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# Genetic correlations between measures of beef quality traits and their predictions by near-infrared spectroscopy in the Piemontese cattle breed

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**ABSTRACT** - The aims of this study were to predict beef quality traits (BQ: colour, shear force, drip and cooking losses) of Piemontese cattle using near-infrared spectroscopy (NIRS) and to estimate genetic parameters for measured BQ and their predictions by NIRS. Heritabilities and genetic correlations for measured BQ and their predictions based on NIRS were estimated through bivariate Bayesian analyses. Heritability estimates for measured BQ were of intermediate magnitude (from 0.10 to 0.63) and similar to those for NIRS predictions. The genetic correlations between BQ measures and their predictions by NIRS were very high for colour traits, high for drip loss, and nil for shear force and cooking loss. NIRS predictions can be proposed as indicator traits in breeding programs for enhancement of colour traits and drip loss.

*Key words:* Genetic parameters, Near-infrared spectroscopy, Beef quality, Piemontese.

**Introduction** - Assessment of beef quality traits (BQ) is difficult to be carried out routinely on a large scale because of costs and time-consuming lab methods. NIRS is one of the most promising techniques for large scale meat quality evaluation (Geesink *et al.*, 2003; De Marchi *et al.*, 2007). From a genetic point of view, the relevance of near-infrared spectroscopy (NIRS) for programs focusing on selection for improved BQ based on indicator traits relies on the genetic variation of NIRS predictions of BQ and on the magnitude of genetic correlation between NIRS predictions and BQ measured by standard methods. The aims of this study were to predict physical BQ of Piemontese cattle breed using NIRS and to estimate genetic parameters for BQ measured by standard methods and predicted by NIRS.

**Material and methods** - 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 is reported in Boukha *et al.* (2007). BQ considered in this study were: shear force (SF, kg), cooking loss (CL, %), drip loss (DL, %), lightness (L\*), redness (a\*), yellowness (b\*), saturation index (SI), and hue angle (H). NIRS spectra were collected using a Foss NIRSystems 5000 over the spectral range of 1,100 to 2,498 nm in reflectance mode every 2 nm. Partial least square (PLS) regression was performed using the Unscrambler software (v.9.6; Camo A/S, Oslo, Norway). PLS is widely used to establish a calibration model and to provide a correlation between reference data and values predicted using spectral data. Models were developed using raw spectra for CL, DL, colour traits and first derivative spectra for SF. Prediction models were developed using PLS regression on a calibration subset (n=300) and the holdout validation was carried out by applying the predic-

tion models on the remaining data (i.e., the validation subset). Estimation of (co)variance components for measures of BQ and predictions by NIRS were performed through 8 separate bivariate Bayesian analysis on the validation subset (n=998). In matrix notation, the 2-trait statistical model utilized can be written as:  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{W}_1\mathbf{c} + \mathbf{W}_2\mathbf{q} + \mathbf{Z}\mathbf{u} + \mathbf{e}$ , where  $\mathbf{y}$  contains observations on measures and NIRS predictions of BQ,  $\boldsymbol{\beta}$  is the vector of fixed effects,  $\mathbf{c}$  is the vector of random herd effects,  $\mathbf{q}$  is the vector of random weeks of laboratory analysis effects,  $\mathbf{u}$  is the vector of animal additive genetic effects,  $\mathbf{e}$  is the vector of random residual effects, and  $\mathbf{X}$ ,  $\mathbf{W}_1$ ,  $\mathbf{W}_2$ , and  $\mathbf{Z}$  are incidence matrices of proper dimensions. All bivariate models included the non genetic effects due to herds and weeks of laboratory analysis. Additional effects included in  $\boldsymbol{\beta}$  were the slaughtering age effect for SF and H, the carcass weight effect for b\*, CL, and DL, and carcass and age at slaughter effects for L\*, a\*, and SI. A priori, animal additive genetic effects were assumed normally distributed  $\mathbf{u} \sim N(\mathbf{0}, \mathbf{G}_0 \otimes \mathbf{A})$ , where  $\mathbf{G}_0$  is the (co)variance matrix between animal effects, and  $\mathbf{A}$  is numerator of Wright's relationship matrix. Parameters were drawn from the posterior distributions using Gibbs sampling, as implemented in the program TM by Legarra *et al.* (2007, available on request from the author at andres.legarra@toulouse.inra.fr). A single chain of 1,000,000 iterations was obtained for each of bivariate analyses, with a burn-in of 50,000. Samples were saved every 250 iterations. The posterior median was used as a point estimate of heritabilities and genetic correlations. Lower and upper bounds of symmetric 95% probability density regions for  $h^2$ , additive genetic correlation ( $r_A$ ) and additive genetic standard deviation were obtained from the estimated marginal densities.

**Results and conclusions** - NIRS predictions were satisfactory for the measurement of L\*, a\*, b\*, H, and SI ( $R^2=0.65, 0.69, 0.81, \text{ and } 0.60$ , respectively) but not for SF, CL, and DL ( $R^2<0.50$ ). These results agree with those reported by De Marchi *et al.* (2007) for the Piemontese cattle breed.

The estimated heritabilities (Table 1) for BQ measures and predictions by NIRS were very heterogeneous ranging from 0.05 to 0.63 for measures and from 0.10 to 0.62 for NIRS predictions. Differences between measures and predictions of BQ in terms of heritability were partially due to the reduction of variation, mostly the residual one, when BQ were predicted by NIRS. Only few investigations were conducted upon the genetic variation of beef colour coordinates. L\*, a\*, and b\* were moderately heritable and in good agreement with the estimates reported by Aass (1996) and Boukha *et al.* (2007).

