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Abstract

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Keywords

Pigs, BLUP, Growth Rate, Backfat, Computer Simulation, Performance Testing

Disciplines

Agriculture | Animal Sciences

Comments

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EVALUATION OF PERFORMANCE-TESTED BOARS USING A SINGLE-TRAIT ANIMAL MODEL¹

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ABSTRACT

Data structure designs for breeding value estimation of performance-tested boars using mixed-model methodology were compared. Computer models were based on estimates of parameters from the literature and from results of a survey of test station managers. Results were compared using accuracy (the correlation of true and estimated breeding values) and prediction error variance (PEV). The single-trait animal model included a fixed effect due to station-season, a random effect due to breeding value for ADG or backfat, and a random error term. Family size, number of families per test, and relationships among animals within and across tests were varied. Prediction error variance decreased faster for small families than for large ones as number of families increased, but increasing numbers of animals per pen was most important, especially if test size was optimized. With no other genetic ties, full-sibs were much more accurately evaluated than half-sibs. Designs that included sire ties among families within a station-season resulted in increased PEV. Increasing the number of full-sibs and(or) increasing the number of families per test would help to optimize PEV and correct this problem. Tying station-seasons with the relationship matrix improved the average accuracy of predicted breeding values. Placing full-sibs in different stations resulted in the greatest accuracy of evaluation, but a large number of half-sib (sire) ties resulted in comparable accuracies. Half-cousin ties did not improve accuracy of evaluation but could result in significant genetic progress by increasing the selection differential.

Key Words: Pigs, BLUP, Growth Rate, Backfat, Computer Simulation, Performance Testing

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Introduction

Although mixed-model methodology has been refined and applied extensively in the dairy and beef cattle industries, the swine industry in the United States has been slow to adopt its use. In recent years, results of mixed-model analyses of swine data have been reported with increasing frequency (Hudson and Kennedy, 1985; Mabry et al., 1987; Keele et al., 1988). Most research on mixed-model methodology has been conducted using design

structures commonly found in cattle data. The purpose of this study was to explore the behavior of mixed-model equations when data structures similar to those found in central boar test stations are used and then to establish guidelines for exploiting data structure to increase accuracy of swine genetic evaluations.

Materials and Methods

Test Station Survey. A survey of 32 central swine testing station managers was conducted to ascertain data structures. Twenty-six managers responded to questions concerning entry requirements (e.g., number of animals, genetic relationships, sexes, and number of pens) of each breed tested during 1984 and 1985. The ranges and means for number of pigs per pen and number of pens per breed and the genetic relationships among pigs within a

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TABLE 1. NUMBER OF PENS BY BREED, NUMBER OF ANIMALS PER PEN, AND RELATIONSHIPS AMONG PENMATES IN CENTRAL TEST STATIONS^a

Breed	No. of pens	
	Total	Avg ^b
Berkshire	37	3
Chester White	38	2
Duroc	407	17
Hampshire	154	6
Landrace	60	3
Poland China	37	2
Spot	84	4
Yorkshire	355	14

No. of animals per pen		Relationships among penmates	Stations
Animals	Stations		
4	5	Half-sibs	7
3	11	Full-sibs	3
2	8	Either	13
1	1	Two litters maximum	6

^aResults are based on responses from 25 central test station managers.

^bAverage number of pens by breed for those test stations that had that breed.

pen were calculated and are presented in Table 1. These numbers were used as guidelines in setting up the various combinations of parameters for the data structure designs modeled in this study.

Animal Model with Relationships. The performance index recommended by the National Swine Improvement Federation for use by central test stations includes ADG, backfat (BF), and feed efficiency (FE) measured as the ratio of feed to gain (National Swine Improvement Federation, 1988). Literature estimates of parameters associated with these traits were summarized (Table 2) using guidelines provided by Hutchens and Hintz (1981). Of considerable interest were the genetic correlations of FE with ADG and BF; indirect

selection for FE may be almost as effective as direct selection and is considerably less expensive (Bereskin and Steele, 1985; Christian and Wood, 1985). The absence of a genetic correlation between ADG and BF, along with a low (.15) phenotypic correlation, also suggested the use of single-trait mixed models as opposed to a multiple-trait model with its correlated variance structure (Hudson and Kennedy, 1985). Thus, ADG and BF were considered separately, and FE was ignored, to avoid complications engendered by multiple-trait models.

The animal model used in this study assumed that breeds were analyzed separately and that the only fixed effect was due to a station-season combination. The only random variable in the model was breeding value. Common environmental effects (c^2) were ignored to keep the designs as simple as possible and because very few estimates of c^2 were available. Genetic trends would be accounted for by inclusion of relationships (Pollak and Quaas, 1981), so the models also ignored such trends.

