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ADDITIVE GENETIC AND ENVIRONMENTAL VARIANCE COMPONENTS FOR MILK TRAITS IN GOAT WITH TEST DAY MODEL

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ABSTRACT

Genetic and environmental dispersion parameters for daily milk yield (DMY), fat (FC), protein (PC) and lactose contents (LC) were estimated on 1805 does of Alpine and Saanen breed. During the period 1991-1996, 24044 monthly test days were obtained from 57 herds in Slovenia. Covariance components for random effects and residual were estimated by REML using Powell's algorithm. The models contained season (year-month interaction) and breed as fixed effects, litter size, day of lactation and parity as independent variables, and common flock, permanent environment and additive genetic effect (animal) as random effects. Heritability for DMY was 0.19 - 0.20, for FC was 0.16 - 0.18, for PC was 0.21 - 0.24, and for LC was 0.21 - 0.23. The greatest part of phenotypic variance of FC, PC and LC remained in residual. FC and PC had a negative genetic correlation with DMY (-0.32 and -0.41). Correlation between FC and PC was positive (+0.57), as between PC and LC (+0.27).

Keywords: goats / test day records / milk traits / genetic parameters / covariance components

ADITIVNE GENETSKE IN OKOLIŠKE KOMPONENTE (KO)VARIANCE ZA LASTNOSTI MLEČNOSTI NA DAN KONTROLE PRI KOZAH

IZVLEČEK

Ocenjevali smo genetske in okoliške parametre za količino mleka (DKM) in vsebnost maščobe (M), beljakovin (B) in laktoze (L) na dan kontrole za obdobje od 1991 do 1996. V raziskavo smo vključili 24044 zapisov 1805. koz srnaste in sanske pasme iz 57 tropov v Sloveniji. Komponente kovariance smo ocenjevali z metodo omejene največje zanesljivosti (REML) z algoritmom Powell. Večlastnostni model živali vsebuje sezono in pasmo kot sistematska vpliva, neodvisne spremenljivke so velikost gnezda, dan laktacije in zaporedna laktacija. Naključni del modela sestavljajo trop, stalno okolje in aditiven genetski vpliv (žival). Heritabiliteta za DKM je od 0,19 do 0,20, za M od 0,16 do 0,18, za B od 0,21 do 0,24 in za L od 0,21 do 0,23. Največji delež fenotipske variance za M, B in L ostane nepojasnjen. Za DKM in M oz. B smo izračunali negativno genetsko korelacijo (-0,32 oz. -0,41), med L in M pa pozitivno (+0,27). Visoka genetska korelacija je med M in B (+0,57).

Ključne besede: koze / zapisi na dan meritve / lastnosti mlečnosti / genetski parametri / komponente kovariance

INTRODUCTION

In the recent years, the interest of farmers for goat breeding has increased in Slovenia. Milk recording system for dairy goats was established late in 1991, while goats were earlier prohibited by law. Total milk yield in lactation has been applied for prediction of breeding values. Swalve (1995) reviewed studies on test day records in dairy cattle and also showed some in small ruminants. In goats, the animal model for test day records gives a feasibility to estimate breeding values before lactation is completed and select (or cull) animals before breeding season. Baro *et al*. (1994), Barillet and Boichard (1994) and Gonzalo *et al*. (1994) studied genetic parameters of test day records for milk yield and components in sheep. Study on test day records of dairy goats was done by Schaeffer and Sullivan (1994). Andonov (1994) tried to apply animal model for test day in dairy goats in Slovenia. The goal of this study was to estimate the covariance components for milk yield and milk components on test day in dairy goats and to verify Andonov conclusions on larger dataset including records since 1993.

