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Simultaneous Genetic Evaluation of Sires and Cows for a Large Population of Dairy Cattle

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ABSTRACT

A strategy for simultaneous sire and cow evaluation of genetic merit was implemented. First lactation records of 1,074,971 Holstein cows in 20,065 herds were included. After inclusion of ancestors, there were 1,741,356 equations: 1,505,938 cow, 229,394 herd-year-season, 6000 sire, and 24 genetic group equations. All known genetic relationships among animals were considered. Genetic group coefficients were assigned based on animals that had one or more parents unidentified. Mixed model equations from an animal model were transformed to solve for total additive genetic merit. The coefficient matrix was sparse with .00039% nonzero elements. Equations were blocked by herds. A final block included sires, groups, and cows that had no daughters or records. Effects of herd-year-season were solved last within each herd. All herd blocks were solved before sire equations. A form of block iteration with successive overrelaxation was used to obtain solutions. A total of 30 rounds were completed. Number of iterations per round for herd blocks decreased from an average of 4.93 in round 1 to the minimum allowed, 3.00, in round 30. The correlation between Northeast Artificial Insemination Sire Comparisons and sire solutions from this study stabilized at .94. At round 30, 96.4, 95.2, 99.4, and 75.0% of solutions for cow, sire, herd-year-season, and group effects changed less than 4.54 kg from the previous round.

INTRODUCTION

The history of dairy cattle breeding has featured continual increase in complexity of methods for genetic evaluation. Information used to evaluate animals has increased from physical appearance, to records of yields, to inclusion of correlated traits and records on relatives. Research on methods of genetic evaluation has concentrated on techniques and problems associated with evaluation of additive genetic merit of sires in deference to consideration that as much as 76% of genetic progress possible in dairy cattle results from sires (12). Genetic evaluation of cows has been a two-stage procedure. Both the USDA Cow Index and the Northeast estimates of transmitting ability incorporate independently calculated estimates of sire genetic merit for genetic evaluation of cows. In the Northeast, sires currently are evaluated from their progeny records with a model including genetic relationships to other bulls (5), genetic groups, maternal grandsires of cows, and herd-year-seasons (1). Inclusion of genetic merit of the maternal grandsire partially accounts for genetic merit of the dam of the cow (9). Cows are evaluated from their records and records of relatives adjusted to a common base within a herd and from external evaluations of their sires (4). These evaluations are within herd and utilize all genetic relationships within the herd, effects of herd-year-seasons, and effects of age at calving. Thus, genetic evaluations of sires subsequently used for cow evaluations do not consider directly genetic merit of mates; dams are not considered related to cows in other herds; and genetic evaluations for cows do not consider directly genetic groups.

Simultaneous sire and cow evaluation would reduce the number of assumptions that have been needed and increase accuracy of evaluation for sires and cows. The purpose of this study was to develop a strategy for simultaneous genetic evaluation of sires and cows including all known relationships (14, 15, 16).

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MATERIALS AND METHODS

The Animal Model

The animal model for a cow with a first lactation record is:

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

where:

y_{ij} is a mature equivalent (ME) milk record,

h_i is the fixed effect of the i th herd-year-season of calving,

a_j is the additive genetic merit of the j th cow as a deviation from the function of group effects,

g_r is the effect of the r th group,

q_{jr} is the fractional contribution of the r th group to the genetic merit of the j th cow,

n is the total number of groups, and

e_{ij} is a random residual.

Genetic merit of animals without records, such as sires or dams for which there are no milk records in first lactation, can be predicted by incorporating the inverse of the relationship matrix and by including their genetic merit in the vector of additive genetic animal effects (6).

