



Heritability estimation of test day milk yield in Patch-faced Maritza sheep breed using different test day models

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Patch-faced Maritza sheep breed – *short information*

- ✓ Bulgarian native sheep breed
- ✓ Dual purpose – meat and milk



- Recognized breeding association;
- Approved breeding program;
- Population size – 8 584;
- 75 flocks (2025);
- Main traits for selection:
 - Prolificacy,
 - Litter weight at weaning,
 - Milk yield.



European Strategy for Animal Genetic Resources-2021

One of the main priority:

- Sustainable use and genetic improvement of AnGR
- From practical point of view genetic improvement of a small breed population involves 5 steps:
 - well designed and appropriate breeding programme;
 - performance recording (productive traits with economical importance)
 - genetic parameter estimation (heritability and repeatability)
 - breeding value estimations (BLUP, Animal model)
 - Optimal Contribution Selection (OCS)



The aims of this research:

- The aim of this study was to choose the appropriate linear models for heritability (h^2) estimations of test day milk yield (TDMY) in the population of Patch-faced Maritza breed.



Material and methods

- Data used for this analysis were provided by the Breeding association of native Maritza sheep breeds;
- Database included **12 955 dairy records for the test day milk yields** of the Patch-faced Maritza breed;
- The analyses includes data for the period **24 years** and were made in **18 flocks**;
- The **pedgree data** includes **2 611** animals;
- The mating system in all flocks was natural mating, and there was not artificial insemination;
- The database included ewes with test day milk yields from 100 to 4000mL, with suckling periods of 30 to 150 days. Each sheep in the database was required to have at least 3 test days. The number of lambs born was defined as a fixed effect with two levels;
- The pedigree information was analyzed by using the PEDIG program (BOICHARD, 2002);
- Descriptive statistics of test day milk yield and fertility was carried out using the SPSS programme;
- Estimates of variance components were performed using VCE software version 5.1.2 (Groeneveld et al., 2008).



Material and methods

9 test day models (TDMs) were formulated and tested for estimation of h^2 of TDMY.

- **3 Repeatability models (REP):**

- $y_{ijklmn} = YS_i + DIM3_j + PAR_k + LS_l + b_1(age)^2 + b_2(sp)^2 + fytd_m + a_n + pe_n + e_{ijklmn}$

- $y_{iklmn} = YS_i + PAR_k + LS_l + b_1(age)^2 + b_2(sp)^2 + b_3(DIM) + fytd_m + a_n + pe_n + e_{iklmn}$

- $y_{iklmn} = YS_i + PAR_k + LS_l + b_1(age)^2 + b_2(sp)^2 + b_3(DIM/314) + b_4(DIM/314)^2 + b_5 \ln(314/DIM) + b_6[\ln(314/DIM)]^2 + fytd_m + a_n + pe_n + e_{iklmn}$

- **3 Random regression models (RRMs) with 1st, 2nd and 3rd degree polynomials**

- $y_{iklmn} = YS_i + DIM3_j + PAR_k + LS_l + b_1(age)^2 + b_2(sp)^2 + fytd_m + \sum_{o=0}^3 a_{on}Z_{on} + \sum_{o=0}^3 pe_{on}Z_{on} + e_{iklmn}$

- **3 RR models with Ali-Schaeffer regression models (ASRM) with 1st, 2nd and 3rd degree polynomials**

- $y_{iklmn} = YS_i + PAR_k + LS_l + b_1(age)^2 + b_2(sp)^2 + b_3(DIM/314) + b_4(DIM/314)^2 + b_5 \ln(314/DIM) + b_6[\ln(314/DIM)]^2 + fytd_m + \sum_{o=0}^3 a_{on}Z_{on} + \sum_{o=0}^3 pe_{on}Z_{on} + e_{iklmn}$



Material and methods

- *To compare the 9 linear models described in previous slide:*
 1. The Akaike information criterion (AIC, Akaike, 1973);
 2. The Bayesian information criterion (BIC, Schwarz, 1978);
 3. The loglikelihood(LogL).

$$AIC = 2 \left[\ln \frac{L(i)}{L(0)} - (v_i - v_0) \right]$$

$$BIC = 2 \left(\ln \frac{L(i)}{L(0)} \right) - (v_i - v_0) \times \ln[n - r(X)]$$

$$-2\text{LogL} = n [\log(2\pi) + \log(SSE/n) + 1]$$



Results and Discussions

The analysis of "pedigree" file shows that:

Table 1. Structure of pedigree file.

Pedigree structure	n	Percentage, %
Pedigrees	1769	
Animals with known sire and dam	911	51.50
Animals with known sire and unknown dam	356	20.12
Animals with known dam and unknown sire	76	4.30
Animals with unknown sire and dam (base parents)	426	24.08
Sires	139	
Dams	703	
All animal in pedgree	2611	

Table 2. Pedigree quality in the Patch-faced Maritza sheep breed database.