The model used for animals with records was as follows:

$$y_{ij} = s_i + b_{ij} + e_{ij}, \quad [1]$$

where y_{ij} = ADG or BF measured on the j^{th} boar in the i^{th} station-season, s_i = fixed effect

TABLE 2. COMPOSITE LITERATURE ESTIMATES^a OF PHENOTYPIC AND GENETIC PARAMETERS FOR AVERAGE DAILY GAIN (ADG), BACKFAT PROBE (BF), AND FEED EFFICIENCY (FE)^b

	ADG	BF	FE
ADG	.40	0	-.60
BF	.15	.50	.30
FE	-.60	.20	.25

^aDetails may be found in Wood (1986).

^bAbove the diagonal = genetic correlations; diagonal = heritability; below the diagonal = phenotypic correlations.

due to the i^{th} station-season ($i = 1, 2, \dots, p$) plus the underlying mean common to all observations, b_{ij} = random effect due to the j^{th} boar in the i^{th} station-season ($j = 1, 2, \dots, n$), and e_{ij} = random error associated with the observation on the j^{th} boar in the i^{th} station-season. For an animal model that includes both animals with records and genetically related animals with no records,

$$y = X\beta + Zu + e, \quad [2]$$

where y is an $n \times 1$ vector (augmented to $t \times 1$ with the addition of a $t - n$ null vector when

$$E \begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} X\beta \\ 0 \\ 0 \end{bmatrix}, \text{ and } V \begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} V & A\sigma_G^2 & I_n\sigma_e^2 \\ A\sigma_G^2 & A\sigma_G^2 & 0 \\ I_n\sigma_e^2 & 0 & I_n\sigma_e^2 \end{bmatrix},$$

where $V = A\sigma_G^2 + I_n\sigma_e^2$, A = additive genetic relationship matrix, σ_G^2 = additive genetic variance, and σ_e^2 = residual variance.

evaluating animals without records) of observations on ADG or BF; X is an $n \times p$ incidence matrix; Z is a $t \times t$ matrix equal to an $n \times n$ identity matrix relating observations to the animals that made them and augmented by null rows and vectors for animals that are to be evaluated but have no records; β is a $p \times 1$ vector of unknown fixed effects; u is a $t \times 1$ vector of random breeding values, which can be partitioned into u_1 , an $n \times 1$ vector representing animals having records, and u_2 , a $(t - n) \times 1$ vector for related animals with no records; and e is an $n \times 1$ vector of random errors. Thus,

If the ratio of the residual variance to the additive genetic variance (σ_e^2/σ_G^2) is known, Henderson's (1973) mixed-model equations may be written as

$$\begin{bmatrix} X'X & X'Z & 0 \\ Z'X & Z'Z & 0 \\ 0 & 0 & 0 \end{bmatrix} + A^{-1}k \begin{bmatrix} \hat{\beta} \\ \hat{u}_1 \\ \hat{u}_2 \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ 0 \end{bmatrix}, \quad [3]$$

where $k = \sigma_e^2/\sigma_G^2 = (1 - h^2)/h^2$; h^2 = heritability of the trait being evaluated and 0 represents rows and columns of zeros required to include evaluation of animals with no records that are related to animals with records.

Station-season effects were absorbed into the random effects on a station-by-station

basis. Solutions for the fixed effects are not presented because they do not influence the solutions for the random effects. The inverse of the relationship matrix (A^{-1}) was built directly by using Henderson's (1975b) method, because inbreeding was not part of any design. This resulted in the following system of equations:

$$\begin{bmatrix} Z'MZ & 0 \\ 0 & 0 \end{bmatrix} + A^{-1}k \begin{bmatrix} \hat{u}_1 \\ \hat{u}_2 \end{bmatrix} = \begin{bmatrix} Z'My \\ 0 \end{bmatrix}, \quad [4]$$

where $M = I_n - X(X'X)^{-1}X'$.

Accuracy and prediction error variance (PEV) were the criteria by which the designs were compared to determine which were optimal, accuracy because it is defined as the correlation between the estimated and true breeding values, and PEV or $\text{Var}(u - \hat{u})$ because the "best" evaluation method has been

defined as the one which in the class of linear unbiased predictors has minimum PEV (Henderson, 1975a).