In matrix notation, the animal model can be expressed as:

$$y = Xh + Za + ZQg + e$$

where:

y is a vector of records,

h is a vector of fixed effects of herd-year-seasons,

a is a vector of additive genetic effects of animals,

g is a vector of group effects,

X , Z , Q are incidence matrices associating records with elements of h , a , and g with the row of Z associated with animals having no records consisting only of zeros, and e is a vector of random residual effects,

with:

$$E \begin{bmatrix} y \\ a \\ e \end{bmatrix} = \begin{bmatrix} Xh + ZQg \\ 0 \\ 0 \end{bmatrix}$$

and:

$$V \begin{bmatrix} y \\ a \\ e \end{bmatrix} =$$

$$\begin{bmatrix} ZAZ'k^{-1} + R & ZAk^{-1} & R \\ Z'Ak^{-1} & Ak^{-1} & 0 \\ R & 0 & R \end{bmatrix} \sigma_e^2$$

for $k = \sigma_e^2/\sigma_g^2$, σ_g^2 = additive genetic variance, σ_e^2 = residual variance and A , the matrix of numerator relationships among the animals.

In this study $k = 3.00$ was assumed, corresponding to heritability of .25.

The mixed model equations can be represented (2) as:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & X'R^{-1}ZQ \\ Z'R^{-1}X & Z'R^{-1}ZA^{-1}k & Z'R^{-1}ZQ \\ Q'Z'R^{-1}X & Q'Z'R^{-1}Z & Q'Z'R^{-1}ZQ \end{bmatrix} \begin{bmatrix} \hat{h} \\ \hat{a} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ Q'Z'R^{-1}y \end{bmatrix}$$

In subsequent discussion, $R\sigma_e^2$ is $1\sigma_e^2$. The A^{-1} coefficients are determined from rules of Henderson (3). Equations can be transformed (8, 10, 11) so that solutions are obtained directly for total additive genetic merit,

i.e., for the j th animal, $\hat{u}_j = \hat{a}_j + \sum_{r=1}^n q_{jr}\hat{g}_r$, and in matrix notation $\hat{u} = Q\hat{g} + \hat{a}$.

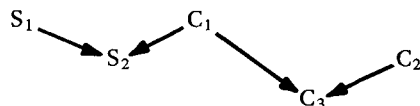
The transformed equations are:

$$\begin{bmatrix} X'X & X'Z & 0 \\ Z'X & Z'Z + A^{-1}k & -A^{-1}Qk \\ 0 & -Q'A^{-1}k & Q'A^{-1}Qk \end{bmatrix} \begin{bmatrix} \hat{h} \\ \hat{a} + Q\hat{g} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ 0 \end{bmatrix}$$

Definition of genetic group effects requires additional explanation (15). The estimate of the total of genetic group effects for j^{th} animal is

$$\sum_{r=1}^n q_{jr} \hat{g}_r$$

for $r=1, \dots, n$ groups. Two parallel sets of genetic groups were assigned. One set contained average genetic merits of unidentified bulls selected to be sires by 2-yr periods based on their probable birth dates. The other set contained average genetic merits of unidentified cows selected to be dams by 2-yr periods based on probable birth date. When the j^{th} animal has an unidentified ancestor that would have been born in the same period as the r^{th} group, then q_{jr} is the additive genetic relationship between the missing ancestor and the j^{th} animal. The r^{th} group was defined by sex of the missing ancestor and by estimated year of birth of the missing ancestor. This allocation of genetic groups accounts for selection beyond that accounted for by known genetic relationships. For example, for the pedigree:



if the total group effect for C_3 is represented by $G(C_3)$, then $G(C_3) = [G(S_2) + G(C_2)]/2$, but because S_2 is identified and has identified parents, then $G(C_3) = G(S_1)/4 + G(C_1)/4 + G(C_2)/2$. The total group effect for animal S_1 , which has two unidentified parents, is one-half average genetic merit of sires selected to be sires of sires that were born one generation before birth of S_1 , plus one-half average genetic merit of dams selected to be dams of sires that were born one generation before birth of S_1 . Total genetic group effect for C_1 or C_2 can be defined similarly.

Example

Assume that the four paths of selection [sires

to produce sires (SS), sires to produce cows (SC), dams to produce sires (DS), and dams to produce cows (DC)] are crossclassified with time: unidentified (or phantom) parents of S_1 and of C_1 would be expected to be born in time T_1 , and parents of C_2 would be expected to be born in time T_2 ; then phantom sire and phantom dam of S_1 would be from groups with effects, SS1 and DS1, phantom parents of C_1 would be from groups with effects, SC1 and DC1, and phantom sire and phantom dam of C_2 would be from groups with effects SC2 and DC2.

