

Short communication

Evaluation of genetic trends for traits of economic importance in South African Holstein cattle

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Abstract

Genetic evaluation for the South African dairy industry has kept pace with global advances in statistical methodology. Increasingly accurate estimated breeding values (EBVs), produced routinely in the past two or three decades, have aided selection decisions. This has been coupled with an increase in the number of traits officially recorded and for which EBVs are calculated. Currently, EBVs are routinely published for more than 20 traits for the major dairy breeds. The current study was conducted to assess the genetic trends realized for traits of economic importance in the South African Holstein population, for the period from 1983 to 2008. Performance and pedigree data of 1 231 930 animals were used to calculate EBVs for these traits by a multi-trait animal model. The resulting EBVs in turn were used to compute annual mean rates of genetic change. Genetic trends for yield decreased by approximately 57% during the decade from 1990 to 2000 and reached stasis in 2005 - 2007. Calving interval and somatic cell count also deteriorated over much or all of the period investigated. Given the widespread availability of genetic evaluations for these traits and the noted potential for selection to implement favourable genetic trends, development of strategies to improve the South African Holstein appears to be urgently needed.

Keywords: Calving interval, estimated breeding value, milk fat, milk protein, milk yield, somatic cell count

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Genetic trend can be monitored with breeding values arrayed by year of birth. Farmers need to monitor genetic trends to ensure their selection decisions are advancing their herd in the direction that they intend. As payment is received for yield traits, they have customarily provided a primary focus for selection (Hansen, 2000). Increasingly accurately estimated breeding values (EBVs), produced routinely in the past two to three decades, have aided these selection decisions. Best linear unbiased prediction (BLUP) using an individual animal model is the global favourite methodology for predicting breeding values for livestock (Hill & Meyer, 1988). Phenotypic and genetic trend lines help farmers to assess selection response and compare alternative methods for genetic improvement (Javed *et al.*, 2007). Therefore, the object of the study was to assess the rate of genetic change in traits of economic importance in the South African Holstein cattle population.

Performance and pedigree data of 1 231 930 animals were obtained from the Integrated Registration and Genetic Information System (INTERGIS) database. The data were originally collected from 3 724 farms participating in the National Milk Recording Scheme run by the Agricultural Research Council on behalf of the South African Department of Agriculture Forestry and Fisheries. Traits analysed for this study were calving interval, somatic cell score and yields of milk, protein and butterfat. The data were used to calculate EBVs for these traits using BLUP methodology for multiple-trait animal models (Henderson, 1984), assuming variance components estimated with REML procedures (Groeneveld & Garcia-Cortes, 1998) for similar models to be the population parameters. Procedures were based on the work of Mostert *et al.* (2004; 2006) and Makgahlela *et al.* (2008). Briefly, a multitrait fixed regression test-day model, including tests of the first

three lactations as repeated measures and fitting the permanent environmental effect across lactations was used for the yield traits. A multitrait model, considering the first three calving intervals as different traits, was used to evaluate calving interval. The resulting EBVs were used to compute the genetic trends and these trends were summarized by polynomial regression on year of birth (coded such that 1983 = 0). Because some of the genetic trends were curvilinear, the first derivative of regression of response on birth year was used to estimate instantaneous rates of change in selected years and to find the year in which the genetic trend was zero.

Figure 1 presents a graph of EBVs and a quadratic regression line describing the genetic trend in milk yield over the period 1983 - 2009. The genetic trend increased at a decreasing rate from 1983 to 2005 with the rate of increase in 1990 being 67 kg (0.13 standard deviations) per year; whereas by 2000 it had decreased to 24 kg (0.05 standard deviations) per year. A positive trend in EBV of 19 kg per year was found for first lactation milk yield in South African Ayrshire cattle using an animal model (Hallowell *et al.*, 1998). In contrast, the annual trend for milk yield EBV of Brazilian Holsteins estimated from an animal model was 9.25 kg per year (Boligon *et al.*, 2005).

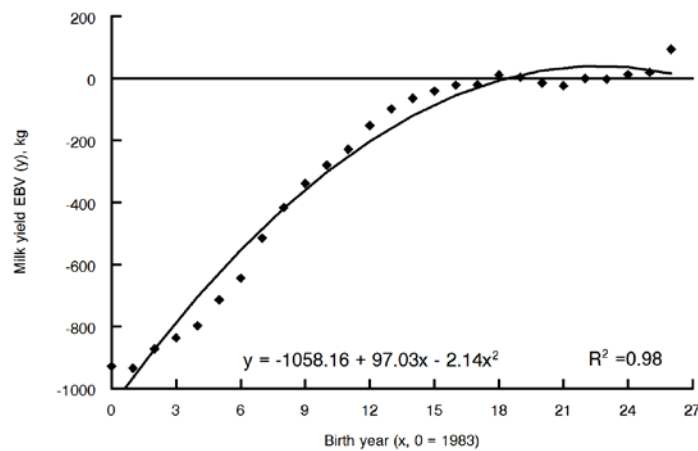


Figure 1 Annual mean estimated breeding values (EBV) for milk yield and quadratic regression line that summarizes the genetic trend.

