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XX CICLO

GENETIC ASPECTS OF BEEF QUALITY IN PIEMONTESE CATTLE AND RELATIONS WITH BREEDING GOAL TRAITS

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SUMMARY

Genetic selection in some countries was directed in favor of high muscle development and low fat development to produce leaner meat. This has been indeed successful in increasing growth rates of beef cattle. Eating meat quality is an important issue for meat scientists, breeders, consumers and the meat industry. The post-slaughter treatment of carcasses, especially chilling rate, ageing and method on hanging, are known to have important effects on eating quality. Compared with progeny testing for carcass traits, live evaluations have the advantage of being inexpensive and of allowing a significant reduction of the generation interval in breeding schemes, but there is no a good live animal predictors of meat eating quality and this is difficult to achieve without progeny testing.

The Piemontese breed is highly specialized for beef production due to double muscling (DM) inherited condition induced by a specific mutation of Myostatin gene (*mh*) located on Chromosome 2. This phenotype is characterized by greater muscle mass with less fat deposition, reduced weight of the skeleton reduced feed intake, and improved feed conversion.

The current breeding goal of the Piemontese population includes traits related to quantitative beef production and maternal calving performance of animals.

This thesis is aimed to study the possibility to introduce, indirectly, meat quality traits among the selected traits. This implies that genetic parameters and heritabilities for all meat quality traits need to be estimated.

Chapter 3 deals with the development and applications of a calibration curve for Near-Infrared spectroscopy (NIRS) aimed to predict chemical and physical compositions of Piemontese beef cattle. NIRS technique is a fast, non-destructive technique for objective and simultaneous analysis of these constituents of organic substances, and moreover it has a lower cost per analysis compared to the analytical laboratory methods. This chapter demonstrates that NIR spectroscopy is a useful tool to predict, with high accuracy, the composition of fatty acids, dry matter, ether extract in Piemontese beef cattle. Furthermore, this study has shown that NIR spectroscopy could not be used to predict physical properties, cholesterol and collagen contents in Piemontese beef cattle, which has been attributed to low analytical data variations used in calibrations. NIRS technique will be applied to a larger dataset for predicting fatty acids and ether extract compositions of Piemontese beef cattle.

Chapter 4 deals with the estimation of genetic parameters and heritabilities for physical meat quality traits, measured in laboratory, on a dataset of 1,080 Piemontese young bulls using a mixed linear Animal model. Univariate analysis was performed through Bayesian integrations. Animal models used for estimating the genetic parameters for meat quality traits have been obtained for the Piemontese population taking into account non-genetic effects of fattening farm, age at slaughter, hot carcass weight and week of meat analysis, and the additive genetic effect of young bull. Estimation of heritabilities of meat quality traits for Piemontese beef cattle were relevant, exploitable for an indirect selection of Piemontese population. Further investigations aiming: to estimate genetic (co)variances among beef quality traits in Piemontese breed and evaluate the genetic and phenotypic correlations among them, and to evaluate the relationship between these traits and the performance traits currently included in the breeding goal of Piemontese population.

Chapter 5 aimed to Predict the fatty acid profiles on a dataset of 733 fresh samples of *Longissimus thoracis* muscle of Piemontese young bulls using the same regression developed by the calibration curve obtained with near infrared reflectance Spectroscopy (NIRS) technique, and to estimate heritabilities and additive genetic variations for NIRS-predicted traits.

Estimate heritabilities obtained in the present study, were homogeneous ranging from 10 for C14:0 to 23 % for C20:4n-6. This homogeneity in the estimation of heritabilities maybe could be due to the use of the same equation of calibration for all fatty acid compositions.

Chapter 6 aimed to estimate variance and covariance components and corresponding genetic parameter estimates, and to estimate genetic and phenotypic correlations among meat quality traits in Piemontese beef cattle. (Co)variance components were estimated using a bivariate mixed animal model and was accomplished using Bayesian methodology and the Gibbs sampling integrations. Generally, genetic correlations among meat quality traits were very heterogeneous and ranged from -0.55 to 0.68. Phenotypic correlations were low and ranged from -0.09 to 0.47.

Chapter 7 deals with the estimation of genetic correlations among beef quality traits and performance traits for Piemontese beef cattle, and to evaluate the possibility to include, indirectly, meat quality traits in the selection objective.

Genetics correlation values among beef quality traits and performance traits in Piemontese populations obtained in this study were very interesting, ranged from 0.01 to 0.85 for positive values, and ranged from -0.60 to -0.15 for negative values. And, that could be useful for an indirect selection for meat quality traits.

