

Continuous Genetic Evaluation of Holsteins for Type¹

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ABSTRACT

Evaluations were based on final score closest to 30 mo of age for 2,072,336 Holstein cows classified from 1952 to 1988. A total of 2,394,809 animals were evaluated, which included 209,089 dams without records and 113,384 sires. Predicted breeding values for animals were obtained using an animal model, which included herd-classification date, animal, and unknown-parent effects. The first evaluation included all records through December 31, 1987 and was the result of 100 rounds of mixed Gauss-Seidel and second-order Jacobi iteration. Forty-eight subsequent sets of evaluations were computed with 20 rounds of iteration each and new information added 1 wk at a time. Solutions for bulls with high reliability ($\geq .999$) showed fluctuations less than .1 point. Most changes in the solutions for sires with lower reliability ($< .999$) occurred during a short period (2 to 4 wk). Solutions for cows changed most the week following availability of their latest records. Of the 118 unknown-parent solutions, only 4 varied more than .1 point. Of these 4, one group corresponding to the unknown dams of cows

born in 1986 through 1987 varied more than 4.5 points. Weekly or biweekly genetic evaluations are computationally feasible and can provide more timely information on young animals.

(Key words: type evaluation, animal model, final score)

Abbreviation key: PBV = predicted breeding value, PEV = prediction error variance, REL = reliability, TPI = type-production index.

INTRODUCTION

Currently, USDA calculates genetic evaluations of US dairy cattle for yield traits with an animal model semiannually. Because of large memory requirements, evaluations are computed on an IBM 3090 supercomputer (10). A system of evaluation within herd has been developed to provide more frequent evaluations and evaluations for animals in unsupervised test plans (11). The within-herd system could be run monthly by regional dairy records processing centers. Because each herd would be analyzed separately, solutions would be similar to but not the same as those from national evaluations.

An optimal evaluation schedule would be continuous evaluations with solutions updated as new records arrive. A frequent evaluation schedule was envisioned for sire models over 20 yr ago (8) but was considered too expensive to implement at that time. Computer hardware was a limiting factor, and appropriate software was not available. Present programming (1, 3, 12) does not require the huge memory of a

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supercomputer. Therefore, continuous evaluations could be implemented at a reasonable cost using smaller computers, even a workstation or a personal computer fully configured with current technology. To disseminate information rapidly, a continuous evaluation system could be accessed electronically through personal computers with modems.

With a continuous evaluation scheme, solutions would change daily as new records arrive. In a connected population, one extra record would change the evaluations of all connected animals although the change would be negligible for most of them. In addition, composition of some management groups would change, and new unknown-parent groups would be introduced and existing ones redefined.

Although day to day or week to week variability of genetic estimates is not necessarily bad and may illustrate the high prediction error variance (PEV) of some evaluations, it could be disturbing to dairy producers. If genetic estimates were different every few days or weeks, breeders might benefit from considering their selection decisions more frequently than under the semiannual evaluation system.

At present, genetic evaluations of Holstein bulls for type are computed semiannually using a sire model; cow evaluations are based on the sire solutions. The cutoff for information used in each genetic evaluation is approximately 1 mo prior to the release of new evaluations. Therefore, the evaluation of a cow classified just after the deadline is not updated until 7 mo later. More frequent evaluations would provide dairy producers with more timely estimates of genetic merit for making breeding and management decisions. The objective of this study was to evaluate the feasibility of computing continuous genetic evaluations for Holstein type traits and to investigate fluctuations in predicted breeding values (PBV) over short time periods.

MATERIALS AND METHODS

Final score closest to 30 mo of age was analyzed for 2,072,336 Holstein cows classified from 1952 through December 2, 1988 by the Holstein Association. Final score ranges from 50 to 100. A total of 2,394,809 animals were evaluated including 209,089 dams without records and 113,384 sires. Data for unknown parents were assigned to 118 un-

known-parent groups based on birth year and four selection paths (sire-son, sire-daughter, dam-son, and dam-daughter). To minimize estimation error for unknown-parent groups, each group consisted of at least 400 animals. Contemporaries were defined by 164,701 combinations of herd and classification date.

The model was the same as the single-record model of Misztal (4):

$$y = Hh + Zu + e$$

where y is a vector of records, h is a vector of fixed herd-classification date effects, u is a random vector of animal breeding values including effects of unknown-parent groups, H and Z are incidence matrices that associate elements of h and u with those of y , and e is a random vector of residual effects. As in the study by Misztal (4), heritability was assumed to be .33.

Mixed Gauss-Seidel and second-order Jacobi iteration on data (5) were used with a Cray-2 supercomputer to calculate PBV. The first 100 rounds of iteration included records with classifications through December 31, 1987. Forty-eight subsequent sets of predictions were computed with 20 rounds of iteration each as new weekly information was added. Weekly reliability (REL) estimates were computed with corrected (see Appendix) methods of Misztal and Wiggans (7). Initially, 8 rounds were performed, followed by 2 rounds weekly. This algorithm did not converge until noncontributing animals (those listed in the Holstein herdbook but with no records for either the animal or its progeny) were not allowed to influence REL of their parents. Noncontributing animals were included in the initial prediction because they could contribute information after they or their progeny were classified at a later date. The convergence criterion was defined as

$$C = \frac{(u^{[i]} - u^{[i-1]})' (u^{[i]} - u^{[i-1]})}{u^{[i]}' u^{[i]}}$$

where $u^{[i]}$ is the vector of PBV at round i .

RESULTS AND DISCUSSION

One round of iteration on the Cray-2 supercomputer required central processing unit time of 18 s for solutions and 80 s for REL. Figure 1 shows the convergence criterion for the first

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