720. Partitioning of genetic trends by flock and gender in Istrian sheep breed

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Abstract

Istrian sheep is Croatian native breed traditionally selected for milk yield, but the success of past selection efforts has never been studied. Genetic trends play an important role in this regard, and their decomposition is effective in identifying the main contributors to trait related genetic change. The objective of this study was to estimate recent genetic trends (2014-2018) obtained under framework of single step genomic BLUP (test-day animal model) and to partition them by gender and flock. The overall genetic trend was positive, but negligible and inconsistent. Males contributed slightly more to the overall genetic trend than females, while the partitioning by flock was inconclusive. The results implicate absence of systematic selection in the recent period and impose a need to conduct selection based on the estimated breeding values. The ongoing transition to single step genomic BLUP in this population will provide sufficiently accurate breeding values to provide faster and consistent selection gain.

Introduction

Istrian sheep is Croatian native multi-purpose breed (milk-meat). The milk recording in this population started in early 2000 following ICAR guidelines, while the BLUP genetic evaluation for dairy traits has been carried out for about a decade. Recently, genotyping of a large part of the population with 50K SNP chip has been conducted. The aim is to upgrade the existing genetic evaluation system to genomic selection in order to increase the accuracy of estimated breeding values (EBVs) (Duchemin *et al.*, 2012; Legarra *et al.*, 2014). There are many uncertainties about success of historical selection work in this population since up to date there has not been a systematic analysis of genetic trends. Monitoring of selection success (genetic trends) can be simply obtained by averaging EBVs per birth year (Blair and Pollak, 1984) or by regressing BVs on birth year. Following the idea of Garcia-Cortes *et al.* (2008), these trends can be partitioned into contributions by the predefined different 'paths' (country, gender, flock, line, etc.). This can provide additional information on the main contributors to selection gain. The method has already been used to assess the contribution of different countries in Brown Swiss cattle (Gorjanc *et al.*, 2011), Croatian Simmental cattle (Špehar *et al.*, 2011), and two pig breeds in Croatia (Škorput *et al.*, 2015). To our knowledge, there are no reports of using this methodology in sheep. In order to analyse the success of previous selection work in the Istrian sheep, we estimated genetic trend for daily milk yield and decomposed it by flock and gender.

Materials & methods

Data. Phenotypic records for daily milk yield (DMY) and pedigree were provided by the Ministry of Agriculture. Phenotypic records were collected following the ICAR guidelines (ICAR, 2018). Before the final inferential statistical analysis, the original data set was 'pruned' leaving a total of 37,703 records obtained from 5,071 ewes. The pedigree file was created using all available relationships to phenotyped ewes and included a total of 7,208 animals. A total of 719 animals were genotyped using the Illumina OvineSNP50K BeadChip® (52,152). Genotyped animals and SNPs were included in the analysis after quality control parameters for call rate per animal, call rate per SNP, and MAF set to 0.9, 0.9, and 0.05, respectively. A total of 26 animals and 5,150 did not pass the above quality control. Monomorphic markers (n=898) and markers with unknown genome position or located on the sex chromosome (n=1,176) were also removed. The final number of genotyped animals and markers was 693 and 45,349, respectively.

Genetic evaluation. The BLUPF90 family of programs (Misztal *et al.*, 2018) was used in genetic evaluation of the reference population. RENUMF90 was used to renumber data sets and prepare parameter files for estimation of variance components (AIREMLF90) and estimation of BVs (BLUPF90). Covariance components were estimated using the AI REML algorithm within single trait repeatability test–day model. The model included the following fixed class effects: parity, litter size, season of lambing, and flock. Days in milk (DIM) and age at lambing were fitted as covariates. DIM was modelled using the Ali–Schaeffer lactation curve (Ali and Schaeffer, 1987) nested within parity and litter size for DMY. Age at lambing was modelled as linear regression nested within parity. The random part of the model included flock–test–day, permanent environmental effect within lactations, direct additive genetic effect (modelled by combining pedigree and genomic relationships), and residual. The same model was used to predict BVs. The matrix notation of the model was:

$$y = Xb + W_c c + W_p p + W_a a + e \tag{1}$$

where: y is a vector of the phenotypic observations for DMY, X is an incidence matrix for the fixed effects; W_c, W_p and W_a are incidence matrices for the flock-test-day, permanent environmental, and additive genetic effects, respectively; b is a vector of unknown fixed effects; c, p and a are vectors of unknown random effects; e is a vector of residuals. Pedigree additive relationship was combined with genomic information following the theory of ssGBLUP (Aguilar *et al.*, 2010). The inverse of numerator relationship matrix A^{-1} in the mixed model equation was replaced by matrix H^{-1} as follows:

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix} \tag{2}$$
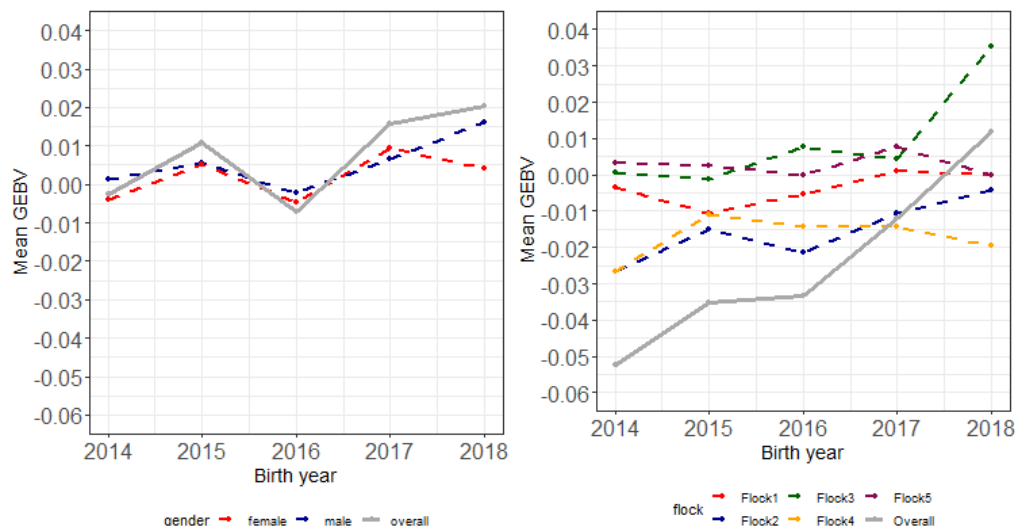
Partitioning of genetic trends. Genetic trends obtained as the average BV by year of birth were estimated for animals born from 2014 to 2018. The BV of an individual can be partitioned as $a_i = 1/2a_s + 1/2a_d + w_i$ where a_i is the BV of the individual, a_s and a_d are BVs of sire and dam, and w_i is the Mendelian sampling term. These partitions of BVs can be allocated into group-specific contributions to the change in genetic mean (Garcia-Cortes *et al.*, 2008). The â was partitioned by the gender and flock using the package AlphaPart 0.8.1. (Obšteter *et al.*, 2021) in R (R Core Team, 2020) following the method proposed by Garcia-Cortes *et al.* (2008) as follows:

$$\hat{a} = TP_1 T^{-1} \hat{a} + TP_2 T^{-1} \hat{a} + \cdots + TP_k T^{-1} \hat{a} \tag{3}$$

where matrix T traces the flow of genes from one generation to the other, i.e. it describes the expected genetic contribution of genes identical by descent between each individual and all its ancestors, while P_i matrix is the 'path' matrix for the ith origin that selects a partition of animals' BV attributed to selection work performed by the ith origin.

Results

Regression of BVs on birth year revealed a negligible positive (0.005 kg per year) overall genetic trend over the period studied. However, the gain was inconsistent throughout the period with significant decreases in 2016 for both genders and in 2018 for ewes (Figure 1a). Decomposition of genetic trend by gender revealed that rams had greater contribution in selection gain than ewes throughout the period, especially in the last examined year where discrepancy was the most pronounced. When BVs were regressed on birth year within gender, the estimated slopes for rams and ewes were 0.007 and 0.005 kg, respectively. Because of the high oscillations in estimated BVs between adjacent years, these regressions were estimated with a relatively high standard errors and were statistically insignificant ($P>0.05$). However, due to the similar number of animals throughout the years, these regressions are still to some extent informative in general

Figure 1. (A) Decomposition of overall genetic trends by gender and (B) flock for DMY.

description of genetic trends. The Figure 1b. shows decomposition of genetic trend by flock for the most informative and most reliable part of this population (flocks with >50 animals). The estimated annual rate for this subpopulation was 0.01435 kg with inconclusive contribution of the flocks' genetics to the overall selection gain.

