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# An Evaluation of Four Procedures to Rank Centrally Tested Boars

## Abstract

Four procedures, one using genetic relationships, were evaluated to rank centrally tested boars from records on 9,093 boars tested in central stations. Breeds with larger numbers of tested boars were found to have more total relationship ties than were breeds with smaller numbers of boars tested. Of the breeds with greater tested numbers, Durocs and Yorkshires were genetically more tied than were the Hampshire or Spotted breeds. Among breeds with fewer observations, Berkshires had the most relationship ties, while Poland Chinas had the fewest. When the number of ties between boars in each season-year with boars in the most recent season-year were evaluated, only the last six or seven-season-year groups were needed to provide sufficient relationship ties with pigs currently tested. The four evaluation procedures were performance value (PV), deviation of the performances value from the station-season-year subclass mean (SSYD), mixed model without relationships (MM) and mixed model including relationships (MMR). The MM procedure produced much lower prediction error variances than did the PV or SSYD procedures; whereas the MMR procedure produced the lowest prediction error variances. Although the MM and MMR procedures gave far more precise estimates than did PV and SSYD, they do involve more complex computing procedures. When the cost of these more complex computations is reasonable, the MMR procedure should be considered to evaluate centrally tested boars because it allows a fair comparison of boars across stations in the same season. The value of across station evaluation is discussed.

## Keywords

Boars, Central Testing, Sire Evaluation, Backfat, Daily Gain

## Disciplines

Agriculture | Animal Sciences | Genetics

## Comments

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# AN EVALUATION OF FOUR PROCEDURES TO RANK CENTRALLY TESTED BOARS<sup>1</sup>

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## Summary

Four procedures, one using genetic relationships, were evaluated to rank centrally tested boars from records on 9,093 boars tested in central stations. Breeds with larger numbers of tested boars were found to have more total relationship ties than were breeds with smaller numbers of boars tested. Of the breeds with greater tested numbers, Durocs and Yorkshires were genetically more tied than were the Hampshire or Spotted breeds. Among breeds with fewer observations, Berkshires had the most relationship ties, while Poland Chinas had the fewest. When the number of ties between boars in each season-year with boars in the most recent season-year were evaluated, only the last six or seven-season-year groups were needed to provide sufficient relationship ties with pigs currently tested. The four evaluation procedures were performance value (PV), deviation of the performances value from the station-season-year subclass mean (SSYD), mixed model without relationships (MM) and mixed model including relationships (MMR). The MM procedure produced much lower prediction error variances than did the PV or SSYD procedures; whereas the MMR procedure produced the lowest prediction error variances. Although the MM and MMR procedures gave far more precise estimates than did PV and SSYD, they do involve more complex computing procedures. When the cost of these more complex computations is reasonable, the MMR

procedure should be considered to evaluate centrally tested boars because it allows a fair comparison of boars across stations in the same season. The value of across station evaluation is discussed.

(Key Words: Boars, Central Testing, Sire Evaluation, Backfat, Daily Gain.)

## Introduction

Henderson (1975b) presented the general linear model as

$$y = X\beta + Zu + e, \quad (1)$$

where  $X$  is an incidence matrix,  $\beta$  is a vector of unknown fixed effects,  $Z$  is an incidence matrix for random effects,  $u$  is a vector of random additive genetic effects and  $e$  is a nonobservable vector of random variables. It is also assumed that  $E(u) = E(e) = O$  and that

$$V \begin{pmatrix} u \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_g^2 & O \\ O & I\sigma_e^2 \end{pmatrix}, \quad \text{where}$$

$A$  is the numerator relationship matrix of animals to be evaluated and  $I$  is an identity matrix. Equations for finding best linear unbiased predictions (BLUP) of the random effects and for estimating estimable linear functions of  $\beta$  are

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}k \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'Y \end{bmatrix}, \quad (2)$$

where  $k = \frac{\sigma_e^2}{\sigma_g^2}$  and  $A^{-1}$  is the inverse of the numerator relationship matrix. The vector  $u$  can include animals for which no records are available but for which estimates of genetic merit are desired. This could include boars that are sires of test station pigs.

