Proceedings of the World Congress on Genetics Applied to Livestock Production, 11.(710)

Impact of Genomic Selection on Genetic Gain of Net Merit of US Dairy Cattle.

F.J. Ruiz-López[1], A. García-Ruiz[1], J.B. Cole[2], G.R. Wiggans[3] & C.P. Van Tassell[2]

[1] National Institute of Forestry, Agricultural and Livestock Research, Ajuchitlán 76680 Querétaro, México.
ruiz.felipe@inifap.gob.mx (Corresponding author)
[2] Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, 20705-5104 Maryland, USA.
[3] Council on Dairy Cattle Breeding, Bowie, 20716 Maryland, USA

Summary

The introduction of genomic selection (GS) in dairy cattle has opened new possibilities to increase the rates of genetic gain. The objective of this study was to measure the impact of GS on Net Merit (NM) genetic gain of US Holstein (HO), Jersey (JE) and Brown Swiss (BS) cattle, using a four-path model of genetic improvement, and to compare these with those predicted by theory. Predicted Transmitted Abilities of NM calculated by the US Council on Dairy Cattle Breeding were used in this study. A total of 36,541,779 HO, 3,283,745 JE and 612,767 BS females and 366,496 HO, 40,369 JE and 16,290 BS bulls, born since 1975 were included in the analysis where generation intervals (GI) and annual genetic gain (GG) were calculated for four paths of selection (Sire of Bulls [SB], Dams of Bulls, Sires of Cows and Dams of Cows). Results showed that the effect of GS on GI was important, especially for the SB path for HO and JE where GI decreased by half compared with previous periods. After introduction of GS, BS maintained the rate of change of GG ($2.8/year) while HO increased it to $21 and JE to $12 (from $1.8 and $0.6, respectively), more than ten and twenty times higher than the previous years for each breed and much higher than the gains predicted in previous studies.

Keywords: genomic selection, genetic gain, dairy cattle.

Introduction

The application of quantitative genetics to dairy cattle breeding from 1960 to 2007 was very successful, increasing milk yield and profitability of the production systems (Brotherstone and Goddard, 2005). Nevertheless, the time required for progeny testing lengthed generation intervals and increased the cost of breeding programs (Schaeffer et al., 2006). The introduction of genomic selection (GS) or marker assisted selection by single nucleotide polymorphisms (SNP) in dairy cattle changed the perspective of genetic improvement, because it promised to bring many advantages by providing the opportunity of decreasing inbreeding rates (Daetwyler et al., 2007), increasing the accuracy of breeding values, decreasing the age of animals to be selected and, therefore, decreasing generation interval (Hayes et al., 2009). As a result of applying GS in livestock populations, the rates of genetic gain have improved (Goddard et al., 2008; García et al., 2016).

Today, 9 years after the introduction of GS in the US dairy cattle, around of 2 million animals have been genotyped; of these, 86.7% are Holstein, 11% Jersey, 1.7% BS and 0.6% from other breeds (CDCB, 2017). For US Holstein cattle, the use of GS has been very successful, especially because this technology has been widely accepted by breeders (García et al., 2016). Although GS was available at the same time for many breeds in the US, factors that could be crucial in GS programs such as reference population size and proportion of genotyped animals are different among them (Hayes et al, 2009).

The objective of this study was to measure the impact of GS on Net Merit (NM) genetic gain of US Holstein (HO), Jersey (JE) and Brown Swiss (BS) cattle, using a four-path model of genetic improvement, and to compare these with those predicted by theory.

Material and methods

Predicted Transmitted Abilities (PTA) of Lifetime Net Merit (NM) calculated by the US Council on Dairy Cattle Breeding (CDCB) were used in this study for HO, JE and BS cattle. A total of 36,541,779 HO, 3,283,745 JE and 612,767 BS females and 366,496 HO, 40,369 JE and 16,290 BS bulls, born since 1975 were included in the analysis.

NM was analysed because it is a genetic-economic selection index with moderate heritability (0.20) and substantial economic value designed for use by commercial dairy producers. Moreover, this index includes milk, fat, protein, productive life, somatic cell score, udder, feet and legs and body size composites, daughter pregnancy rate, service sire calving difficulty, daughter calving difficulty and calving ability as traits to improve. It is important to mention that the importance of these traits in NM has changed over the years, reducing the emphasis on yield traits and introducing other fitness features (Cole et al., 2009).

Annual Genetic Gain and genetic trend.

