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Effect of Selection Index Versus Mixed Model Methods of Prediction of Breeding Value on Response to Selection in a Simulated Pig Population

DANIEL A. SORENSEN
National Institute of Animal Science, PB 39, DK-8830 Ørum Sdrl, (Denmark)

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ABSTRACT

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Selection response for a single trait was compared in two sets of simulated pig populations that attempted to resemble the Danish pig population structure from 1980 until 1986. In one set, breeding values were computed using a selection index (SI) which included the candidate's performance, that of its full and half sibs and of its progeny, if available. Data were first adjusted for fixed effects (station-seasons) using either an ordinary least squares (OLS) or a generalized least squares (GLS) procedure and a fixed mean (FM) or a moving mean (MM) was used to deviate each candidate's information from, the latter (MM) being an attempt to correct for genetic trend. In the other set of simulations, breeding values were computed using a reduced animal model (RAM) with a complete relationship matrix. When heritability is 0.5, after 5 cycles, response relative to RAM was 0.81 for SI/OLS/FM and 0.84 for SI/GLS/FM. When approximate corrections for genetic trend were implemented and boars in the SI/GLS/MM simulation were allowed to mate not more than in two consecutive cycles, response relative to RAM was 0.96. When heritability is 10%, these figures are, respectively, 0.75, 0.84 and 0.89. The three factors that contribute to the smaller response using SI are: (1) the sources of bias introduced in the construction of the selection index owing to genetic trend; (2) the bias of the OLS estimator of fixed effects owing to genetic trend and (3) the smaller accuracy of the SI relative to RAM.

INTRODUCTION

The current method for prediction of breeding values used in the Danish pig breeding system is based on the classical selection index (Christensen et al., 1986). On theoretical grounds, it is well established that mixed model procedures, using an animal model with full pedigree information available on each candidate for selection, should lead to higher genetic progress (Henderson, 1973). However, before new methods are implemented, and consequently major changes in the breeding program are effected, it is desirable to quantify the advantage of alternative methods in terms of improved genetic progress and to gain insight into their computing requirements. While the superiority of mixed-model methods is well established, the actual difference in response achieved over other methods of breeding value evaluation, will depend on the trait in question and the structure of the data. Owing to the existence of test stations in Denmark, the data on which the computations are carried out are fairly balanced. Furthermore, the traits under selection have relatively high heritability and it is therefore questionable whether these advantages are large enough to justify such changes.

Unless simplifying assumptions are made, comparisons of predictors of breeding value in terms of expected genetic progress over repeated cycles of selection in a typical pig breeding program are analytically untractable. One approach that has been followed is to specify the true model and to describe alternative estimators as compromises of it in terms of operational models. Expectations can be taken under the true model to compare biases and prediction error variances can be computed for various estimators. The expressions that result from such an exercise are functions of variance matrices and design matrices and their products, and particular cases can be analysed using numerical examples. A classic paper is Henderson (1975a). Another approach that has been followed has used real data and computed approximate prediction error variances as a judging criterion. In one such study, Carlson et al. (1984) showed considerable reductions in prediction error variances using mixed models over other methods. An alternative and arguably more informative approach is to use computer simulation and to compare actual selection responses achieved. In the only previous simulation study in pig populations, Belonsky and Kennedy (1988) have shown that in their population structure, relative to a full animal model, phenotypic selection led to responses of 0.64 and 0.91 for heritability values of 10 and 60%, respectively.

The present study shows computer simulation results of 5 cycles of selection where candidates are evaluated either combining several sources of information in a selection index, in one set of simulations, or using mixed model methods under an animal model in the other. In the selection index study, a comparison was made between the use of ordinary or generalised least squares estimators of fixed effects, and between the use of a fixed or a moving (or rolling) mean, as alternative approaches in the presence of genetic trend.

METHODS

The structure of the data simulated attempted to resemble the Danish situation from 1980 until 1986, in which only one group from each breeding sow was sent to a test station. The group which was sampled from the sow's first litter. consisted of one gilt, one boar and one castrate. At the end of the testing period, gilt and castrate were slaughtered. Female replacements were taken from those littermates that were not sent to the test station, and which therefore did not have a phenotypic record. The criterion on which they were selected was the average predicted breeding value of their sire and dam. Male replacements were taken from the performance-tested boars, from their sires or from more distant ancestors, according to the predicted breeding value that the candidates scored. There was thus an overlapping generation structure on the male side but females bred only once.

