

The selection index and single- and multi-trait animal model evaluation of Polish Black-and-White cows

Wojciech JAGUSIAK, Andrzej ŻARNECKI

Department of Genetics and Animal Breeding, Agricultural University, Kraków, Poland

Abstract: The selection index and single- and multi-trait animal models were used for genetic evaluation of 100,983 cows. Genetic and environmental (co)variances of five milk production traits were estimated using MTDFREML. The highest heritabilities were found for fat and protein contents in all three lactations (0.29-0.33), and the lowest for protein yield in the third lactation (0.08). Phenotypic and genetic correlations between yield traits in adjacent lactations were higher than between the first and third lactations. Correlations between breeding values for fat content were higher than for yield traits. The magnitude of correlations between the index and animal model evaluations depended on the number of lactation records included in both procedures. Usually the relationships between breeding values based on the same lactations were close to unity. The correlations between single-trait and multi-trait evaluations decreased with increasing numbers of lactations in the model. This was the result of using variances and covariances of later lactations in the multi-trait model.

Key words: animal model, breeding value, dairy cattle, selection index.

Introduction

Until recently, the BLUP single-trait animal model was used in Poland to evaluate sire breeding values, and cow breeding values by the selection index. This approach was adopted for practical reasons, as in some other countries (HILL, SWANSON 1983). Limited computer facilities allowed the BLUP methodology to be applied for sire evaluation using first lactation records, but it was more difficult to evaluate cow breeding values on the basis of more lactations of a particular cow. Selection based on first-lactation records minimizes the generation interval, and estimates of breeding values are not biased by selection, but it has been argued that the rankings of both sires and cows can change over lactations.

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Correspondence: W. JAGUSIAK, Department of Genetics and Animal Breeding, Agricultural University, Al. Mickiewicza 24/28, 30-059 Kraków, Poland, email: jaga@ar.krakow.pl.

The development of improved BLUP animal model evaluation procedures and the availability of more powerful computers have made the use of subsequent lactation records more feasible (WIGGANS et al. 1988). It has been theoretically proved that the BLUP multi-trait animal model yields more accurate breeding value predictions and more precise estimates of fixed effects than the selection index. MEYER (1983) found that the inclusion of later lactation records increased the accuracy of BLUP predictions, mostly a result of the improved (co)variance structure of the data.

This study compares genetic evaluations of cows obtained from the national cow indexing system with single- and multi-trait animal model BLUP methodology.

Material and methods

Records of 102,108 Black-and-White cows that calved for the first time between April 1991 and September 1994 in five regions of northern and western Poland were extracted from the files of the Computing Centre in Olsztyn. After formal edits, three subsets of data were created: (i) 100,983 cows with first lactation records, (ii) 67,332 cows with first and second lactation records, and (iii) 31,599

Table 1. Data characteristics

	Subsamples		
	I	II	III
Number of animals:			
Cows with records	100983	67332	31599
Dams	84798	61257	30592
Sires	2725	2349	1711
Other ancestors	2588	2329	1819
Total	191094	133267	65721
Number of lactations:			
First	100983	67332	31599
Second	67332	67332	31599
Third	31599	31599	31599
Total	199914	166263	94797
Number of herd-year-season subclasses in:			
First lactation	16668	12287	7109
Second lactation	12701	12701	7335
Third lactation	7473	7473	7473
Total	36842	32461	21917

cows with first three lactation records. All lactation records contained data on milk yield, fat yield, protein yield, fat content and protein content. Table 1 presents the characteristics of these three subsets used for multi-trait evaluation of breeding values. The cows were daughters of 2725 sires, with an average of 37 daughters per sire. The average number of records per herd-year-season subclass was 6.1 in the first lactation, 5.7 in the second and 4.8 in the third.

Variance components needed for genetic evaluation were estimated on the basis on three data subsets limited to 2725 sires with at least 10 daughters. In the first subset were 92,877 cows with first lactation records, 60,674 cows with first and second lactation records and 26,649 cows with first, second and third lactation records.

For cows with evaluated multi-trait animal model breeding values 90,291 selection indexes were obtained from the Computing Center. Indexes for protein yield and protein content were not available.

Cow indexes were calculated according to a procedure similar to that described by HILL and SWANSON (1983). The construction of the index was based on cow's three own lactation records when available and estimated breeding values of sire and dam.