Similar to milk yield, the genetic trend of butterfat yield was quadratic over time, increasing until 2005 (Figure 2). The increase per year of butterfat yield slowed from 2.1 kg (0.12 standard deviations) per year in 1990 to 0.7 kg (0.04 standard deviations) per year a decade later. Based on results from an animal model, Abdallah & McDaniel (2000) reported a trend in butterfat yield EBV of 3.46 kg/year for Holstein cattle on experimental farms in North Carolina, USA. On the other hand, Koonawootrittrion *et al.* (2009) found no significant genetic trend in butterfat yield, based on the EBV of Holstein and Holstein-cross cattle in Thailand derived from an animal model.

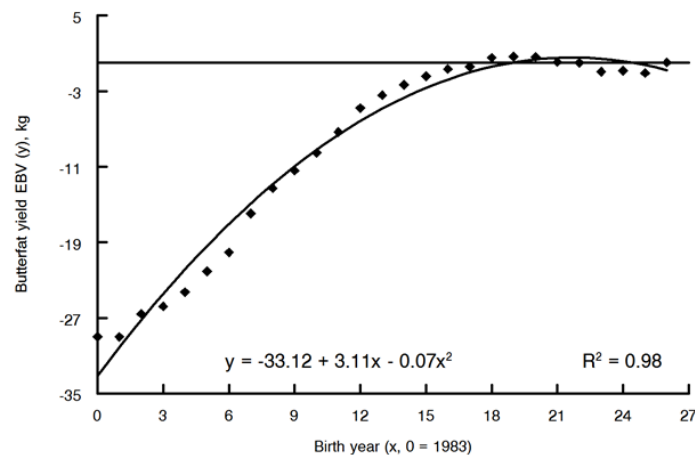


Figure 2 Annual mean estimated breeding values (EBV) for butterfat yield and quadratic regression line that summarizes the genetic trend.

Protein yield also increased at a decreasing rate and reached stasis in 2007 (Figure 3). Whereas the rate of increase in protein yield was 2.1 kg (0.17 standard deviations) per year in 1990, it had declined to 0.9 kg (0.05 standard deviations) per year in 2000. In two Norwegian experimental herds selected to improve protein yield, a genetic trend, based on EBV from an animal model analysis, of 0.7 kg/year was attained between 1989 and 1998, while the corresponding genetic trend in the general Norwegian dairy population was 0.47 kg/year from 1976 to 1996 (Heringstad *et al.*, 2003). Andersen-Ranberg *et al.* (2005) reported an annual genetic increase in first lactation protein yield of 0.63 kg/year from 1978 to 1998.

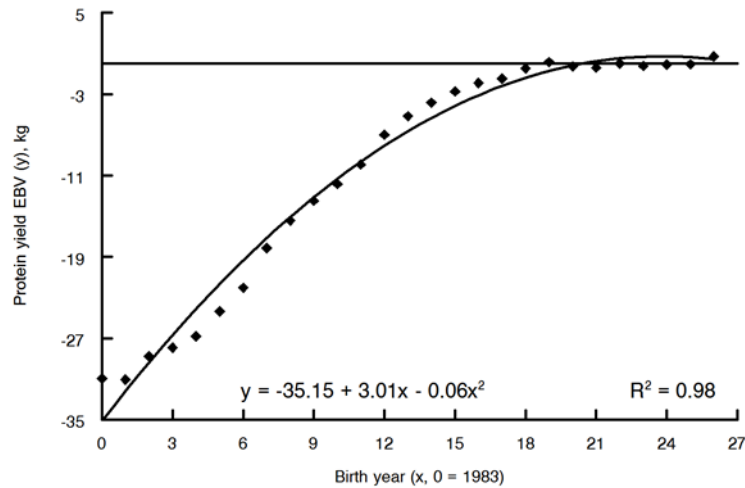


Figure 3 Yearly mean estimated breeding values (EBV) for protein yield and quadratic regression line that summarizes the genetic trend.