The addition of  $A^{-1}$  to the equation ties together records on related individuals. Thus,

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additional information on the individual is obtained by properly weighting performances of animals expected to have a portion of their genes in common with the individual being evaluated and thereby increasing the accuracy of prediction. Secondly, genetic differences between subgroups such as herd-year-seasons are more closely accounted for by tying subgroups together through genetic relationships.

Henderson (1975a,b) defined the best evaluation procedure to be that which is unbiased and has the smallest possible prediction error variance. Kennedy and Moxley (1975) found that including relationships among dairy bulls reduced the average prediction error variance by 18% compared with a model that grouped bulls according to date of birth. Pollak et al. (1977) reported in beef cattle that the prediction error variance increased from 3.5 to 22.2% when genetic relationships were ignored. Also, values for younger sires increased more. These results indicate that use of relationships will reduce prediction error variance in differing amounts, depending on the model and the existing relationships.

Most, if not all, central swine testing stations in the United States currently rank boars using either an undeviated individual performance value or the performance value deviated from the test group mean. Evaluations do not compare boars across stations, years or seasons. The main purpose of this study was to evaluate alternative mixed model procedures used in other species. Should the procedures result in more accurate estimates of genetic values, their use should permit a more rapid rate of genetic progress.

#### Experimental Procedure

Performance figures for average daily gain (ADG) and average backfat (ABF) on 9,093 boars centrally tested in four Iowa stations and one Nebraska station over 5 yr were utilized in this study. A more complete description of the data and nongenetic adjustments are contained in Carlson (1983). With use of information provided by the testing stations and the respective breed associations, the sire, dam and paternal and maternal grandsire of each pig were identified as completely as possible. The number of pigs/breed and percentage lacking sire, paternal grandsire, dam and maternal grandsire information are listed in table 1. Across all breeds, sires

could not be traced on 2.3% of the tested boars, paternal grandsires on 4.1%, dams on 11.6% and maternal grandsires on 19.1%.

Four evaluation procedures then were compared. They were: 1) performance value (PV); 2) deviation of the performance value from the station-season-year subclass mean (SSYD); 3) mixed model without relationships (MM) and 4) mixed model with relationships (MMR). These procedures were compared on the basis of their prediction error variance by using the guidelines offered by Henderson (1975a).

For the PV procedure, the boars are ranked on  $X$ , their performance value for the trait (ADG, ABF). The variance of this value is simply the variance of  $X$  across all breeds and station-season-years. This procedure is currently used in some central swine test stations. In the SSYD procedure, the value of a boar is  $X - \bar{X}$ , where  $\bar{X}$  is the station-season-year subclass mean. The mean of  $X - \bar{X}$  is zero, the variance of this estimate is  $\left(\frac{n-1}{n}\right)$  times the within station-season-year variance, and  $n$  is the number of pigs in the station-season-year. The SSYD procedure is recommended for central swine test station use by the National Swine Improvement Federation (Hubbard, 1981).

For MM and MMR procedures, the prediction error variances are approximated by  $\left(\frac{1}{C_{ii}}\right) \sigma_e^2$ , where  $C_{ii}$  is the diagonal element of the coefficient matrix for the particular animal if iterated solutions are obtained, or is  $(C^{ii}) \sigma_e^2$ , where  $C^{ii}$  is the inverse element corresponding to a particular animal when solutions are obtained through a direct inverse.