Variance components were estimated by the use of the REML (BOLDMAN et al. 1995) according to the following linear model:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

where \mathbf{y} is a vector of observations on 305-day lactations for the first three lactations (milk, fat, protein yields, fat and protein contents); \mathbf{X} and \mathbf{Z} are incidence matrices for fixed and random effects respectively; \mathbf{b} is the vector of fixed effects, \mathbf{u} is the vector of animal breeding values; \mathbf{e} is the vector of random error effects. The assumptions are: $E(\mathbf{y}) = \mathbf{X}\mathbf{b}$, $E(\mathbf{u}) = \mathbf{0}$, $E(\mathbf{e}) = \mathbf{0}$, $V(\mathbf{u}) = \mathbf{G}$, $V(\mathbf{e}) = \mathbf{R}$, $\text{Cov}(\mathbf{u}, \mathbf{e}') = \mathbf{0}$, which gives $V(\mathbf{y}) = \mathbf{Z}\mathbf{G}\mathbf{Z}' + \mathbf{R}$. As all relationships were utilized, $\mathbf{G} = \mathbf{A} \otimes \mathbf{G}_0$ where \mathbf{A} is the numerator relationship matrix and \mathbf{G}_0 is the additive genetic (co)variance matrix between lactations. $\mathbf{R} = \mathbf{I} \otimes \mathbf{R}_0$, where \mathbf{R}_0 is the residual (co)variance matrix for three lactations and \otimes is the Kronecker product.

Single and multi-trait BLUP animal model breeding values were calculated using a computer program written for routine evaluation. The linear model in this case was as follows:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{Q}\mathbf{g} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

where \mathbf{y} , \mathbf{b} , \mathbf{u} , \mathbf{e} , \mathbf{X} and \mathbf{Z} are as above, \mathbf{g} is the vector of fixed effects of genetic groups; \mathbf{Q} is an incidence matrix.

Animals with unknown parents were assigned to genetic groups (WESTELL et al. 1988). Bull-sires were assigned to three genetic groups, and cow-dams were assigned to four genetic groups, by age.

A single-trait animal model was used for breeding value estimations in data subset (i), consisting of cows with first lactation records. Single- and two-trait animal models were applied in data subset (ii), consisting of cows with first and sec-

ond lactation records. In subset (iii) with cows with first, second and third lactation records, single-, two- and three-trait animal models were used.

Pearson correlation coefficients were calculated between evaluations of breeding values obtained by different methods on the basis of different data subsets:

1. I_1, I_2, I_3 – index based on first (I_1), first two (I_2) or first three (I_3) lactation records;
2. S_1, S_2, S_3 – single-trait animal model breeding values based on first (S_1), second (S_2) or third (S_3) lactation records;
3. D_1, D_2 – breeding values for first (D_1) and second (D_2) lactation based on a two-trait animal model;
4. T_1, T_2, T_3 – breeding values for first (T_1), second (T_2) and third (T_3) lactation based on a three-trait animal model.

Different fractions of the best cows were selected on the basis of the breeding values obtained from single- and two-trait animal models and the index, and their rankings were compared with the ranking based on the three-trait animal model.

Results

Table 2 shows estimates of the heritabilities, phenotypic and genetic correlations of milk production traits in three lactations. The highest heritabilities were found for fat and protein content in all three lactations (0.29-0.33). Among the yield traits the highest was the heritability of milk yield in the first lactation (0.23), and the lowest was protein yield in the third lactation (0.08). In general, for all traits except protein content the heritabilities decreased in successive lactations.

Phenotypic correlations between yield traits in adjacent lactations ranged from 0.36 to 0.40, and were lower between the first and third lactations. Correlations between fat contents were higher (0.50-0.54).

Genetic correlations were much higher, ranging from 0.79 to 0.93 for yield traits between adjacent lactations and from 0.79 to 0.82 between the first and third

Table 2. Heritabilities (h^2), phenotypic (r_p) and genetic (r_g) correlation estimates of milk production traits in consecutive lactations

Trait	h^2			r_p			r_g		
	I	II	III	I * II	I * III	II * III	I * II	I * III	II * III
Milk yield [kg]	0.23	0.15	0.12	0.39	0.32	0.40	0.92	0.82	0.93
Fat yield [kg]	0.19	0.14	0.10	0.36	0.28	0.38	0.93	0.80	0.92
Protein yield [kg]	0.17	0.12	0.08	0.37	0.27	0.38	0.93	0.79	0.91
Fat content [%]	0.33	0.30	0.29	0.54	0.50	0.54	0.98	0.97	0.99
Protein content [%]	0.32	0.29	0.31	0.40	0.41	0.42	0.89	0.88	0.97

lactations. Genetic correlations close to unity were found for fat content and protein content in the second and third lactations.