Initially 40 males and 200 females were sampled and their mating generated 600 offspring, distributed in 15 station–seasons. Groups were allocated to station–seasons randomly, sampling from the uniform distribution. The next crop of 200 females was selected on the basis of the predicted breeding value of the best 100 parental averages of the 200 available. Each of the 100 selected families contributed 2 gilts as parents of the next generation. This was repeated each selection cycle. On the male side, at the first cycle of selection, the first 40 were selected among the 240 males available, but as the program proceeded, the 40 males selected each cycle were chosen among all those available in the system until that time. Those with the highest predicted breeding value, regardless of age, were selected. At each cycle, the 40 males and 200 females generated a new set of 600 performance tested offspring. In some runs, a restriction was placed on the number of cycles a sire could be used, but if this was not the case, at the fifth cycle of selection, the 40 new sires were selected among the 1040 males available in the system. The program ended after the fifth selection cycle. At this stage there were 4840 animals, of which 3600 had records distributed across 90 station–seasons with an average of 40 records per station–season.

Contrary to what goes on in practice, only one trait was simulated. An animal's record was contributed by the sum of a station–season effect, an additive genetic value and a residual or pure environmental effect. Effects were sampled from a normal distribution with specified mean and variance. Station–season effects accounted for 40% of the total phenotypic variance and were considered as fixed effects. Additive values and pure environmental values were considered as random effects. The true model for the ij record was therefore:

$$Y_{ij} = b_i + a_{ij} + e_{ij} \tag{1}$$

where b_i is the ith station–season and a and e are the additive genetic and pure environmental values, respectively. At generation zero, breeding values were sampled from a normal distribution with mean zero and variance $\sigma^2 h^2$, where σ^2 is the phenotypic variance (within station–seasons) and h^2 is the heritability in the base population. Later on, offspring breeding values were sampled from a normal distribution with mean equal to $1/2(a_s + a_d)$ and variance $1/2\,\sigma^2 h^2(1-\bar{F})$, where a_s and a_d are the breeding values of the sire (s) and dam (d) and $\bar{F}$ is their average inbreeding coefficient. The implied genetic model in this simulation is known as the infinitesimal model with free recombination and has been discussed among others by Bulmer (1980). Under the model, the genetic variance in the population declines through the joint effects of inbreeding and gametic disequilibrium.

The selection index for the ith individual is of the form:

$$I_i=\sum_j b_{ij}\,(Y_{ij}-E(Y_{ij}))+E(I_i) \qquad (2)$$

where Y_{ij} is the jth record or source of information associated with i, and the b_{ij}'s are the usual selection index weights. The term $E(Y_{ij})$ is the expected value of the jth record contributing information to i, and $E(I_i)$ is the expected breeding value of i. Implied in eqn. (2) is that records have been adjusted for station–season effects. In this simulation, the selection index for males used information on the candidate's full and half-sibs, its own performance and its progeny, if available. Young gilts were selected on the basis of the average index value of their parents. The index of their dams used information on half and full sibs and progeny.

The computation of the index involved two steps, namely, the correction of the data for station–season effects, and the collection of information on each candidate to compute the selection index.

The correction of data for station–season effects was carried out using either ordinary least squares (OLS) or generalised least squares (GLS) procedures. The model used with the OLS estimator included station–seasons and sires, as practised in the Danish system until 1986 (Andersen and Vestergaard, 1984). All existing records were used to obtain the OLS estimate of the estimable function (station–season i minus station–season 1) which was subtracted from the record belonging to the ith station–season. In the absence of genetic trend and assuming breeding values have zero expectation, the OLS estimator of this function is unbiased under the true model (1), and $E(Y_{ij})$ in eqn. (2) is equal to b_1, the effect of station–season 1.