The MMR procedure is the same as the MM procedure with the addition of a relationship matrix. The inverse of the relationship matrix was first formed by using procedures outlined by Quaas (1976). The maternal and paternal grandsires, the sire and the dam of each tested boar were used to establish the relationship matrices. Because breeding values were not desired for the maternal or paternal grandsires, nor for the dams, the original inverse of the relationship matrix was reduced by absorbing the grandsire and dam equations into the sire and pig equations. It therefore contained only the inverse of relationships between tested boars and their

TABLE 1. NUMBER OF BOARS OF EACH BREED AND PERCENTAGES MISSING ANCESTRAL INFORMATION

| Breed         | Number of pigs | % missing sire identification | % missing paternal grandsire identification | % missing dam identification | % missing maternal grandsire identification |
|---------------|----------------|-------------------------------|---|------------------------------|---|
| Berkshire     | 175            | 0                             | 0   | 5.1                          | 5.1   |
| Chester White | 493            | 2.0                           | 2.0   | 9.1                          | 12.4  |
| Duroc         | 3,179          | 1.0                           | 1.8   | 8.0                          | 10.2  |
| Hampshire     | 1,909          | 2.6                           | 5.0   | 15.5                         | 20.8  |
| Landrace      | 168            | 3.6                           | 26.8  | 5.4                          | 33.9  |
| Poland China  | 180            | 1.7                           | 1.7   | 10.6                         | 10.6  |
| Spotted       | 1,196          | 1.9                           | 3.2   | 12.4                         | 48.8  |
| Yorkshire     | 1,793          | 5.0                           | 6.7   | 16.1                         | 16.6  |

sires. The equations in (2) were then positioned with  $u$  subdivided such that  $u_1$  contained additive genetic effects of sires and  $u_2$  additive genetic effects of boars. Further,  $Z$  could be portioned into  $\begin{pmatrix} Z_1 \\ Z_2 \end{pmatrix}$  with the  $Z_1$  elements relating to sires and  $Z_2$  relating to their tested progeny. As individual performance information was not available on the sires of the tested boars, the  $Z_1'Z_1$ ,  $Z_1'Z_2$ ,  $Z_2'Z_1$  matrices and  $Z_1'Y$  vector were null. Because  $A^{-1}$  included sires, additive genetic effects of the sires of the boars could be estimated.

Henderson (1975a,b) showed that the  $k$ -value for a given trait is equal to the inverse of the heritability of the trait minus one. Hubbard (1981) places the heritability of ADG at .30. Thus,

$$k_{ADG} = \frac{1}{.30} - 1 = 2.33 \text{ because } \frac{1}{h^2} - 1 =$$

$$\frac{1}{\frac{\sigma_g^2}{\sigma_e^2 + \sigma_g^2}} - 1 = \frac{\sigma_e^2}{\sigma_g^2}$$

The heritability of ABF according to Hubbard (1981) is .50. So the

$$k_{ABF} = \frac{1}{.50} - 1.0 = 2.0 - 1.0 = 1.0.$$

Because heritabilities of these traits were considered equal across breeds,  $k$ -values for ADG and ABF, respectively, were the same for each breed. These  $k$ -values are needed in (2) to obtain BLUP of the additive genetic merit.

To evaluate the relative benefit of using the relationship matrix for breeds with different numbers of boars and relationships, investigations were made of one of the four

smaller breeds (Berkshire) with the most relationships, one of the smaller breeds with the fewest relationships (Poland China) and a breed (Duroc) with the most relationships. The actual and approximate prediction error variances were obtained after iteration and inversion for the smaller breeds and by iteration only for the larger breed chosen. The Gauss-Seidel procedure was used to iterate the solutions. Details on programming procedures can be obtained from the author.

Separate analyses were conducted for each breed using the LSML76 program and procedures outlined by Harvey (1975) to obtain the within-dam variances for ADG and ABF. These values were then weighted by the degrees of freedom for each breed to obtain weighted averages for these two traits. The weighted average variances were then used to calculate prediction error variances for ADG and ABF in the MM and MMR procedures.