Table 3 shows correlations between the indexes and breeding values evaluated by single-trait and multi-trait animal models. The index based on the first lactation (I_1) fat yield showed the highest correlations (0.725) with animal model single-trait evaluations also based on first lactation fat yields (S_1) and with multi-trait

Table 3. Correlations between cow indexes and breeding values estimated using single-, two- and three-trait animal models

Methods of BV evaluation	Milk yield [kg]	Fat yield [kg]	Fat content [%]
$I_1 * S_1$	0.742	0.725	0.835
$I_1 * D_1$	0.730	0.709	0.818
$I_1 * D_2$	0.689	0.672	0.814
$I_1 * T_1$	0.729	0.729	0.816
$I_1 * T_2$	0.692	0.674	0.812
$I_1 * T_3$	0.685	0.658	0.811
$I_2 * S_1$	0.730	0.707	0.825
$I_2 * D_1$	0.815	0.804	0.896
$I_2 * D_2$	0.804	0.791	0.896
$I_2 * T_1$	0.816	0.805	0.890
$I_2 * T_2$	0.806	0.793	0.889
$I_2 * T_3$	0.796	0.775	0.887
$I_3 * S_1$	0.679	0.651	0.784
$I_3 * D_1$	0.767	0.751	0.863
$I_3 * D_2$	0.771	0.753	0.863
$I_3 * T_1$	0.797	0.784	0.898
$I_3 * T_2$	0.813	0.799	0.900
$I_3 * T_3$	0.818	0.800	0.900

BV = breeding value.

animal model evaluations that included first lactation yield as a basic trait (0.709 with D_1 and 0.729 with T_1). Correlations with multi-trait evaluations (D_2 , T_2 and T_3) based on second or third lactation fat yield did not exceed 0.7. Evaluations for milk yield showed a similar pattern. Higher correlations were found between breeding values for fat content, in all cases above 0.8.

Indexes consisting of the first, second and third lactation fat yields (I_2) correlated highest with two- and three-trait animal model evaluations (0.791-0.805).

Table 4. Correlations between cow breeding values estimated using single-, two- and three-trait animal models

Methods of BV evaluation	Milk yield [kg]	Fat yield [kg]	Fat content [%]	Protein yield [kg]	Protein content [%]
S ₁ *S ₂	0.572	0.525	0.680	0.537	0.571
S ₁ *S ₃	0.491	0.424	0.652	0.433	0.589
S ₁ *D ₁	0.946	0.933	0.918	0.937	0.923
S ₁ *D ₂	0.853	0.841	0.903	0.829	0.805
S ₁ *T ₁	0.935	0.922	0.892	0.929	0.883
S ₁ *T ₂	0.841	0.828	0.874	0.822	0.758
S ₁ *T ₃	0.804	0.769	0.868	0.776	0.775
S ₂ *S ₃	0.638	0.605	0.718	0.605	0.626
S ₂ *D ₁	0.770	0.757	0.886	0.759	0.809
S ₂ *D ₂	0.869	0.854	0.901	0.867	0.921
S ₂ *T ₁	0.768	0.756	0.865	0.759	0.781
S ₂ *T ₂	0.855	0.839	0.875	0.856	0.865
S ₂ *T ₃	0.834	0.822	0.876	0.836	0.843
S ₃ *D ₁	0.554	0.499	0.701	0.505	0.634
S ₃ *D ₂	0.581	0.531	0.705	0.537	0.645
S ₃ *T ₁	0.617	0.565	0.816	0.550	0.791
S ₃ *T ₂	0.692	0.654	0.832	0.634	0.835
S ₃ *T ₃	0.772	0.759	0.840	0.741	0.850
D ₁ *D ₂	0.968	0.972	0.999	0.964	0.959
D ₁ *T ₁	0.991	0.991	0.972	0.994	0.959
D ₁ *T ₂	0.952	0.955	0.965	0.954	0.902
D ₁ *T ₃	0.915	0.902	0.961	0.908	0.904
D ₂ *T ₁	0.962	0.967	0.971	0.961	0.923
D ₂ *T ₂	0.981	0.979	0.966	0.986	0.938
D ₂ *T ₃	0.948	0.935	0.963	0.948	0.927
T ₁ *T ₂	0.971	0.974	0.999	0.967	0.966
T ₁ *T ₃	0.945	0.934	0.997	0.931	0.973
T ₂ *T ₃	0.989	0.984	1.000	0.984	0.998

BV = breeding value.

The correlation between the three-trait index (I_3) and single-trait animal model estimates of breeding values was low (0.651), and increased in the case of two- and three-trait animal model evaluations. The highest correlation (0.800) was recorded for T_3 .

