GENETIC EVALUATION OF GROWTH RATE AND BACKFAT OF PIGS BY BEST LINEAR UNBIASED PREDICTION

Evaluación Genética de Rata de Crecimiento y Espesor de Grasa de Cerdos Con "Best Linear Unbiased Prediction (BLUP)"

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INTRODUCTION

Procedures based on best linear unbiased prediction (BLUP) have been widely used for genetic evaluation in dairy cattle and to some extent in beef cattle. In Canada, routine dairy and beef sire evaluation is by BLUP. Little attention has been given to the application of BLUP to genetic evaluation in pig populations, although Ronningen (1979) has initiated some discussion in this area.

In Canada, pigs are performance recorded on the home farm for growth rate, measured as age to 90 kg, and backfat depth. Also some young boars are sent to test stations for performance testing under more standard conditions. This paper considers the application of BLUP to the genetic evaluation of pigs by progeny test and by combining individual performance with the performance of relatives from growth rate and backfat records.

BEST LINEAR UNBIASED PREDICTION

Theory and development of BLUP is given by Henderson (1973). Consider the general mixed linear model

\[ y = Xb + Zu + e \]

with \( \text{Var}(u) = G; \text{Var}(e) = R; \) and \( \text{Var}(y) = ZGZ' + R, \) where \( y \) is a vector of observations, \( X \) and \( Z \) are fixed incidence matrices, \( b \) is a vector of fixed effects, \( u \) is a vector of random variables and \( e \) is the error vector. Then the BLUP of \( u \) can be obtained from (Henderson, 1973).

\[
\begin{pmatrix}
\hat{b} \\
\hat{u}
\end{pmatrix} =
\begin{pmatrix}
X'R^{-1}X & X'R^{-1}Z \\
Z'R^{-1}X & Z'R^{-1}Z + G^{-1}
\end{pmatrix}^{-1}
\begin{pmatrix}
X'R^{-1}y \\
Z'R^{-1}y
\end{pmatrix}
\]

The vector \( \hat{u} \) usually contains predictors of function of breeding values. The model (1) is perfectly general and allows for multiple as well as single trait evaluation. It should be noted, that \( \hat{u} \) is BLUP only if the fixed effects and the distribution of the random variables are specified correctly. In practice, these specifications are rarely exact. Rather, compromises between a conceptually ideal model and what is practical computationally are made. The following

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consider possible fixed and random effects to be included in genetic evaluation for growth rate and backfat. References are made also to their applicability to genetic evaluation in the Canadian population.

**Fixed Effects**

Important fixed effects influencing growth rate and backfat might include i) herd- (or station)-year-season, ii) weight of pig at testing, iii) sex of pig, iv) genetic group and v) breed composition.

Effects of herd-year-season are well recognized. Dempfle (1977) has defined criteria for determining optimum herd-year-season class size for sire evaluation in dairy cattle and the principles outlined are appropriate for other species. In pig breeding, boars tend to be used over a relatively short time span, but seasonal effects on growth rate and backfat are not great. Both of these are considerations in determining herd-year-season subclass size. For our data, splitting the year into two six-month "seasons" gives average herd-year-season numbers of 55 to 60 pigs for the Yorkshires and Landrace and approximately 30 pigs for Hampshires and Durocs.

Although we measure growth as age to 90 kg, pigs are actually probed and complete test in groups. Weights of most pigs deviate from the 90 kg standard which necessitates inclusion of weight in the model. In our data, heritability of weight at probe is zero. Accordingly, adjustment for weight will not bias genetic evaluations for growth and backfat.

Effects of sex of pig also need inclusion. The concern here is that in our data, male pigs exhibit considerably less variation than females for both traits. This may be due to a real difference between the sexes, differences in management of the sexes, or might be the result of relatively greater intensity of selection of males as candidates for performance testing. Jonsson (1975) has provided discussion on sex and housing effects on genetic and environmental variation for growth rate and backfat. In our data, only half as many males as females are tested in the Landrace and Yorkshire breeds, but approximately equal numbers of males and females are performance tested in the Hampshire and Duroc breeds. Substantially smaller variances of males for backfat depth are consistent across all four breeds which suggests a real sex difference either biological or caused by how the sexes are managed. However, for growth rate, male variances are considerably smaller than female variances for Yorkshires and Landrace, but are only marginally smaller for Hampshires and Durocs which suggests preselection of candidates for performance testing might be important.

