

Accuracy of genomic predictions for GC measured and MIR predicted fatty acid composition of sheep milk

A. Cesarani¹, G. Gaspa¹, F. Correddu¹, M. Cellesi¹, C. Dimauro¹, & N.P.P. Macciotta¹

¹ University of Sassari, Dipartimento di Agraria, Viale Italia, 39 07100 Sassari
macciott@uniss.it (Corresponding Author)

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 gas chromatography (GC) methodology for measuring milk FA composition. Moreover, genomic selection (GS) could enhance the efficiency of 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 genomic BLUP approach. Prediction accuracies for validation animals were rather low (<0.30), but always higher for GEBV in comparison with EBV. Moreover, no substantial differences were observed between GC and MIR phenotypes.

Keywords: fatty acids, genomic selection, estimated breeding value