The total number of groups, $n = 6$. Then:

$$\begin{aligned} G(S_1) &= \sum_{r=1}^n q_{S_1 r} \hat{g}_r \\ &= (SS1)/2 + (DS1)/2. \\ \text{Similarly } G(C_1) &= (SC1)/2 + (DC1)/2 \\ G(C_2) &= (SC2)/2 + (DC2)/2. \\ \text{Finally } G(C_3) &= (GS_1)/4 + G(C_1)/4 + G(C_2)/2 \\ &= (1/4)[(SS1 + DS1)/2 + (SC1 + DC1)/2] + (1/2) [(SC2 + DC2)/2] \\ &= (1/8) (SS1 + DS1 + SC1 + DC1) + (1/4) (SC2 + DC2). \end{aligned}$$

There was no differentiation between sires of sires and sires of cows. Similarly, no differentiation was made between dams of sires and dams of cows. Thus, $G(C_3) = (S1 + D1)/4 + (S2 + D2)/4$ with only S or D needed to identify male or female groups.

Generation intervals of 10, 9, 7, and 5 yr were estimated to assign birth years to unidentified parents for the four paths of selection (Table 1).

Accounting for all unknown ancestors is tedious, if not impossible, if the animal model is used directly. Use of the QP transformed animal model equations reduces assignment of genetic group coefficients to a few simple rules (14, 15). These rules require determining whether the sire or dam of each animal is unknown. Groups may be defined by sex of

the missing parent and by year of birth of the animal. This method of allocating genetic groups to account for selection is similar to that of Thompson (13) and Henderson (2).

Data

First lactation milk records (2×, 305-d, ME) of Holstein cows were obtained from Northeast Dairy Records Processing Laboratory (DRPL). Cows included grade and registered animals with artificial insemination sires. Two seasons assigned were December to April and May to November. A record was a first lactation record if the cow first freshened between 612 and 1067 days after birth. The acceptable range for milk records was 454 kg to 18,144 kg.

All pedigrees were traced as far as possible to define relationships. All sires and dams of heifers whose records passed edits were brought into the file. When additional animals were brought into the data set, a search was undertaken to establish their parentage.

Table 2 presents distribution of records by herds and sires. Table 3 summarizes animals having records and relatives brought in by the tracing process. Of 1,505,938 cows in the file, 498,228 were known to be registered. The population was classified into mutually exclusive categories according to information available and number of progeny. Sires were categorized by whether they had daughters with records. Dams were crossclassified by whether they had a record and whether they had daughters with records. Category of "non-parent" was applied to cows with records that had no daughters with records.

A total of 1,074,971 cows had first lactations on file. Dams of 7.8% of these had known first lactations in a different herd. No dam was identified for only 7.0%. Table 3 indicates that approximately half of the cows were "nonparents."

Generation intervals for the four selection paths were estimated from all parent and progeny pairs having valid years of birth (Table 1). Cows with records had a year of birth. Other animals were ancestors of cows with records. If an ancestor did not have a known year of birth, an approximate year of birth was assigned by subtracting the appropriate generation interval from the year of birth of the oldest progeny. Average generation intervals were used to approximate year of birth for any animal missing that information and to approximate year of birth of any missing parent to assign an appropriate group. Table 4 shows number of unidentified sires and dams categorized by approximate year of birth. Unidentified parents were not subdivided into groups born before 1950, corresponding to the assumption of no genetic progress before then.

Implementation of Evaluation Procedures

Solving the mixed model equations (MME) presented a challenge. The number of equations was large (1,741,356), and the coefficient matrix was sparse. The number of nonzero elements in the left-hand sides (LHS) was 12,070,894.

Equations when grouped by herd have a natural blocking structure that suggested block

TABLE 1. Average generation intervals.¹

	Paths of selection			
	Dams to produce cows	Dams to produce bulls	Sires to produce cows	Sires to produce bulls
Number of parent and progeny pairs	662,018	1226	1,073,674	3863
Generation interval, yr				
X	4.86	2.88	8.47	9.73
SD	2.34	2.46	2.81	3.46

¹ Individual generation intervals were rounded downward to the nearest full year.

