Accuracy of genomic predictions for sheep milk fatty acid composition

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Summary

The increasing consumer's demand for high quality and healthier foods is drawing a great attention on milk fatty acid (FA) composition. However, the inclusion of these traits as breeding goals in traditional selection plans is hampered by cost and logistic problems. Medium infrared spectroscopy (MIR) is a valid and cheap alternative to the traditional laboratory gas chromatography (GC) methodology for predicting milk fatty acids composition. Moreover, genomic selection (GS) could represent a valid option for breeding for these traits. Objective of this research was to estimate breeding values for milk FA composition in dairy sheep using two different phenotypes (GC vs MIR) and two breeding strategies (traditional vs GS). Milk FA composition, pedigree relationships, and SNP genotypes were available for 769 Sarda breed ewes, divided in two groups: 669 in training and 100 validation cohorts, respectively. Traditional EBV were estimated using a BLUP animal model whereas GEBV were estimated using a single step approach. Prediction accuracies for validation animals were rather low (<0.30), but always higher for GEBV in comparison with EBV. Moreover, no differences were observed between GC and MIR phenotypes.

Keywords: Fatty acids, genomic selection, estimated breeding value.

Introduction

Milk fatty acid (FA) content and composition represent interesting potential breeding objectives for dairy animals because of healthy properties of these components for humans (i.e. C18:2cis9,trans11 was associated to antiatherogenic effect) (Banni *et al.*, 2003). Moreover, previous studies in dairy sheep confirmed the existence of genetic variability for sheep milk FA profile (Boichard *et al.*, 2014). However, FA recording on large scale using the standard gas chromatography (GC) methodology is problematic due to the high costs, logistic problems and a huge variability due to the several effects that can affect their content in milk. In addition to the diet, breed, stage of lactation, flock and farming area affect milk FA composition in sheep (De La Fuente *et al.*, 2009). A valid and cheaper alternative to the GC method for milk FA measurement is the medium infrared spectroscopy (MIR). Moreover, this simplified measurement method could be combined with genomic selection (GS) for enlarging the number of animals involved in the breeding plan. Objective of this research was to estimate breeding values for milk FA composition in dairy sheep using two different phenotypes (GC vs MIR) and two breeding strategies (traditional selection vs GS).

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Material and methods

Data

Milk FA composition (see table 1) for 769 Sarda breed ewes was measured by GC using a 7890A GC System (Agilent Technologies, Santa Clara, CA, USA) or predicted by MIR spectra. One record per ewe was available. Animals were genotyped using the Illumina Infinium Ovine SNP50 v1 BeadChip: after data editing, 44,619 SNPs across 27 chromosomes were retained for the analysis. Animals were divided in two groups: 669 ewes were considered as training cohort (TC) and the 100 youngest animals as validation cohort (VC). The phenotypic values of VC animals were masked in order to mimic the candidate animals without own records.

Breeding values

EBV and genomic breeding values (GEBV) were estimated with the following animal model:

$$y_{ijklnop} = \mu + PAR_j + DIM_k + LM_l + ALT_n + anim_o + FTD_p + e_{ijklnop} \qquad (1)$$

where $y_{ijklmnop}$ is the FA trait; μ is the overall mean; PAR is the fixed effect of the j-th parity class (eight classes = 1, …, 7, >7); DIM is the fixed effect of the k-th days in milking interval (five intervals: < 110, 110 to 140, 141 to 170, 171 to 200, >200); LM is the fixed effect of the l-th class of lambing month (1: January; 2: February to March; 3: October to November; 4: December), ALT is the fixed effect of the n-th altitude of location of flocks (mountain>= 500 mt above the sea level; hill= < 500 and >= 200 m a.s.l; *plain* < 200 m a.s.l.); *anim*, is the random additive genetic effect of the o-th animal; (o = 1, …, 6,252), *FTD* is the random effect of the p-th flock-test date combination (p = 1, …, 66); and $e_{ijklmnop}$, is the residual term.