Modeling Procedures

The computer programs required for generation of coefficient matrices and the resulting

TABLE 3. DATA STRUCTURE DESIGNS EMPLOYED TO EVALUATE MIXED-MODEL METHODOLOGY^a

Item	Genetic relationship within pens		
	None	Half-sib	Full-sib
Family size	1	2,3,4,8	2,3,4
No. of families ^b	10,15,20,32,40,48,50,64,75,100,128,200	5,16,25	5,16,25
Ties within station ^c No. of ties	None	None	Half-sib 0,1,2,3,4,5
Ties across station ^d	None	None	Half-sib Half-cousin Full-sib 0,1,2,3,4,5
No. of ties			0,1,2,3,4,5

^aSelected combinations within the table were modeled due to biological or computational constraints.

^bFor the data sets with no genetic relationships within pens, the number of families equals the total number of unrelated animals; these are the same as numbers of animals in corresponding designs modeling half-sib and full-sib families. The 5, 16, and 25 families for the half-sib and full-sib models correspond to the number of pens in each of three stations.

^cTwo or more full-sib families within a station had the same sire.

^dHalf-sib: one or more families in each station were sired by the same boar; half-cousin: sires of one or more families in each station were half-sibs; full-sibs: littermates were placed in each of the three stations.

PEV were written in FORTRAN 66. Composite literature values (Wood, 1986) for standard deviations of gain (.12) and backfat (.10) were used to generate error variances, which were calculated as standard normal deviates. The variance ratios (k) were obtained from the h^2 . After the animal equations with fixed effect absorbed were built, constants needed to adjust the equations for information from the relationship matrix were added to the appropriate elements of the coefficient matrix. That matrix was inverted by using the LINV1F routine in IMSL (1984), and PEV were calculated from the diagonal elements of the inverse. After all $\text{Var}(u - \hat{u})$ had been accumulated for each class, the average was calculated.

Designs. Data structure designs (Table 3) were modeled by using information from Table 1 and parameter estimates from Table 2. A direct inverse of the coefficient matrix was desired, so numbers of pens and stations and total numbers of animals were kept small, yet they were of a magnitude consistent with information from the station survey.

Designs examining relationships included animals with no relatives, half-sib families, and full-sib families. Family size (number of sibs) varied from one for unrelated boars to eight for half-sibs. This last design was reflective of a possible progeny test using paternal half-sibs, whereas family sizes of two, three, and four are commonly found in test station situations (Table 1). Total number of animals was constrained by the numbers of families involved. A midvalue of 16 was

chosen based on the average number of pens of Durocs tested during the survey period. Some of the recommendations made by Robison (1982) suggested that 25-pen tests could be realistic, and a test consisting of five pens was chosen as an arbitrary minimum. The number of unrelated animals was based on the total number of animals in the multiple-member families.

Genetic relationships among families within and across stations are of interest for several reasons. Relationships among families within stations may increase accuracy of evaluation, but if families are too closely interrelated, a decrease in accuracy may actually occur (Wood et al., 1991). The question is whether a balance can be found. When tests are tied by genetic relationships, boars in different tests may be fairly compared, and accuracy of evaluation may also increase. Thus, designs that included genetic ties within and across tests were modeled. The basic data structure already described was used as a foundation relative to family size and number of pens.

A genetic tie was defined as a pedigree relationship between animals in different families through a common relative. Types of genetic ties included the following: 1) sire (half-sib) ties, in which different litters had the same sire. This tie was used within and across stations; 2) paternal grandsire (paternal half-cousins) ties, in which sires of litters in different stations were half-sibs; and 3) full-sib ties, generated by assigning members of a litter to different stations. The ties chosen were

representative of the purebred swine industry, wherein sons of popular sires produce the boars being tested in central stations (half-cousin); the traditional sire evaluation model (half-sib); or the possibility of more closely tying neighboring evaluation stations on a regional basis (full-sib). Also of interest was the question of how additional ties of the same kind would affect accuracy. Therefore, within each type of tie, number of ties was varied. In addition to individual PEV and accuracies for individual boars and sires, average PEV were calculated for each class of animals. Average daily gain ($h^2 = .40$) and BF ($h^2 = .50$) were evaluated for each of these designs. Because results are similar for both traits, ADG was used in discussing general results. Details of the computer programs may be found in Wood et al. (1991).

One set of designs was used to model sire ties among full-sib families within different size (5, 16, 25 pens) tests. To determine the effect of adding genetic ties across stations, designs using sire, paternal-grandsire, and full-sib ties were modeled. These three types of ties were used to connect sets of three stations of different sizes (5, 16, and 25 full-sib families). To simplify the designs, each time a genetic tie was generated, all stations in a set were so tied. For example, for sire ties, the number of sires decreased by two for each tie added.