TABLE 2. Numbers of herds, cows, records per herd, herd-year-seasons, and cows and sires per herd-year-season.

Category	Number
Herds	20,065
Cows	1,074,971
Cows per herd	
Mean	53.6
Minimum	1
Maximum	1644
Herd-year-seasons	
Year-seasons per herd	
Mean	11.4
Minimum	1
Maximum	64
Cows per herd-year-season	
Mean	4.7
Minimum	1
Maximum	100
Sires per herd-year-season	
Mean	3.5
Minimum	1
Maximum	38

iteration. Many cows without records had daughters with records. Such cows were allocated to the herd in which the majority of their daughters made records to reduce the number of coefficients between herds.

Two strategies for iterating large sparse matrices were used. For each block only non-zero elements of the coefficient matrix were stored. Equations were ordered so that as many coefficients per row were left of the diagonal as possible. In the following example, X indicates a nonzero coefficient in the LHS:

$$\begin{bmatrix} X & X & X & X \\ X & X & 0 & 0 \\ X & 0 & X & 0 \\ X & 0 & 0 & X \end{bmatrix} \begin{bmatrix} A \\ B \\ C \\ D \end{bmatrix} = \begin{bmatrix} E \\ F \\ G \\ H \end{bmatrix}$$

The equation for A has three coefficients right of the diagonal and no coefficients to the left, whereas B, C, and D have no coefficients right of the diagonal and one each left of the diagonal. If the equations are reordered, B, C, D, A, then:

$$\begin{bmatrix} X & 0 & 0 & X \\ 0 & X & 0 & X \\ 0 & 0 & X & X \\ X & X & X & X \end{bmatrix} \begin{bmatrix} B \\ C \\ D \\ A \end{bmatrix} = \begin{bmatrix} F \\ G \\ H \\ E \end{bmatrix} [1]$$

Now B, C, and D each have one coefficient right of the diagonal, and A has no coefficients right of the diagonal. Reordering has computational advantages. Because the mixed model equations are symmetric, coefficients can be half-stored with no information lost. When equations are half-stored, solving the equations requires special handling. In [1], if the coefficient matrix is represented by M:

$$B = (F - m_{1,4}A)/m_{1,1}$$

Coefficients left of the diagonal of M, such as $m_{4,1}$, need not be stored, because the right-hand sides (RHS) of subsequent equations can be adjusted for solutions already obtained. For example, the same solution for A is obtained if either:

$$A = (E - m_{4,1}B - m_{4,2}C - m_{4,3}D)/m_{4,4}$$

or:

$$A = E^*/m_{4,4}$$

is used, where:

$$E^* = (E - m_{1,4}B - m_{2,4}C - m_{3,4}D).$$

As soon as the solution for B is calculated, the RHS of A can be adjusted by subtraction of $m_{1,4}B$. Thus, coefficients left of the diagonal need never be stored. Strategy of ordering within a herd was to minimize number of coefficients right of the diagonal. This ordering is important with sire equations where there may be many off-diagonal coefficients. By ordering equations and adjusting RHS of sire equations for daughter solutions before solving sire equations, the only off-diagonals right of the diagonal that need to be carried with the sire equations are those of equations that are not already solved, such as for other sires or group equations.

Within herd, cow registration numbers were sorted in ascending order on the premise