MATERIAL AND METHODS

Data analysed were obtained from the central database of the Slovenian selection program for small ruminants. For the period 1991 - 1996, 24044 records were used. Dataset contained test day records for milk yield and milk components of 1805 does in 57 flocks. Milk samples from 1316 Alpine and 489 Saanen goats were taken from the first to the eleventh lactation at different stages of lactation. Measurements were taken after a suckling period, in many cases after a peak of lactation curve had been reached. Pedigree file contained 1876 animals. Among animals, 51.49% had at least one parent known, and the rest (48.51%) were base animals. The amount of records increased over six years, mainly because new breeders were included. The data were collected under production environment. A goat had at most six lactations. Therefore, diverse ages were expected.

During the observation period, the average daily milk yield was 1.98 kg (Table 1). The averages for milk components were similar to the literature values for Alpine and Saanen breed (Stark, 1988; Shafika *et al*, 1993; Zeng *et al*., 1996), only Souci *et al*. (1994) and Alichanidis and Polychroniadou (1996) reported higher protein content. Over the observed period, daily milk yield and protein content were increasing, while fat and lactose content showed fluctuation.

Table 1. Descriptive statistics for milk traits in goats in Slovenia for the period 1991 – 1996

	No. of records	Mean	Standard deviation	Min	Max
Daily milk yield (kg)	23 982	1.98	0.92	0.06	7.09
Fat content (%)	23 552	3.35	0.86	0.15	11.21
Protein content (%)	23 622	2.84	0.53	0.13	9.03
Lactose content (%)	22 814	4.38	0.33	0.11	9.68

Because the species almost disappeared in Slovenia, all animals regardless of their productivity, were included in the recording system, in order to establish a sizeable population. Some goats were kept in poor environment. In most flocks, conditions were improved over observation period and thus, increasing overall production level. Differences in production level among flocks as well as among animals were expressed in large standard deviation and were also proven in wide range between maximum and minimum values. The most extreme values were excluded from analyses, which represents 2.16% records. The narrower bounds would result in biased estimation of covariance components.

Covariance components were estimated for daily milk yield and milk components by single-trait and four-trait models. Separate analyses (single-trait) were done with different models to find appropriate model for each trait. A multi-trait analysis was used for simultaneous estimation of covariance components for all four traits in order to estimate covariances between traits.

Different models were used for the analyses of test day records for daily milk yield (model 1) and fat, protein, and lactose content (model 2). Litter size (x_{ijklm}), day in milk (z_{ijklm}), and parity (w_{ijklm}) were included as independent variables in model 1, while model 2 contained only milking day as an independent variable. Furthermore, season (year-month interaction, S_i) and breed (B_j) were fitted in both models as fixed, while common flock (f_k), permanent environment (p_{jkl}), and additive genetic (a_{il}) effects were considered as random. Permanent environment represents common environment for all test days within parity (lactation) for each animal. In data analysed, there were 4156 levels of permanent environmental effects in 1805 animals with record, while common flock effect is environment which is common for all animals within the same flock.

$$y_{ilklm} = S_i + B_j + b_I(x_{ijklm}) + b_{II}(z_{ijklm} - \bar{z}) + b_{III}(w_{ijklm}) + b_{IV}(w^2_{ijklm}) + f_k + p_{jkl} + a_{il} + e_{ijklmn} \qquad [1]$$

$$y_{ilklm} = S_i + B_j + b_{II}(z_{ijklm} - \bar{z}) + f_k + p_{jkl} + a_{il} + e_{ijklmn} \qquad [2]$$

Models 1 and 2 can be generalised in matrix form as:

$$y = X\beta + Z_1 f + Z_2 p + Z_3 a + e \qquad [3]$$

where **y** is a vector of observations on daily milk yield and milk components, $\boldsymbol{\beta}$ is a vector of fixed effects, **f** is a vector of flock effect, **p** is a vector of permanent environmental effect, **a** is a vector of additive genetic effect of animals, **e** is a vector of residual, $\mathbf{X}$, $\mathbf{Z}_1$, $\mathbf{Z}_2$ and $\mathbf{Z}_3$ are incidence matrices. Expectations and covariance matrices of random vectors are described in the following equations.