The correlations between animal model evaluations are shown in Table 4. The highest correlations, usually close to unity, were between breeding values

based on the same lactations. Only the correlations between single-trait breeding values (S_1 , S_2 , and S_3) were below 0.7. For fat yield, the correlation between D_1 and D_2 was 0.972, between T_1 and T_2 – 0.974, between T_1 and T_3 – 0.934, and between T_2 and T_3 – 0.984. Slightly lower were the correlations between two-trait and three-trait animal model breeding values. Usually the correlations between breeding values based on adjacent lactations were higher. The correlations between single-trait and multi-trait evaluations decreased with increasing numbers of lactations in the model. This was the result of using variances and covariances of later lactations.

In the case of single traits, the correlations between index and animal model evaluations were lower than those between the index based on two lactation records and the two-trait animal model (D_1 and D_2). The correlations between three-trait evaluations (I_3 and T_1 , T_2 , T_3) were of a magnitude similar to those between two-trait evaluations; about 0.8 for yield traits and about 0.9 for fat content. Slightly lower were the correlations between indexes based on two or three traits and animal model evaluations based on smaller numbers of traits, e.g. I_2 and S_1 , S_2 , S_3 , D_1 or D_2 (Table 3). The index based on first-lactation records (I_1) showed the lowest correlations with animal model evaluations.

Discussion

Before the introduction of the BLUP animal model, in many countries sires were evaluated by the BLUP sire model, and cow breeding values were evaluated by the selection index (HILL, SWANSON 1983). HENDERSON (1973) proved that mixed model methodology using all relationships enables greater genetic progress than does selection based on the selection index. The genetic parameters needed for BLUP breeding value evaluation were estimated using single-trait and multi-trait REML animal models. Estimates of heritabilities of yield traits from multivariate analyses cited in the literature were similar to those in our study, that is, heritabilities of first lactation yields were usually higher than those of second and third lactation yields, and in general were much higher than our estimates. VISSCHER and THOMPSON (1992) reported heritabilities ranging from 0.29 to 0.40 for yield traits and from 0.34 to 0.64 for fat and protein contents.

In most studies, genetic correlations between yield traits in adjacent lactations ranged between 0.80 and 0.99. MEYER (1984) reported an average estimate of 0.91 obtained by multivariate analysis, and thus free of selection bias.

Genetic correlations across lactations are less than one, and the use of multiple lactations adds more information, thus directly increasing the accuracy of selection. The multi-trait model also improves the (co)variance structure of the data through better connectedness due to additional ties between sires and fixed effects (MEYER 1984, VISSCHER et al. 1992). For the same reasons, higher genetic gain

can be expected from selection based on multi-trait evaluation of breeding values than from that based on a single-trait procedure (MEYER 1983). The multi-trait animal model predicted the genetic trend with higher accuracy than did single-trait and repeatability models (SIGURDSSON, ARNASON 1995).

Theoretically, an animal model with all pedigree information gives higher genetic progress than does the selection index. SORENSEN (1988) studied genetic progress in a simulated pig population, comparing an animal model and a selection index. The smaller response obtained with index selection was caused by bias due to the genetic trend, corrections for fixed effects and lower accuracy. NORMAN et al. (1991) compared Modified Contemporary Comparison, a procedure based on the selection index, with animal model evaluations, and found correlations between evaluations obtained from these two procedures ranging from 0.92 to 0.96. Our correlations were smaller and, as could be expected, the highest correlations were obtained between indexes and animal model evaluations based on three lactations.

Using the first three lactations instead of the first lactation also produces additional ties between sires and fixed effects through non-zero covariance. Selection based on BLUP multivariate predictions of breeding values should result in a greater genetic progress than selection based on a selection index or single-trait animal model.

Conclusions

The heritabilities of milk, fat and protein yields were generally low and decreased in consecutive lactations. In the second and third lactations the estimates for yield traits were much below the magnitude found in other studies. Genetic correlations between lactations were high, especially between adjacent lactations.

The breeding values evaluated by the index were highly correlated with single-trait or multi-trait animal models. The highest correlations were found when evaluations were based on the same lactation records. Similarly, when single-trait and multi-trait animal model estimates of breeding values were compared the highest correlations were found when the same lactation was used in the single-trait evaluation and as a basic lactation in the multi-trait model. The genetic correlations, however high, in all cases ranged from 0.82 to 0.93. This suggests that implementation of a multi-trait system in place of a selection index will result in substantial changes in cow ranking.

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