TABLE 3. Survey of animal counts.¹

	Sires		Dams without records		Dams with records		Nonparents with records ²
	That have daughters with records	That have no daughters with records	That have daughters with records	That have no daughters with records	That have daughters with records	That have no daughters with records	
Total animals	5114	886	386,724	44,614	317,794	9032	748,145
Sire identified	4952	602	99,777	6143	317,794	9032	748,145
Dam identified	4947	557	85,958	5543	300,810	8617	690,051
Single progeny							
Cow	620	93	271,848	37,779	203,199	8507	0
Son	0	476	0	2823	0	0	125
Daughters with records							
2-5	1199	0	100,390	0	107,501	0	0
6-10	479	0	464	0	636	0	0
11-50	1144	0	0	0	1	0	0
≥51	1631	0	0	0	0	0	0
Maximum	19,541	0	10	0	11	0	0
Sons							
2-3	92	127	69	485	139	1	29
≥4	197	64	3	21	11	0	2
Maximum	252	39	4	5	5	2	5
Daughters without records							
2-5	662	66	2620	3474	804	514	0
6-10	304	31	1	0	0	0	0
11-50	584	26	0	0	0	0	0
≥51	408	5	0	0	0	0	0

¹ After this summary was prepared 371 dams without records were eliminated before solution of the equations.² "Nonparent" designates cows with records without daughters with records, although some may be dams of bulls.

TABLE 4. Approximate years of birth of unidentified sires or dams and the number of cows with unidentified sires or dams in each group.¹

Projected year of birth of parent ²	Dam		Sire	
	Number	Group	Number	Group
≤1949	52,321	1	99,343	15
1950–1951	28,238	2	22,886	16
1952–1953	28,241	3	26,424	17
1954–1955	27,832	4	26,612	18
1956–1957	32,380	5	25,546	19
1958–1959	33,369	6	26,284	20
1960–1961	32,536	7	25,081	21
1962–1963	35,226	8	28,064	22
1964–1965	34,148	9	34,281	23
1966–1967	36,890	10	10,958 ³	24
1968–1969	42,081	11		
1970–1971	18,493	12		
1972–1973	7688	13		
≥1974	6099	14		

¹ Approximate year of birth estimated by subtracting average generation intervals from year of birth of animals with unidentified parent(s).

² Years are not partitioned before 1950.

³ Total unidentified sires with approximate year of birth after 1965.

that older cows had smaller numbers. Equations for herd-year-seasons were last equations within a herd. Thus, for herd-year-season equations all except diagonal coefficients are left of the diagonal. Herd equations were ordered before sire equations. Thus, the only off-diagonals to be stored for sire equations resulted from sire relationships to other sires and coefficients connecting sires and groups. Group equations were ordered last. After inclusion of cows without records in herds where their daughters had records, maximum number of equations to be solved per herd was 1935. Maximum number of off-diagonal coefficients right of the diagonal that had to be retained per cow was 21.

Initial solutions for genetic merit for sires were twice the estimated transmitting ability calculated by the June 1983 Northeast Artificial Insemination Sire Comparison (NEAISC). Initial solutions for herd-year-seasons were calculated by averaged milk yields of all cows freshening in each herd-year-season. Most initial solutions for cows were zero. One-fiftieth of the cows had Northeast estimates of genetic merit which were used as initial estimates. Many more cows actually had

Northeast estimates of genetic merit, but these were not included because of an error in matching. After coefficients for a herd were stored in core, RHS of cow equations with linkages outside the herd were adjusted for linked solutions by coefficients to the right of the diagonal corresponding, e.g., to bulls, groups, or cows in other herds. Solution of all equations was considered a "round" of solutions. Within each round, groups of equations were iterated before the subsequent group of equations was processed. Within-herd equations were iterated as many as five times per round. If the convergence criterion was met and at least three iterations had been completed, the within-herd iteration was terminated for that round. The convergence criterion was met when [e.g., Jennings (7)]:

$$\frac{\|r^{(n)}\|}{\|b\|} < .001.$$

where for $Ax^{(n)} = b$:

A is the coefficient matrix,
 $x^{(n)}$ is the vector of solutions from the n^{th}

round of iteration, and

- b is the vector of RHS, in the case of herd blocks the nonzero RHS correspond to records of cows making records and herd-year-season totals (the convergence factor for the sire and group equations was calculated with RHS adjusted for cow and herd-year-season solutions, instead of the corresponding RHS, which are zero), $r^{(n)} = b - Ax^{(n)}$ is the residual term with $\|r^{(n)}\| = [\sum_i (r_i^{(n)})^2]^{.5}$ and $\|b\| = [\sum_i b_i^2]^{.5}$.