### Results and Discussion

The number of relationships across all station-season-year subclasses is shown in table 2 for each breed. A tie is defined as a nonzero genetic relationship between two animals. Generally, the more pigs represented in the breed, the more total ties. The percentage of filled cells was also calculated by dividing the number of nonzero relationships within a breed by the number of total possible relationships had all pigs within a breed been related. This measure seemed to be inversely related to breed size, with the smaller breeds having a larger percentage of filled cells. For a pig to be unrelated to all others, his sire and dam had to be un-

TABLE 2. SUMMARY OF RELATIONSHIPS BY BREED

| Breed         | Number of pigs | Total number of ties | Mean ties/pig | % of filled cells | Minimum ties/pig | Maximum ties/pig |
|---------------|----------------|----------------------|---------------|-------------------|------------------|------------------|
| Berkshire     | 175            | 3,471                | 39.7          | 22.8              | 1                | 78               |
| Chester White | 493            | 4,808                | 19.5          | 4.0               | 0                | 53               |
| Duroc         | 3,179          | 103,284              | 65.0          | 2.0               | 0                | 223              |
| Hampshire     | 1,909          | 38,876               | 40.7          | 2.1               | 0                | 111              |
| Landrace      | 168            | 2,059                | 24.5          | 14.7              | 1                | 19               |
| Poland China  | 180            | 1,032                | 11.5          | 6.4               | 1                | 23               |
| Spotted       | 1,196          | 22,683               | 37.9          | 3.2               | 0                | 109              |
| Yorkshire     | 1,793          | 52,504               | 58.6          | 3.3               | 1                | 192              |

related to all other animals and his penmates had to have either died or had their records excluded from the analysis.

The percentage of season-year groups tied within a station is shown in table 3 by station. These are direct ties; i.e. a pig in station-season-year<sub>ijk</sub> is related to a pig in station-season-year<sub>imn</sub>. For a breed represented in every station-season-year subclass, there were 45 possible ties in the Ames, Ida Grove and New Hampton stations. The Durocs, Hampshires and Yorkshires were represented in each station-season-year subclass and, thus, could possibly tie together 207 season-years within station. This was less for the other breeds because not all breeds were represented in each test.

In Durocs, Hampshires and Yorkshires, from 81 to 100% of the season-years were tied within a station, whereas the ties of season-years within a station were much lower for the Berkshire, Chester White, Landrace, Poland China and Spotted breeds.

Season-years within a station were also evaluated for indirect ties. An indirect tie

is when season-year *i* and *j* are directly tied, as are season-year *j* and *k*, while season-year *i* and *k* are not. These are now tied because the direct ties exist.

The percentage of season-years within stations not tied directly, indirectly or both are listed in the last column of table 3. Values ranged from 0 to 6.0% across breeds. Because almost all season-years within a station were tied for each breed, it seems that animals currently tested can be compared with their predecessors through common ancestry.

An important computational question that arises is which records must be included to aid in the evaluation of a set of boars just completing a test season. Listed in table 4 are the number of ties for the most current test season included in this analysis with preceding season-years for the Duroc, Hampshire, Spotted and Yorkshire breeds.

As expected, the further back data were kept, the number of ties with pigs currently being tested increased, but at a decreasing rate. The third column of table 4 lists the percentage of ties with pigs currently being

TABLE 3. PERCENTAGE OF SEASON-YEARS TIED GENETICALLY WITHIN STATION

| Breed         | Station |           |        |          |             | Total | Untied <sup>a</sup> |
|---------------|---------|-----------|--------|----------|-------------|-------|---------------------|
|               | Ames    | Ida Grove | Lisbon | Clarkson | New Hampton |       |                     |
| Berkshire     | 82      | 50        | 33     | 47       | 50          | 58.8  | 1.7                 |
| Chester White | 100     | 17        | 0      | 53       | 58          | 52.5  | 5.5                 |
| Duroc         | 98      | 93        | 100    | 100      | 93          | 96.6  | .0                  |
| Hampshire     | 100     | 100       | 89     | 81       | 98          | 94.2  | .0                  |
| Landrace      | 80      | 70        | 20     | 20       | 100         | 63.2  | 2.6                 |
| Poland China  | 80      | 14        | 32     | 0        | 10          | 43.1  | 6.0                 |
| Spotted       | 93      | 64        | 47     | 42       | 76          | 66.2  | .5                  |
| Yorkshire     | 100     | 87        | 100    | 92       | 96          | 94.7  | .0                  |
| Mean          | 92      | 67        | 62     | 68       | 77          | 75.0  | 1.7                 |

<sup>a</sup>Percentage of no direct or indirect genetic ties.