	Average for generation	Average for ancestors
Female animals	2.75	35.73
Male animals	2.47	24.83
Average	2.63	30.99

Pedigree quality analysis shows:
 -known generations are 2.75 for females, 2.47 for males or the average



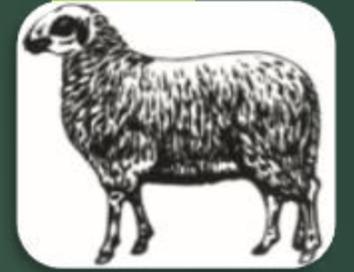
Results and Discussions

Table 3. Descriptive statistics of traits for Patch-faced Maritza breed.

Traits	n	\bar{x}	SD	Min	Max	CV, %
Test day milk yields (TDMY), <i>mL</i>	12 955	748.59	416.22	100	4000	56
Age at lambing of ewe (age), <i>days</i>	2881	1244.57	574.06	308	3627	46
Suckling period (sp), <i>days</i>	2881	62.50	18.22	30	149	29
Stage of lactation (DIM), <i>days</i>	12 955	134.10	49.22	30	308	37
Litter size (LS), <i>n</i>	2881	1.37	0.48	1	2,>2	35

TDMY was 748.59 mL. Coefficient of variation is relatively high – 56%.

TDMY is significantly lower than specialized dairy sheep breeds - East Frisian, Asaf, Lacon



Results and Discussions

Table 4. Additive genetic variance (σ_a^2), flock-year-test-day variance (σ_{fytd}^2), permanent environmental variance (σ_{pe}^2), residual variance (σ_e^2), heritability (h^2) and repeatability (r_w) coefficients of test day milk yield using REP models (REP 1, 2 and 3) for the Patch-faced Maritza sheep breed calculated as a ratio between the general phenotypic variance (taking into account the animal age in terms of lambing day for the Patch-faced sheep breed).

REP Models	$\sigma_a^2 \pm SE$	$\sigma_{pe}^2 \pm SE$	$\sigma_{fytd}^2 \pm SE$	$\sigma_e^2 \pm SE$	$h^2 \pm SE$	$r_w \pm SE$
REP 1	0.271±0.056	0.072±0.047	0.200±0.013	0.457±0.012	0.271± 0.056	0.343±0.061
REP 2	0.275±0.056	0.072±0.047	0.182±0.013	0.472±0.012	0.275± 0.056	0.346±0.061
REP 3	0.263±0.055	0.077±0.047	0.206±0.013	0.454±0.012	0.263± 0.055	0.340±0.060

Heritability estimates (h^2) are slightly higher or similar compared to those obtained for other breeds like Chios, Bovec, Improved Bovec and Istrian Pramenka breeds. There are no significant differences in the h^2 values calculated by the three models.



Results and Discussions

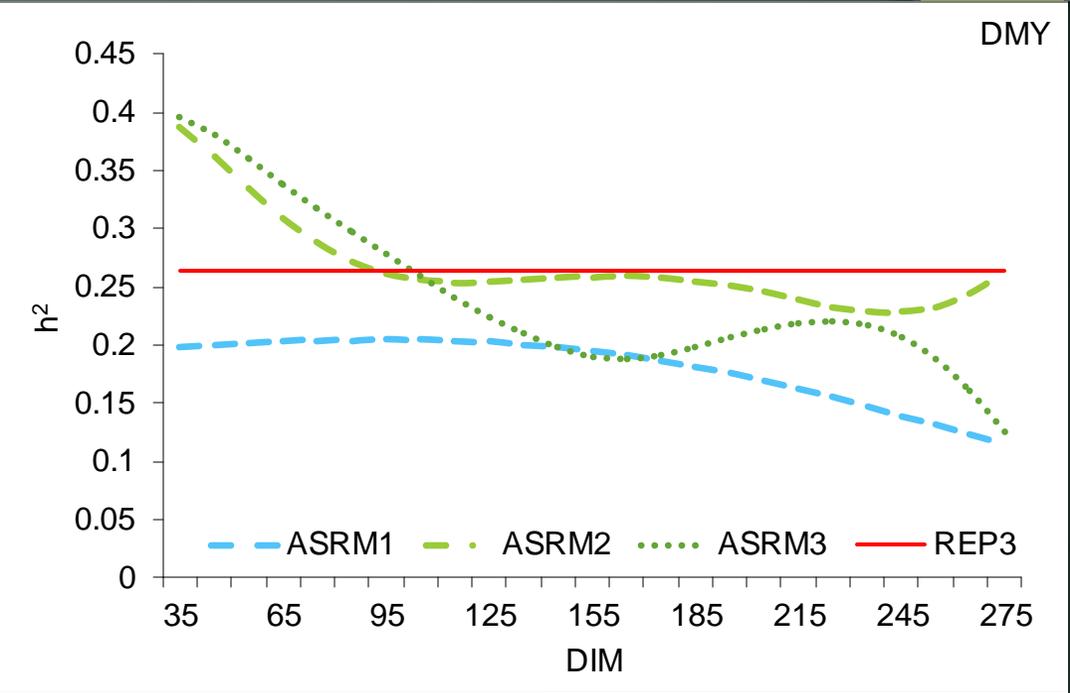
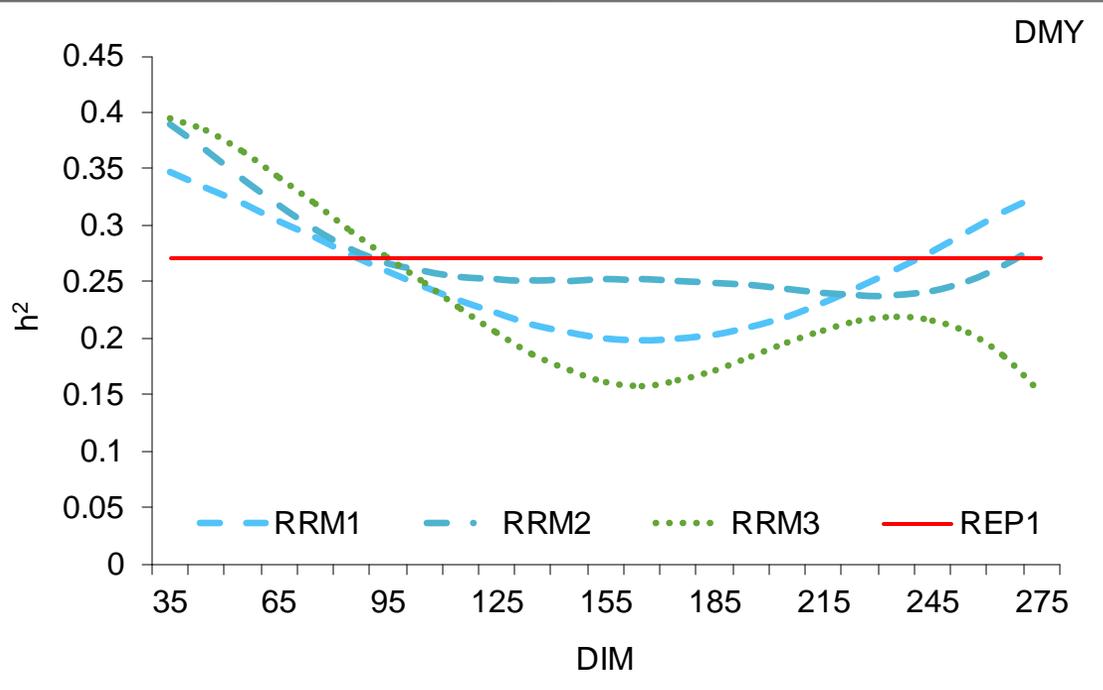


