

ML, REML, MINQUE and Henderson 3 estimates of variance and covariance components for milk yield, fat and protein content of Braunvieh and Brown Swiss X Braunvieh sires

Estimacion de componentes de variancia y de covariancia para produccion de leche, porcentaje de grasa y de proteinas de toros Braunvieh y Brown-Swiss X Braunvieh mediante ML, REML, MINQUE y Henderson 3

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INTRODUCTION

Variance components are essential for designing breeding schemes and for accurate estimation of breeding values. They differ from one population to another and, thus, have to be estimated from data of the population for which they are used. No recent estimates were available for the Swiss Braunvieh population where extensive crossbreeding with American Brown Swiss has been practiced. The purpose of this Paper is (1) to obtain estimates of variance components to be used routinely for sire and cow evaluation, (2) to investigate differences in variation between the pure Braunvieh and the crossbred populations, and (3) to compare different methods of estimation.

DATA AND METHODS

Data were first lactations from 1978 to 1981. Three data sets of progeny of sires with ≥ 20 daughters were analysed (Table 1). Lactations with < 80 days were eliminated, lactations with 80 to 269 days were extended to 305 days by multiplicative factors. Lactations were precorrected multiplicatively for age at calving, service period (i.e., time between calving and conception), and additively for alpine pasturing. Sires were assumed unrelated. The statistical model for the analyses was

$$y = Xb + Zu + e$$

where

y is the vector of observations (three traits were used: milk yield, fat and protein content)

b is an unknown vector of fixed effects including herd level-region-year-season groups and sire groups (according to year of birth)

X is the design matrix for the fixed effects

U is an unknown vector of random sire effects

Z is the design matrix for the random effects

e is a vector of random residuals

Table 1: Distribution of data.

	Data set		
	Br1	Br2	F1
Observations	14989	13076	17551
Herd groups	1527	1629	2235
Sire groups	2	2	4
Sires	367	303	135

Br1 = progeny of Braunvieh sires born 1971 - 1972
 Br2 = progeny of Braunvieh sires born 1973 - 1975
 F1 = progeny of Brown Swiss x Braunvieh sires born 1972 - 1975
 Herd group = Herd level-region-year-season groups

$$\begin{aligned} E(y) &= Xb \\ E(u) &= 0 & \text{Var}(u) &= I\sigma_u^2 \\ E(e) &= 0 & \text{Var}(e) &= I\sigma_e^2 \end{aligned}$$

The mixed model equations (MME) were

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + Ik^* \end{bmatrix} \begin{bmatrix} b \\ u \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

where $k = \sigma_e^2 / \sigma_u^2$ and k^* is the guessed value of k .

σ_e^2 and σ_u^2 were estimated by Maximum Likelihood (ML), Restricted Maximum Likelihood (REML) and Minimum Norm Quadratic Unbiased Estimation (MINQUE) via MME using formulae given in Searle (1979), and Henderson's Method 3 (H3) (Henderson, 1953). The assumption of normality was made for ML and REML. Iterative MINQUE was used to compute the REML estimates because fewer rounds of iteration were needed. For MINQUE, priors for the k 's were 15 for milk yield and 9 for fat and protein content. Formulae derived by Dempfle (unpublished) were used to obtain standard errors of MINQUE estimates from absorbed MME, and of H3 estimates from absorbed Least Squares equations.

REML estimates for covariance components were obtained in the same manner as by Rothschild et al. (1979) and Clement (1978) :

$$\sigma_{i,j} = (1/2) [\sigma_{(i+j)}^2 - \sigma_i^2 - \sigma_j^2]$$

where

$\sigma_{i,j}$ is the REML estimate for the covariance component between traits i and j

σ_i^2 is the REML estimate for the variance component of trait i , and

$\sigma_{(i+j)}^2$ is the REML estimate for the variance component of the sum of traits i and j .

