

## USE OF TEST DAY RECORDS IN GENETIC EVALUATION OF MILKING SHEEP IN SLOVAKIA

M. Oravcová<sup>1</sup>, E. Groeneveld<sup>2</sup>, M. Kovač<sup>3</sup>, D. Peškovičová<sup>1</sup> and M. Margetín<sup>1</sup>

<sup>1</sup>Research Institute of Animal Production, Hlohovská 2, 94992 Nitra, Slovakia

<sup>2</sup>Institute for Animal Science and Animal Behaviour Mariensee, Federal Agricultural Research Center (FAL), D 31535 Neustadt, Germany

<sup>3</sup>University of Ljubljana, Groblje 3, SI 1230 Domžale, Slovenia

### INTRODUCTION

At present, breeding programs aimed at raising milk yield of sheep in Slovakia, are based on phenotype values of dams. For more efficient selection, a multivariate genetic evaluation of milk sheep has been done. Predicting accurate breeding values needs all effects affecting the traits to be accounted for and the estimates of variance-covariance components to be known.

Genetic evaluation of milk yield can either be based on cumulative lactation or individual test day records. The latter have a number of advantages and are quickly becoming the basis for state of the art of genetic evaluation. One main advantage, apart from operational ease lies in a better possibility to account for sources of variation affecting each test day. The traditional approach of trivially aggregating test day into lactation records and then subjecting them to sophisticated statistical analyses accounting for an optimum differentiation of genetic and environmental effects (Swalve, 1998) does not make much sense.

The objective of this study was to present the simultaneous estimates of genetic parameters and covariance components for milk production traits (daily milk yield, fat and protein percentages) of two most numerous sheep breeds in Slovakia - Improved Valachian (IV) and Tsigai (T) using a multiple trait animal model based on test day records.

### MATERIAL AND METHODS

**Animals and traits.** Test day records were collected by the State Breeding Institute under the AC method during the period from 1995 to 2000. Only purebred animals and lactations with at least 3 (IV) and 4 test day records (T) were used. Milk yield, fat and protein percentages within the ranges recommended by the ICAR regulations were taken into account. The data files comprised 90,011 (IV) and 40,094 records (T), respectively. The average number of known ancestors per individual was 5.4 (IV) and 4.7 (T). In both breeds, more than 50 % of the animals had both parents known. Conversely, almost 30 % of the animals were individuals with both parents unknown. The pedigree files comprised 26,808 (IV) and 11,980 (T) animals.

**Statistical analyses.** The covariance components were estimated using the following three-trait fixed regression test day animal model:

$$y_{ijklmn} = N_j + B_k + P_l + b_{1l} A_{ijklmn} + b_{2l} (DIM_{ijklmn} / 150) + b_{3l} (DIM_{ijklmn} / 150)^2 + \\ + b_{4l} \ln(150 / DIM_{ijklmn}) + b_{5l} \ln^2(150 / DIM_{ijklmn}) + fym_m + a_{il} + pe_{il} + e_{ijklmn}$$

where

|                   |   |  |
|-------------------|---|--|
| $y_{ijklmn}$      | - | n-th test day measurement (milk yield, fat and protein content)  |
| $N_j$             | - | fixed effect of j-th number of milking   |
| $B_j$             | - | fixed effect of k-th litter size   |
| $P_l$             | - | fixed effect of l-th parity  |
| $b_{1l}$          | - | regression coefficient on age $A_{ijklmn}$ within parity   |
| $b_{2l} - b_{5l}$ | - | regression coefficients on various functions of days in milk $DIM_{ijklmns}$ covariates to account for the shape of the lactation curve<br>- according to Ali and Schaeffer regression (1987), applied for sheep |
| $fym_m$           | - | random environmental effect of flock-year-month of measurement   |
| $a_{il}$          | - | additive genetic effect of animal with complete relationship included  |
| $pe_{il}$         | - | random permanent effect of animal  |
| $e_{ijklmn}$      | - | random residual error  |

There were 3 levels of parity (1, 2 and 3+), 2 levels of litter size (1 and 2+) and 2 levels of number of milking per day (2 and 3), 605 and 397 levels of composite environmental effect  $fym$ , 22336 and 9481 levels of non-genetic effect of animal (IV and T, respectively).

Restricted maximum likelihood method on the basis of analytical gradients (Neumaier and Groeneveld, 1998) implemented in the Variance Components Estimation Package VCE 4.0 (Groeneveld and García Cortés, 1998) was used to estimate the covariance structure of the above model, separately for each breed.

## RESULTS AND DISCUSSION

Descriptive statistics (means and standard deviations) of both breeds under study is given in table 1. Slightly higher phenotype values were found in T breed. Tables 2 and 3 show heritabilities and genetic correlations between the traits for each breed separately. Variance-covariance matrices for additive genetic effect could be found in table 4.