Records of somatic cell counts were recorded only from 1990 onwards. Somatic cell counts have been shown to be closely associated with clinical and subclinical mastitis and thus are a valuable indicator trait for improvement of udder health (Urioste *et al.*, 2011). Udder health, as represented by somatic cell score (log scale), exhibited a genetic trend that was qualitatively similar to the trends exhibited by the yield traits (Figure 4). Genetic improvement in clinical mastitis is feasible as demonstrated in a study by Heringstad *et al.* (2003) in which selection of sires against incidence of clinical mastitis in their daughters established a genetic trend in the incidence of $-0.91\%/year$. However, selection for increased milk production appeared to be antagonistic to reducing the incidence of clinical mastitis as a genetic trend of 0.23% per year was observed in cows whose sires had been selected for increased 305-d milk yield.

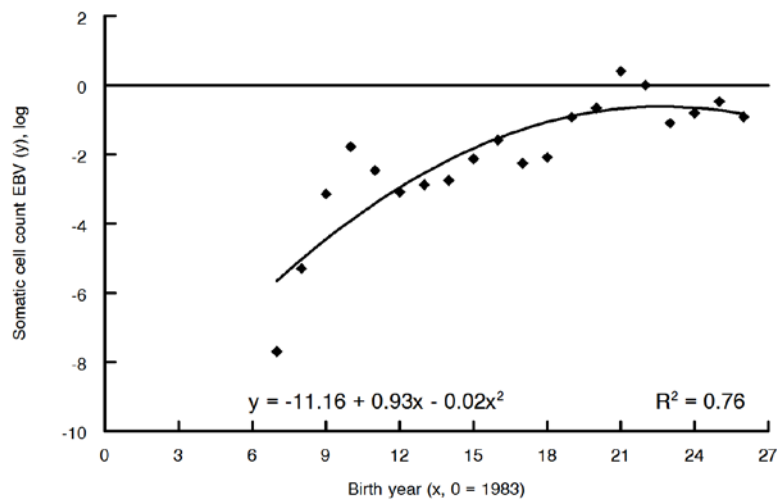


Figure 4 Annual mean estimated breeding values (EBV) for somatic cell count (log) and quadratic regression line that summarizes the genetic trend.

Increasing the level of milk production has also been shown to be antagonistic to successful reproduction (Nebel & McGilliard, 1993; Huang *et al.*, 2008). However, recent work has called this assertion into question (Norman *et al.*, 2009; Belo *et al.*, 2013). In the present study, the genetic trend in calving interval is linear with an average rate of increase of 1.34 days (0.09 standard deviations) per year (Figure 5). Another study, also conducted in South Africa, reported a similar increase of 1.25 days in the Holstein population between 1980 and 2004 (Makgahlela *et al.*, 2008). Effa *et al.* (2011) reported a decrease in calving interval of -0.882 days from a dairy cattle crossbreeding programme conducted between 1974 and 2008. Similar results were found by Ojango & Pollott (2001), in which the genetic trend in calving interval was -0.9 days per year.

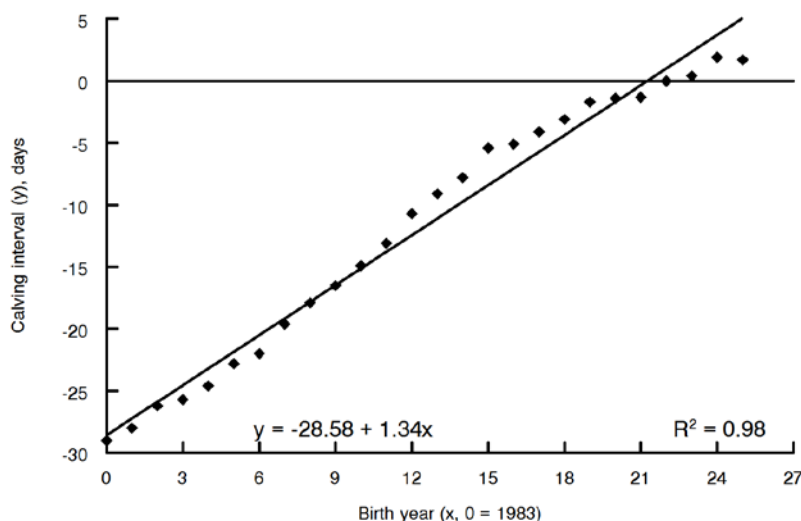


Figure 5 Yearly mean estimated breeding values (EBV) for calving interval and linear regression line that summarizes the genetic trend.

In conclusion, while there were consistent increases in the EBV for yield traits until approximately 2000, the results show a remarkable decay in these genetic trends since that time. Genetic trends for yield decreased by 58% in the decade from 1990 to 1999. Calving interval and somatic cell count also deteriorated over the period studied. However, the rate of deterioration in somatic cell score appeared to have abated. Given the widespread availability of genetic evaluations for these traits and the noted potential for selection to implement favourable genetic trends, development of strategies to improve the South African Holstein appears to be urgently needed.

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