

Effects of Genomic Selection on Breeding Value Estimation and International Comparisons

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Traditional genetic evaluation versus genomic evaluation

Traditional selection schemes have been based on BLUP estimated breeding values, that combine in so called animal models phenotypic information from an animal and all its known relatives. In dairy cattle breeding the reliabilities range e.g. for milk production traits from 0.25 – 0.35 for a PA (parent average) to 0.99 for an AI bull that has thousands of progeny in the respective genetic evaluation system. Progeny testing breeding programmes are efficient but rather costly, because until recently there was no way to determine whether a young animal got the average sample of genes from its parents (the PA) or a better or poorer sample. Genetic progress can be achieved identifying offspring, that receive due to Mendelian Sampling a better set of genes from its parents.

Since recently dairy cattle can be genotyped for 54000 single nucleotide polymorphisms (SNP) markers, which represent single base changes within the DNA sequence at a cost of about 200 € per animal. This is much more efficient than the genotyping of microsatellite markers that have been used for some years in marker assisted BLUP evaluations.

Research has shown, that with more or less evenly spaced genetic markers (SNPs) and a representative reference group of bulls, associations between traits in the breeding goal, e.g. milk yield, type traits, somatic cell counts, longevity, fertility, etc. can be estimated that result in breeding values based on SNP data (eg Meuwissen et al, 2001, Schaeffer 2006). Since SNP data can be retrieved from a very young animal the genetic evaluation based on SNP data (=genomic evaluation) the reliability of a genomic EBV is considerably higher than a parent average (figure 1). This reliability is mainly based on the amount and quality of the data to derive the association between the SNP data and the traditional BLUP EBVs. With 3000-4000 bulls in the reference sample the reliability of a DGV (direct genomic value) is about 50-60% and with this nearly doubled compared to a PA.

Many national projects have been initiated, that implement this new technique in national genetic evaluation systems (table 1).

Figure 1: Increase in reliability of the BVs for AI bulls

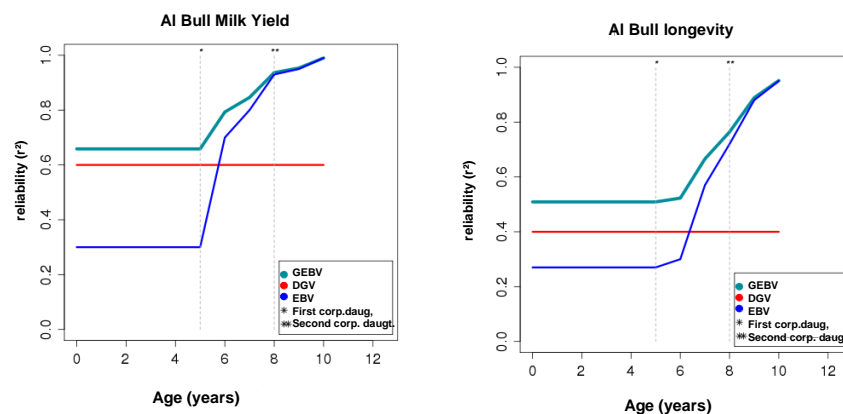


Table 1: Implementation of genomic evaluations (Status Jan. 2009)

Country	Project started	Chip	Size of reference population	GEBV	Official Implementation	Internal Implementation
USA	2003	Illumina	4.422 sires + 947 cows	✓	Jan. 2009	2008
CDN	2003	Illumina	4.127	✓	April 2009 ?	?
NZL	2005	Illumina	1.450	✓	2010 ?	(Aug. 2008)
AUS	2005	Illumina	1.600	✓	2010 ?	
NLD	2005	MG1 / MG2	1.500	✓	2009 ?	Aug. 2008
FRA	2007	Illumina	1.750	(MAS+gZW)	?	Fall 2008
DFS	2007	Illumina	2.012	?	?	Aug. 2008
POL	2008	Illumina	1.227	✓	2010	2009
(DEU /HOL)	2008	Illumina	3.000	✓	2010	2009

International comparisons

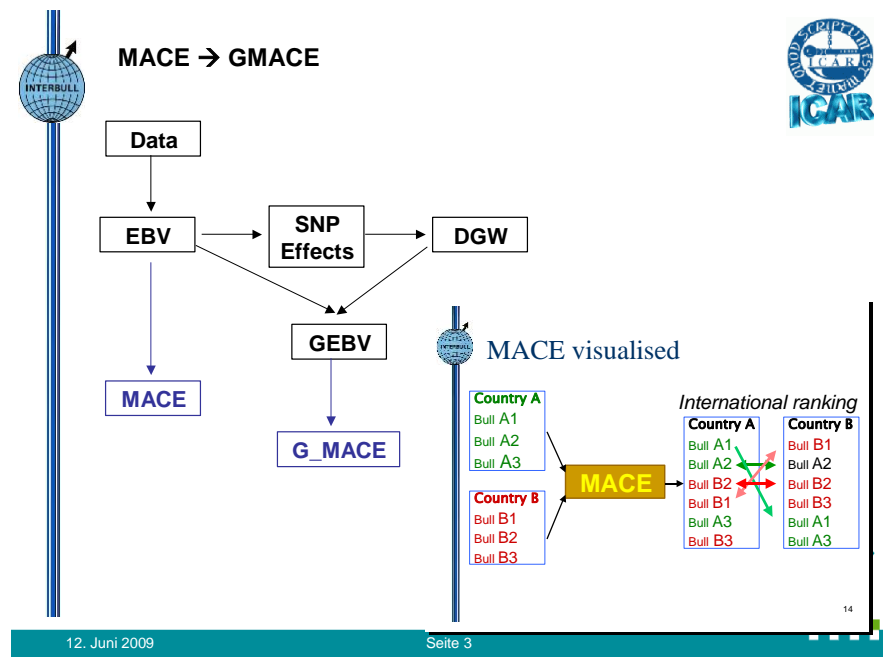
Interbull has addressed the topic of genomic evaluation already since its Interbull meeting in Dublin, 2007. In June 2008 (joint ICAR/Interbull session, Niagara Falls) and January 2009 (Interbull workshop, Uppsala) the relevant research and development work has been discussed within the Interbull framework. A detailed work plan has been developed that allows the stepwise implementation of genomic EBVs also in international comparisons after a validation procedure for national genomic EBVs has been developed until August 2009.

The steps are:

1. MACE conversion formulas can be used on an interim basis from August 2009 onwards
2. Genomic MACE (GMACE) is aimed to be implemented by early 2010
3. Application of the importing countries prediction equations on genotypes of traded animals can be envisioned by 2010/2011

Options 1 to 3 have increasing requirements of data that has to be available at Interbull but has also increasing benefit for the optimal ranking of imported animals (semen) in the importing country.

Figure 2 displays the principle of GMACE:



References

- Interbull 2009: Proceedings of the Interbull international workshop Genomic Information in Genetic Evaluations Uppsala, Sweden, January 26-29, 2009, bulletin N° 39, 2009
- Meuwissen T. H. E., B. J. Hayes, and M. E. Goddard, 2001, Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps, *Genetics*, Vol. 157, 1819-1829
- Schaeffer, L.R., 2006, Strategy for applying genome-wide selection in dairy cattle. *J. Anim. Breed. Genetics* 123, 218-223