Upgrading breeding value estimation in beef cattle

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Summary

This paper gives a summary of the possibility for applying genomic information for breeding value estimation in beef cattle breeding. This process is called genomic prediction and is now widely used in dairy cattle globally as well as in some beef and sheep populations. The advantage of genomic prediction is a more accurate estimate of the genetic merit of an individual at a young age thereby facilitating greater annual genetic gain, predominantly through shorter generation intervals. Genomic predictions are more advantageous for sex-linked (e.g., milk yield), low heritability (e.g., fertility) and difficult-to-measure (e.g., feed intake) traits. The larger the reference population, on average, the more accurate the genomic predictions; additionally, the closer genetically the reference population is to the candidate population, the greater the accuracy of genomic predictions. Research is continuing on strategies to generate accurate genomic predictions using a reference population consisting of multiple breeds (and crossbred). Retrospective analysis of real-life data where genomic predictions have been operation for several years clearly shows a benefit of this technology.

Keywords: SNP information, genomic evaluation, beef cattle

Introduction

A recent possibility to improve breeding value estimation and selection in beef cattle breeding is the use of genomic information. Applying of genomic information in animal breeding is not new. Monitoring of major-gene variants and lethal recessive mutations has been used for decades in screen animals, especially AI bulls. DNA information in the form of microsatellites has been used to trace animal products as well as being routinely used in parentage verification and assignment. Recent advancements in genomic technologies have facilitated the (low-cost) genotyping of animals for thousands of tiny DNA variants termed single nucleotide polymorphisms (SNPs). Statistical methodology was

developed (and is being refined) to simultaneously estimate the effect of these thousands of SNPs for a range of different performance traits. Large populations, termed reference populations, of animals with both DNA information (i.e., genotype) and performance information are required to estimate the SNP effects. The SNP genotype of a candidate animal times the SNP effect is used to calculate the breeding value of that candidate animal for that SNP; when summed across all SNPs, an overall breeding value, termed a direct genomic value, for that animal for that trait is derived. The direct genomic value is blended with pedigree information to produce a genomic (-enhanced) breeding value (GEBV).

Materials and methods

During the study relevant literature for genomic breeding value estimation for dairy herds moreover, when it was applied, beef herds was collected and evaluated. Furthermore, the experience of breed associations of oversee countries was analysed, too. The aim of this review is to provide an overview of the developments that occurred over the past decades to lay the foundation for genomic prediction with special regard to application in Hungarian beef cattle breeding.

Results and discussion

Traditionally the breeding value estimation is based on the phenotypic performance of the relative groups of the candidate animals. The development and implementation of official genomic evaluations for beef cattle has occurred later than its 2009 introduction in dairy. Interest in the more wide-spread application of genomic technology in cattle breeding has, however, rapidly intensified in recent years. This growing excitement has been fuelled by the rapidly declining cost of acquiring a genotype but also advancements in the statistical methodology to effectively and efficiently analyse the vast quantities of genomic data being generated. In Europe genomic evaluations in beef cattle are currently not official in any country, but research on genomic evaluation or access to unofficial genomic proofs exists in many countries (Berry et al., 2016).

While heretofore applications of genomics in cattle breeding exploited knowledge on only few pieces of DNA (e.g., Merial/Igenity marker panels), today's application of genomic selection utilises information on tens or hundreds of thousands of pieces of DNA of an individual. The increased information available per results in a new-proven more accurate genetic evaluation (Berry, 2016).

Single nucleotide polymorphisms are abundant, bi-allelic, single locus markers located at approximately 3 kb intervals in the *Bos taurus* genome with an estimated total of nearly 40 million SNP which were identified during sequencing (Seidel, 2010).

The technology commonly used internationally heretofore in genomic evaluation and selection programs exploits DNA information at 54 001 locations, or less, across the animal's DNA. There are different platforms used to determine the genotype of an animal is referred to as a SNPchip (pronounced „snip-chip"). For example the base Illumina is a low density (LD) panel for 6 909 SNPs, while the total Illumina for 45 521 SNPs (Berry, 2016), however the newly developed BovineHD chip features 777 962 SNPs including the mitochondrial DNA (Marle-Köster et al., 2013).