RIASSUNTO

La razza bovina Piemontese è una razza Italiana specializzata da carne che trasforma molto bene il foraggio in carne e che fornisce un'alta resa alla macellazione. Morfologicamente presenta ossa piccole, pelle fine ed elastica, un ridotto tenore di grasso sottocutaneo ed una carne tenera e magra.

Le finalità generali di questa tesi sono state:

- su un dataset di 148 campioni messa a punto e applicazione della metodologia "spettroscopia nel vicino infrarosso (NIRS)" per la predizione di parametri fisici (perdita di gocciolamento, perdita di cottura, forza di taglio, e il colore), la composizione chimica e il profilo di acidi grassi della carne bovina di razza Piemontese, e questo si è compiuto attraverso lo studio di fattibilità di una curva di calibrazione in grado di predire questi parametri. NIRS si è rivelato un metodo utile ed efficace, con alta accuratezza, per la predizione della composizione acidica della carne bovina Piemontese, d'altra parte non ha dato dei risultati molto soddisfacenti per la predizione dei parametri fisici, colesterolo e collagene.

  Per cui si è fatto ricorso al metodo analitico per la misurazione di parametri fisici.
- la stima dei parametri genetici e stime di ereditabilità dei caratteri legati alla qualità della carne bovina di razza Piemontese applicando un'analisi univariata di un modello animale misto usando l'inferenza statistica Bayesiana. Il modello misto includeva come effetti non genetici gli effetti dell'azienda (FF), età dell'animale alla macellazione in classi, peso della carcassa in classi, e turno o settimana di lavorazione. L'effetto *random* dell'animale è stato incluso nel modello come effetto genetico additivo. Le stime di ereditabilità per i caratteri di qualità della carne Piemontese ottenute in questo capitolo sono interessanti e utili ai fini selettivi per i medesimi.
- La stima dei parametri genetici e stime di ereditabilità del profilo acidico misurato con la metodologia NIRS. Questa tecnica è stata estesa ad un dataset di 733 campioni. Questo capitolo ha dato dei risultati omogenei dove le stime di ereditabilità erano compresi tra 10 e 23 %. Questa

omogeneità potrebbe essere dovuta al fatto che è stata utilizzata un'unica equazione di calibrazione per tutti gli acidi grassi.

- La stima dei componenti di (co)varianze attraverso un'analisi bivariata, e stime di correlazioni genetiche e fenotipiche tra i caratteri della qualità della carne bovina di razza Piemontese. Le correlazioni genetiche tra i caratteri qualitativi della carne sono risultate comprese tra -0.55 e 0.68. Le correlazioni fenotipiche sono risultate basse comprese tra -0.09 e 0.47.
- Successivamente Sono stati stimati i componenti di (co)varianze tra i caratteri di qualità della carne e caratteri di conformazione rilevati su animali vivi della razza Piemontese ai fini di valutare la possibilità di introdurre, indirettamente, nell'attuale obiettivo selettivo della razza Piemontese qualche carattere di qualità della carne, vista l'importanza e l'influenza di questi caratteri sulla scelta d'acquisto del consumatore. Le correlazioni genetiche tra i caratteri di qualità e i caratteri di conformazione nella razza Piemontese sono compresi tra 0.01 e 0.85, per le correlazioni positive, e tra -0.60 e -0.15 per le correlazioni negative. Questi risultati sono importanti e utili ai fini della selezione per i caratteri di qualità.

CHAPTER 1

General introduction

1. GENERAL INTRODUCTION

1.1 Animal breeding and eating meat quality

Eating meat quality is becoming an increasingly important issue for meat scientists, breeders, consumers and the meat industry in richer countries.

In most European countries over 50 % of beef production is from pure dairy or dual purpose breeds. Beef cattle breeding in temperate countries is less homogeneous than dairy cattle breeding. For this, many European countries have only a small specialized beef cattle breeding industry; in many cases this comprises purebred terminal sire breeds to supply beef bulls for crossing in diary or dual purpose herds. Italian beef breeds account for a high proportion of total production, after France, in Europe.

It was demonstrated that beef breeds were characterized by lower values for collagen content, compression and shear force in raw and cooked meat respectively, compared to dairy or dual purpose breeds.

Genetic selection in some countries was directed in favor of high muscle development and low fat development to produce leaner meat. This has been indeed successful in increasing growth rates of beef cattle. This is important because, nowadays, consumers seek meat of high and consistent quality and the concept of quality includes now not only eating meat quality but also nutritional value, healthiness and any other consideration important for consumers.

Therefore, in animal breeding extensive interest has been renewed in the carcass characteristics of the double muscled beef cattle, especially due to the fact that consumer demand is moving toward leaner meat.

