

## CANADIAN GENETIC EVALUATION FOR DAIRY CATTLE PRODUCTION TRAITS

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### SUMMARY

A review of the national genetic evaluation for dairy cattle production traits is presented. Some of the history of the development of the records processing is discussed as it relates to the development of the evaluation system and the nature and quality of the data available. The model and iteration techniques are covered in general. Genetic and phenotypic trends estimated from the evaluations are shown for the ten year period of 1983 to 1992.

### INTRODUCTION

The national dairy cattle genetic evaluation for production traits has evolved along with the needs of the dairy industry. What began as a herdmate comparison of milk and fat yield for the national Record of Performance (ROP) program has become an Individual Animal Model (IAM) evaluation for milk, fat and protein yield, calving ease and milking speed. Milk recording has a strong history in Canada, beginning with the federal ROP program in 1904. ROP was privatized from 1985 to 1990 but the federal presence in milk recording remains strong in the roles of audit, standards implementation and monitoring and support. National standards ensure the continued high quality, accuracy and consistency of the data received from the four dairy record processing centres (DRPCs): Dairy Herd Analysis Service (serving Quebec and the Maritimes), Ontario DHI, Alberta DHI (serving Manitoba, Saskatchewan and Alberta) and British Columbia DHI. The dairy industry is a strong partner in the genetic evaluation process through dairy cattle improvement committees like the dairy cattle Genetic Evaluation Board (GEB) which is made up of representatives from its two subcommittees; the Technical Committee (researchers) and the Industry Consultative Committee (industry stakeholders - artificial insemination, breed associations and producers). The GEB meets twice per year at the beginning of the genetic evaluation run in order to review the results of research projects and chart the future of the evaluations.

### MATERIALS AND METHODS

The evaluations are computed semi-annually and released in January and July using data from the four DRPCs in combination with the historical database of ROP and DHI records dating back to the mid-1950's. Over 8,000,000 lactation records, 4,000,000 cows and 100,000 bulls are evaluated in the Ayrshire, Brown Swiss, Canadienne, Guernsey, Holstein and Jersey breeds (about 90% Holstein).

#### Pre-adjustment of records

Milk, fat and protein yield is measured in kilograms and then expressed in Breed Class Average (BCA) units; a form of expressing mature equivalent (ME) yield. BCAs are computed

as  $BCA = \frac{\text{cow's yield in kg}}{\text{average yield for age and month}} \times 100$ . BCAs can be easily converted to MEs by

substituting the average yield of a "mature cow" for the "100" in the above equation. BCAs are computed using 305-day yields (actual or predicted). Records in progress (RIP) with at least 90 days in milk are extended to 305-days and used in the evaluation. RIP are adjusted for heterogeneity of residual variance during the iteration process by substituting different elements for the diagonal

element of  $R^{-1}$ ; the element is the ratio of the variation in the RIP in specific days in milk categories and test types to the variation in a standard completed record. Lactation records are also adjusted for heterogeneity of within-herd phenotypic variation. A phenotypic standard deviation is estimated for each herd-year-parity (HYP) subclass using a similar approach to weighting of HYP values from previous years for the same herd, the regional weighted average HYP value (RYP) and the degrees of freedom (d.f.) as Van Raden and Wiggans (1991):

$$\hat{\sigma}_{HYP} = \frac{30\hat{\sigma}_{RYP} + \frac{1}{3}d \cdot f \cdot \hat{\sigma}_{HYP-2} + \frac{2}{3}d \cdot f \cdot \hat{\sigma}_{HYP-1} + d \cdot f \cdot \hat{\sigma}_{HYP}}{30 + \frac{1}{3}d \cdot f \cdot \hat{\sigma}_{HYP-2} + \frac{2}{3}d \cdot f \cdot \hat{\sigma}_{HYP-1} + d \cdot f \cdot \hat{\sigma}_{HYP}}$$

The ratio of the estimated HYP standard deviation and the regional base standard deviation is then used to adjust the deviation of the record from the mean of the herd-year-season-parity (HYSP)

subclass as  $y_{adjusted} = (y_{actual} - \bar{y}_{HYSP}) \times \frac{\hat{\sigma}_{base}}{\hat{\sigma}_{HYP}} + \bar{y}_{HYSP}$  where  $y$  represents the BCA yield. The regional base standard deviation is the weighted average of the RYP standard deviations for all supervised lactations initiated two calendar years prior to the current one; which corresponds to the selection of cows for the genetic base.

### Evaluation Model

These pre-adjusted lactation yields are then analyzed as single traits using the following individual animal model (IAM):

$$y_{ij} = h_i + a_j + \sum_{r=1}^{n_g} q_{jr} g_r + p_j + e_{ij}$$

where:

$y_{ij}$  is the observation (milk, fat or protein yield)

$h_i$  is the effect of the  $i$ -th HYSP subclass (fixed, management)

$a_j$  is the additive genetic value of the  $j$ -th animal (random) deviated from the group effect function,

$q_{jr}$  is the contribution of the  $r$ -th phantom parent group to the  $j$ -th animal,

$g_r$  is effect of the  $r$ -th phantom group (fixed),

$p_j$  is the permanent environmental effect for the  $j$ -th cow (random),

$e_{ij}$  is the residual effect (random), and

$n_g$  is the number of groups.

All relationships are incorporated with pedigree traced as far back as available data allows. Phantom parent groups are assigned on the basis of sex of parent, origin (foreign or domestic) and birthdate of the offspring and assumed generation intervals for the four different selection paths. Once assigned, phantom parent grouping follows Westell *et al* (1988).