Annual Genetic Gain (GG) was calculated as the quotient of the sum of Selection Differential (SD) of four paths of selection and the sum of Generation Intervals (GI) of the same paths (Rendel and Robertson, 1950), which are Sire of Bulls (SB), Dams of Bulls (DB), Sires of Cows (SC) and Dams of Cows (DC). SD were calculated for each path of selection as the difference between the NM predicted breeding values (PBV) of the parent deviated from the average NM-PBV of the appropriate base group in that same birth year. GI was calculated as the age of the parent (sire or dam) when the offspring was born (Van Tassell and Van Vleck, 1991). Genetic trend was calculated using the nonlinear procedure by segmented linear regression (SAS 9.3) and validated with the Interbull methods as in García et al (2016).

Results and discussion

From 1991 through 2005, GI were constant for all paths of selection for all breeds with the exception of BS for which it was slightly larger. In the period when GS was introduced (2006-2010), GI slightly decreased for HO and JE. From 2011-2016, the effect of GS on GI was large, especially for the SB path for HO and JE where GI decreased by half compared with the previous period. For these breeds, GI for SC, DB and DC, decreased substantially, but did not reach the magnitude of the SB path. For BS, GI for all paths of selection also decreased but the change was not as obvious as for HO and JE (Table 1). The reduction of GI is associated with the degree of adoption of GS by breeders, and the averages observed in these US dairy populations suggest a high adoption for HO and JE, although these breeds can still achieve shorter GI according to GS theory (Sheaffer et al., 2006).

Estimated SD for BS, HO and JE (Table 2) show nearly uniformly increasing trends across all four paths of selection, except for the DC paths of BS and JE. The negative trend behaviour of the DC path in BS and JE, could be due to the need of replacements which relaxes the selection of DC. The NM–SD averages were superior for HO during the whole period, and the rates of SD were also higher for this breed across years in all paths of selection.

Table 1. Generation intervals from 1991 to 2016 of Brown Swiss (BS), Holstein (HO) and Jersey (JE) US cattle including four paths of selection.

Breed	Period/Year of birth[1]					
	Path of Selection[2]	1991-1995	1996-2000	2001-2005	2006-2010	2011-2016
BS	SB	8.0	8.1	8.0	7.9	5.9
	SC	7.3	7.4	7.3	7.3	6.5
	DB	5.4	5.0	5.1	5.5	4.9
	DC	4.9	4.8	4.7	4.5	4.3
HO	SB	7.6	6.8	6.8	6.6	3.1
	SC	7.2	6.8	6.7	6.7	5.3
	DB	4.6	4.2	4.2	4.0	3.0
	DC	4.1	4.1	3.9	3.7	3.5
JE	SB	7.2	7.1	6.9	6.4	3.7
	SC	6.6	6.5	6.6	6.5	5.0
	DB	4.6	4.8	5.1	4.8	3.8
	DC	4.2	4.3	4.1	3.8	3.4

[1] Results were grouped in periods of five years; except for 2011-2016 which included six years.
[2]The paths of selection include Sires of Bulls (SB), Sires of Cow (SC), Dams of Bulls (DB) and Dams of Cows (DC).

Figure 1 shows that after introduction of GS, BS maintained the rate of change in GG ($2.8) while HO and JE increased theirs ($1.8 to $21 and $0.6 to $12, respectively), much larger than the gains predicted in a simulation study by Pryce et al. (2010), which ranged from 59% to 120% greater than progeny testing. The NM - GG rate observed in HO and JE can be explained by many factors, such as population size, number of genotyped animals or the adoption of GS (Hayes et al, 2009).

Table 2. Selection Differentials from 1991 to 2016 of Brown Swiss (BS), Holstein (HO) and Jersey (JE) US cattle including four paths of selection.