1.2 Genetic effects on beef meat quality

Besides slaughtering conditions and technological considerations, meat characteristics depend directly on the muscle biology of live animals, which is regulated by genetic, nutritional and biological factors. Among the latter, the genetic factors are of prime importance because genetic improvement is permanent and cumulative when inherited by the next generations.

It is well known that different cattle breeds or genotypes differ in their muscle characteristics due to marked differences in animal physiology. Consequently, beef meat may differ in quality depending on the animal genotype.

Compared with progeny testing for carcass traits, live evaluations have the advantage of being inexpensive and of allowing a significant reduction of the generation interval in breeding schemes, but there is no a good live animal predictors of meat eating quality and this is difficult to achieve without progeny testing.

The post-slaughter treatment of carcasses, especially chilling rate, ageing (ageing speed of fast-glycolytic muscle fibers is known to be important, which may favor tenderness) and method on hanging, are known to have important effects on eating quality.

1.3 Myostatin gene mutation and muscular hypertrophy

Double muscling (**DM**) or muscular hypertrophy is an inherited condition manifested by a generalized hypertrophy of muscles, most prominently in the regions of the proximal fore- and hind quarters, and prominent muscular protrusion, with intermuscular boundaries and grooves clearly visible beneath the skin (Mènissier, 1982). Other physical characteristics include fineness of the limb bones, a higher incidence of underdeveloped external genetalia, and enlarged tongues in newborn calves (Kieffer & Cartwright, 1980).

This phenotype is characterized by greater muscle mass; the overall increase in muscle mass, which is due to an increase in the number of muscle fibers (hyperplasia) and to a lesser extent to fiber enlargement (hypertrophy), differs among muscles. DM animals have a higher proportion of lean meat than normal cattle. Their meat is pale and tender, mainly due to an elevated proportion of white fast-twitch glycolytic fibers and a lower collagen content. They contain less bone and less fat deposition, with a higher proportion of ‘expensive’ cuts of meat (Menissier, 1982; Shahin and Berg, 1985); the lower fat content is detrimental for flavor but nevertheless healthy, because those fats remaining tend to be polyunsaturated varieties (Smet et al., 2000). DM animals are characterized also by reduced weight of the skeleton (Vissac, 1968), reduced feed intake, and improved feed conversion (Hanset et al., 1987; Arthur, 1995; Cundiff et al., 1996; Wheeler et al., 1996, 1997).

These characteristics in cattle have led to the selection of this phenotype for specific uses in Europe despite its association with reduced female fertility, susceptibility to respiratory illness, and the need for Caesarian section due to high incidence of dystocia (Hanset, 1991). Cattle showing the DM characteristic are, however, reported to show varying degrees of subfertility, calving difficulty, lower calf viability and increased stress susceptibility (Menissier et al., 1974; Vissac et al., 1974; Arthur et al., 1988).

Muscular hypertrophy in cattle is due to a specific mutation in myostatin gene (*mh*) (Kambadur et al., 1997; McPherron and Lee, 1997; Grobet et al., 1997). The locus causing DM in cattle has been mapped to the centromeric end of bovine chromosome 2 (Charlier et al., 1995; Dunner et al., 1997; Smith et al., 1997; Casas et al., 1998).

There are at present six identified mutations of myostatin sequence that give rise to muscular hypertrophy by inactivating this gene. In Piemontese breed, there is a guanine to adenine transition mutation at position 938 (G938A) causing a substitution of a critical tyrosine with a cysteine in the signaling portion of the protein. This mutation produce an inactive myostatin protein (Grobet et al., 1998; Dunner et al., 2003).

1.4 Piemontese breed

The Piemontese breed is the most numerous Italian beef breed, and accounting for around 300.000 cattle registered in the Italian Herd books, the interest about this breed is appeared because Piemontese cattle are highly specialized for beef production due to DM characteristic.

A recent research (Anaborapi, 2004) has estimated a frequency of 0.98 for the mutated allele in the Piemontese populations, whereas all AI bulls were essentially homozygous for DM. Double muscling characteristic in Piemontese breed, as well as in all other DM breeds, exerts positive effects on dressing percentage, carcass conformation and eating meat quality, but its influence on maternal traits such as calving performance is generally negative (Ménissier, 1982).

The current breeding goal of the Piemontese population includes traits related to quantitative beef production such growth potential, muscularity and maternal calving performance of animals which are selected by performance testing on station of young bulls (ANABORAPI, 2003).

Therefore, selection is organized in two stages: young bulls are station-tested, at the genetic station located in Carrù owned by the Italian Piemontese Association (ANABORAPI), on own performance for beef production traits and selected animals are then progeny tested for direct and maternal calving ease (Carnier et al., 2000).