EBV were estimated with a BLUP methodology by structuring the animal genetic covariance with the pedigree relationship matrix (**A**). GEBV were estimated with a single step approach (ssGBLUP) combining genomic and pedigree relationship matrix (**H**). Variance components were estimated using airemlf90, whereas for GEBV prediction blupf90 program was used. Moreover, prediction accuracies of GEBV were expressed as square root of reliability, calculated from prediction error variance (PEV) and then averaged in TC and VC for each fatty acid.

Results and discussion

Prediction accuracies are reported in Table 1. As expected, larger values were observed for TC in comparison with VC animals, for both phenotypes (GC and MIR) and breeding strategies (BLUP vs ssGBLUP). In the BLUP approach, EBV accuracies were in most of cases generally larger for GC compared to MIR phenotypes, whereas GEBV accuracies showed an opposite trend. Accuracies for VC were rather low, slightly larger for ssGBLUP in comparison with BLUP (0.23±0.05 and 0.17±0.06, respectively). Values obtained in the present work are in agreement with previous reports for genomic prediction of meat FA composition in beef cattle (Chiaia *et al.*, 2017; Zhu *et al.*, 2017). Results of the present study, although low in absolute terms probably because of the reduce size of sample of animals considered, showed that MIR predicted FA MIR are valid substitutes of GC measures for breeding purposes. Moreover, the inclusion of genotype information to the breeding value prediction can improve its accuracy, also in young animals without phenotypic information.

Table 1. EBV accuracy of sheep milk fatty acids obtained with gas chromatography (GC) or predicted by medium infrared spectra (MIR). Accuracy for training cohort (TC) and validation cohort (VC) predicted using pedigree (BLUP) or pedigree and SNP genotypes combined with single-step genomic approach (ssGBLUP).

| | TC (n=669)[1] | | | | VC (n=100)[2] | | | |
| | BLUP | | ssGBLUP | | BLUP | | ssGBLUP | |
Trait	GC	MIR	GC	MIR	GC	MIR	GC	MIR
C4:0	0.59	0.66	0.66	0.78	0.21	0.23	0.31	0.36
C6:0	0.33	0.43	0.60	0.68	0.12	0.15	0.27	0.31
C8:0	0.52	0.42	0.61	0.66	0.18	0.15	0.27	0.30
C10:0	0.56	0.49	0.60	0.62	0.19	0.17	0.27	0.28
C12:0	0.57	0.55	0.56	0.55	0.20	0.19	0.25	0.25
C18:0	0.65	0.57	0.53	0.54	0.22	0.20	0.24	0.24
C18:1t11	0.70	0.60	0.42	0.41	0.23	0.20	0.19	0.19
C18:1c9	0.58	0.26	0.62	0.50	0.20	0.09	0.27	0.22
C18:2ω6	0.11	n.a.	0.26	0.11	0.04	n.a.	0.14	0.14
C18:3ω3	0.11	0.24	0.22	0.39	0.04	0.09	0.12	0.18
CLAc9t11	0.60	0.58	0.40	0.41	0.20	0.20	0.19	0.19
MUFA[3]	0.35	n.a.	0.57	0.48	0.12	n.a.	0.26	0.22
PUFA[4]	0.36	0.56	0.37	0.50	0.13	0.19	0.18	0.22
ω6:ω3[5]	0.73	0.46	0.54	0.50	0.23	0.16	0.24	0.22
TFAnoVA[6]	0.49	0.48	0.47	0.58	0.17	0.17	0.21	0.26
Denovo[7]	0.46	0.43	0.55	0.56	0.16	0.15	0.25	0.25

[1] Cohort of sheep with own records born before 2012.
[2] Cohort of sheep born after 2012 with own records masked to mimic a validation set of younger sheep.
[3] Sum of the individual monounsaturated fatty acids.
[4] Sum of the individual polyunsaturated fatty acids.
[5] Ratio between the sum of individual PUFA ω6 fatty acids and the sum of individual PUFA ω3 fatty acids.
[6] Trans Fatty Acid (TFA) without Vaccenic acid (VA).
[7] Fatty acids synthetized de novo in mammary gland.

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