The reliability of genomic evaluation depends on the density of SNP panel. The lower density, lower cost genotype platform is less reliable than the higher density, higher cost platform (*Table 1*). Therefore a lower density platform can be used to generate higher density genotype information.

Table 1. *Genetic correlations (r_g) between traits and their genomic indicators in case of different SNP density used by the American Angus Association*

	Number of SNP-s; (panel)	
Trait	384 (Igenity)	50 000 (Pfizer)
	Genetic correlation; r_g	
Calving ease direct	0.47	0.33
Birth weight	0.57	0.51
Weaning weight	0.45	0.52
Yearling weight	0.34	0.64
Dry matter intake	0.45	0.65
Yearling height	0.38	0.63
Yearling scrotal	0.35	0.65
Docility	0.29	0.60
Milk	0.24	0.32
Mature weigt	0.53	0.56
Mature height	0.56	0.56
Carcass marbling	0.65	0.57
Ribeye area	0.58	0.60
Carcass fat	0.50	0.65
Carcass weight	0.54	0.48

Source: Spangler (2012)

In a research in Ireland (Berry, 2016) genomic evaluations were undertaken using 104 169 beef genotypes including a combination of AI sires, natural mating sires and cows. To test whether genomic information could aid in the prediction of future performance, a genetic evaluation was undertaken using data up to the year 2008; the genetic

merit of animals born after the year 2008 was predicted based on DNA information only and compared to their genetic merit in the year 2015 (which included their performance information). The prediction accuracy varied per trait but was approximately 0.60 to 0.70. The improvement in reliability for the individual traits is in *Table 2*.

Table 2. *Heritability (h²), traditional reliability, genomic reliability and progeny equivalents of the improvement in reliability from including genomic information*

Trait		Reliability		Progeny equivalent
	h²	Traditional BV	Genomic BV	
Calving difficulty – direct	0.10	0.34	0.52	21.8
Calving difficulty – maternal	0.04	0.34	0.52	56.2
Calf mortality – direct	0.02	0.35	0.53	113.6
Gestation length	0.40	0.28	0.49	4.6
Docility	0.35	0.23	0.47	6.3
Weaning wt	0.25	0.15	0.38	5.9
Age at first calving	0.31	0.21	0.46	6.3
Calving interval	0.02	0.16	0.44	95.7
Survival	0.02	0.14	0.43	139.5
Carcass wt	0.40	0.25	0.48	4.6
Carcass fat	0.35	0.22	0.46	5.4
Carcass conformation	0.32	0.21	0.46	6.1
Feed intake	0.43	0.12	0.42	4.2

Source: Berry (2016)

The relative improvement in reliability (in terms of progeny equivalents) was greatest for the lower heritability traits of fertility and survival; this is particularly relevant since it actually takes longer in the life of a bull to receive information on the fertility performance of his daughters. Having genomic information on an animal is equivalent to the animal have fertility performance on almost 100 daughters – not bad for an animal that is potentially only 3 weeks of age.

The accuracy of genomic evaluations in a selection of US cattle population is in *Table 3* (Saatchi et al., 2011, 2012). As it can be seen in the table the genetic correlation (r_g) between direct genomic values and phenotype are positive in every case and varies from 0.32 to 0.85. It seems there are no differences between breeds as for the accuracy of genomic values.

Genomic evaluation and genomic selection are based on the principle of relating genetic markers to phenotypic performance. A large database of the reference population is therefore required of genotyped animals with all relevant phenotypes pertinent to the system of production where the genomic prediction will be applied. This large database of phenotyped and genotyped animals is generally referred to as the reference population or training population and is used to estimate the

genetic marker effects. The reliability of genomic evaluation depends on the number of reference population and the heritability of trait as well (*Table 4*).