The objective of the performance testing in the Piemontese breed is the evaluation of young bulls for growth rate and live fleshiness.

Live assessments of muscularity are simple methods to carry out, and have the advantage to be inexpensive and to allow a significant reduction of the generation interval in breeding schemes. But can not determine the chemical composition and physical traits of meat quality.

Whereas the progeny testing for carcass traits requires the slaughtering of the animals, and allows the assessments of beef quality traits in the laboratory.

Some researches were achieved on the determination of genetic parameters of carcass and beef quality traits (Mohiuddin, 1993 and Koots et al. 1994a, 1994b). However, few investigations have been conduced on double-muscled cattle breed (Gengler et al., 1995). No previous investigations have been realized for the Piemontese breed on genetic aspects of beef quality, and no information are currently available on the amount of genetic variations exhibited by these traits.

The study concerning genetic relationship between meat quality traits and the current breeding goal of the Piemontese population is unexplored. Then meat quality traits are currently not included in the Piemontese breeding goal.

This thesis is aimed to study the possibility to introduce, indirectly, meat quality traits among the selected traits. This implies that genetic parameters and heritabilities for all meat quality traits need to be estimated.

Chapter 3 deals with the development and applications of a calibration curve for Near-Infrared spectroscopy (NIRS) aimed to predict chemical and physical composition of Piemontese beef cattle.

Chapter 4 deals with the estimation of genetic parameters and heritabilities for physical meat quality traits, measured in laboratory, of Piemontese young bulls using a linear Animal model.

Chapter 5 deals with the estimation of heritabilities and additive genetic variations for NIRS-predicted traits.

Chapter 6 deals with estimation of genetic and phenotypic correlations for beef quality traits. Bivariate traits estimation of genetic (co)variances components were estimated using Bivariate Animal model.

Chapter 7 deals with the estimation of genetic (co)variances and correlations among meat quality traits and performance traits measured on station for Piemontese beef cattle.

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CHAPTER 2

Materials and methods

2. MATERIALS AND METHODS

2.1 Animals

Data used in this study were from 1080 Piemontese young bulls which were selected within the progeny of 139 AI sires. Young bulls were fattened in 166 different fattening farms, basically fed with restricted concentrate based on corn meal, soy meal, barley meal, sugar beet pulp, wheat bran, molasses, mineral and vitamin supplements and *at libitum* hay. Animals were slaughtered at the same commercial abattoir from March 2005 to September 2007 (211 slaughter groups, mean ± SD: 6 ± 3 bulls per group), and they were 527 ± 66 d old. After slaughtering the average hot carcass weight ± SD was 428 ± 46 kg.

Carcasses were graded for fleshiness using the EU grading system (Commission of European Communities, 1982). **(S)EUROP** classification is a means of describing beef and sheep carcasses in terms that indicate the suitability and value of a carcass for a particular end usage (e.g. retail sale, catering, processing, etc). The class of 'S' has been introduced for double-muscled animals.

The main elements of the schemes, which are similar for beef and sheep, are weight, conformation and fatness. Meat buyers use the language of classification to specify their requirements. Within any purchasing scheme, classification is linked to price and it generally provides the basis for the transaction between the farmer and abattoir.

In this thesis SEUROP classification has been rearranged into scores (EUS: S+ = 6.33, S = 6, S- = 5.66, E+ = 5.33, E = 5, E- = 4.66, U+ = 4.33, U = 4, U- = 3.66) for statistical analyses.

2.2 Data collection

Individual samples of *Longissimus Thoracis* muscle were collected 24 h after slaughtering, and were taken between the 5th and 6th thoracic vertebra. After collection, each sample was immediately weighed and vacuum-packaged. For assessment of beef quality, all samples were transferred to the meat laboratory in the Department of Animal Sciences of the University of Padova using a portable chilling device at 4 °C. At arrival, the samples were stored in a chilling room at 4 °C for 8 ± 2 d.

2.3 Near Infrared Reflectance Spectroscopy methodology

Spectroscopy is the study of the interaction between radiation (electromagnetic radiation, or light, as well as particle radiation) and matter. Spectroscopy is often used in physical and analytical chemistry for the identification of substances through the spectrum emitted from or absorbed by them.

Near infrared (NIR) Reflectance Spectroscopy is the subset of spectroscopy that deals with the near-infrared region of the electromagnetic spectrum (from about 750 nm to 2500 nm) . It examines the reflected light and reveals how much energy was absorbed at each wavelength. Typical applications include pharmaceutical, medical diagnostics, food and agrochemical quality control. As with all spectroscopic techniques, it can be used to identify compounds or investigate sample composition.