Results and Discussion

Numbers of Animals and Degree of Relationship

It has been shown that increasing the total number of unrelated animals within fixed-

effect subclasses is advantageous in increasing accuracy of evaluation (Henderson, 1973; Ojala et al., 1985; Wood et al., 1991). As shown in Table 4, there was some decrease in accuracy of evaluation when fixed effects were included in the model; evaluation of animals based on individual performance does not account for this source of variation. When accounting for adjustment of the station-season effect in this study, almost 48 pigs (16 half-sib families of three pigs each) were needed to exceed the accuracy of individual performance records of unrelated pigs for ADG (Figure 1 and Table 4); four half-sibs in each of 16 families (64) were required for BF. Although certain fixed effects can be ignored in mixed-model analyses, there are ramifications (such as bias) that must be considered (Henderson, 1973, 1975a). Such decisions must be made on a case-by-case basis.

When family structure is considered, however, the effect of increasing numbers of pigs becomes more complicated because numbers must be distributed between more and/or larger families. With unlimited test space, the ideal situation would be more and larger families. In practice, however, the opportunity to place one more boar in a pen (or replace a barrow with a boar) or to remodel or reorganize an existing station is more feasible than building a larger facility.

Figure 1 illustrates the differences in accuracy of evaluation for various numbers of half-sib families as family size increases. The graph is for ADG, but the pattern for BF is very similar. For every pen size, increasing the number of families was most beneficial when test size was small; beyond 16 families, the

TABLE 4. EXPECTED CORRELATIONS BETWEEN TRUE AND ESTIMATED BREEDING VALUES CALCULATED FOR EVALUATION OF INDIVIDUAL PERFORMANCE RECORDS AND BEST LINEAR UNBIASED PREDICTION OF AVERAGE DAILY GAIN (ADG) AND BACKFAT PROBE (BF)

Method of evaluation	Correlation	
	Formula	Result
Individual performance record	$r_{u\hat{u}} = \sqrt{h^{2a}}$	ADG = .632 BF = .707
Best linear unbiased prediction	$r_{u\hat{u}} = \sqrt{1 - \frac{V(u-\hat{u})}{\sigma_G^2}}^b$	ADG: .60 to .70 BF: .67 to .75

$$^a h_{ADG}^2 = .40; h_{BF}^2 = .50.$$

^bValues varied with number and distribution of animals as well as with the relationship among those animals. These results represent the extremes found in this study.

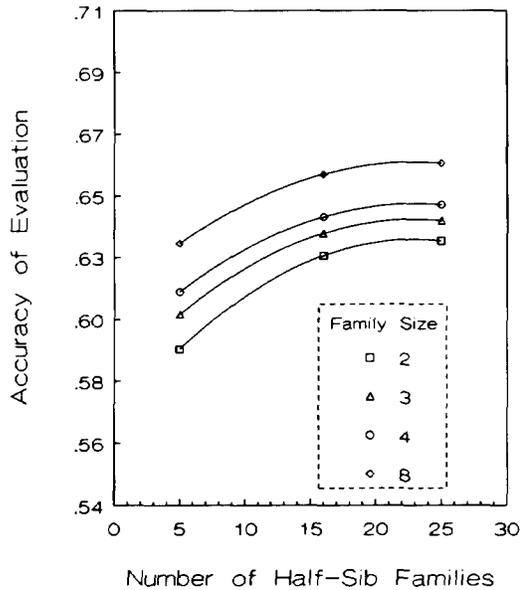


Figure 1. Average accuracy of evaluation of average daily gain as influenced by number of families and half-sib family size.

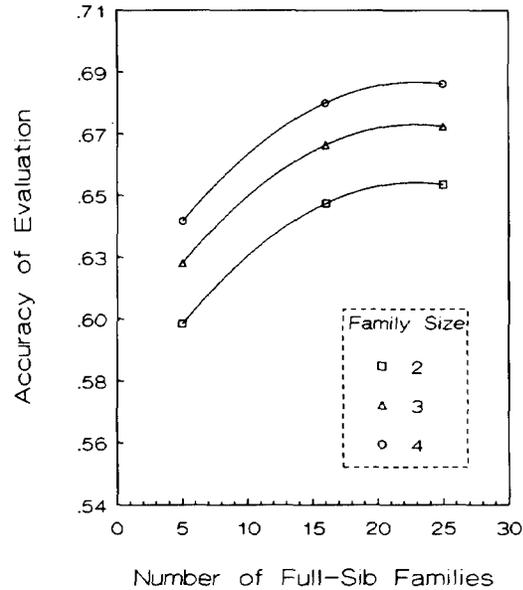


Figure 2. Average accuracy of evaluation of average daily gain as influenced by number of families and full-sib family size.

slopes of the lines moved toward zero but the differences between family sizes remained parallel. Accuracy also improved somewhat faster for smaller half-sib families than for larger families as number of families increased (e.g., an increase in total numbers is more beneficial when numbers are small to begin with), because the change was proportionately smaller for the large families. With full-sib families, however, the rate of improvement was similar for family sizes of two, three, or four animals (Figure 2).