Table 1. Posterior median and standard deviation for the additive genetic ( $\sigma_A$ ) and residual ( $\sigma_E$ ) standard deviation, and heritability ( $h^2$ ) of measures and predictions by NIRS of BQ<sup>a</sup>.

Item <sup>b</sup>	Measures			NIRS predictions		
	$\sigma_A$	$\sigma_E$	$h^2$	$\sigma_A$	$\sigma_E$	$h^2$
SF, kg	0.15 (0.05)	0.46 (0.02)	0.10 (0.07)	0.06 (0.02)	0.18 (0.01)	0.10 (0.06)
CL, %	0.65 (0.30)	2.70 (0.09)	0.05 (0.05)	0.18 (0.05)	0.40 (0.02)	0.17 (0.09)
DL, %	0.61 (0.15)	1.07 (0.07)	0.24 (0.11)	0.16 (0.04)	0.40 (0.02)	0.14 (0.07)
L*	1.66 (0.28)	2.48 (0.17)	0.31 (0.09)	1.25 (0.24)	2.09 (0.14)	0.26 (0.10)
a*	1.17 (0.20)	1.70 (0.13)	0.32 (0.10)	0.94 (0.14)	1.24 (0.09)	0.36 (0.09)
b*	0.64 (0.18)	1.63 (0.07)	0.13 (0.07)	0.60 (0.12)	0.94 (0.07)	0.29 (0.11)
H	2.37 (0.21)	1.81(0.24)	0.63 (0.10)	2.16 (0.21)	1.69 (0.24)	0.62 (0.10)
SI	0.95 (0.24)	2.26 (0.11)	0.15 (0.08)	0.92 (0.20)	1.68 (0.10)	0.23 (0.09)

<sup>a</sup> $h^2$ =calculated as  $\sigma_A^2/(\sigma_A^2+\sigma_E^2)$  where  $\sigma_A^2$  is the additive genetic variance and  $\sigma_E^2$  is the residual variance.

<sup>b</sup>SF=shear force; CL=cooking loss; DL=drip loss; L\*=lightness; a\*=redness; b\*=yellowness; H=hue angle [ $H=\tan^{-1}(b^*/a^*)$ ]; SI=saturation index ( $SI = \sqrt{a^{*2} + b^{*2}}$ ).

SI showed a moderate heritability, whereas H displayed the highest  $h^2$ . Heritability of SF was low, according to Riley *et al.* (2003). Table 2 shows the posterior medians, standard deviation, and bounds of the high posterior density (HPD) intervals (95%) for genetic ( $r_A$ ) and phenotypic ( $r_p$ ) correlations between BQ measured and predicted by NIRS. The genetic correlation between measures of BQ and predictions by NIRS were very high for colour traits, whereas the phenotypic correlation was lower. The relationships between SF, CL, DL, and their predictions were nil for SF and CL and moderate for DL, albeit the  $r_A$  exhibit a large degree of uncertainty. The poor predictability of CL is in agreement with that reported by other authors attempting to estimate CL in beef and pig meat samples by NIRS (Leroy *et al.*, 2003). The results of the present study verified that NIRS technology offers an alternative to conventional methods to evaluate BQ. Heritabilities of BQ predicted by NIRS were similar to those measured, only for SF and H. Heritabilities of SI,  $b^*$ ,  $a^*$ , and CL predicted by NIRS were higher than those measured, whereas  $h^2$  of DL was lower. The genetic correlations between BQ measured and BQ predicted by NIRS were very high for colour traits and moderate for DL. NIRS predictions can be proposed as indicator trait for an indirect improvement of BQ only for colour traits and DL.

Table 2. Posterior median and bounds of the 95% high posterior density region (HPD) for the genetic ( $r_A$ ) and phenotypic ( $r_p$ ) correlation between measures of BQ traits and predictions by NIRS.

Correlation <sup>a</sup>	$r_A$		$r_p$	
	Median	HPD	Median	HPD
SF with pSF	0	-0.85 – 0.86	0.02	-0.05 – 0.09
CL with pCL	0	-0.83 – 0.84	0.04	-0.03 – 0.11
DL with pDL	0.72	-0.07 – 0.98	0.24	0.17 – 0.32
$L^*$ with $pL^*$	0.85	0.53 – 0.98	0.60	0.55 – 0.65
$a^*$ with $pa^*$	0.98	0.83 – 0.99	0.67	0.62 – 0.71
$b^*$ with $pb^*$	0.93	0.44 – 0.99	0.47	0.38 – 0.54
H with pH	0.99	0.96 – 0.99	0.76	0.72 – 0.79
SI with pSI	0.95	0.61 – 0.99	0.61	0.55 – 0.66

<sup>a</sup>SF=shear force; pSF=shear force predicted by NIRS; CL=cooking loss; pCL=cooking loss predicted by NIRS; DL=drip loss; pDL=drip loss predicted by NIRS;  $L^*$ =lightness;  $pL^*$ =lightness predicted by NIRS;  $a^*$ =redness;  $pa^*$ =redness predicted by NIRS;  $b^*$ =yellowness;  $pb^*$ =yellowness predicted by NIRS; H=hue angle [ $H=\tan^{-1}(b^*/a^*)$ ]; pH=hue angle predicted by NIRS; SI=saturation index ( $SI = \sqrt{a^{*2} + b^{*2}}$ ); pSI=saturation index predicted by NIRS.

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