$$\mathbf{E}\begin{bmatrix}\mathbf{y}\\ \mathbf{f}\\ \mathbf{p}\\ \mathbf{a}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{X}\boldsymbol{\beta}\\ \mathbf{0}\\ \mathbf{0}\\ \mathbf{0}\\ \mathbf{0}\end{bmatrix}; \qquad \mathbf{V}\begin{bmatrix}\mathbf{f}\\ \mathbf{p}\\ \mathbf{a}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{F} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{P} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{G} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{R}\end{bmatrix} = \begin{bmatrix}\mathbf{I}_1 \otimes \mathbf{F}_0 & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{I}_2 \otimes \mathbf{P}_0 & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{A} \otimes \mathbf{G}_0 & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \sum^{\oplus} \mathbf{R}_{\mathbf{k0}}\end{bmatrix} \qquad [4]$$

$\mathbf{F}_0$, $\mathbf{P}_0$ and $\mathbf{G}_0$ denote scalar in single-trait model or 4x4 matrices in four-trait model containing covariance components for common flock, permanent environmental and additive genetic effects, respectively. Residual covariance matrix **R** in single-trait model was a diagonal matrix. In four-trait model, the block-diagonal **R** matrix can be described as a direct sum of different 4x4 matrices ($\mathbf{R}_{k0}$) due to missing values. Beside full records (in 95.4% cases) there were ten different patterns of missing values.

Covariance components for additive genetic, common flock, permanent environmental within lactation and residual effects for test day measurements were estimated by restricted maximum likelihood (REML) using derivative free algorithm (Powell), as implemented in PeRun (Kovač, 1992). The optimisation was performed on standardised scale, while the stopping criteria for rations were three significant digits. The maximum number of iteration was restricted to 5000, and maximum number of rounds to 20. The maximum number of evaluations per linear search was limited to 8 in univariate and in multivariate.

RESULTS AND DISCUSSION

Phenotypic variances for milk traits estimated with single-trait and four-trait model were practically identical (Table 2). Phenotypic correlation between daily milk yield and fat content was negative (-0.25), and so was between daily milk yield and protein content (-0.19). Low phenotypic correlation was estimated between daily milk yield and lactose content (0.09), also between lactose and protein content (0.12). Baro *et al.* (1994) in goats and Kennedy *et al.* (1982) in sheep reported a close to zero phenotypic correlation between daily milk yield and protein content. Pander *et al.* (1992) also found a negative but high phenotypic correlation between lactation milk yield and fat (-0.32) and between lactation milk yield and protein (-0.45) content calculated from eight test day records in cows. The phenotypic correlation estimated between lactation fat and lactation protein content was 0.56 in dairy cattle (Pander *et al.*, 1992), higher than in our case. Phenotypic covariances between lactose and other milk components as well as daily milk yield were positive, but close to zero.

Table 2. Phenotypic variances (on diagonal), covariances (above diagonal) and correlations (below diagonal) of test day for milk traits estimated with single-trait (italic) and four-trait model

	Daily milk yield (kg)	Fat content (%)	Protein content (%)	Lactose content (%)
Daily milk yield (kg)	***0.72*** **0.69**	-0.16	-0.07	0.02
Fat content (%)	-0.25	***0.58*** **0.58**	0.13	0.03
Protein content (%)	-0.19	0.40	***0.18*** **0.17**	0.01
Lactose content (%)	0.09	0.12	0.09	***0.10*** **0.10**

Heritabilities (h^2) of all milk traits estimated in single-trait model were actually equal to the estimates in four-trait model (Table 3). Similar heritabilities for milk yield per lactation, fat and protein content were estimated with single-trait (0.18) and multiple-trait model (0.17) in dairy goats by Analla *et al.* (1996). Schaeffer and Sullivan (1994) reported higher heritabilities for test day milk (0.29), fat (0.27) and protein percentage (0.31) in goats. Higher heritabilities were also estimated by Barillet and Boichard (1994) in sheep: 0.25, 0.24 and 0.35 for daily milk yield, fat and protein content, respectively. A high heritability (0.28) for daily milk yield in dairy sheep was estimated by Sanna *et al.* (1994). Baro *et al.* (1994) also reported a high heritability for daily milk yield (0.35), but low heritability for protein percentage (0.13) in milking ewes as estimated by Andonov (1994). Heritability for daily milk yield (0.30) was higher, but he found similar heritability for fat content in our earlier data in Slovenian population of goats.