In populations that show genetic trend, under the sire model, the OLS estimator of the difference between station–season i and station–season 1 is biased upwards. An alternative estimator that seems to be unbiased by some forms of selection is the GLS (Henderson, 1975b). In order to quantify the effect of using an improved estimator of fixed effects on selection response, in a set of simulation runs, station–seasons were estimated using GLS under an animal model with a complete relationship matrix. The model included station–seasons as fixed and breeding values as random effects. At each cycle, all the animals present in the system were processed. The inverse of the additive genetic relationship matrix was computed using the algorithm proposed by Quaas (1976) and multiplied by $(1-h^2)/h^2$, where as before, h^2 is the base population heritability which was assumed known. The mixed model equations were stored on disc and solutions were obtained using Gauss–Seidel iteration. To reduce the size of the coefficient matrix, the breeding value of those animals that at the time of evaluation did not contribute offspring were absorbed. After the records were corrected using the GLS estimates of station–season effects, the selection index was computed using standard procedures.

In selected populations, with overlapping generations, evaluation of breeding values using classical selection index are biased owing to genetic trend. Operationally, one can either ignore genetic trend or attempt ad hoc corrections for it. In this study one set of simulations ignored genetic trend, and the general mean from which the sources of information were deviated (i.e. $E(Y_{ij})$), was computed as the average of the adjusted records of the initial 600 unselected animals. This approach will be referred to as the fixed mean. In another set of simulations, an ad hoc adjustment for genetic trend was attempted. This was done by computing $E(Y_{ij})$ from the adjusted records providing information to the new candidates for selection (rather than from a fixed base as in the previous set), and their average index summed to zero. In both approaches, $E(I_i)$ in eqn. (2) was assumed to be zero. The second approach is the one currently used in the Danish pig breeding program, and will be referred to as the moving mean.

In populations under selection, Henderson (1975b) has shown that, under one cycle of culling type selection, solutions to the mixed model equations, lead under certain conditions, to unbiased estimates of estimable functions of fixed effects and of predictions of breeding value. Simulation work by Sorensen and Kennedy (1986) indicated that use of mixed model procedures under an animal model with the complete relationship matrix, leads to predictions of breeding value with no detectable bias when selection operated over several generations. The other set of simulations in this study, evaluated breeding values with the same animal model used in the generalised least squares correction of fixed effects described above. The predicted breeding value of the absorbed animals was obtained from:

$$\hat{a}_o = 1/2(\hat{a}_s + \hat{a}_d) + w(y_o - \hat{b}_i - 1/2(\hat{a}_s + \hat{a}_d))$$

where: $w = 1/2\ h^2(1-\bar{F})/(1/2\ h^2(1-\bar{F})+1-h^2)$, (Kennedy and Sorensen, 1987). In the expressions above, $\hat{a}_o$, $\hat{a}_s$ and $\hat{a}_d$ are the predicted breeding values of the offspring, sire and dam respectively, y_o is the offspring record, $\hat{b}_i$ is the estimate of its station–season effect, h^2 is the base population heritability and $\bar{F}$ is the average inbreeding coefficient of the parents. This is known as the reduced animal model (Quaas and Pollak, 1980) and it is computationally advantageous when the proportion of the records contributed by individuals that have no progeny is high. In this simulation, at the fifth cycle of selection there were more than 3450 such records out of the total of 4840.

The criterion of comparison between the methods was the selection response measured each cycle as the average true genetic value of the 600 performance tested offspring. Runs with no selection are also shown. In these, the criterion of comparison is the accuracy of the methods. In both the animal model and the selection index, the heritability of the base population was assumed to be known.

RESULTS

Correlations are shown in Table 1 between true breeding values (from the distribution of simulated genotypes) and predicted breeding values (i.e. accuracy) using either an animal model or a selection index for heritabilities of 10 and 50%. In each replicate, breeding values were predicted using both methods. In the selection index case, station–seasons are estimated using either the OLS procedure or the GLS procedure. Correlations computed in this way account for the reduction in accuracy owing to the estimation of fixed effects from the data. The data have been generated by random sampling and mating of males and females (no selection) and comprised 4840 paired observations.