Table 3. *Genetic correlations between direct genomic values and phenotype in several different beef breed populations*

Trait	Red Angus	Angus	Hereford	Simmental	Limousine
	Genetic correlation (r_g)				
Birth weight	0.75	0.64	0.68	0.65	0.58
Weaning weight	0.67	0.67	0.52	0.52	0.58
Milk yield	0.51	0.51	0.37	0.34	0.46
Rib eye area	0.75	0.75	0.49	0.59	0.63
Marbling	0.85	0.80	0.43	0.63	0.65
Direct calving ease	0.60	0.69	0.68	0.45	0.52
Maternal calving ease	0.32	0.73	0.51	0.32	0.51

Source: Saatchi et al. (2011, 2012)

Table 4. *Expected reliability of genomic evaluations for different numbers of reference (phenotyped and genotyped) animals in case of different heritability (h^2) of traits*

Heritability, h^2	0.03	0.15	0.35	0.90
Number of animals in reference population	Reliability			
0	0.00	0.00	0.00	0.00
20 000	0.30	0.60	0.70	0.75
40 000	0.44	0.69	0.75	0.78
60 000	0.51	0.72	0.76	0.78
80 000	0.57	0.74	0.76	0.79
100 000	0.60	0.75	0,.7	0.79

Source: Berry and Kearny (2016)

Within breeds, the improvement in the accuracy of genomic predictions with increasing size of the reference population is non-linear and is dependent on how accurately the phenotypic measures reflect the true breeding value (i.e. heritability) of the animals (Daetwiler et al., 2007; Marle-Köster et al., 2013). The lower the accuracy of the phenotypes, as is, on average, the case for lower heritable traits such as fertility (Veerkamp and Beerda, 2007) and health (Berry et al., 2016), the lower the accuracy of genomic predictions for the same reference population size, the greater the relatedness of the reference population size. For the same reference population size, the greater the relatedness of the reference population to the population where the prediction equations will be applied, the greater will be the accuracy of the genomic prediction (Habier et al., 2007, Marle-Köster et al., 2013).

Based on the above mentioned research in beef cattle, it was obvious that a very large population of genotyped and phenotyped animals

would be required to develop an accurate genomic evaluation that worked well across breeds.

In general beef cattle have more breeds, but smaller populations than dairy cattle within a country. Therefore, a combined reference population of various breeds to increase the size of the reference population is usually used for genomic prediction. Weber et al. (2012) investigated the accuracy of genomic prediction for six growth and carcass traits for populations including many breeds. The study reported that genomic predictions using multibreed reference populations were more accurate than those obtained using single-breed reference population. The accuracies, on average 5 traits (birth weight, weaning weight, yearling weight, rib eye area and marbling score), were 0.30 for combined reference population consisted of both purebred and crossed animals, larger than with breed proportion of Angus 0.25 and those with breed proportion of Hereford 0.25. This value for single breed Angus or Hereford populations was 0.17. Chen et al. (2013) reported that the combined reference population increased accuracies of 1–2% points in Angus and 3.4% points in Charolais. Bolormaa et al. (2013) assessed the accuracy of genomic predictions for 19 traits including feed efficiency, growth and carcass and meat quality traits in Australian beef cattle popolations. The study showed that combined reference population performed in 4% better than a single-breed reference population.

Conclusions

The new technology called genomic evaluation and genomic selection will increase the reliability of genetic evaluations of cattle; the extent to which the reliability improves will depend on the number of animals with genotype and performance information available. The increased reliability from genomics means greater confidence that the published values of a given animal will translate into progeny performance or in other words less fluctuations in proofs over time. This all results in accelerated genetic gain.

In Hungary, as it is worldwide, application of genomic evaluation, genetic estimation and selection is in practice in Holstein breeding.

However, in Limousine breed, there are some first steps for applying genomic selection, beef cattle breeders generally do not use this possibility.

It is envisaged that genomic selection will be important for Hungarian beef cattle breeders in the future. Of course, there are some difficulties today in applying genomic evaluation. However, collaborating with international beef cattle breeder's associations, moreover creating combined multibreed reference populations within the country would

help to apply genomic prediction and selection. The advantage of genomic prediction is a more accurate estimate of the genetic merit of an individual at a young age thereby facilitating greater annual genetic gain, predominantly through shorter generation intervals.

Acknowledgements

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