NIR methodology is ground on selective absorption properties, proper to infrared region, of chemical components of a sample. The sum of these properties, combined with radiation dispersion properties (radiation-scattering) of the sample, determines the reflectance. Infrared reflectance contains information concerning the chemical composition of the matter, these information could be extracted treating adequately the reflectance data.

Firstly, the procedure consisted in calculating the reflectance in two different wavelengths, usually the maximum and the minimum of the absorption point, respectively, of the analyzed component. The ratios of them, calculated in different samples, could be correlated with the concentration of one of the chemical components of this sample. This correlation is developed in an equation useful for predicting the concentration of a chemical component directly from the reflectance values (AA.VV., 1989).

This can be done with a monochromatic beam, which changes in wavelength over time, or by using a Fourier transform instrument to measure all wavelengths at once. From this an absorbance spectrum can be produced showing at which wavelengths the sample absorbs. Analysis of these absorption characteristics reveals details about the molecular structure of the sample. This technique works almost exclusively on samples with covalent bonds.

Multivariate (multiple wavelength) calibration techniques (e.g., principal components analysis or partial least squares) are often employed to extract the desired chemical information from the reflectance data. Careful development of a set of calibration samples and application of multivariate calibration techniques is essential for near infrared analytical methods.

In the NIR spectroscopy Instrumentation there is a source, a detector, and a dispersive element (such as a prism, or more commonly a diffraction grating) to allow the intensity at different wavelengths to be recorded. Depending on the sample, the spectrum can be measured in transmission or in reflection. The phenomenon In the second case is named *diffuse reflectance*.

Diffuse reflectance relies upon the focused projection of the spectrometer beam into the sample where it is reflected, scattered and transmitted through the sample material (figure1). The back reflected, diffusely scattered light (some of which is absorbed by the sample) is then collected by the accessory and directed to the detector optics.

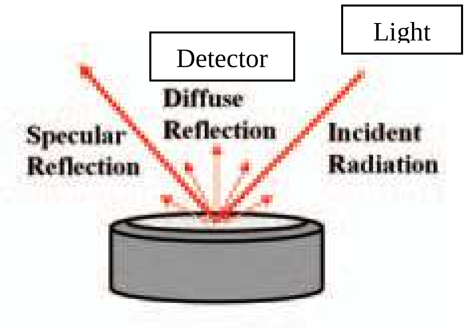

Figure 1: incident radiation, diffuse reflection, specular reflection.

We express diffuse reflectance (*R*) using a logarithmic scale, Log (1/*R*), where the minimum value is 0, the maximum value is 2. R is correlated with the concentration of the chemical component (*c*) according to Beer-Lambert law:

$$log(1/R) = kc$$

where *k* is a factor that considers the absorbance (figure2).

The combination of bands is developed by an interaction between two or more simultaneous vibrations, and the result frequencies is the sum of the fundamental multiple frequencies (Osborne, 2000).

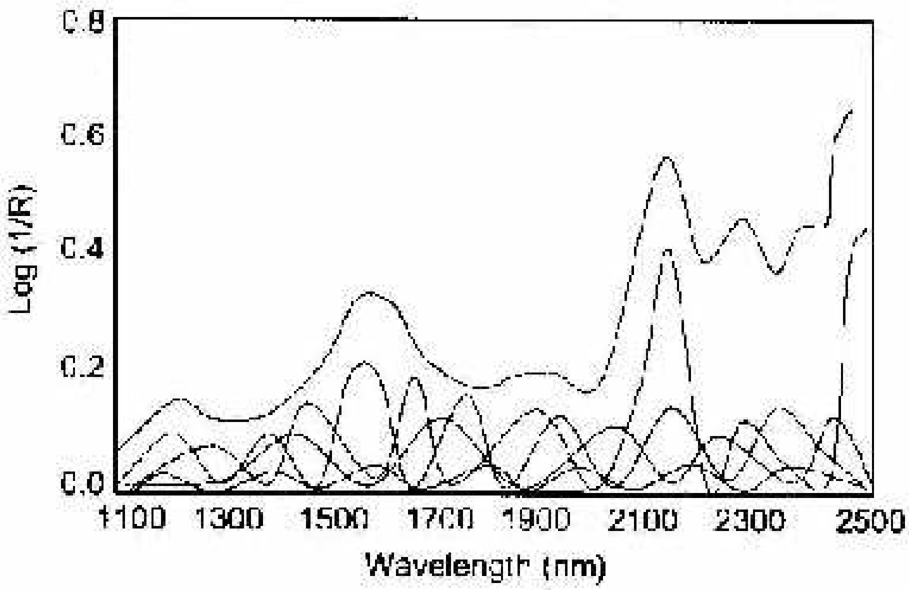

Figure 2: spectrum of a minced cereal, and some absorbance of their components.