The simulation results of Table 1 show that at heritability values of 50%, the accuracy of selection index with an OLS correction for station–seasons, relative to the accuracy of the animal model is 0.96. This figure increases to 0.97 when a GLS correction is used. At heritability values of 10%, these figures are 0.85 and 0.90, respectively. When predicting breeding values using an animal model, all related animals contribute to the predictions by means of the additive relationship matrix, in contrast with the selection index which uses a limited amount of information. At smaller heritability values, the impact of the use of the animal model on accuracy is higher because relatives contribute relatively more to an animal's evaluation than they do at higher heritability values. In this random mating situation, if estimability holds, OLS estimates of fixed effects are unbiased but have larger sampling variance than their GLS counterparts. This is reflected in the increased accuracy obtained using GLS adjustments of station–seasons. The effect of the use of the GLS adjustments on accuracy is higher at smaller heritability values. This is because with un-

TABLE 1

Simulation results showing the correlation (%) between true breeding value and predicted breeding value obtained using selection index and using the animal model. Random sampling of males and females (no selection)[1]

Heritability	Selection index		Animal model
	OLS[2]	GLS[3]	
0.1	43.9	46.6	51.7
0.5	74.5	75.2	77.3

[1] Number of records = 4840; two replicates for each run.

[2] Ordinary least squares correction of fixed effects.

[3] Generalised least squares correction of fixed effects.

balanced cross-classified data, the variance of the GLS estimator decreases with decreasing heritability.

The results of 5 cycles of selection using an animal model to predict breeding values or using selection index with a fixed mean and an OLS adjustment for fixed effects for heritability of 50%, are shown in Table 2. This is a rather hypothetical situation in that there is no correction for genetic trend and it is assumed that all sires remain alive during the selection period. It is presented here because it highlights the deficiencies inherent in the injudicious use of selection index. The average true breeding value per cycle computed from the 600 performance tested individuals is shown together with the standard deviation over 20 replicates. This replicate variation represents the drift variance that tends to fluctuate rather erratically in the initial stages of the breeding program, owing to the overlapping generation structure. Similar fluctuations are found with the average inbreeding coefficient. Both phenomena are as predicted by theory (Johnson, 1977a, b). After 3 cycles of selection, the program that uses the animal model begins to show a clear advantage over the one that uses selection index with an OLS adjustment of station–seasons. After the fifth cycle, the response of selection index relative to that of the animal model is 0.81.

There are two factors that contribute to the superiority of the animal model.

TABLE 2

Selection response using animal model (AM) and selection index (SI) with a fixed mean and an ordinary least squares correction for station–seasons. Heritability is 50%

Cycle	BV[1] (SD)		FE bias (%)[2]		F(%)[3]		Accumulated number of sires	
	AM	SI	AM	SI	AM	SI	AM	SI
1	1.55 (0.20)	1.60 (0.16)	−0.28	−0.65	1.0	0.8	74	73
2	3.14 (0.34)	3.11 (0.22)	−0.13	0.56	3.0	2.9	104	92
3	4.61 (0.26)	4.30 (0.39)	0.00	2.67	3.6	4.1	136	101
4	6.07 (0.27)	5.21 (0.32)	−0.12	4.28	4.8	3.4	164	106
5	7.39 (0.35)	6.02 (0.41)	0.04	5.80	5.2	4.7	195	110

[1] BV (SD) = average true breeding value of the crop of offspring (600 observations/cycle/replicate); SD = standard deviation from 20 replicate runs. (i.e. $\mathrm{SE} = \mathrm{SD}/\sqrt{20}$).

[2] FE bias (%) = percent fixed effect bias calculated as: (estimated average fixed effect of cycle *t* minus estimated fixed effect one) minus the corresponding parameter values. This value is expressed relative to the true mean of cycle *t*.

[3] F(%) = average percent inbreeding coefficient among the 600 offspring of each cycle.

The first one is related to the OLS estimator of the fixed effect. In the presence of genetic trend, the OLS estimator of station–season differences, with the model used, (i.e., station–seasons and sires) is biased. The sire effect in the model accounts for only part of the genetic trend but the remaining part goes in to the station–season effects. Differences between any given station–season and the base station–season are biased upwards, and this bias increases with increasing genetic trend. As a consequence, records of young candidates are overcorrected and this encourages repeated use of older boars. This effect is shown in the column FE bias in Table 2. The results of the animal model on the other hand, show no detectable bias in the estimates of fixed effects in the presence of genetic trend.