At each iteration the i th solution was scaled by an overrelaxation factor, w , (7), such that the estimate of x for the $(n+1)$ round was:

$$x_i^{(n+1)} = x_i^n + w(b_i - \sum_{j=1}^{i-1} a_{ij}x_j^{(n+1)} - a_{ii}x_i^n - \sum_{j=i+1}^t a_{ij}x_j^n)/a_{ii}$$

when there are t equations. Relaxation factors varied from 1.25 to 1.50 by round (Table 5). After solutions for a round for a herd were calculated, the RHS of equations with outside linkages to that herd were adjusted for the new solutions. Solutions for the 9522 sires, dams without herds or records, and groups were handled a row at a time. Maximum number of off-diagonal coefficients right of the diagonal for any one sire was 121 after equations had been reordered. This number possibly could have been reduced if sires had been ordered such that equations for younger bulls came before equations for their sires. For each round equations for sires, groups, and dams without herds were iterated five times after all herd equations had been completed. After 30 rounds equations still were converging.

RESULTS AND DISCUSSION

Monitoring convergence involved effort because a major concern had been that the

equations might fail to converge. Convergence was monitored by our 1) ensuring that convergence factors decreased in magnitude as number of rounds increased; 2) observing intermediate solutions for representative effects of herd-year-season, sire, cow and group; and 3) ensuring that average absolute change for solutions decreased as number of rounds increased. Convergence factors were monitored separately for herd equations (which included herd-year-seasons and cows with herds) and sire equations (which included sires, groups, and dams that had neither herds nor records). Time per round decreased from 262 min for round 1 to 252 min for round 30 because of fewer iterations within a round.

Table 6 presents convergence factors for herds, sires, and the entire set of equations. Convergence factors given for herds and sires are summarized as factors after all iterations per round had been completed. Convergence factors did not decrease continually as number of rounds increased. For example, the convergence factor for the sire block in round 5 was .00019 compared with .00324 for round 10 and was the result of altered relaxation factor (Table 5). Any time the relaxation factor was altered, the balance in the equations was disturbed, and the convergence factor increased. In round 9 the relaxation factor was altered to 1.50, whereas it had been 1.25 in rounds 1 through 8. In general, magnitude of the convergence factors decreased with increasing number of iterations and with increasing number of rounds. Table 6 also

TABLE 5. Relaxation factors used with successive overrelaxation.

Rounds	Cow and herd-year-season equations	Sire, group and dam-without-herd equations
1-8	1.25	1.25
9-13	1.50	1.50
14-20	1.50	1.25
21-23	1.25	1.25
24-26	1.25	1.25
27-28	1.25	1.50
29-30	1.25	1.25

TABLE 6. Convergence factors¹ at end of specified rounds for herds,² sires,³ and total equations⁴ and average number of iterations per herd per round to reach the convergence criterion.^{5,6}

	Round					
	1	5	10	15	20	30
Herd	.00143	.00027	.00033	.00028	.00024	.00012
Sires	.00099	.00019	.00324	.00028	.00030	.00223
Total	.00108	.00020	.00296	.00028	.00029	.00206
Mean iterations per herd	4.93	3.04	3.13	3.08	3.05	3.00

¹ Convergence factor was the ratio of norm of residuals to norm of RHS.

² Herd equations include all herd-year-season equations and equations of cows within herds.

³ Sire equations include equations for sires, dams without herds, and groups.

⁴ Altering of relaxation factors as shown in Table 5 seriously affected the convergence factors.

⁵ A minimum of three interactions per herd was required. Fewer iterations per herd indicate that the convergence criterion is being met sooner.

⁶ Altering the relaxation factors as shown in Table 5 seriously affected the rate of convergence and the number of iterations per herd.

shows that average number of iterations per herd per round decreased from 4.91 in round 1 to 3.00 in round 30. Increase of average number of iterations per herd in round 10 was a result of altered relaxation factor in round 9.

Table 7 presents convergence factors for sire and group equations by iteration and round. Magnitude of the factors decreased as number of iterations increased and as number of rounds increased. The initial convergence factor for each round is an indicator of overall conver-

gence.