Discussion

Analysis of genetic trends is important to monitor the success of past breeding activities and to carefully plan future breeding actions. The main intention of this study was to examine recent genetic trends in the Istrian sheep with special attention to determining the main contributors to the genetic trend. We used all the available phenotypic, pedigree, and genomic information to estimate genetic trends. The obtained results suggest that selection had a negligible positive overall trend, but oscillations in average BVs between years suggest that selection was not systematically conducted. The BVs used in this analysis were post-hoc obtained (after selection had been done), so it is ungrateful to derive firm conclusions on this issue. By not having the same information on genetic merits of the animals (potential disproportion of current and past BVs), as well as information which breeders selected based on EBVs, we can only hypothesise that selection on many of the examined flocks was 'happening by chance' rather than following the estimated BVs. In addition, partition of genetic trend by gender indicates that breeders in this population paid more attention to the selection of rams. There are many indications that rams are selected (based on different criteria among the breeders), while ewes are often 'recruited' by chance (often the ones not slaughtered for meat). According to the national breeding programme (Mioč *et al.*, 2011), animals should be selected based on the BVs, but since this is not obligatory, it is obviously sporadically applied. Decomposition of genetic trend by flock was inconclusive because none of the flocks studied had positive trend throughout the study period. Inconsistent genetic trends among flocks can be partially explained by differences in breeders selection criteria, but also as a consequence of limited genetic connectedness between the flocks. It is well known that many sheep populations, including this one, suffer from poor connectedness which leads to inability of the BLUP procedure to disentangle average genetic level from flock effects. Implementation of genomic information in genetic evaluation can alleviate this issue to some extent (Yu *et al.*, 2017) and therefore the results obtained probably nicely reflect true genetic trends in this population. A great precaution is needed

in ranking the flocks according to their estimated genetic merit, thus the obtained results should serve the best on within-flock level. The initial steps towards genomic selection in this population have been taken and continuous genotyping should additionally enlarge the reference population, likely leading to even more accurate predictions. To conclude, the results obtained indicate a very slow and inconsistent genetic gain for DMY and additional efforts need to be made to make it faster and more consistent. Breeders should be more decidedly advised to select replacements based on the estimated BVs. High accuracy of genomic BVs should serve as a strong argument in this regard. The connection between advisors and breeders should be more firm to adopt and carry out the proposed selection methods in order to bring this breed much closer to the world-famous dairy sheep breeds.

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References

Aguilar I., Misztal I., Johnson D.L., Legarra A., Tsuruta S. *et al.* (2010) J. Dairy Sci. 93(2):743-752. https://doi.org/10.3168/jds.2009-2730.

Ali T.E., and Schaeffer L.R. (1987) Can. J. Anim. Sci. 67(3):637-644. https://doi.org/10.4141/cjas87-067.

Blair H.T., and Pollak E.J. (1984) Anim. Sci. J. 58(4):878-886. https://doi.org/10.2527/jas1984.584878x.

Duchemin S.I., Colombani C., Legarra A., Baloche G., Larroque H. *et al.* (2012) J. Dairy Sci. 95(5): 2723-2733. https://doi.org/10.3168/jds.2011-4980.

García-Cortés L.A., Martínez-Ávila J.C., and Toro M.A. (2008) Animal 2(6):821-824. https://doi.org/10.1017/S175173110800205X.

Gorjanc G., Potočnik K., García-Cortés L.A., Jakobsen J., and Durr J. (2011) Proc. of the 2011 Interbull Meeting, Stavanger, Norway.

International Committee for Animal Recording (ICAR) (2018) Section 16. Guidelines for Performance Recording in Dairy Sheep and Dairy Goats. Available at: https://www.icar.org/index.php/icar-recording-guidelines/.

Legarra A., Baloche G., Barillet F., Astruc J.M., Soulas C. *et al.* (2014) J. Dairy Sci. 97(5):3200-3212. http://doi.org/10.3168/jds.2013-7745.

Mioč B., Pavić V., Barać Z., Vnučec I., Prpić Z. *et al.* (2011) Program uzgoja ovaca u Republici Hrvatskoj. Hrvatski savez uzgajivača ovaca i koza, Zagreb.

Misztal I., Tsuruta S., Lourenco D.A.L., Masuda Y., Aguilar I. *et al.* (2018) Manual for BLUPF90 family of programs. Athens: University of Georgia.

Obšteter J., Holl J., Hickey J.M., and Gorjanc G. (2021) Genet. Sel. Evol. 53:30. https://doi.org/10.1186/s12711-021-00600-x.

R Core Team (2020) R: A Language and Environment for Statistical Computing; R Foundation for Statistical Computing: Vienna, Austria. Available at: https://www.R-project.org.

Škorput D., Gorjanc G., Kasap A., and Luković Z. (2015) Animal 9(10):1605-1609. http://doi.org/10.1017/S1751731115001056.

Špehar M., Ivkić Z., Bulić V., Barać Z., and Gorjanc G. (2011) Agric. Conspec. Sci. 76(4):1-4.

Yu H., Spangler M.L., Lewis R.M., Morota, and Gorjanc G. (2017) G3: Genes, Genomes, Genetics 7(10):3543-3556. http://doi.org/10.1534/g3.117.300151.