2.4 Physical analyses

Drip loss percentage (**DL%**), during the conservation at 4° C for 8 days, was calculated as [(the difference between the sample weight at collection and the sample weight after 8 days ripening/sample weight at collection) * 100].

Meat color was measured on five positions, after removing a 1 to 2-cm slices from the surface of the sample, and after 1-h of exposing the samples to air at 4°C (ASPA, 1996), with a Minolta CM-508 Spectrophotometer equipped with a D65 illuminant, according to the method of CIE (1976).

A *Lab* color space is a color-opponent space with dimension ***L*** for luminance and ***a*** and ***b*** for the color-opponent dimensions, based on nonlinearly-compressed CIE XYZ color space coordinates. With "Lab" color spaces we create a space which can be computed via simple formulas from the *XYZ* space, but is more perceptually linear than *XYZ*. *Perceptually linear* means that a change of the same amount in a color value should produce a change of about the same visual importance. When storing colors in limited precision values, this can improve the reproduction of tones.

Reflectance measurement closely relates to what the eye and brain see. In addition, the procedure is rapid and relatively easy. Reflectance measurements are affected by muscle structure, surface moisture, fat content and pigment concentrations.

- Lightness (**L***) is measured as the amount of incident light reflected by a surface, ranged between 0 (Black) and 100 (white).
- Redness parameter (**a***), where negative values represent green and positive values represent red color.
- Yellowness parameter (**b***), where negative values represent blue and positive values represent yellow color.

In opponent color spaces, such as CIE *L*a*b** (CIELAB) hue may be computed together with saturation (or chroma) by converting a color's chromaticity coordinates from rectangular coordinates into polar coordinates. Hue is the angular component of the polar representation, while chroma is the radial component.

- Hue angle (**H***) value is determined as arctangent (a*/b*) x [360°/(2 x 3.14)].
- Chroma or saturation indexe (**C***) value is determined as $\sqrt{(a^{*2}+b^{*2})}$.

Cooking loss percentage (**CL%**) was measured using 2-cm thick steaks sealed in a polyethylene bag and heated in a water bath to an internal temperature of 75 °C for 55 min (ASPA, 1996). CL% was calculated as the ratios[(difference between the steak weight before cooking and the steak weight after cooking) / steak weight before cooking] * 100.

Shear force (**SF**), we used a mechanical measure for texture analysis of cooked meat in water bath, measures were obtained on five cylindrical cores of 1.13 cm in diameter taken parallel to muscle fibers. The core samples were obtained from the steaks used to determine cooking loss. Shear force was measured by a TA-HDi Texture Analyser (Stable Macro System) with a Warner-Bratzler shear attachment, 100-kg load cell and crosshead speed of 2 mm/s, and interpreted using texture expert software (ASPA, 1996).

2.5 Chemical analyses

pH was measured on a fresh side of the sample, at five random positions, with a pH-meter (Basic 20, Crison) using a penetrating electrode containing a temperature sensor. The pH-meter was calibrate a priori with two buffer solutions: at pH 4.00 and 7.00).

Ash was determined by incinerating samples at 550°C until to have a clear ash, in accordance with standards of the Association of Official Analytical Chemists (AOAC, 2000).

Crude protein was calculated by subtracting the sum of ash (%) and ether extract (%) from 100 %.

Cholesterol content was obtained by high performance liquid chromatography (HPLC) according to Casiraghi et al. (1994). The sample (0.5 g) was saponified using 5 ml ethanol 96% and 2 ml KOH 50%. The mixture was incubated in a water bath at 70 °C for 10 min and kept in agitation. An extraction by 35 ml hexane/ether diethyl was performed. Upon cooling, 20 ml distilled water was added, after that a centrifugation was applied for the separation of the two phases. The organic phase on the top was extracted and heated to dryness in a water bath at 35 °C. The dried extract was resuspended in 5 ml HPLC mobile phase. Cholesterol content of the extract was quantified by HPLC.

Hydroxyproline is one of three predominant amino acids constituting ***collagen***. Therefore, the collagen content were determined by the determination of the Hydroxyproline content using a Hydroxyproline-kit according to Teerlink et al. (1989) and Mazzi et al. (1990); with previous acid hydrolysis (HCl 6 N) and filtration. 0.5 grams of freeze-dried homogenized meat was put in a 30 ml tube and HCl 6N (30 ml) solution was added. The solution was mixed with a vortex 3 times every 60 min, and after that kept overnight in a drying oven at 103.5 °C overnight. The day after, the mixture was filtrated with a Millipore (0.45 µm) filter and was read with a hydroxyproline-kit.