Common flock effect explained up to 33% of phenotypic variation in daily milk yield and 11% in milk components. Especially for fat and protein content higher flock effect might be expected due to the large influence of feeding level (regime) on milk components. Low values for permanent environmental effect were estimated for all milk components, and differences between single-trait and four-trait model were closed to zero. Permanent environmental effect within lactation explained 17 to 20% of phenotypic variance for daily milk yield and between 4 to 8% of phenotypic variance in milk contents. In single-trait model and in four-trait model the estimates for residual were almost identical, values for all milk components were high (from 0.59 to 0.69). This means that the large proportion (59 to 69%) of phenotypic variation for milk components remained unexplained, while in daily milk yield the residual accounted only 31% of phenotypic variation.

Table 3. Estimates of variance proportion in single-trait and four-trait model

	Daily milk yield (kg)		Fat content (%)		Protein content (%)		Lactose content (%)	
	Single-Trait	Four-trait	Single-trait	Four-trait	Single-trait	Four-trait	Single-trait	Four-trait
h^2	0.20	0.19	0.18	0.16	0.24	0.21	0.23	0.21
f^2	0.33	0.30	0.11	0.10	0.11	0.11	0.11	0.11
p^2	0.17	0.20	0.04	0.04	0.06	0.08	0.06	0.08
e^2	0.31	0.31	0.68	0.69	0.59	0.59	0.60	0.61

h^2 heritability (additive genetic effect); f^2 common flock effect; p^2 permanent environmental effect; e^2 residual

Genetic correlations (Table 4) were negative between daily milk yield and milk components and positive among milk components. In other words, if daily milk yield is improved, fat and protein content would be decreased. The same is true for lactose, although changes (if any) are expected to be much smaller. A high positive correlation (0.57) is expressed in our records between fat and protein content: the increase in fat content would cause the increase in protein content. Likewise, selection only on protein or fat content (percentage) was connected with the strong fall of milk yield (de Jager and Kennedy, 1987).

Table 4. Estimates of correlations between milk traits in four trait model

	Daily milk yield (kg)	Fat content (%)	Protein content (%)	Daily milk yield (kg)	Fat content (%)	Protein content (%)
	Additive genetic effect			Common flock effect		
Fat content (%)	-0.32			-0.56		
Protein content (%)	-0.41	0.57		-0.18	0.35	
Lactose content (%)	-0.14	0.27	0.01	0.20	0.19	0.15
	Permanent environmental effect			Residual		
Fat content (%)	-0.24			-0.16		
Protein content (%)	-0.05	0.09		-0.17	0.40	
Lactose content (%)	0.35	0.10	0.23	0.09	0.06	0.08

The environmental components of covariance showed a negative correlation between daily milk yield and the two most important components: fat and protein. The additive genetic correlation between lactose content and daily milk yield was negative, while the residual correlation was very low. On the other hand, common flock and permanent environment correlations are positive, nullifying the genetic components. As a consequence the phenotypic correlation between lactose content and daily milk yield was low (0.09).

CONCLUSIONS

The paper gave the estimates of genetic and environmental components for daily milk yield and milk components. Estimates of variance components evaluated in single-trait analysis were close to estimates in multiple-trait analysis.

Heritabilities for daily milk yield (0.19 to 0.20), fat (0.16 to 0.18), protein (0.21 to 0.24) and lactose content (0.21 to 0.23) were lower than estimates found in the literature.

Results showed the negative genetic correlations between daily milk yield and milk components (from -0.14 to -0.41), while genetic correlations among milk components were positive.

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