Grouping of sires is routinely used in dairy and beef sire evaluation primarily to account for different populations sampled and to remove bias due to genetic trend. Possible grouping criteria for swine data may be according to sire population, ie. artificial insemination (AI), multiple herd, or single herd and by year of birth of sire and dam. The consequences of ignoring groups have been considered in theory and as applied to dairy sire evaluation by Kennedy (1981) and the same principles apply to pigs.
Maximum use of the data can be realized by combining records of all breeds in a single analysis with breed treated as a fixed effect. Eriksson et al. (1979) have used this approach for evaluating beef bulls. Computational complications arise when variances and heritabilities differ across breeds, and an expedient approach is to evaluate animals within breed. In our data, Hampshires show considerably less variation than the other breeds for backfat, and variation for growth rate is relatively constant across breeds for males but not for females. Also, preliminary examination of the data indicate that heritabilities differ by breed (Kennedy et al., 1982).

Several of the fixed effects already discussed are included in the model to account for, at least in part, some forms of selection. For example, treating herds as fixed accounts for non-random distribution of sires with herds (Henderson, 1973) and grouping accounts for genetic trends unaccounted for by the relationship matrix. Other "fixed" effects might be considered to account for other forms of selection. In these data, preselection as to which animals are performance tested has taken place. The average number of pigs tested per litter is less than four. If the pretest records of all candidates for selection were available, inclusion of these records in a multiple trait analysis would remove bias from this type of selection (Pollak and Quaas, 1981; Eriksson, 1981). Unfortunately, such records are not available. Inclusion of a fixed effect for the proportion or number of pigs in the litter tested might be an alternative to correct for selection bias.

Also, sires and dams may not be mated at random. Ideally, the inclusion of dams as random variables in the model would account for this, but this might not be possible computationally. An alternative, although less desirable approach, might be to treat the dam's record as a fixed effect in the model, as done by Schaeffer et al. (1978) in dairy sire evaluation for conformation traits.

2. Random Effects and Their Distribution

For our application of BLUP to pig evaluation, the vector \( \mathbf{u} \) from (1) can be partitioned into subvectors \( \mathbf{u}_1 \), and \( \mathbf{u}_2 \) representing breeding values of animals and litter effects respectively. An additive genetic model is assumed,

\[
\begin{align*}
\mathbf{Var}(\mathbf{u}_1) &= \mathbf{A} \sigma^2_a, \\
\mathbf{Var}(\mathbf{u}_2) &= \mathbf{I} \sigma^2_l, \\
\mathbf{Cov}(\mathbf{u}_1, \mathbf{u}_2) &= \mathbf{0},
\end{align*}
\]

where \( \mathbf{A} \) is the numerator relationship matrix between animals, \( \mathbf{I} \) is the identity matrix, \( \sigma^2_a \) is the additive genetic variance and \( \sigma^2_l \) is the litter variance. Solution of (2) requires \( \mathbf{A}^{-1} \) and this can be obtained, for most applications, using computational procedures given by Henderson (1976) and Quaas (1976). It should be noted that the specification of the distribution of \( \mathbf{u}_1 \) in (3) is quite general and \( \mathbf{u}_1 \) can contain animals which have performance records or animals related to those with performance records. Simplifications can be made, whereby for example, \( \mathbf{u}_1 \) might represent only sires of performance recorded pigs.
The model (1) is also general with respect to the distribution of e. For many applications, R can be assumed to equal \( \sigma^2_0 \), where \( \sigma^2 \) is the error variance. In application to our data, where there is concern about the homogeneity of variances associated with sex effects, R might have different diagonal elements depending upon whether the observation was on a male or female. Similarly, combining observations of different breeds in a single analysis might dictate R being a diagonal matrix.