Final solutions for groups (Table 8) show that dam groups have negative solutions whereas solutions for sire groups generally are positive. There is little indication of any trend across groups. This may be attributed to the number of relationships among animals in the data set. Increasing relationships in an evaluation decreases the need for genetic grouping (8). Solutions seemed to converge slowly to a final value from a single direction. For both

TABLE 7. Convergence factors¹ for sire and group equations per round for five iterations.²

Iterations within round	Round					
	1	5	10	15	20	30
1	.07058	.01515	.02437	.01829	.01555	.01351
2	.01907	.00399	.00667	.00608	.00611	.00667
3	.00746	.00130	.00540	.00227	.00240	.00467
4	.00280	.00052	.00474	.00081	.00087	.00333
5	.00099	.00019	.00324	.00028	.00030	.00223

¹ Convergence factor was the ratio of norm of residuals to norm of RHS.

² Altering of relaxation factors as shown in Table 5 seriously affected the convergence factors.

TABLE 8. Approximate solutions for group effects at end of the thirtieth round.

Dam group	Round 30 solution (kg)	Sire group	Round 30 solution (kg)
1	-274	15	71
2	-269	16	43
3	-307	17	8
4	-354	18	11
5	-329	19	-40
6	-327	20	-56
7	-310	21	-32
8	-289	22	27
9	-279	23	44
10	-291	24	76
11	-205		
12	-201		
13	-49		
14	-84		

the sire and dam groups, convergence was slower for groups with missing parents born earliest in the data set.

Table 9 presents averages and standard deviations of solutions for cows, herd-year-seasons, sires, and groups. In general, according to selection index principles $\sigma_I = r_{IT}\sigma_T$, where σ_I is standard deviation of the index, σ_T is standard deviation of true merit, and r_{IT} is correlation between the index and true merit. In this study σ_T is a constant; hence, the only reason for differences in σ_I is r_{IT} . An increase in accuracy would result in a larger σ_I . At 30 rounds of iteration, the standard deviation (SD) for sire solutions of genetic merit was 491 kg, which is larger than the

SD for any other animal category, as expected. Dams without records, but allocated to herds, are evaluated from records of relatives (primarily daughters). The degree of sire identification is less for dams without herds (Table 2) so the accuracy would be expected to be low; the SD was 204 kg. The SD for solutions of dams without herds and without records was 236 kg. They were included in the data set and not allocated to herds because they are dams of sires. Accuracy of the evaluations of their sons increases accuracy of their own evaluations. The SD for dams that made records is 384 kg. These dams have a high accuracy because their sires were known (Table 2), they made records themselves, and they had progeny in the data set. The SD for the category of nonparents is 410 kg, the greatest for any category of cows. Generally the SD of their solutions would be expected to be greater than that of dams without records but less than that of dams with records because nonparents have no progeny with records. Average year of birth of nonparents was 1972. This category of animal was the youngest in the data set so their accuracy may have improved because of increased accuracy of evaluation of their sires.

Table 10 presents average solutions and SD of a subset of solutions containing only those cows and sires that had Northeast estimates of genetic merit. Northeast estimates of genetic merit for cows calculated from only first lactation records within herd were available from DRPL (4). The Northeast sire evaluations calculated from first lactation records of their progeny in June 1983 are transmitting abilities. Averages in Table 10 for

TABLE 9. Average approximate solutions (kg) and standard deviations for cows, herd-year-seasons, sires, and groups at end of thirtieth round.

Type of solution	Number	Mean	SD
Herd-year-seasons	229,394	6872	1074
Sires	6000	-118	491
Groups	24	-142	155
Cows			
Dams without records with herds	427,469	-137	204
Dams without records without herds	3498	-182	236
Nonparents	747,989	-46	410
Dams with records	326,982	-91	384

TABLE 10. Correlations of Northeast solutions for genetic merit (kg) with solutions at end of thirtieth round of simultaneous evaluation.