Table 2: Estimates of σ_e^2 and standard errors / σ_u^2 when $k^* = k$

Trait	Data set	σ_e^2				SE / σ_u^2		
		ML	REML	MINQUE	H3	k	MINQUE	H3
Milk kg	Br1	242141	270377	270378	270334	9	.11120	.11122
	Br2	248231	286163	286202	286031	9	.12088	.12091
	F1	312416	358473	358496	358399	9	.10329	.10330
Fat %	Br1	.07787	.08694	.08695	.08692	15	.18529	.18537
	Br2	.07715	.08895	.08903	.08888	15	.20142	.20151
	F1	.08086	.09257	.09257	.09258	15	.17213	.17216
Protein %	Br1	.04922	.05496	.05497	.05496	30	.37042	.37074
	Br2	.04915	.05667	.05670	.05663	30	.40263	.40302
	F1	.04882	.05602	.05602	.05602	30	.34419	.34433

Table 3: Estimates of σ_u^2 and standard errors / σ_u^2 when $k^* = k$

Trait	Data set	σ_u^2				SE / σ_u^2		
		ML	REML	MINQUE	H3	k	MINQUE	H3
Milk kg	Br1	20243	19290	19289	19509	9	.09781	.10636
	Br2	25032	23558	23396	22429	9	.10848	.12209
	F1	31032	30017	29761	29379	9	.14581	.17645
Fat %	Br1	.01550	.01518	.01509	.01503	15	.11224	.11786
	Br2	.01827	.01768	.01708	.01458	15	.12461	.13402
	F1	.00929	.00908	.00907	.00909	15	.15707	.18182
Protein %	Br1	.01257	.01237	.01231	.01166	30	.14590	.14774
	Br2	.01160	.01126	.01102	.00975	30	.16174	.16534
	F1	.00826	.00811	.00810	.00726	30	.18023	.19567

RESULTS AND DISCUSSION

Estimates for σ_e^2 and σ_u^2 are in Tables 2 and 3. The ML estimates for σ_e^2 were smaller, and for σ_u^2 larger, than estimates obtained by the other methods because the degrees of freedom due to the fixed effects are not taken into account by ML. This was also pointed out by Rothschild and Henderson (1979). REML and MINQUE estimates were similar. Because REML estimates can be obtained by iterating MINQUE, it is concluded that satisfactory results were obtained already after one round of iteration. σ_e^2 and σ_u^2 estimates for milk yield were larger in the F1 group than in the Braunvieh groups, indicating a scale effect. For fat and protein content, considerable smaller σ_u^2 estimates were found in the F1 group.

Table 4: Effect of various k^* and k on variance of MINQUE variance components from the F1 group.

k	k^*					
	3	15	30	79	159	H3
3	.00119	.00119	.00121	.00136	.00176	.00119
	.01746	.01882	.02093	.02575	.03070	.02931
15	.02964	.02963	.02964	.02982	.03026	.02964
	.02757	.02467	.02555	.02963	.03447	.03306
30	.11855	.11849	.11847	.11861	.11909	.11856
	.04547	.03401	.03248	.03506	.03960	.03829
79	.82210	.82161	.82118	.82081	.82116	.82216
	.14461	.08019	.06396	.05721	.05958	.05965
59	.33015	.32809	.32615	.32357	.32282	.33039
	.44037	.20716	.14448	.10798	.10283	.10861

1st line = $\text{Var}(\hat{\sigma}_u^2) / \sigma_u^4$

2nd line = $\text{Var}(\hat{\sigma}_u^2) / \sigma_u^4$

Standard errors (SE) of the estimates are given in units of $\hat{\sigma}_u^2$ for three $k^* = k$. MINQUE and H3 were equally efficient for estimating $\hat{\sigma}_u^2$. SE of $\hat{\sigma}_u^2$ estimated by MINQUE, however, were 1 to 21 % smaller than SE of $\hat{\sigma}_u^2$ estimated by H3. The superiority of MINQUE also depends on the structure of the data. Increasing k gave larger SE for $\hat{\sigma}_u^2$ and $\hat{\sigma}_e^2$ estimates. The effect of various k and k^* on standardized variance of variance components is demonstrated in Table 4 for MINQUE estimates from the F1 group. The influence of a bad k^* is much more important for $\hat{\sigma}_u^2$ than for $\hat{\sigma}_e^2$. Only if the difference between k and k^* becomes large, H3 results in smaller variances.

