, IRL, ITA, ISR, FRA, NLD, AUT, CHE, USA, ESP
	JER	7	DNK, FIN, SWE, NZL, USA, AUS, CAN
	RDC	6	DNK, FIN, SWE, NZL, CAN, NOR
	SIM	3	AUT, CHE, ITA
Female fertility traits			
	BSW	3	CHE, AUT, USA
	HOL	14	DNK, AUS, FIN, SWE, NZL, IRL, ITA, ISR, FRA, NLD, AUT, CHE, USA, ESP

	JER	7	DNK, FIN, SWE, NZL, USA, AUS, CAN
	RDC	6	DNK, FIN, SWE, NZL, CAN, NOR
	SIM	3	AUT, CHE, ITA
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Workability traits			
	BSW	3	CHE, AUT, ITA
	HOL	11	DNK, AUS, FIN, SWE, NZL, IRL, ITA, FRA, NLD, AUT, CHE
	JER	7	DNK, FIN, SWE, NZL, AUS, CAN
	RDC	6	DNK, FIN, SWE, NZL, CAN, NOR
	SIM	3	AUT, CHE, ITA
	FRM	1	FRA (Montbeliard)
	NOR	1	FRA (Normade)
Other	ITA		SIM beef traits (daily gain, muscling)
	AUT		other health traits (BSW, SIM)

Table 9. Which categories of animals are being (or will be) genotyped?

Foundation animals			
	Current	11	DNK, FIN, SWE, ITA(BSW), CAN, IRL, DEU(SIM), NZL, CHE, USA, NLD
	Future, 2009	5	DEU(HOL), ITA(SIM), FRA, ISR, ESP
Active proven bulls			
	current	14	DNK, ITA(HOL), ITA(BSW), CAN, DEU(HOL), IRL, CHE, NZL, FIN, SWE, AUT, USA, NLD, AUS
	Future, 2009	6	FRA, GBR, ISR, DEU(SIM), ITA(SIM), ESP
	Future, 2010	1	POL
Young unproven bulls			
	current	10	DNK, CAN, DEU(HOL), IRL, NZL, FIN, SWE, NLD, USA, AUS
	Future	2	ITA(HOL), ITA(BSW)
	Future, 2009	5	CHE, FRA, AUT, ISR, GBR
	Future, 2010	3	DEU(SIM), POL, ESP
Bull dams			
	current	7	DNK, CAN, FIN, SWE, AUT, USA, NLD
	Future	1	ITA(HOL)
	Future, 2009	5	CHE, FRA, NZL, DEU(HOL), IRL
	Future, 2010	1	ESP
	Future, 2011	1	POL
Milking cows			
	current	5	DNK[1], CAN, FIN[1], SWE[1], USA, AUS
	Future, 2009	3	DEU(HOL), FRA, IRL
Heifers			
	current	6	DNK[1], CAN, FIN[1], SWE[1], USA, NLD
	Future, 2009	3	DEU(HOL), FRA, IRL

[1] GS of heifer and milking cows is in relation to bull dam selection

Table 10. Which categories of animals are being (or will be) evaluated with genomic information?

Foundation animals			
	current	7	DNK, CAN, IRL, FIN, SWE, USA, NLD
	Future, 2009	4	ISR, NZL, DEU(HOL), ESP
	Future, 2010	1	AUT
	Future, 2011	1	FRA
Active proven bulls			
	current	9	DNK, CAN, DEU(HOL), IRL, FIN, SWE, AUS, USA, NLD
	Future	1	ITA(HOL)
	Future, 2009	2	NZL, ISR, ESP
	Future, 2010	2	POL, AUT
	Future, 2011	1	FRA
Young unproven bulls			
	current	9	DNK, CAN, DEU(HOL), IRL, FIN, SWE, AUS, USA, NLD
	Future	2	ITA(HOL), ITA(BSW)
	Future, 2009	4	CHE,FRA, ISR, NZL
	Future, 2010	4	DEU(SIM), GBR, AUT, POL, ESP
Bull dams			
	current	7	DNK, CAN, FIN, SWE, AUS, NLD, USA
	Future	2	ITA(HOL), IRL
	Future, 2009	4	CHE, ISR, DEU(HOL), NZL
	Future, 2010	1	AUT, ESP
	Future, 2011	3	DEU(SIM), FRA, POL
Milking cows			
	current	5	DNK[1], CAN, FIN[1], SWE[1], USA
	Future	2	DEU(SIM), IRL
	Future, 2009	3	ISR, NZL, DEU(HOL)
	Future, 2011	1	FRA
Heifers			
	current	6	DNK[1], CAN, FIN[1], SWE[1], USA, NLD
	Future	1	IRL
	Future, 2009	3	ISR, NZL, DEU(HOL)
	Future, 2011	1	FRA

[1] GS of heifer and milking cows is in relation to bull dam selection

Table 11a. Does your country cooperate with other country(ies) in genomic evaluations?

