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Innovative tools for phenotypic characterization and genetic improvement of meat quality in the Piemontese breed

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Genetic improvement of meat quality is complicated by the large number of traits involved and is limited by difficulties and costs related to sample collection and analytical procedures, which involve time-consuming lab methods.

The main aim of „QualiPiem“ project was to perform a comprehensive investigation on the possibility for the improvement of meat quality traits in the Piemontese breed, focusing on the application of innovative tools as Vis-NIR spectroscopy and genomics.

The study was carried out sampling 1,327 Piemontese young bulls, all registered in the Italian Piemontese Herdbook. Animals were fattened in 135 farms and slaughtered at the same commercial abattoir. Information about farms fattening system was collected through on field surveys.

At slaughter, the following carcass traits were recorded: carcass weight, SEUROP conformation, age at slaughter and carcass daily gain.

Twenty-four hours after slaughter, absorbance spectra were collected directly at the abattoir with two very different portable spectrometers after the division of carcasses in two quarters on the exposed Longissimus thoracis muscle. Then, individual samples of the Longissimus thoracis muscle were collected between the fifth and sixth thoracic vertebrae and transferred to the laboratory. After 8 d of ageing physical attributes of meat samples were assessed by measurement of lightness (L^*), redness (a^*), yellowness (b^*), pH (pH8d), purge loss (PL, %), cooking loss (CL, %) and Warner Bratzler shear force (WBSF, N). All young bulls were genotyped with the “GeneSeek Genomic Profiler Bovine LD” array containing 30,111 SNPs.

Six main fattening systems were identified within the Piemontese breed. Carcass traits were deeply affected by production system, while little effects on meat quality, limited to L^* , were observed.

All the meat quality traits showed not negligible heritabilities ranging from 0.12 (PL) to 0.32 (WBSF), allowing their improvement through selection. They also displayed genetic relationships with carcass traits, indicating a possible correlated response to selection for growth rate and muscularity, traits currently included in the breeding goal of the Piemontese breed. Infrared predictions of colour traits and PL were satisfactory, whereas pH8d, CL and WBSF predictabilities were rather poor, as a consequence of the large slaughter batch and residual variances affecting reference analyses. However, all the predicted traits, except WBSF, showed moderate heritabilities and were highly genetically correlated with measured traits, allowing their use for selection purposes.

The very simple, small, and cheap spectrometer (Micro-NIRS) yielded results not much inferior to the reference one (Vis- NIRS).

Genomic heritabilities were higher than pedigree-based heritabilities for PL and all colour traits, while they were similar for the other meat quality traits. The accuracy of prediction of genomic breeding values was satisfactory, ranging from

0.216 (pH) to 0.380 (WBSF) and allows to consider genomic selection as a valid tool to improve meat quality traits in the Piemontese breed.

The general results indicate that the genetic improvement of meat quality traits which are difficult to select with traditional methodologies could take advantage from the application of new phenotyping technologies, such as Vis-NIR spectroscopy, and by genomics.

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