Heritabilities for the 3 analysed data sets are in Table 5. Heritability estimates of milk yield for the F1 and the second Braunvieh groups were practically identical. Due to small $\hat{\sigma}_u^2$, much smaller heritabilities of fat and protein content were estimated for the F1 group. Thus, expected selection response in the two traits would be considerable smaller than in the Braunvieh groups. Clement (1978) reported similar observations comparing genetic parameters for Bavarian Braunvieh and its crosses with Brown Swiss. Compared with the review of Maijala and Hanna (1974), our estimates are in the upper range for all traits.

The genetic correlations are in Table 6. Larger absolute values were found in the population of crossbred sires. The correlations between milk yield and fat and protein content were negative, except for the correlation between milk and fat percentage for one data set of pure Braunvieh sires. Clement (1978) found also a larger negative genetic correlation between milk yield and fat content for crossed sires than for Bavarian

Table 5: Estimates of heritabilities

Trait	Data set	Method of estimation			
		ML	REML	MINQUE	H3
Milk kg	Br1	.309	.266	.266	.269
	Br2	.366	.304	.302	.291
	F1	.361	.309	.307	.303
Fat %	Br1	.664	.595	.592	.590
	Br2	.766	.663	.644	.564
	F1	.413	.357	.357	.358
Protein %	Br1	.814	.735	.732	.700
	Br2	.764	.663	.651	.588
	F1	.579	.506	.505	.459

Table 6: REML estimates for genetic correlations.

Trait	Data set		
	Br1	Br2	F1
Milk kg x Fat %	-.164	.111	-.307
Milk kg x Protein %	-.253	-.251	-.480
Fat % x Protein %	.354	.406	.403

Braunvieh sires (-.83 versus -.28). A wide range of estimated genetic correlations was also given in the review of Majala and Hanna (1974).

SUMMARY

Variance components for error and sire effects were estimated separately for groups of 367 and 303 Braunvieh and 135 Brown Swiss X Braunvieh sires by ML, REML, MINQUE and Henderson's New Method for milk yield, fat and protein content. ML estimates for error components were smaller, for sire components larger, than by the other methods. Standard errors of variance components are given for MINQUE and Henderson's New Method. Heritabilities for milk yield and genetic correlations were larger for progeny of crossed sires, heritabilities for fat and protein content were smaller. Estimates from REML variance components for heritability of milk yield were .27 and .30 for the two groups of Braunvieh sires and .31 for the group of crossed sires. Heritabilities for fat content were .60, .66, .36, for protein content .74, .66, .51. Genetic correlations between milk yield and fat content were -.16, .11, -.31, between milk yield and protein content -.25, -.25, -.48, and between fat and protein content .35, .41, .80.

RESUMEN

Se estimaron componentes de variancia para el error y el efecto del padre para la producción de leche y el porcentaje de grasa y de proteínas para 3 grupos diferentes de toros (367 y 303 Braunvieh y 135 Brown-Swiss) mediante ML, REML, MINQUE y el Nuevo Metodo de Henderson. Las estimaciones ML de los componentes de variancia para el error fueron menores, para el efecto del toro fueron mayores, que mediante los otros metodos. Se menciona el error estandard de cada componente de variancia para MINQUE y el Nuevo Metodo de Henderson. La ~~heritabilidad~~ de la producción de leche y las correlaciones genéticas fueron mayores para hijas de toros cruzados, las ~~heritabilidades~~ para porcentaje de grasa y proteínas menores. Las estimaciones de la ~~heritabilidad~~ para la producción de leche mediante componentes de variancia segun REML fueron .27 y .30 para los dos grupos Braunvieh y .31 para el grupo de toros cruzados. Las heritabilidades para el porcentaje de grasa fueron .60, .66, .36 y de proteínas .74, .66, .51. Las correlaciones genéticas entre la producción de leche y el porcentaje de grasa fueron -.16, .11, -.31, entre la producción de leche y el porcentaje de proteínas -.25, -.25, -.48 y entre los porcentajes de grasa y de proteínas .35, .41, .80.

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