The second and most important factor that contributes to the differences between the methods is the lack of correction for genetic trend in the construction of the index which generates two related problems. Firstly, evaluations of repeatedly-used boars are biased upwards because no account is taken of the fact that they are mated to genetically-superior dams. The information that contributes the bias is also the one that contributes most to the accuracy. In contrast, predicted breeding values obtained using selection index of young sons of heavily-used sires, are biased downwards because considerable information comes from genetically-inferior half-sibs whose dams belonged to earlier generations. Secondly, deviations from the fixed mean contributing information to the evaluations of young candidates include a component due to genetic trend that should not be regressed, but that should contribute additively to the animal's evaluation. This contributes further to the downward bias of the evaluation of young candidates. These two problems, together with the bias of the OLS estimator of differences between station–seasons lead to an increase of the generation interval. This is illustrated in the last two columns of Table 2. In each new cycle, 40 sires are selected among those available in the system. Using selection index with a fixed mean and OLS adjustments of fixed effects, out of the 40 sires, 33, 19, 9, 5 and 4 are young boars, in Cycles 1 through 5, respectively. As a consequence, the generation interval on the male side increases at a high rate. On the other hand, when breeding values are predicted using the animal model, approximately 32 of the 40 selected males at each cycle are young boars. It should be clear that if the 40 sires selected each cycle were to be young boars, the accumulated number from Cycles 1 through to 5 would be 80, 120, 160, 200 and 240.

The effect of using a selection index with a fixed mean with a GLS adjustment for station–seasons on selection response is shown in Table 3. Relative to the animal model, response at Cycle 5 increases from 0.81 to 0.84. This small improvement arises because with an unbiased estimator of fixed effects, records of young candidates are not overcorrected, and thus the generation interval is slightly reduced.

In breeding programs where a selection index is used, some type of ad hoc

TABLE 3

Selection response using selection index with a fixed and a moving mean. In the latter, sires are allowed to be used repeatedly (r) or limited to a maximum of two consecutive matings (l). In all cases, data had been precorrected using generalised least squares. Heritability is 50%

Cycle	Fixed mean		Moving mean			
	BV[1](r)	Accumulated number of sires	BV[1](r)	BV[1](l)	Accumulated number of sires (r)	Accumulated number of sires (l)
1	1.60	71	1.58	1.57	76	74
2	3.05	87	3.17	3.13	106	105
3	4.34	100	4.55	4.60	130	136
4	5.36	113	5.90	5.92	152	160
5	6.21	122	7.01	7.10	170	184

[1] Average true breeding value of the crop of offspring (600 observations/cycle/replicate). Standard error of the difference between two means at Cycle 5 is 0.12 units (20 replicates).

correction for genetic trend is often implemented. In the Danish pig-breeding program, this is achieved using the moving mean that has the effect of reducing the underevaluation of young boars and the overevaluation of old boars. The effect of using a moving mean on selection response is shown in Table 3. At Cycle 5, response using selection index with a moving mean relative to that using the animal model is 0.95. This approximate correction for genetic trend has a very substantial effect on reducing the bias in the predicted breeding values and hence the rate of turnover per cycle is higher. However, comparison between Tables 2 and 3 shows that repeated use of sires is considerably more frequent than with the animal model, because the bias in the evaluations is still present. The effect of using selection index with a moving mean, and restricting the use of boars to a maximum of two consecutive cycles, is shown in the last column of Table 3. On average, of the 40 boars in use at any one cycle, 28 are young boars and response at Cycle 5 relative to the animal model is 0.96.

In the other set of simulations, boars were used for one cycle only so that the breeding program ran with non-overlapping generations. Progeny did not contribute information to the index which was now restricted to the individual's own performance, their full sibs and half sibs. Relative to the animal model, response at Cycle 5 was a little under 0.96 (not shown). In this situation, differences between predicted breeding values using selection index are unbiased. However, the accuracy of selection index is lower than that of the animal model and the non-overlapping generation structure does not give opportunity to the few genetically-superior animals of previous generations to contribute as parents. Intervention to reduce the generation interval is not needed using the animal model, and candidates can be ranked and selected according to their predicted breeding values, regardless of age.