Breed	Path of Selection	Period				
		1991-1995	1996-2000	2001-2005	2006-2010	2011-2016
BS	SB	5	100	160	251	238
	SC	22	60	90	132	161
	DB	-37	67	123	181	207
	DC	35	27	26	20	3
HO	SB	211	205	242	370	521
	SC	154	155	183	256	387
	DB	77	77	123	192	350
	DC	35	31	28	27	32

JE	SB	232	207	210	272	357
	SC	194	175	194	225	302
	DB	79	105	127	175	236
	DC	30	26	20	19	30

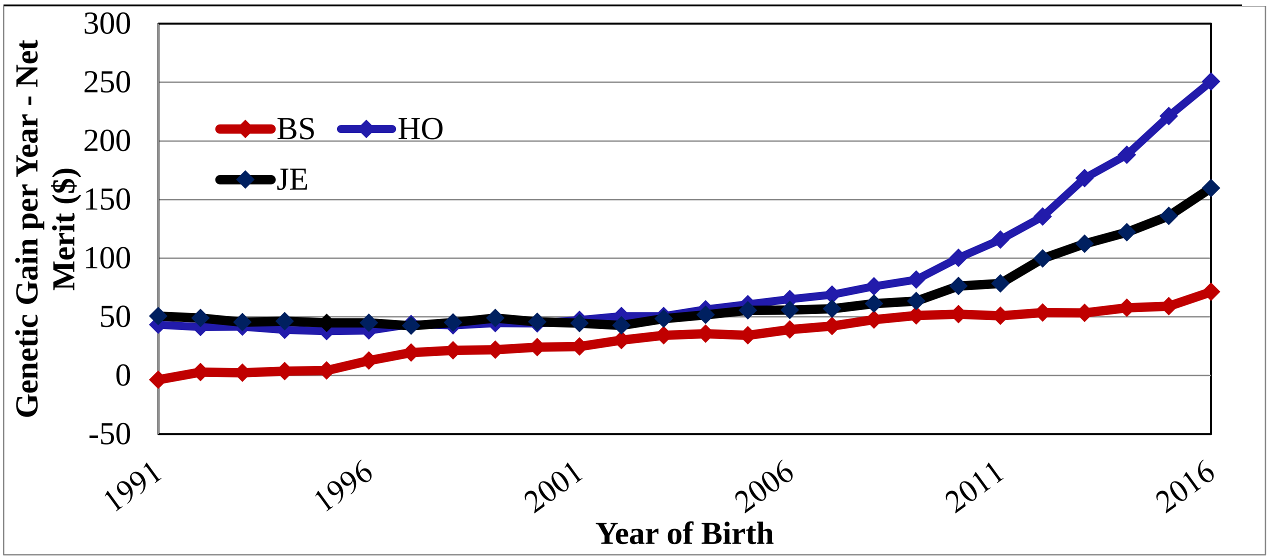

Figure 1. Trends of Genetic Gain of Net Merit for Brown Swiss (BS), Holstein (HO) and Jersey (JE) US cattle.

Conclusions

With the introduction of GS GI in HO, JE and BS have decreased but there is still an opportunity to shorten GI, especially in the DC path. NM - SD averages and GG show a constant and positive trend in the three US dairy breeds, especially in HO and JE.

List of References

Brotherstone, S., Goddard, M. 2005. Artificial selection and maintenance of genetic variance in the global dairy cow population. Philos Trans R Soc Lond B Biol Sci, 360(1459): 1479–1488.

Cole, J.B., VanRaden, P.M. and Multi-State Project S-1040. 2009. AIPL Research Report NM$4: Net merit as a measure of lifetime profit: 2010 revision. Accessed Nov. 13, 2013. http://aipl.arsusda.gov/reference/nmcalc.htm.

Daetwyler, H. D., B. Villanueva, P. Bijma, and J. A. Woolliams. 2007. Inbreeding in genome-wide selection. J. Anim. Breed. Genet. 124:369–376

García-Ruiz, A., J. B. Cole, P. M. Vanraden, G. R. Wiggans, F. J. Ruiz-López, & C. P.Van Tassell, 2016. Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. Proc. Natl. Acad. Sci. USA. 113: E3995–E4004.

Goddard, M. E. 2008. Genomic selection: Prediction of accuracy and maximization of long term response. Genetica doi:10.1007/ s10709-008-9308-0.

Hayes, B. J., Bowman, P. J., Chamberlain, A. J. and Goddard, M. E. 2009. Invited review: Genomic selection in dairy cattle: Progress and challenges. J Dairy Sci 92(2):433–443.

Rendel, J.M., Robertson, A. 1950. Estimation of genetic gain in milk yield by selection in a closed herd of dairy cattle. J Genet 50(1):1–8.

Schaeffer, L.R. 2006. Strategy for applying genome-wide selection in dairy cattle. J Anim Breed Genet 123(4):218–223.

Van Tassell CP, Van Vleck LD (1991) Estimates of genetic selection differentials and generation intervals for four paths of selection. J Dairy Sci 74(3):1078–1086.