Genetic Variation Of Lipid Content And Fatty Acid Profile Of Beef Estimated By Near-Infrared Spectroscopy

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Introduction

Chemical composition, and especially fat and fatty acids (FA), contributes importantly to various aspects of meat quality and plays a fundamental role in its nutritional value (Wood *et al.*, 2008). Typical methods used for FA determination as well as meat chemical composition are destructive and time-consuming. Near infrared spectroscopy (NIRS) is being increasingly used in food analysis because it gives fast, non-destructive, clean, and cost effective measurements (Sierra *et al.*, 2008). Variation in FA composition across cattle breeds have been reported in many studies (Huerta-Leindez *et al.*, 1993; Siebert *et al.*, 1996). Nevertheless, estimates of genetic parameters for meat composition and fatty acids content are scant and mostly available in pigs. Therefore, the objective of this study was to estimate genetic variation for meat chemical composition and fatty acid profile predicted by NIRS in beef.

Material and methods

Animals, beef samples and data. The study was carried out on 1,298 Piemontese young bulls protected by quality label denominated "Vitellone Piemontese della Coscia". The young bulls were progeny of 109 AI sires, fattened in 124 farms located in the Piemonte region (Italy) and all slaughtered at the same commercial slaughterhouse from March 2005 to July 2006 (average age at slaughter: 523±73 d). A description of meat sample collection and quality assessment as well as meat chemical composition and fatty acid profile analyses is reported in Boukha *et al.* (2007) and De Marchi *et al.* (2007) respectively. Briefly, a subset of 148 samples of *longissimus thoracis* was analyzed for meat chemical composition and fatty acid profile whereas NIR spectra were obtained for all samples (N = 1,298) using a Foss NIRSystem 5000, with fresh minced (FM) meat samples. The calibration equations used were those obtained by De Marchi *et al.* (2007). Only the equations showing coefficients of determination in cross-validation above or equal to 0.60 for the prediction of dry matter, lipid, C10:0, C12:0, C14:0, C16:0, C18:0, C16:1, C17:1, C18:1n9ct, C18:1n11tr, C18:2c9t11, C20:2, saturated fatty acids (SFA), monoinsaturated fatty acids (MUFA), and polyunsaturated fatty acids (PUFA) have been used.

Genetic analysis. Variance components and related parameters for predicted chemical composition and fatty acid profile were analyzed using a Bayesian approach and Monte Carlo Markov-Chain (McMC) methods (Sorensen and Gianola, 2002). The model accounted

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for the systematic effect of carcass weight (class 1: less than 387 kg; class 2: from 387 to 410 kg; class 3: from 411 to 430 kg; class 4: from 431 to 450 kg; class 5: from 451 to 474 kg; class 6: greater than 474 kg), the fattening herd (124 levels), the week of laboratory analysis (92 weeks), and the additive genetic effect. Flat prior distributions were assigned to systematic effect and to genetic effect, fattening herd and week of lab analysis. Parameters were drawn from the posterior distributions using Gibbs sampling as implemented in TM program (available at: http://cat.toulouse.inra.fr/~alegarra/). A single chain of 800,000 iterations was obtained for each analyses, with a burn-in of 50,000. Samples were saved every 200 iterations. The posterior median was used as a point estimate of heritabilities. Lower and upper bounds of the highest 95% confidence region for h^2 as well as the posterior probability for values of h^2 greater than 0.10 were obtained from the estimated marginal densities.

Results and discussion

Table 1 summarises the descriptive statistics for chemical composition and FA profile estimated for the 1,150 *longissimus thoracis* samples from Piemontese young bulls.