At heritability values of 0.5, the difference in the final response at Cycle 5 between an OLS or a GLS estimator of station–seasons when a moving mean is used and use of boars is restricted to two consecutive cycles is of less than 1% in favour of the latter (not shown). With a shorter generation interval, records contributing information are less spread apart and the bias of the OLS estimator has less effect on the ranking of the candidates.

Table 4 summarises selection response and inbreeding coefficients per cycle when heritability is 10%. Response at Cycle 5 using selection index with a fixed mean and an OLS correction of station–seasons, relative to that using the animal model is 0.75. The advantage of the animal model is considerably higher than at 50% heritability, as expected. The GLS correction of station–seasons increases this figure to 0.84. With a correction for genetic trend (moving mean) response using selection index relative to that using the animal model is 0.87 or 0.89 for unrestricted use of sires across cycles or for a restricted use of sires to not more than two consecutive cycles, respectively. At heritability values of 0.1, the advantage of using GLS over OLS in this improved structure is about 1% (not shown).

Inbreeding coefficients in the selection index case are a little higher at low heritabilities, but the differences are not as clear as in the case of the animal model, probably because in the selection index case, the populations have not reached such a stable age distribution. At low heritability values, relatives' records contribute more to an animal's evaluation than they do at high herit-

TABLE 4

Selection response using animal model and selection index. Heritability is 10%[1]

Cycle	Animal model		Selection index. Fixed mean				Selection index. Moving mean			
			OLS (r)		GLS (r)		GLS (r)		GLS (l)	
	BV	F(%)	BV	F(%)	BV	F(%)	BV	F(%)	BV	F(%)
1	0.44	1.0	0.41	0.6	0.41	1.1	0.43	0.7	0.41	1.2
2	0.85	2.9	0.80	2.4	0.89	5.1	0.86	5.0	0.88	3.4
3	1.29	4.9	1.20	4.7	1.27	4.5	1.25	4.9	1.28	4.9
4	1.75	7.1	1.43	3.8	1.60	5.1	1.64	6.0	1.68	6.6
5	2.22	8.9	1.66	5.9	1.87	5.3	1.93	7.1	1.98	6.9
Accumulated number of sires at Cycle 5	190		110		125		160		182	

[1] Abbreviations: OLS = Ordinary least squares correction of station-seasons; GLS = generalised least squares correction of station-seasons; r = sires allowed to be used repeatedly across cycles; l = use of sires limited to a maximum of two consecutive cycles; BV = average true breeding value of the crop of offspring (600 observations/cycle/replicate); F(%) = average percent inbreeding coefficient among the 600 offspring; Average standard error of the BV at Cycle 5 = 0.03 (50 replicates).

abilities. There are therefore less differences among breeding values of related individuals and among those selected more will be related than when heritability is high. Similar results *were obtained by Belonsky and Kennedy (1988)* and are as should be expected from theory (Robertson, 1961).

DISCUSSION

The purpose of this simulation was to quantify the advantage of mixed-model techniques over selection index in terms of improved selection response, in the context of a pig population structure. Clearly the results hold strictly for the true model simulated and for the assumed data structure. However, they can be regarded as useful guidelines for other pig breeding programs where animals are centrally tested. Further, the advantage of the animal model over selection index is likely to increase with more complicated models and with data that are less balanced, such as the one generated by an on-herd recording program. Use of selection index resulted in responses that ranged from 81 to 96% to those achieved using the animal model, for heritability values of 50%. At 10% heritabilities, this ratio ranged from 75 to 89%. At high heritability values, correction for genetic trend was the largest contributing factor to this range. At low heritabilities, use of an OLS or a GLS correction for station–seasons had relatively more impact on response than correcting for genetic trend. Belonsky and Kennedy (1988) obtain responses under phenotypic selection relative to the animal model of 64 and 91% for heritabilities of 10 and 60%, respectively. The figures for the improved index in this study are 89 and 96%, for heritabilities of 10 and 50%. The range is smaller in this simulation owing primarily to the advantage of using several sources of information rather than only the individual's own record, when heritability is low.