Ether extraction (**EE**) was carried out by continuous extraction by petroleum ether, at heat, on 0.5 grams of freeze-dried sample, using a Foss soxtec system in accordance with submersion method of the standards of the Association of Official Analytical Chemists (AOAC, 2000). This method permits to extract crude lipid content.

Fatty acid (**FA**) profiles were determined by gas-chromatography technique after Folch extraction (Folch et al., 1957), at cooling.

The gas chromatographic analysis, after a trans-estherification of the extracted, was performed on a Shimadzu GC 17A equipped with an Omegawax 250 capillary column, length 30 m, internal diameter 0.25 mm (SUPELCO Bellafonte, PA, USA Cod.24136), and a FID detector.

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CHAPTER 3

Use of Near Infrared Reflectance Spectroscopy for prediction of meat quality traits

ABSTRACT:

The aim of this chapter was to develop a calibration curve for NIR spectroscopy to predict carcass components in Piemontese beef cattle. Data used in this study were from 148 Piemontese young bulls. These bulls were randomly selected from a pool of 1080 animals. On fresh *Longissimus thoracis* samples the chemical composition (pH, dry matter, ether extract, ash, crude protein, cholesterol and collagen), fatty acid profiles and physical properties (cooking loss, drip loss, shear force and color parameters) were determined. Absorption spectra were made in reflectance mode between 1,100 and 2,498 nm of the near-infrared region at intervals of 2 nm. The resulting spectra were stored as absorbance, log (1/R), on WINISI II version 1.02 software. The Best calibrations tested by cross-validation showed coefficient of determination in calibration (R^2) and standard errors of cross validation (SECV) of 0.92 and 0.21% (dry matter), 0.99 and 0.20% (ether extract), 0.86 and 0.09% (ash), and 0.99 and 0.20% (crude protein).

Calibrations for all other chemical components showed very poor predictive ability. The calibration was most accurate for the major fatty acids with the exception of linoleic acid (C18:2n-6ct), arachidonic acid (C20:4n-6), PUFA, ω 3 and ω 6 where R^2 values were 0.69, 0.02, 0.71, 0.74 and 0.66, respectively.

Physical traits were not successfully predicted, likely attributable to the low variation or to the limited number of samples used in this study.

Key Words: NIR spectroscopy, Meat quality, Piemontese beef cattle, Regression.

INTRODUCTION

Amongst the instrumental methods tested for predicting eating meat quality, there are several spectroscopic methods. In Northern Ireland studies, near infrared reflectance spectroscopy gave useful predictions for compositional aspects on pork meat (dry matter, crude protein, intramuscular fat). Correlations with juiciness were high, but correlations with eating quality scores for tenderness and flavour were poor (Park *et al.,* 2002).

Near infrared reflectance (NIR) spectroscopy has become widely used in the food and agricultural industries to measure the chemical constituents of animal and plant tissues such as water, protein and fat contents (Burns and Ciurczak, 1992). It is a fast, non-destructive technique for objective and simultaneous analysis of these constituents of organic substances, and moreover it has a lower cost per analysis compared to the analytical laboratory methods. The application of NIR spectroscopy for the prediction of quality characteristics in foods can be useful in determining the chemical and physical attributes of meats (Windham and Morrison, 1998).

Hildrum et al. (1994) reported that the NIR spectra of beef muscles change during the ageing process, reflecting those observed in meat color, tenderness, flavor and juiciness; other studies showed that NIR spectroscopy might be able to predict variation in tenderness of beef steaks. Further applications include the quantitative prediction of textural and sensory properties of beef meat (Venel et al., 2001; Prieto et al., 2006; Yongliang et al., 2003). Using NIR to predict fatty acid composition and cholesterol levels in meat has also received increased interest considering their implications for human health and product quality (Wood et al., 2004). Laboratory methods to determine the chemical and physical components of meat are very expensive and time-consuming.

The aim of this study was to develop and validate a calibration curve for NIR spectroscopy to predict chemical, physical and fatty acids compositions in Piemontese beef cattle.

3.2 MATERIALS AND METHODS

3.2.1. Animals

Data used in this study were the chemical composition, fatty acid profiles and physical properties of meat samples collected from 148 Piemontese young bulls. These bulls were progeny of 59 sires selected randomly from a pool of 1080 animals. Animals were sampled from 82 fattening farms feeding an *ad libitum* diet based on corn meal, soybean meal, barley meal, sugar beet pulp, wheat bran, molasses, mineral and vitamin supplements, and hay. Animals were slaughtered at a single commercial abattoir from March 2005 to September 2007.