TABLE 4. RELATIONSHIP TIES OF SEASON-YEARS ONE THROUGH NINE WITH SEASON-YEAR 10 ACROSS STATIONS FOR DUROC, HAMPSHIRE, SPOTTED AND YORKSHIRE BREEDS

| Season-year | Number of ties | % of total | Cumulative % of total |
|-------------|----------------|------------|-----------------------|
| 1           | 641            | 2.5        | 100.0                 |
| 2           | 736            | 2.8        | 97.5                  |
| 3           | 1,208          | 4.6        | 94.7                  |
| 4           | 1,587          | 6.1        | 90.1                  |
| 5           | 1,947          | 7.5        | 84.0                  |
| 6           | 3,225          | 12.4       | 76.5                  |
| 7           | 4,250          | 16.3       | 64.1                  |
| 8           | 5,734          | 22.0       | 47.7                  |
| 9           | 6,679          | 25.7       | 25.7                  |

tested if that season-year and all others before it were included, compared with nine previous season-years. Keeping the previous nine season-years rather than the last six would add only 10% more ties. Keeping nine season-years rather than seven would add only 5% more ties. All nine season-years were used in these analyses to utilize as many ancestral ties as available. For practical test station use, however, it would seem that data from only the last six or seven season-years would need to be included in an analysis.

The percentages of direct ties between stations within a season-year are presented in table 5. When a potential buyer of centrally tested boars evaluates the records on the boars to be sold, he is interested in boars tested in a particular season-year. Thus, the number of ties between stations in that season-year indicates the extent that boars in a certain station were evaluated relative to those in another. Column 2 of table 5 lists the per-

TABLE 5. POSSIBLE PERCENTAGE OF STATIONS TIED GENETICALLY WITHIN A SEASON-YEAR AND THOSE UNTIED

| Breed         | Possible % direct ties | % untied <sup>a</sup> of possible |
|---------------|------------------------|-----------------------------------|
| Berkshire     | 60                     | 4                                 |
| Chester White | 46                     | 13                                |
| Duroc         | 100                    | 0                                 |
| Hampshire     | 97                     | 0                                 |
| Landrace      | 42                     | 14                                |
| Poland China  | 10                     | 26                                |
| Spotted       | 74                     | 2                                 |
| Yorkshire     | 99                     | 0                                 |

<sup>a</sup>Untied either directly or indirectly.

centage of all possible direct station ties within a season-year for each breed. The values for Durocs, Hampshires and Yorkshires were 100, 97 and 99%, respectively. The Berkshire, Chester White, Landrace, Spotted and Poland China breeds did not tie stations within season-years as well due to the lower number of boars tested. The third column lists the percentage of stations within a season-year that were not tied either directly or indirectly. These values range from 0 to 26% of the possible season-year within station ties.

Examination of tables 3, 4 and 5 reveals that the Duroc, Hampshire and Yorkshire breeds have season-years within stations, stations within season-years and station-season-year combinations well-tied. The Spotted breed is intermediate, with the Berkshire, Chester White, Landrace and Poland China breeds not nearly as well-tied as the three larger breeds. Of the latter four breeds, the Berkshire boars were the most related while Poland China boars were the least related.