The selection-index procedure could probably be improved by adopting more sophisticated corrections for genetic trend than the moving mean and by deviating the information within comparable generation subclasses, rather than using an overall mean of half-sibs, say, across generations. Also, more sources of information could be incorporated. The latter could be done in a recursive manner, as in the direct updating procedure developed by Christensen (1980, 1981). Indeed, this method results in a close approximation to the use of a complete relationship matrix, and therefore it hardly requires ad hoc corrections for genetic trend. Under the present data structure differences between the rates of response achieved using mixed-model methods under an animal model and the direct updating procedure are likely to be small, and will depend largely on the way fixed effects are estimated in the latter. When computer power is a limiting factor the direct updating can be a useful alternative.

~~The accuracy of the~~ selection index relative to that of the animal model, in

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RESUME

Coulon, J.B., d'Hour, P. et Petit, M., 1988. Evolution de la production et de la composition du lait à la mise à l'herbe: effet du type de transition. *Livest. Prod. Sci.*, 20: 119-134 (en anglais).

Cinquante et une vaches laitières (24 primipares la 1ère année, 27 multipares la 2ème année) ont été mises à l'herbe du jour au lendemain sans recevoir de fourrage conservé au pâturage (Lot 1), du jour au lendemain mais en recevant du foin pendant les 2 premières semaines de pâturage (Lot 2), en rentrant à l'étable la nuit et en recevant du foin pendant les 2 premières semaines de pâturage (Lot 3). La mise à l'herbe a eu lieu dans de bonnes conditions climatiques (absence de froid et de pluie abondante) et alimentaires (herbe de qualité) et n'a été accompagnée d'aucun trouble sanitaire. A la mise à l'herbe, la production laitière et le taux protéique ont augmenté plus fortement ($P<0{,}01$) chez les animaux des Lots 1 et 2 (respectivement +2,9 et +2,7 kg jour^{-1} de lait et +3,5 et +3,0 g kg^{-1}) que chez ceux du Lot 3 (+0,5 kg jour^{-1} de lait et +0,8 g kg^{-1}). Ces écarts n'ont pas persisté après la 3ème semaine de pâturage, lorsque tous les animaux étaient conduits de la même manière. Ces résultats sont discutés en fonction du niveau de production des animaux, de leur mode de conduite et du type de pâturage utilisé.

KURZFASSUNG

Coulon, J.B., d'Hour, P. und Petit, M., 1988. Einfluß der Übergangsfütterung auf die Milchproduktion beim Weideaustrieb von Milchkühen. *Livest. Prod. Sci.*, 20: 119-134 (auf englisch).

Mit einer Gesamtzahl von 51 Milchkühen (24 Färsen im ersten Jahr, 27 Kühe im zweiten Jahr) wurde ein Versuch zum Weideaustrieb durchgeführt. In jedem Jahr wurden folgende drei Behandlungen verglichen: In der Behandlung 1 kamen die Kühe nach dem Austreiben — abgesehen vom Melken — nicht in den Stall zurück und erhielten kein Heu. In der Behandlung 2 wurde bei gleichem Vorgehen wie in Behandlung 1 über 2 Wochen Heu beigefüttert. In der Behandlung 3 kamen die Tiere über Nacht in den Stall zurück und erhielten gleichfalls über 2 Wochen eine Heubeifütterung.

Der Weideaustrieb erfolgte zu Zeiten guter klimatischer Bedingungen (keine Kälteeinbrüche und keine stärkeren Niederschläge) und unter guten Fütterungsverhältnissen (Grasqualität) und war nicht durch gesundheitliche Störungen beeinträchtigt. Bei Weideaustrieb stiegen Milchleistung und Eiweißgehalt in der Milch von der letzten Woche im Stall zur zweiten Woche auf der Weide in den Behandlungen 1 und 2 (+2,9 bzw. 2,7 kg Milch pro Tag und +3,5 bzw. 3 g Eiweiß je kg Milch) stärker an als in Behandlung 3 (+0,5 kg Milch pro Tag und +0,8 g Eiweiß je kg Milch). Diese Differenzen verschwanden nach der dritten Woche auf der Weide, wenn die Behandlung aller Tiere gleich war. Die Ergebnisse werden in Hinsicht auf das Leistungsniveau, die Behandlung der Kühe und den Weidetyp diskutiert.