YES	DNK-FIN-SWE CAN-USA NLD-NZL IRL-NZL AUT-DEU

Table 11b. If probably in future.

Probably in future	FRA, DEU(SIM), DEU(HOL), ZAF, SVK, LVT, GBR, ESP, AUS

Table 12. Which is the SNP array that your country is using?

Customized CRV Illumina 60K BeadChip	1	NLD
Illumina Bovine SNP50 BeadChip,	21	ITA(HOL), ITA(SIM), ITA(BSW), CAN, JPN, DEU(HOL), IRL, CHE, DEU(SIM), NZL, DNK, SWE, ISR, FRA, FIN, USA, AUT, AUS, GBR, NOR, ESP
Affymetrix 25 K Bovine array	1	NOR

Table 13. Which methodology is being used to estimate SNP effects?

Baruch and Weller (2008) J. Dairy Sci. 91: 4365-4371.	1	ISR
Bayes A	1	IRL
Bayes B in development (among other methods), QTL BLUP (presently)	1	FRA
Bayes B	1	AUS[1]
Bayesian SNP model, Calus *et al.*, Genetics 178:553-561, 2008	1	NLD
BLUP	2	CAN, NZL
Non-linear deterministic model,	2	DEU(HOL), USA

[1] Still being researched, options include Bayes A, B and Dairy CRC methodologies

Table 14. What data is used for estimation of SNP effects?

Both national DYDs and degressed proofs based on MACE EBVs	1	IRL
Deregressed proofs - based on MACE EBVs	3	USA, NZL, CAN
Deregressed proofs - based on national EBVs	1	AUS
DYDs – national	3	DEU(SIM), DEU(HOL), FRA[1]
EBVs - international/MACE	1	ITA(SIM)
EBVs – national	1	NLD[2]
Phenotypic records	1	ISR

[1] DYDs - national, national YDs genotyped female

[2] EBVs - national, EBVs national + EBVs international/MACE

Table 15. What weighting factors are used in genomic evaluation?

Deregressed reliability	1	NZL[1]
EDC	2	FRA, DEU(HOL)
None	1	NLD
Reliability	3	AUS, USA, CAN[1]

[1] Like EDC but also available for cows - B Harris comment

[2] EDC for DGVs but REL for blending DGVs with national or MACE EBVs and Pas

Table 16. Is a polygenic effect included in genomic evaluation?

No	4	USA, CAN, NZL, HOL(SIM)
Yes	1	AUS
Yes, 5% genetic variance	1	DEU(HOL)
Yes, about 0.00	1	NLD
Yes, polygenic component, QTL variance removed	1	FRA

Table 17. What reliability method is used for GEBV?

Different REL for each genotyped animal,	1	NLD
Direct matrix inversion, then discounted to estimate realized	1	USA
Direct matrix inversion for REL approximation	4	CAN[1], NZL, EU(HOL), FRA

[1] Direct matrix inversion yields a different REL for each genotyped animal

Table 18. What kind of information is your country willing to provide for international genetic evaluations
through Interbull?

Any information necessary	1	IRL
DYDs	1	POL
GEBVs	3	ISR, CAN, USA
Identification of genotyped animals	5	ISR, CAN, USA, DEU(SIM), ITA(BSW)
Conventional EBVs	8	ISR, CAN, USA, DEU(SIM), ITA(BSW), SVK, SVN, ITA(HOL), ESP[1]
National EBVs blended with direct genomic values	2	CAN, USA
Direct genomic values (DGV)	1	CAN
Probably all of the above except DYDs	1	AUS

[1] Conventional evaluations. As genotype ownership is still not defined, it cannot be said more at the moment.

Table 19. Which is the expected role of Interbull in genomic evaluations?

AUS	Continue the current service for as long as a significant proportion of countries/animals/traits is not included in genomic evaluations. Provide a service similar to the current for BVs excluding genomic information, for as long as it improves reliability of Genomic BVs. Facilitate the exchange of genotype information among countries (allowing for country specific estimation of GEBVs), ideally Interbull would keep a database of all genotypes of genotyped animals and use these to estimate (country specific) SNP effects, as well as make genotypes available to countries (this is most helpful for small breeds). Promote international collaboration to estimate SNP effects. Be a platform for exchange of ideas.
BEL	As an importing country, Belgium (Walloon Region) is making extensive use of EBVs provided by Interbull. In the future we expect services from Interbull to continue allowing us to access most reliable international EBVs. It is the responsibility of all exporting countries to allow accurate and unbiased estimation of international EBVs through Interbull.
CAN	To continue to provide fair and technically sound international bull evaluations using official national evaluations for various traits from all participating countries. This should allow for the use official national evaluations that have genomic information included from some countries as well as traditional national evaluations from other countries.
CHE	Set standards, promote exchange of information on methods used, promote exchange of information on genotyped animals
DEU(HOL)	Facilitate exchanging genotype data among countries.
DNK	Depends very much of the role (effect) of genomic information in future breeding scheme - difficult to answer exact
ESP	Promote country collaboration and genotype sharing, establish new requisites for incorporating national proofs into international evaluations, specially for countries using already genomic evaluations. Also research into new methods and new services as i.e. "genomic MACE" for estimation of genotype effects on different countries, probably countries with small progeny test programs, as large ones will not participate, at least initially. Also, perhaps Interbull could deliver de-regressed international proofs into each national scale (but for all bulls not only those evaluated nationally) for being used for SNP estimation, as a new service.