*Prediction Error Variances.* The within-dam variances for ABF and ADG for the Berkshire, Duroc and Poland China breeds are shown in table 6. Weighted by the respective degrees of freedom, the average variance for ABF is .04583 cm<sup>2</sup> and for ADG is .00495 (kg/d)<sup>2</sup>. These weighted average variances were used to estimate prediction error variances for the MM and MMR procedures across the three breeds.

The mean prediction error variances for the PV, SSYD, MM and MMR procedures for the Berkshires, Poland Chinas and Durocs for ABF are given in table 7. For ABF, the SSYD procedure reduced the estimated variance by 14.1% compared with the PV method. The difference between the PV and SSYD procedure is that, because the station-season-

TABLE 6. WITHIN-DAM VARIANCES FOR AVERAGE BACKFAT AND AVERAGE DAILY GAIN IN BERKSHIRES, DUROCS AND POLAND CHINAS

| Breed            | df    | Within dam variance  |                          |
|------------------|-------|----------------------|--------------------------|
|                  |       | ABF, cm <sup>2</sup> | ADG, (kg/d) <sup>2</sup> |
| Berkshire        | 41    | .07836               | .00616                   |
| Duroc            | 1,924 | .04439               | .00498                   |
| Poland China     | 55    | .07214               | .00639                   |
| Weighted average | 2,020 | .04583               | .00495                   |

TABLE 7. PREDICTION ERROR VARIANCES FOR AVERAGE BACKFAT AND AVERAGE DAILY GAIN BY BREED

| Method <sup>a</sup> | Average backfat (cm <sup>2</sup> ) |           |              |        | Average daily gain (kg/d) <sup>2</sup> |           |              |        |
|---------------------|------------------------------------|-----------|--------------|--------|--|-----------|--------------|--------|
|                     | All                                | Breed     |              |        | All                                    | Breed     |              |        |
|                     |                                    | Berkshire | Poland China | Duroc  |  | Berkshire | Poland China | Duroc  |
| PV <sup>b</sup>     | .08125                             |           |              |        | .00864                                 |           |              |        |
| SSYD <sup>b</sup>   | .06987                             |           |              |        | .00686                                 |           |              |        |
| MM, inverted        |                                    | .02844    | .02722       |        | .00163                                 | .00162    |              |        |
| MM, iterated        |                                    | .02565    | .02537       | .02307 | .00160                                 | .00159    |              | .00151 |
| MMR, inverted       |                                    | .02360    | .02450       |        | .00131                                 | .00141    |              |        |
| MMR, iterated       |                                    | .01939    | .01941       | .01346 | .00112                                 | .00113    |              | .00076 |

<sup>a</sup>PV = performance value, SSYD = station-season-year deviation, MM = mixed model and MMR = mixed model with relationship matrix included.

<sup>b</sup>Estimates of prediction error variances do not account for number of pigs in each breed.

<sup>c</sup>Solutions were obtained only from iteration due to the size of the matrix to be inverted.

year subclass mean has been subtracted from the performance value, pigs are evaluated within a station-season-year subclass, and the variance of these estimates is  $(\frac{n-1}{n})$  times the variance within a station-season-year. For both PV and SSYD the number of pigs/breed is ignored in estimation of the variance of each procedure. Because the within-station-year variance for ABF is substantially less than the total variance, the variance of the SSYD estimates is less.

Predicting performance of boars under the MM procedure drastically reduced the prediction error variances in all three breeds for ABF. In the Berkshire breed, the exact prediction error variance obtained was 59.3% less than that of the SSYD procedure, while the approximate prediction error variance from the iteration routine was 63.3% smaller than that under SSYD. Reductions in prediction error variance of similar magnitude occurred in the Poland China breed. These were 61.0 and 63.7%, respectively.

For both MM and MMR in the Berkshire and Poland China breeds the estimated prediction error variances from the iterated procedure are quite similar to those obtained by inversion. It must be realized, however, that the prediction error variances obtained from inversion are exact, while those from iteration are approximate. For larger breeds, such as the Durocs, solving the equations by iteration is a much more economical procedure computationally than is inversion. Solutions and approximate prediction error variances for larger breeds therefore seem

to be satisfactorily estimated by using iteration.