When full-sib and half-sib families are compared (Figures 1 and 2), it can be seen that increases in accuracy were not linear. Under the assumption of no c^2 , the addition of extra full-sibs had more than double the impact of adding the same number of half-sibs. When tests were as large as 25 families, two full-sibs contributed almost as much information as eight half-sibs, if families were not related. Therefore, if test size is small, the first priority would be to test full-sibs, and if pen dimensions allow, then increase the number of animals per family. Increasing the number of pens per test would also be worth the return in improved accuracy, especially if half-sib families are being tested. When test size is

optimized, however, or it reaches approximately 15, attention should be focused on increasing family size. A two-part approach to the problem could include reorganizing tests to define contemporary groups (like state and national breed tests) more accurately and concurrently rewriting entry requirements to fill pens most efficiently for optimum accuracy of evaluation for individual tests.

If c^2 had been included in the model, it is probable that the effect of adding more full-sibs would not have been as dramatic. In progeny testing, the presence of c^2 , if ignored, can limit improvement in accuracy (Pirchner, 1983). Yet, accounting for c^2 in design and analysis can be extremely difficult; this is one reason why use of paternal half-sibs has become the method of choice for progeny testing in beef cattle (Berger, 1983). When dealing with evaluation of individuals based on their own records and those of relatives, the situation is even more complicated, because of probable confounding with dams and pretest environment (Carlson, 1980). Conversely, Falconer (1981) pointed out that competition may cancel out some of the effects due to c^2 .

Mixed-model methodology offers the possibility of accounting for c^2 . Henderson (1973)

TABLE 5. PREDICTION ERROR VARIANCE OF AVERAGE DAILY GAIN (ADG) AND BACKFAT PROBE (BF) FOR BOARS WITH SIRE TIES ACROSS FULL-SIB FAMILIES, WITHIN TESTS

No. of families	Family size	No. of sires	Prediction error variance ^a			
			ADG		BF	
			Tied	Untied	Tied	Untied
5	2	4	.00378	.00370	.00289	.00282
5	2	3	.00381	.00373	.00293	.00285
5	2	2	.00398 ^b	.00389 ^c	.00310 ^b	.00302 ^c
16	2	15	.00336	.00338	.00247	.00248
16	2	14	.00336	.00338	.00247	.00248
16	2	11	.00337	.00339	.00249	.00249
16	2	6	.00340 ^b	.00340 ^c	.00253 ^b	.00252 ^c
25	2	24	.00329	.00333	.00240	.00242
25	2	23	.00329	.00333	.00241	.00243
25	2	20	.00330	.00333	.00241	.00243
25	2	15	.00331	.00334	.00242	.00244
25	2	10	.00330	.00332	.00243	.00244
5	3	4	.00363	.00356	.00277	.00270
5	3	3	.00368	.00360	.00282	.00275
5	3	2	.00386 ^b	.00378 ^c	.00300 ^b	.00293 ^c
16	3	15	.00321	.00323	.00236	.00236
16	3	14	.00321	.00323	.00236	.00237
16	3	11	.00322	.00324	.00238	.00238
16	3	6	.00327 ^b	.00327 ^c	.00243 ^b	.00242 ^c
25	3	24	.00314	.00317	.00229	.00231
25	3	23	.00314	.00318	.00230	.00231
25	3	20	.00315	.00318	.00230	.00232
25	3	15	.00316	.00319	.00231	.00233
25	3	10	.00316	.00318	.00233	.00233

^aPEV = Var(u - ũ).

^bThis prediction error variance is for boars with ties to more than two families.

^cThis prediction error variance is for boars with single direct ties.

and Kennedy et al. (1985) have used different approaches to address this problem, but a final solution has not been found. One management suggestion, if indirect selection for FE is assumed, would be to randomly assign half- or full-sibs to pens to reduce c^2 . Another possibility would be to use electronically controlled feeding stalls, but such a system would be expensive.