FRA	First of all, it is expected that Interbull will continue to supply unbiased international breeding values based on phenotypic data only. This supposes corrections for biases due to genomic pre-selection of some bulls.It is also expected that Interbull will contribute to regulate the announced quality of genomic EBV 1) by defining what is the minimum requirements for a correct genomic evaluation, a correct way of combining genomic and classical evaluations and a correct way to compute reliabilities (we fear that artificially inflated reliabilities will distort fair comparisons); 2) by allowing the international community to a posteriori assess the quality of genomic selection schemes (by having a posteriori indicators of the true breeding value of the bulls based on phenotypic records); 3) by facilitating any collaboration between countries (on a voluntary basis), for example for the exchange of genotypes.
GBR	Keeper of SNP keys per country. Provider of MACE proofs incorporating SNP effects. Quality control. Validation of software and results
HUN	Interbull may coordinate cooperation on exchange of genomic information and research work on this topic across country.
IRL	Storage and analysis of genotypes and phenotypes. Ideally we would like to see Interbull generate the most accurate SNP effects for Ireland based on the genotype and phenotype information supplied by all other countries (if this is not feasible the phenotypic and genotype information from all countries signed up should be available to a member country to generate their own genomic key). Interbull should then provide international breeding values for all bulls as is currently done. Perhaps there is also a role for Interbull to provide a mechanism whereby when a country genotypes a young bull, the country gets back the breeding values based on all countries to trigger if a young bull who isn't very suited to the country he is born but may be a good test candidate in another country.
ISR	I'll will have to think about this more
ITA(HOL)	We expect that Interbull will continue to provide accurate estimates of the genetic levels of animals for all traits and on the scale of various countries, regardless of additional genomic information being available for some countries/animals/traits.
ITA(SIM)	Doing research in order to evaluate how GEBS from some countries could affect correlations among countries. After that, setting up clear rules and guidelines concerning inclusion of Genomic BVs, in particular about their reliabilities.
NLD	It is expected that via Interbull young bulls, having a GEBV but no daughters yet, are converted to other countries base and scale, and that genomically enhanced EBVs are converted.
NZL	To include national centre genomically enhanced BVs for bulls prior to progeny test, to provide genomically enhanced MACE BVs as "next best" estimates for country combinations that are unable to arrange SNP data sharing. Alternatively, to become a SNP clearing house - but it is hard to see why national centers would need MACE if the Centre provided them with SNP data for all bulls of interest.
POL	The role should be similar to that which INTERBULL played in implementing and running the EBV evaluation

USA	MACE results allow genotypes for foreign bulls (such as those from Canada) to be easily included in genomic equations. USDA genomic evaluations will be publicly available on our web site. We hope that MACE can convert GEBVs to other scales so that foreign breeders will have easy access to the best young bulls and more accurate information on proven bulls.
ZAF	Giving guidance on the use of GEBVs and GMACE, assist in integrating (especially developing economies) in global evaluations involving genomic information.

Conclusions

This survey has given a good overview of the status of genomic selection in dairy cattle in December 2008, but it has to be stressed that it is the situation at that time, development is rapid and a new survey in a year from now would most likely give very different result. Results tell us that as many as ten countries are planning to start using genomic information in their genetic evaluations of dairy cattle within the next two years and within the big group 'not defined yet' some countries might also start soon.

Independent research groups in the countries that are using genomic information have started the development of new methodologies. We can see that there are several methods mentioned for estimation of SNP effects, different reliability methods used and different data used for estimation of SNP effects.

From the comments about the role of Interbull in the future the wishes can be divided into three groups. (1) Service, to continue doing traditional international genetic evaluations free of genomic information, do genomic international evaluations and evaluations for young bulls with genotypic information but no daughters. (2) Facilitating exchange, the exchange could cover several areas such as genotypic data and methodologies. (3) Other, including issues such as setting standards and guidelines, validation, research and quality control.

Table 20. List of respondents.

Name	*Organization*	*Country*	*Email*
Gert Nieuwhof	ADHIS	Australia, AUS	gert.nieuwhof@dpi.vic.gov.au
Christian Fuerst	ZAR-ZuchtData	Austria, AUT	fuerst@zuchtdata.at
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Martin Verner	Czech Moravian Breeders Corporation	Czech Republic, CZE	vernerm@plemdat.cz
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