

## Implementation and first year results on the use of genomic selection in dairy cattle in Ireland

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**Introduction** Genomic selection in Holstein-Friesian dairy cattle was launched in Ireland in February 2009. The objective of this document is to outline the implementation and the uptake of genomic estimated breeding values (GEBVs) in Ireland for Spring 2009. We also outline the results of the first group of Holstein-Friesian bulls that were selected on GEBVs compared to their progeny test proofs obtained in the August 2009 evaluations.

**Materials and methods** Berry *et al.* (2009) described in detail the methodology used for the estimation of GEBVs in Ireland. Briefly, the training population was made up of just over 1,000 Holstein-Friesian bulls, genotyped using the Illumina Bovine50 Beadchip. Direct genomic values (DGVs) are estimated in Ireland using mixed models equations by replacing the traditional numerator relationship matrix with a genomic relationship matrix as outlined by VanRaden (2008). The dependent variable included in the genomic evaluation are the deregressed traditional EBVs of the animal as outlined by Berry *et al.* (2009). Genomic EBVs (GEBVs) are the combination of the DGVs and the traditional EBVs. This blending procedure is done because not all animals in the pedigree are genotyped (genotypes of no females are currently included in the genomic evaluation) and therefore not all information is included in the genomic evaluation. The uptake of the use of genomically selected (GS) bulls was assessed on 349,000 AI insemination records collected via technician handhelds from January to June 2009. Initial results on the predictive ability of genomic selection was assessed by looking at the correlation of the daughter proven EBV to the DGVs, the GEBVs, and the parent average proof for 35 young test sires used in the 2006 national progeny test program and who received a daughter proof in the August 2009 evaluation. These bulls were marketed in the Spring 2009 breeding season as GS bulls with no daughter information.

**Results** The accuracy of genomic selection using forward prediction is reported elsewhere (Berry *et al.*, 2009). After consultation with representatives from the Irish dairy industry it was decided to publish GEBVs of individual bulls without progeny on the list of active bulls for the Spring 2009 breeding season. Bulls included on the active bull list had to have sufficient progeny born to have reliability for direct calving difficulty of  $\geq 50\%$  in the country of origin. Also the reliability of the GEBV for EBI, had to be  $\geq 35\%$ . In 2008, prior to the introduction of genomic evaluations, each sire on the active bull list had to have a reliability of EBI of  $\geq 58\%$ . Compared to 2008, the average EBI of the bulls on the list was higher, but the reliability was lower. In addition, younger sires replaced sires that had occupied the list for many years, but the number of bulls with daughters in Ireland decreased. The usage for the daughter proven bulls with daughters in Ireland (DP-IRL) was the highest at 37% of inseminations with GS bulls accounting for 34%, and proven bulls but with no Irish daughters (DP-INT) at 29%. The mean number of bulls used per herd was 3 for DP-IRL bulls, 2.7 for DP-INT bulls and 4 for GS bulls. The very positive uptake of GS bulls can be attributed to the difference in genetic merit between these bulls and the daughter proven bulls. The weighted average EBI of the GS bulls was €69, more than one standard deviation (€62), ahead of the DP-IRL bulls. The weighted average across all three groups of bulls used in 2009 was €38 more than the bulls used in 2008. The correlation and mean difference between parent average, DGV, GEBV and daughter EBV are given in Table 1. In terms of the predictive ability of genomic information the correlation between parent average and daughter proofs were consistently lower than those of the GEBV and the DGV. At this stage the DGVs are the best predictors of progeny performance however one must recognize the limitations of this analysis due only 35 bulls being included in this comparison, the average reliability of the sires is 80%, and the daughter records are not completed lactation records.

**Table 1** Correlations and mean difference between daughter proofs and GEBV, DGV, and parent average for 35 GS bulls selected when in lay-off in Spring 2009 but now with greater than 70% reliability for production traits based on daughters milking in 2009.

	Correlation			Mean Difference		
	GEBV	DGV	PA	GEBV	DGV	PA
Milk (kg)	0.64	0.65	0.63	65	50	77
Fat (kg)	0.51	0.57	0.4	2	2	3
Prot (kg)	0.59	0.65	0.53	2	1.5	2.2

**Conclusion** Overall the implementation of genomic evaluations in Ireland has been very successful. The uptake of the GS bulls has been very encouraging with farmers using several bulls as recommended to reduce the risks. Initial results on how the technology is working are promising and the introduction of genomic evaluations will generate greater genetic gain in the future. Research work is underway to increase the size of the training population, by incorporating multiple-trait across country (MACE) evaluations, to improve the accuracy of GEBVs.

### References

- Berry, D., Kearney, F. and Harris, B., 2009. Interbull Bulletin 39, 34-37.  
 VanRaden, P.M., 2008. Journal Dairy Science 91, 4414-4423.