Genetic Ties Within Station

When a sire has more than one set of littermate progeny on test at the same time in the same location, a design structure is created that involves half-sib (sire) ties in a fairly small data set. Although not observed frequently in central tests, this structure will occur often in an on-farm performance program. In situations involving mixed-model evaluation of data sets with small numbers per subclass and closely related animals, however,

the presence of nonzero off-diagonal elements generated by A^{-1} may have a detrimental effect on breeding value estimates (Wood et al., 1991). Thus, designs involving differing numbers of sire ties within station were compared in this study to ascertain their effects on accuracy of evaluation.

In modeling these designs, two subsets of data were generated, based on the pattern of genetic ties. With small numbers of ties, the first subset consisted of full-sib boars with direct ties across families because they had the same sire, and the second subset contained full-sib boars with no ties across families. When the number of ties grew large enough, the two subsets contained boars with ties across several families and boars with a single direct tie across families. For example, in a test consisting of five litters (Table 5), one sire tie resulted in the two related litters having one PEV (.00378) and the other three unrelated litters having another (.00370). When five

TABLE 6. AVERAGE PREDICTION ERROR VARIANCES OF AVERAGE DAILY GAIN AND BACKFAT PROBE FOR BOARS IN TESTS TIED BY HALF-SIBS^a

No. per family	Total no.	No. of sires	No. of ties	Average prediction error variance ^b	
				Average daily gain	Backfat probe
2	92	46	0	.00338	.00248
		44	1	.00337	.00247
		42	2	.00336	.00247
		40	3	.00336	.00246
		38	4	.00335	.00246
		36	5	.00334	.00245
3	138	46	0	.00323	.00237
		44	1	.00322	.00236
		42	2	.00321	.00235
		40	3	.00320	.00235

^aThree stations with 5, 16, and 25 pens, two or three boars per pen, depending on the design. Half-sib ties were generated by placing full-sib families sired by the same boar in each of three stations. Thus, the number of sires decreased by two each time a tie was added.

^bPEV = $\text{Var}(u - \hat{u})$.

litters were sired by two boars, however, the first subset consisted of three litters from one sire; the second contained the two litters sired by the second boar. In other words, all litters were tied directly with at least one other, and some were tied more tightly than others.

As discussed by Wood et al. (1991), designs with large numbers of genetic ties within a fixed effect may under some circumstances result in increased PEV. As shown in Table 5, increasing ties among animals increased PEV in all cases investigated except the large (25-family) test. For ADG in that instance, the design with 10 sires resulted in a slightly lower PEV, compared with the design with 15 sires, but no such change was observed for BF. Having three full-sibs within a family, rather than two, helped decrease PEV, as did increasing the number of families within a test from 5 to 25. Seventy-five animals present in 25 families of three littermates each had the lowest PEV. Evaluation of BF, with its greater h^2 , resulted in lower PEV than for ADG, but the higher h^2 also resulted in a slower rate of change in PEV. As might be expected, more dramatic changes in PEV occurred in the smaller tests.

Conversely, as test size increased, the differential between PEV of related boars and their testmates increased, and the PEV of testmates was greater than that of the directly related boars. The one exception to the pattern was in the five-pen tests. In family sizes of two and three, the PEV of related boars was greater

than that of their testmates. Mathematically, the result was due to nonzero off-diagonal elements in A^{-1} (Wood et al., 1991).

Ties Across Tests

Half-Sib Ties. A half-sib, across-station tie was defined as litters having the same sire but located in different station-seasons. Table 6 contains average PEV of individual boars for such designs. The sparseness of the relatively large matrix containing 92 or 138 boars (two or three per family, respectively) led to the expected results. As number of ties increased, the average PEV for all boars gradually declined. Figure 3 shows in more detail that boars in tied stations were more accurately evaluated than those in stations with no ties, assuming the same family size. Figure 3 also demonstrates that tying smaller families across station-seasons increased accuracy as much as increasing family size. For example, 10 animals with a tie to the other two stations had the same accuracy as 15 animals (five families of three full-sibs) with no ties to other stations. As previously noted for small data sets, however, both accuracies were lower than that obtained by ranking on individual performance because of fitting the fixed effect due to station-season. Larger tests consisting of pens of three full-sibs and no ties, however, were still more accurately evaluated than the same size tests with two full-sibs per family and one genetic tie, and families consisting of three

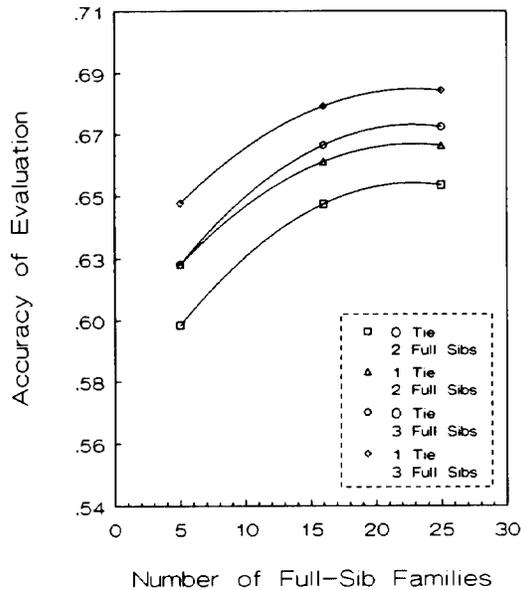


Figure 3. Average accuracy of evaluation of average daily gain measured on boars with or without half-sib ties across stations.