Figure 1. Estimation of heritability trajectories of TDMY depending on the DIM in first, second and third linear polynomials, with fixed linear regressions for the sheep age in terms of the lambing day (RRMs)

Figure 2. Estimation of heritability trajectories of TDMY depending on the DIM with ASRMs of first-, second- and third-order linear polynomials and with fixed linear regressions for the age in terms of lambing day. (ASRMs)

Fig. 1 shows that the trajectories of h^2 calculated by the three RRM models are similar, but for most of the lactation period they reveal to a lesser extent the genetic diversity compared to the REP models.

The trend is similar in the trajectories of h^2 calculated by the three ASRM models (Fig. 2).

The six regression models (RRMs and ASRMs) have an advantage over the REP models at the beginning of lactation until the 90th day, after which they reveal to a lesser extent the genetic diversity compared to the REP models.



Results and Discussions

Table 5. Compare the log-likelihood (LogL), Akaike information criterion (AIC) and Bayesian information criterion (BIC) to select the best model.

Models	LogL	AIC	BIC
REP1	4259.0034	4267.00	4273.43
REP2	4065.9908	4073.99	4080.42
REP3	3872.7736	3880.77	3887.20
ASMR1	4628.5093	4644.51	4659.72
ASMR2	4821.5971	4849.60	4878.66
ASMR3	5270.5195	5314.52	5362.91
RRM1	5014.7391	5030.74	5045.94
RRM2	5175.1345	5203.13	5232.19
RRM3	5620.0958	5664.10	5712.48

A comparison of REP1 with RRM1, RRM2 and RRM3 was performed. The comparison shows that for the used database REP1 is more suitable compared to the three RRMs.

In the second type of comparison of REP2 with REP3 and all ASRMs, REP3 is the most suitable, because all three criteria have the lowest values and determine REP3 as “the best fit model”.



Conclusions

- The RRM3 with third-order polynomials demonstrated more genetic diversity until the 95th day of lactation, but AIC, BIC and LogL estimates were higher than REP (which is not good).
- The regression models with 1st and 2nd degree polynomials were insufficient to reveal genetic diversity to a higher degree than REP model 1.
- The trend in the trajectories of h^2 calculated by the three random regression models with Ali and Schaeffer regression models (ASRMs) were similar to those of random regression models without incorporated Ali and Schaeffer regression.
- Although the known advantages of the random regression models for heritability estimations, AIC, BIC and LogL estimates indicated that in this data base (breed) repeatability models achieved a better balance between complexity and fitness and smaller prediction error compared to random regression models.

Thank you for your attention!



Patch-faced Maritza sheep breed