### Iteration of solutions

The iteration of the mixed model equations (MME, Henderson, 1973) is a hybrid of different methods: iteration on the data (Schaeffer and Kennedy, 1986), setting up coefficients and solving (without storing coefficients) and block iteration. One round of iteration includes one round of iteration on the management effects solutions and ten rounds of iteration on the animal and group effects solutions. This strategy was developed to maximize the convergence progress and minimize

the input / output (I/O) overhead involved with processing the lactations and herd information. The management effect solutions are derived using iteration on the lactation record file combined with reading and writing the herd solutions. The animal and permanent environmental effect solutions are derived by reading the pedigree data file sorted youngest to oldest (to insure all offspring adjustments are accumulated prior to solving parental equations) and accessing animal and group solutions and adjusted right hand sides in random access memory (RAM). Relationships and coefficients (Henderson, 1976 and Westell *et al*, 1988) are not stored but rather determined for every animal each time the animal equation is solved. Group effect solutions are computed using block iteration; multiplying the group by group block of the equations by their adjusted right hand sides. The group by group block of the equations is determined prior to beginning iteration and the inverse is computed and checked for stability (elements of similar magnitude) in order to validate the group definition. Experience has shown that a well-conditioned group by group matrix inverse results in successful and stable iterations. Foreign evaluation information for parents is incorporated in a post-iteration step that replaces parent information derived during iterations with a blend of converted foreign information and domestic results (blended in proportion to the respective repeatabilities). The repeatability of the solutions is approximated following Meyer (1989), modified for multiple records and different weights in  $R^{-1}$ . As a selection tool, an economic index referred to as Lifetime Profit Index (LPI - Dekkers, 1992 and Gibson *et al*, 1992) is computed combining production and conformation traits as follows (the weighting is about 70% production, 30% conformation on a genetic standard deviation basis):

$$LPI = 6(3 \times \text{ETA Fat} + 8 \times \text{ETA Protein}) +$$

$$4(3 \times \text{ETA Final Class} + 2 \times \text{ETA Feet \& Legs} + 4 \times \text{ETA Mammary system} + \text{Capacity})$$

## RESULTS AND DISCUSSION

The IAM has been used in Canada for the national dairy cattle production genetic evaluations since 1989 with modifications incorporated (heterogeneous within-herd variance adjustments, inclusion of foreign evaluations and new reports and statistics). Figures 1, 2 and 3 below show the genetic (EBV) and phenotypic (average ME kg production) trends for Canadian Holstein cows by year of first calving for milk, fat and protein respectively.

Figure 1

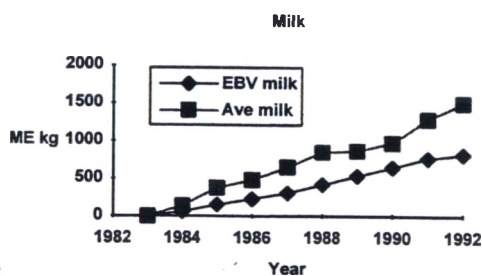


Figure 2

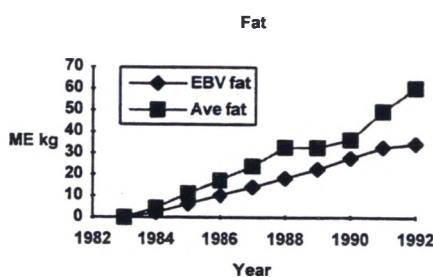
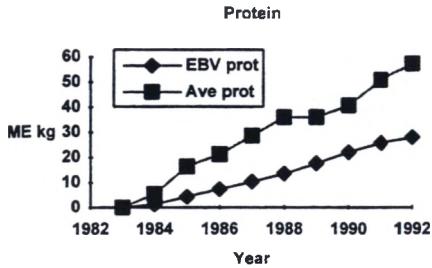


Figure 3



### CONCLUSIONS

Through continual upgrades and flexible reporting, the national genetic evaluation system for dairy cattle provides users with a valuable selection and marketing tool to compete in today's global marketplace.

### REFERENCES

- DEKKERS, J.C.M. 1992. Breeding profitable cows with LPI, now and in the future. *Holst. Journal*, June 1992 p. 20.
- GIBSON, J.P., N. GRAHAM, E.B. BURNSIDE. 1992. Selection indexes for production traits of Canadian dairy sires. *Can. J. An. Sci.* 72:477.
- HENDERSON, C.R. 1973. Sire evaluation and genetic trends. Page 10 in *Proc. Anim. Breeding Genet. Symp. in Honor of Dr. J.L. Lush*. Am. Soc. Anim. Sci. and Am. Dairy Sci. Assoc., Champaign, Ill.
- HENDERSON, C.R. 1975. Use of all relatives in intraherd prediction of breeding values and producing abilities. *J. Dairy Sci.* 58:1910.
- HENDERSON, C.R. 1976. A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. *Biometrics* 32:69.
- MEYER, K. 1989. Approximate accuracy of genetic evaluation under an individual animal model. *Genet. Sel. Evol.* 21:317.
- QUAAS, R.L. and E.J. POLLAK. 1980. Mixed model methodology for farm and ranch beef cattle testing programs. *J. Anim. Sci.* 51:1277.
- SCHAEFFER, L.R. and B.W. KENNEDY. 1986. Computing solutions to mixed model equations. Page 392 in the *Proc. Third World Congr. Genet. Appl. Livest. Production*, Lincoln, NE.
- VAN RADEN, P.M and G.R. WIGGANS. 1991 Derivation, calculation and use of national animal model information. *J. Dairy Sci.* 74:2737.