For multiple trait evaluation, if the data are ordered by traits within animal, \( \text{Var}(u_1) = A^*V, \text{Var}(u_2) = I^*L, \) and \( \text{Cov}(u_1, u_2') = 0 \), where V is a matrix of additive genetic variances and covariances between traits on the same animal, L is a matrix of litter variances and covariances between traits and \( * \) represents the direct product operator (see Searle, 1966). Similarly, R would be of the form \( R = I^*E \) where E is a matrix of error variances and covariances between traits. Multiple trait evaluation is more difficult computationally but has been applied in practice as, for example, in the beef sire evaluation program in Canada (Schaeffer and Wilton, 1981). The chief advantage of multiple trait evaluation is to remove bias from selection practised in stages when records upon which selection was practised are available.

If genetic correlation between the sexes is less than one or the genetic variances are unequal, treating observations on different sexes as different traits might be necessary. Similarly, if breeds differ in genetic variation or genetic correlations, multiple trait evaluations would be required if the breeds are to be combined in a single analysis. Also, Standal (1977) has reported that genetic correlations between station and home test measures of the same characteristic are less than one, and this might necessitate a multiple trait analysis if home and station test data are to be combined.

APPLICATIONS

In this section, two possible applications of BLUP to genetic evaluation of pigs using our data are discussed. The first is a straightforward sire evaluation based on progeny performance and the second combines individual performance with performance records of relatives.

For evaluation based on progeny performance, \( u_1 \) constitutes a vector of transmitting abilities of sires and dams with \( \text{Var}(u_1) = \sigma_s^2 \) where \( \sigma_s^2 = 1/4 \sigma_a^2 \). A further simplification might restrict \( u_1 \) to represent sires only. If dams were ignored, covariances between dams, sires and dams, and litters of related dams would not be accounted for, but the consequences of this might not be too serious. Either analysis is not difficult computationally. Litter and herd-year-season equations can be absorbed into the sire, (dam) and remaining fixed effects equations which are solved for iteratively. The absorption is relatively simple because of the nesting of litters.
within herd-year-season and involves only the inverses of diagonal matrices. For our data, particularly if restricted to sire evaluation only, the analysis is quite simple as, at present, only 1162 Yorkshire, 754 Landrace, 299 Hampshire and 355 Duroc sires are involved.

The limitation of this analysis is that it provides progeny test evaluation only, and does not take advantage of the performance record of the individual being evaluated. Use of the individual animal model (3) makes maximum use of the data by combining the animal's own performance with all information on its relatives. In this application, Z of (1) is an identity matrix augmented by columns of zeros, the latter corresponding to animals with no individual records but with records on relatives. The order of Z is the number of animals to be evaluated.

The number of equations to be solved exceeds the number of observations. Our data set at present has 38634, 28295, 7310 and 2065 Yorkshire, Landrace, Hampshire and Duroc observations and although most likely the Hampshire and Duroc equations can be solved iteratively, the Yorkshires and Landrace may be too large to solve, at least on a routine basis. There are real advantages to using the individual animal model for pig evaluation though, and it may be possible to perform the computations once, on the whole data set, save the computed breeding values, and subsequently only use the new data for new equations. This recursive estimation approach has been suggested by Sallas and Harville (1981) and might be adaptable to our data if the only fixed effects involved are herd-year-seasons with litters nested within them (Schaeffer, personal communication). This would necessitate prior adjustment of the data for other fixed effects.

SUMMARY

Models are presented for the genetic evaluation of pigs based on home and station test records using best linear unbiased prediction procedures. Methods of accounting for the effects of herd- or station-year-season, sex of pig, genetic trends, nonrandom mating of sires and dams and pre-selection of pigs for testing are considered. Genetic evaluation by progeny test as well as by combining individual performance with performance records of relatives is outlined, and application of the procedures and computational strategies appropriate for the Canadian swine population is discussed.

RESUMEN

Se presentan modelos para la evaluación genética de cerdos a partir de datos locales y en estaciones de prueba usando BLUP. Métodos que corrigen efectos de rebaño o estación-año-época del año, sexo del cerdo, mejora genética, apareamiento no al azar de machos y hembras y preselección de cerdos para prueba son considerados. Evaluación genética por test de progenie como también combinación de performance individual con datos de performance de parientes es sumarizada y se discute la aplicación de los procedimientos y estrategias de computación para la población de cerdos de Canadá.
References


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