The MMR procedure reduced prediction error variance for ABF in the Berkshires by 17.0% compared with the MM method. Under iteration, MMR approximate prediction error variance was 24.4% less than that of MM. The MMR prediction error variance in Polands for ABF was 10% less than approximate prediction error variance for MM. The reduction of the error variance of prediction, comparing MMR with MM in Durocs, was 41.7% lower for MMR. These values generally are equal to or higher than those found by Kennedy and Moxley (1975), Pollak et al. (1977) and Tong et al. (1980). In addition to the much lower prediction error variances, MMR allows animals in different subgroups to be more accurately compared (Henderson, 1975b). Thus, under MMR, boars tested in the same season but in different stations can be evaluated free of any subgroup effect.

Because individual breeding values based on one record are being predicted in this analysis, the percentage of information added to an animal by including relationships is much higher than in a typical sire evaluation in dairy cattle. Thus, the decreases in the prediction error variance by including the relationship matrix should be at least as large as those of a dairy sire analysis. Kennedy and Moxley (1975) reported that the maximum number of bulls to which any particular bull was related was 16. The maximum numbers of ties/pig in Berkshires, Durocs and Poland Chinas, respectively, were 78, 223 and 23, with respective averages of 39.5, 65.0 and 11.5.



Thus, including the relationship matrix in these analyses, tied more records to a particular animal than did the study by Kennedy and Moxley (1975). That study had 11.3% of all possible relationship ties filled; while for the Berkshires, Durocs and Poland Chinas in this study, values were 22.8, 2.0 and 6.4%, respectively.

The greater frequency of relationships within Berkshires compared with that of Poland Chinas explains the larger decrease in error variances of prediction for the Berkshires relative to that of the Poland Chinas as well as for the large increase in accuracy for Durocs when the relationship matrix is included.

The actual and approximate prediction error variances resulting from the inverted and iterated procedures for both the MM and MMR methods are quite similar in Berkshires and Poland Chinas. The two procedures would be equal if all off-diagonal elements of the matrix to be inverted or iterated were zero. How far apart the two procedures lie thus depends on the number and magnitude of the off-diagonals relative to the size of the diagonals. Because the relationship matrices used here undoubtedly have smaller diagonals and larger and more numerous off-diagonals than those of a cattle sire analysis, the prediction error variances from inversion would not be expected to be as close to those from iteration as was found by Ufford et al. (1979).

The procedures ranked in a similar manner for ADG. The results are shown in table 7. Reductions in prediction error variances were larger for ADG than ABF. For brevity, results are not discussed. The larger reduction for ADG, as compared with ABF, is attributed to the difference in heritability of the traits. A trait with a lower heritability, such as ADG, benefits more from including information on relatives than does a more highly heritable trait, such as ABF.

The application of MM procedures requires consideration of benefits and problems associated with use of these methods for swine data from test stations.

While the MMR procedure resulted in the lowest prediction error variances for both ADG and ABF compared with the other procedures, certain problems must be overcome before the procedure is widely used. Testing costs would certainly rise due to the extra computing involved. Also, the MMR

procedure is a more complex computing procedure than either PV or SSYD, and an operator familiar with its use would be required to process records. This could be circumvented if a computer program were written specifically for evaluation of central test station records and required that the operator only submit the appropriate data.

The extra time involved in computing the MMR analysis is a factor as well. However, the pedigree information could be obtained and entered into the data base several weeks before the boars are expected to complete the test. Performance data could be quickly entered using interactive computer modules. Thus the extra time required should be minimal.

Central tests might be arranged so all boars' records from many test stations could be evaluated simultaneously. Buyers could then compare boars across many stations before purchasing one boar. The mixed model procedures, while more difficult computationally, should provide more precise estimates of genetic values and should result in better sire selection and thus more genetic progress.

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