Table 1. Descriptive statistics for the studied traits

Trait	Mean	SD[1]	CV[2]
Chemical composition (g/100 g FM)			
Dry matter	27.63	0.65	2.4
Lipid	1.98	0.62	31.3
Major fatty acids (g/100 g FM):			
C14:0	0.032	0.015	49.9
C16:0	0.460	0.152	33.0
C16:1	0.029	0.015	51.7
C18:0	0.398	0.117	29.4
C18:1n9ct	0.566	0.236	41.7
C18:1n11tr	0.059	0.022	37.1
Minor fatty acids (mg/100 g FM):			
C10:0	1.358	0.044	3.2
C12:0	1.125	0.334	29.7
C17:1	9.971	3.601	36.1
C18:2n9t11-CLA	6.439	2.517	39.1
C20:2	2.943	1.248	42.4
Fatty acids groups(g/100 g FM)			
ΣSFA	0.885	0.292	33.0
ΣMUFA	0.673	0.302	44.9
ΣPUFA	0.243	0.031	12.8

[1] SD = standard deviation
[2] CV = coefficient of variation

In general, the chemical composition (i.e., dry matter and lipid) was within the range of literature values for the same breed (Russo and Preziuso, 2002) and similar to those obtained by Sierra *et al.* (2008) for other breeds. FAs were organized as major and minor (below 1%), being expressed in mg/100 g fresh minced meat. Major FAs (percentage over 1% of the total

FA quantified) accounted for more than 77% of the total lipid content. Most of them showed a broad range of variability, especially C14:0 and C16:1. When looking at the FA groups, the samples set was found to encompass a wide variability of both SFAs and MUFAs (as the main components of intramuscular fat), while the coefficient of variation of PUFAs was relatively limited.

Point estimates (median of the marginal posterior density of the parameter) of heritability for chemical composition and FA profile are given in Table 2. Moderate heritability values were found for all the investigated traits. The posterior probability of heritability being higher than 0.10 was greater than 85% for all the FA with the only exception of one major FA (C18:0) and one minor FA (C12:0). To our knowledge, no heritability estimates have been reported before for the chemical composition and FA profile of beef estimated using NIRS. The preliminary results of a study on the physical quality traits obtained both by reference analyses and NIRS prediction on the same samples evidenced similar or even higher h^2 values for both measured and predicted traits (Cecchinato *et al.*, 2009). Similarly, very promising results have been obtained also estimating h^2 values of milk coagulation properties both measured and predicted by mid-infrared-spectroscopy (De Marchi *et al.*, 2008; Cecchinato *et al.*, 2009). The results of the present trial suggest that exploitable genetic variation seems to exist also in the case of fat and FA content of beef .

Table 2. Features of the marginal posterior distribution for chemical composition and fatty acid content

	h^2			
Trait	PM[1]	LB95%[2]	UB95%[3]	*P* [4]
Chemical composition (g/100 g FM)				
Dry matter	0.168	0.08	0.30	89
Lipid	0.199	0.09	0.34	95
Major fatty acids (g/100 g FM):				
C14:0	0.225	0.10	0.40	95
C16:0	0.197	0.09	0.35	95
C18:0	0.119	0.04	0.24	63
C18:1n9ct	0.241	0.12	0.40	98
C18:1n11tr	0.171	0.07	0.32	87
C16:1	0.252	0.12	0.43	98
Minor fatty acids (mg/100 g FM):				
C10:0	0.187	0.08	0.34	91
C12:0	0.118	0.04	0.28	61
C17:1	0.222	0.11	0.37	97
C18:2n9t11-CLA	0.165	0.06	0.32	85
C20:2	0.156	0.08	0.27	88
Fatty acids groups(g/100 g FM):				
ΣSFA	0.163	0.06	0.31	86
ΣMUFA	0.235	0.10	0.41	95
ΣPUFA	0.218	0.11	0.37	96

[1] PM = median of the posterior density
[2] LB95% = lower bound of 95% probability density region
[3] UB95% = upper bound of 95% probability density region
[4] *P* ($h^2 > 0.10$) = posterior probability for values of h^2 greater than 0.10

Conclusion

Though preliminary, this study contributes to improve knowledge on the possibility of using the cheap and rapid NIRS technique for the prediction of lipid and fatty acid content of beef on a high number of animals and on the possibility of using these data for the study of the genetic variability, and possibly improvement, of FA profile of beef, important because of its association with human health.

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