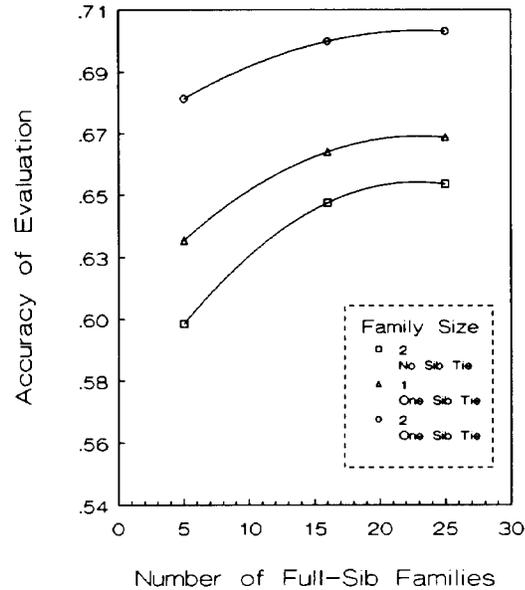


Figure 4. Influence of family size on average accuracy of evaluation of average daily gain measured on boars with or without full-sib ties across stations.

full-sibs with ties all had higher accuracies of evaluation than those obtained from ranking on individual performance (Figure 3 and Table 4).

As number of ties increased, however, the same pattern as in Table 5 emerged: the rate of increase in average accuracy leveled off. If individual accuracies are carried out far enough, it can be seen that the mixed-model equations behaved similarly to those reported by Wood et al. (1991), with directly related boars being less accurately evaluated as number of ties increased. In general, however, the increase in accuracy of untied animals in the same test more than compensated for the small decrease in the accuracy for closely related boars. For very small numbers of animals per test, the connections with larger groups through genetic ties more than offset the nonzero off-diagonals, resulting in an improved accuracy throughout. Mabry et al. (1987) analyzed data from central test stations that included a reference sire to provide ties across station. They noted that inclusion of the reference sire increased accuracy of evaluation but concluded that naturally occurring ties were sufficient.

Paternal Half-Cousin Ties. Paternal half-cousin ties are generated as a result of using

half-sib sires to produce litters tested in different stations. This situation is common in the purebred swine industry wherein sons of a popular boar are sold and used by a number of breeders. The breeders, in turn, place litters sired by these sons in central test stations. If these ties are common enough, it might be possible to dispense with some of the restrictions and cooperation necessary to generate designed ties such as those provided by reference sires.

Relative to half-sib ties, however, half-cousin ties were quite weak in improving accuracy: curves representing the addition of one half-cousin tie were indistinguishable from 0-tie curves in Figure 3. One may compare animals across stations after adding these ties, but an excessively large number of ties would be required to improve accuracy appreciably. Indeed, one paternal half-cousin tie is only 1/16 as strong as a half-sib tie. But the selection differential may be increased by comparing more animals fairly across test and by choosing a smaller proportion of the total, and this may be sufficient reason for using half-cousin ties.

Full-Sib Ties. Full-sib ties are generated by sending one or more littermates to different test stations. This is the most designed of the ties considered because these are unlikely to

occur without prior planning, but locations of stations in the United States would lend themselves to a regional network consisting of tightly linked groups of stations tied on a national basis by half-sib ties such as those provided by AI sires.

In contrast to the other ties, these are quite strong when numbers are comparable. Even if single full-sibs are sent to different stations, the tie is strong enough to increase accuracy above that of tests with no ties and two full-sibs per pen, as shown in Figure 4. As discussed earlier, some caution must be exer-

cised in interpreting these results because c^2 is not in the model. The other major drawback is that there is a lower biological limit to the number of ties possible, relative to half-sib and half-cousin ties, inasmuch as AI technology allows the production of many more paternal half-sibs than full-sibs. It also seems that the beneficial effect of additional families is masked somewhat by the presence of a full-sib tie; the slope of the tied lines is much flatter than that of the untied lines. Again, with increasing numbers of ties, the rate of improvement also levels off.