**Table 1. General statistics**

| Trait                | Improved Valachian (IV) |       |       | Tsigai (T) |       |       |
|----------------------|-------------------------|-------|-------|------------|-------|-------|
|                      | n                       | avg   | s     | n          | avg   | s     |
| Daily milk yield, ml | 91011                   | 605.9 | 268.7 | 40094      | 633.9 | 318.4 |
| Fat content, %       | 80964                   | 7.7   | 1.6   | 47,206     | 8.1   | 1.8   |
| Protein content, %   | 90001                   | 5.8   | 0.7   | 47,206     | 6.0   | 0.8   |

**Table 2. Heritabilities (on diagonal) and genetic correlations (above diagonal) - IV**

|                  | daily milk yield    | fat content         | protein content     |
|------------------|---------------------|---------------------|---------------------|
| Daily milk yield | <b>0.10 ± 0.003</b> | -0.32 ± 0,02        | -0.31 ± 0,02        |
| Fat content      |                     | <b>0.06 ± 0.002</b> | 0.52 ± 0,02         |
| Protein content  |                     |                     | <b>0.07 ± 0.002</b> |

**Table 3. Heritabilities (on diagonal) and genetic correlations (above diagonal) - T**

|                  | daily milk yield    | fat content         | protein content     |
|------------------|---------------------|---------------------|---------------------|
| Daily milk yield | <b>0.19 ± 0.004</b> | -0.24 ± 0.02        | -0.30 ± 0.02        |
| Fat content      |                     | <b>0.12 ± 0.004</b> | 0.56 ± 0.01         |
| Protein content  |                     |                     | <b>0.14 ± 0.004</b> |

**Table 4. Variance-covariance matrices for additive genetic effect**

|                  | daily milk yield |                | fat content |            | protein content |            |
|------------------|------------------|----------------|-------------|------------|-----------------|------------|
|                  | (IV)             | (T)            | (IV)        | (T)        | (IV)            | (T)        |
| Daily milk yield | <b>6256.6</b>    | <b>15346.5</b> | -9.0        | -17.4      | -4.2            | -9.9       |
| Fat content      |                  |                | <b>0.13</b> | <b>0.3</b> | 0.03            | 0.1        |
| Protein content  |                  |                |             |            | <b>0.03</b>     | <b>0.1</b> |

**Table 5. Variance components for random effects in IV subsets (daily milk yield)**

|                 | No_100  | No_300  | No_600  |
|-----------------|---------|---------|---------|
| $\sigma_A$      | 4634.2  | 3067.0  | 681.6   |
| $\sigma_{fym}$  | 23309.5 | 25515.5 | 24038.0 |
| $\sigma_{perm}$ | 10212.1 | 7516.2  | 5119.0  |

In comparison to IV breed, approximately twice higher heritabilities for all traits investigated were estimated for T breed (tables 2 and 3) : 0.10 vs. 0.19, 0.06 vs. 0.12 and 0.07 vs. 0.14. In contrast, slightly higher negative genetic correlations between daily milk yield and composite percentages were observed for IV : -0.32 vs. -0.24 and -0.31 vs. -0.30. Besides, strong positive correlations between fat and protein percentages were found (0.52 and 0.56 for IV and T, respectively). Lower heritabilities for IV were mainly caused by lower additive genetic variance 6256.6 vs. 15346 for daily milk yield, 0.13 vs. 0.3 for fat percentage, 0.03 vs. 0.1 for protein percentage (table 4). In order to find a reason, the whole data file was divided into the subfiles according to the flock size (with maximum number of 100 heads – No\_100, minimum number of 300 heads – No\_300 and minimum number of 600 heads – No\_600). Variance-covariance components and genetic parameters were estimated separately for relevant data sets (table 5). Apparently, the additive genetic variance (for milk yield) decreased with increasing size of flock (about 35 and 75 %, respectively). In contrast, less drastic changes in other environmental components were observed. These results indicate that there might be some problems with identification of rams, mainly in large flocks.

Heritabilities for milk yield and protein percentage (T) were similar to those obtained by El-Saied et al. (1998a, 1998b) for Spanish Churra sheep (0.18 and 0.14 for test day milk yield depending on the period analyzed, and 0.16 for protein percentage). Also, the genetic correlation between daily milk yield and protein content was almost the same (-0.38). These results were quite different from those reported by Baro et al. (1994) for the same breed. He found higher heritability for daily milk yield (0.34), but similar heritability for protein

percentage (0.13). The positive genetic correlation between daily milk yield and protein content (0.08) did not agree with our and El-Saied's findings. The estimates for Slovenian sheep breeds reported by Brežnik (1999) ranged from 0.16 to 0.22, from 0.08 to 0.14 and from 0.06 to 0.13 for daily milk and composite percentages (fat and protein, respectively).

Compared to heritabilities estimated from lactation records collected during the same period 1995 – 2000, those were lower for both breeds under study (unpublished results): 0.08 (IV) and 0.12 (T) for milk yield, 0.06 (IV) and 0.11 (T) for fat percentage, 0.08 (IV) and 0.12 (T) for protein percentage. This is in agreement with Swalve (1998) and Meyer et al. (1989), who reported higher heritabilities for test day yields in comparison to 305-day yields for dairy cattle breeds, while, El-Saied (1998b) found slightly higher heritabilities for standardized lactations 0.18 vs. 0.14 (Spanish Churra breed).

## CONCLUSION

The results indicate differences in heritabilities between the breeds under study. In spite of heritability estimates for the Improved Valachian breed being extremely low, these analyses may be the first step in the introduction of genetic evaluation of milk traits in Slovakian sheep.

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