Type of solution	Number	Correlations	Standard deviations	
			Northeast estimates	Simultaneous estimates
Sires	2491	.94	629	587
Cows				
Dams without records with herds	190,672	.42	472	238
Dams without records without herds	167	.41	524	288
Nonparents	496,895	.75	487	417
Dams with records	231,297	.71	485	393

sires are for estimated breeding values (EBV) or twice average transmitting abilities.

Correlations between Northeast estimates of cow genetic merit, Northeast estimates of sire EBVs, and their corresponding solutions

after 30 rounds of block iteration in Table 10 indicate general agreement of estimates of sire merit but less agreement for estimates of cow merit. Several explanations are possible for this discord. The amounts of information

TABLE 11. Changes of solutions from round to round.

Range of change	Round A to Round B ¹						
	1-2 kg	4-5 kg	9-10 kg	14-15 kg	19-20 kg	24-25 kg	29-30 kg
Cow genetic merit (1,505,938)							
d, ¹ kg	59.98	9.47	6.14	4.98	4.12	3.51	3.07
SD, ² kg	105.50	10.25	5.24	4.38	3.73	3.06	2.86
≤4.5 kg, %	21.2	62.0	75.2	81.6	84.3	95.9	96.4
>11.3 kg, %	54.5	4.3	.6	.2	.1	0	0
Sire genetic merit (6000)							
d, kg	151.80	41.16	13.68	7.27	5.46	4.75	3.80
SD, kg	167.92	42.94	12.63	6.18	4.43	3.79	3.25
≤4.5 kg, %	7.0	21.2	49.1	75.0	87.1	91.4	95.2
>11.3 kg, %	80.9	51.4	13.6	1.7	.5	.2	0
Group effects (24)							
d, kg	19.69	18.22	19.42	12.54	10.72	10.01	7.58
SD, kg	14.16	14.63	12.67	9.53	7.79	8.05	5.94
≤4.5 kg, %	37.5	45.8	37.5	50.0	50.0	58.3	75.0
>11.3 kg, %	37.5	41.7	41.7	16.7	4.2	4.2	0
Herd-year-season effects (229,394)							
d, kg	61.37	7.54	4.78	3.26	2.60	2.41	2.03
SD, kg	80.27	9.11	4.84	3.27	2.50	2.07	1.71
≤4.5 kg, %	17.8	74.8	90.3	97.7	98.9	99.2	99.4
>11.3 kg, %	62.8	3.5	.7	.3	.2	0	0

¹ d = Average absolute deviation of change: end of round A to end of round B, e.g., round 1 to round 2.

² SD = Standard deviation of change.

that contribute to estimates for sires and cows are different in the estimation procedures.

The major cause of differences between procedures may be in the grouping procedures. The Northeast cow evaluation procedure does not group cows directly. The only grouping is by inclusion of sire estimates of genetic merit. In the NEAISC sire evaluations, bulls were grouped roughly by registration number in batches of 100 (R. W. Everett, 1984, personal communication).

Table 11 presents distributions of changes from round to round and average change per round of solutions for genetic merit for cows and sires and for groups and herd-year-seasons. Average changes per round continued to decrease for all types of solutions as number of rounds increased. By 30 rounds, 96% of solutions of cow genetic merit, 95% of sire solutions, 75% of group solutions, and 99% of herd-year-season solutions were changing by less than 4.5 kg from round to round.

SUMMARY AND RECOMMENDATIONS

A joint sire and cow evaluation procedure was developed. This procedure should be superior to the current Northeast procedures for evaluating sires and cows because it reduces the number of assumptions.

Joint evaluation is feasible in time and money. The amount of additional editing is minimal. The time to complete each round of iteration could be reduced from 4 h by at least 2 h by more efficient programming of the iteration program and use of disks to store equations that were stored on tape. Starting iterations with solutions from a previous evaluation also would result in faster convergence. Faster computers with increased memory are inevitable and will further reduce the time required.

The procedure is readily extendable to multiple records and multiple traits. The number of nonzero coefficients carried would be increased, but the coefficient matrix still would be sparse.

The method of grouping should account more precisely for type of missing information

and, thus, define selection more accurately than previous methods.

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