TABLE 7. AVERAGE PREDICTION ERROR VARIANCES OF EVALUATIONS FOR SIRES OF BOARS^{ab}

Design	NO	N	NS	NT	Average prediction error variance ^c	
					ADG	BF
Half-sibs across stations, three stations with 5, 16, and 25 pens	2	92	46	0	.00486	.00406
			44	1	.00484	.00404
			42	2	.00481	.00401
			40	3	.00477	.00398
			38	4	.00474	.00394
	3	138	36	5	.00470	.00391
			46	0	.00461	.00383
			44	1	.00457	.00380
			42	2	.00454	.00377
			40	3	.00450	.00373
Paternal half-cousins across stations, three stations with 5, 16, and 25 pens	2	92	46	1	.00486	.00406
				2	.00485	.00406
				3	.00485	.00405
				4	.00484	.00405
				5	.00484	.00404
	3	138	46	1	.00460	.00383
				2	.00459	.00382
				3	.00459	.00382
				4	.00458	.00381
				5	.00458	.00381
Full-sibs across stations, three stations with 5, 16, and 25 pens	1	46	44	1	.00521	.00440
			42	2	.00519	.00438
			40	3	.00517	.00437
			38	4	.00515	.00435
			36	5	.00513	.00433
	2	92	44	1	.00484	.00405
			42	2	.00482	.00403
			40	3	.00480	.00401
			38	4	.00477	.00399
			36	5	.00475	.00396

^aNO = number of boars per family; N = total number of boars; NS = number of sires; NT = number of ties; ADG = average daily gain; BF = backfat.

^bCommon environmental effects are not included in the model.

^cPEV = $\text{Var}(u - t)$.

Accuracy of Sire Evaluations. One advantage of using the animal model is that animals with records and related animals with no records of their own can be evaluated simultaneously. A measure of accuracy of those evaluations is also obtained. Sire average PEV are summarized in Table 7. Because the portion of the relationship matrix directly concerned with sires was relatively sparse (they were assumed to be unrelated except for half-cousin ties), the average PEV decreased as more information about greater numbers of progeny was assumed. With related sires (half-cousin ties), average PEV decreased very little. These results are in agreement with work on sire models by Henderson (1975c,d), Ojala et al. (1985), and Wilmink and Dommerholt (1985). Thus, one possibility is the use of market pigs to evaluate sires and(or) young boars. This may be the most efficient use of on-farm information and also would help when selection for market hog performance through traits of boars is less than perfect (Standal, 1977; Roberts and Curran, 1981).

On the other hand, classical experiments have shown the danger of using full-sibs to evaluate parents (Lush, 1935, 1945; Falconer, 1981; Pirchner, 1983), and that experience must be taken into account when deciding whether to emphasize young boars or sires. Also, in contrast to other traits evaluated under a sire model, ADG and BF are more highly heritable. But, several recent studies (Belonsky and Kennedy, 1988; Keele et al., 1988) have indicated that even with high heritability, BLUP results in greater accuracy of evaluation than selection on phenotype or index. Keele et al. (1988) also concluded that BLUP is robust to errors in estimated heritability.

Although this study has addressed the problem of optimizing accuracy for centrally tested animals, it has not addressed the problem of testing too few animals overall. One method of increasing numbers of tested animals would be to combine on-farm tests with central tests. This has the added appeal of evaluating boars on the basis of their relatives' market performance, because there is some indication that the traits measured in the station are not those of greatest importance at the packing plant (Standal, 1977; Roberts and Curran, 1981). But, Van Diepen and Kennedy (1989) concluded from an analysis of Canadian data that the correlations were large enough to expect some genetic progress from

using boars and gilts evaluated in central tests. One major disadvantage of incorporating on-farm evaluations is the large increase in number of fixed effects, so it would be necessary to ensure that data sets were reasonably large.

Implications

Inclusion of genetic relationships in mixed-model analyses of centrally tested boars resulted in greater rate of improvement in accuracy for average daily gain than for backfat. Conversely, increasing the number of boars within station-seasons improved the evaluation of backfat more because fixed effects were more accurately estimated. Increasing family size when families were not related resulted in increased accuracy of evaluation. Tying station-seasons by using genetic relationships resulted in a total increase in accuracy, far outweighing the decrease in accuracy for closely related boars. Use of relationship matrices may also allow fair comparison of more boars. It is possible in the context of a central test situation to specify covariances among animals through imposition of entry requirements. Likewise, specific genetic ties could prove especially valuable if on-farm performance tests are linked to the central tests.

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