3.2.2 Tissue samples

Individual samples of *Longissimus thoracis* muscle were collected 24 h after slaughter between the 5th and 6th thoracic vertebra. Samples were weighed, vacuum-packaged and refrigerated for a period of 8 ± 2 d at 4 °C, and then analyzed for meat quality characteristics in the meat laboratory of the department of Animal Sciences at the University of Padova.

3.2.3 Chemical and Fatty Acids Analyses

The pH was measured (see Chapter 2). Sub-samples of 100g were freeze-dried. Chemical analyses (cholesterol, crude protein, ether extract, fatty acid profiles) were determined in accordance with standards of the Association of Official Analytical Chemists (AOAC, 2000) (see chapter 2).

The fatty acid composition of meat products has become increasingly important in recent years, because of the association between the fatty acid composition of dietary fat (and in particular saturated fats) and cardiovascular and other lifestyle diseases humans.

Dietary advice in Europe is to decrease the fat content of the diet, maintain the ratio of the polyunsaturated to saturated fatty acids (P:S) at about 0.4 and to increase the intake of n-3 polyunsaturated fatty acids (PUFA) relative to n-6 PUFA (WHO, 2003).

3.2.4 Physical Analyses

Drip loss, cooking loss, shear force and color were computed as described in the chapter 2.

3.2.5 Near Infrared Reflectance Spectroscopy measurements

Minced fresh samples were used for NIR spectroscopy analyses. Measurements of the NIR spectra were obtained using a FOSS NIR Systems model 5000 with small ring cup cells. Measurements were made in reflectance mode between 1,100 and 2,498 nm of the near-infrared region at intervals of 2 nm. All spectra were collected in duplicate and the average spectrum was used for NIR analysis. The resulting spectra were stored as absorbance, *log (1/R)* where R is reflectance, on WINISI II version 1.02 software (InfraSoft International, Port Matilda, PA, USA).

3.2.6 Calibrations and validations

The association of NIR spectroscopy measures with the chemical composition and physical properties of the samples, in this study, was derived from WINISI software. With WINISI, mathematical transformations are applied to reduce noise due to the interferences between absorption bands, and to minimize deviations caused by the physical form of the sample; the mathematical treatments also provide a best interpretation of spectral information.

Formally, derivatives and smoothing are performed on spectra to optimize accuracy. First and second derivatives were taken and were denoted by 1,4,4 and 2,5,5, respectively. The first number indicates the derivative order. The second number (gap) denotes interval of points from which the derivative was calculated; a gap of 4, for example, indicates that the derivative is calculated between data point *n* and the point *n+3*. The third number refers to the smoothing by which data points are averaged with their neighbors in a spectra, thereby enhancing low absorbance peaks; a smoothing of 4 means that the average was calculated between the data point and 4 neighbor points on spectra.

Cross-validation was performed during model development. The data set was partitioned into four subsets. Three subsets were used for calibration while the remaining subset was used to validate the results of the calibration analysis. This process was repeated such that each subset was used once as the validation data.

Calibrations were performed by modified partial least squares (MPLS) regression. The accuracy of calibration equations was evaluated with: coefficient of determination (R^2), which determines variability expressed by calibration equations; standard error of calibration (SEC), which corresponds to the mean square deviation between analytical data and the estimated values in calibration; coefficient of determination of cross validation (R^2_{cv}); and, standard error of cross validation (SECV), calculated by the average between the standard error of the four cross validation analyses.

The optimal number of factors used to obtain the calibration equation model (MPLS terms) for the different constituents was that which produced minimum overall error between modeled and reference values (SECV) and high R^2 values.

3.3 RESULTS AND DISCUSSION

3.3.1 Analyses

Summary statistics for the chemical composition and cholesterol content of the samples of fresh *Longissimus Thoracis* muscle used for calibration (n=148) are shown in Table 1.

Ether extract (%) had the highest coefficient of variation (CV=60%) and a SD of 1.31. For pH, crude protein %, and ash the CV was very low (1, 2.4 and 3.9 %, respectively), and the SD had a narrow range of variation (0.05, 0.58 and 0.04, respectively).

Descriptive statistics of chemical composition appeared consistent with the values reported for Piemontese bulls by Russo and Preziuso (2002).

Table 1. Summary Statistics for chemical composition, cholesterol and collagen contents of fresh *Longissimus Thoracis* muscle (n=148).

Trait	Mean	Min	Max	S.D.	C.V (%)
Ph	5.50	5.34	5.74	0.05	0.98
Dry matter, %	27.87	25.84	33.31	1.22	4.36
Ether extract, %	2.2	0.01	9.21	1.31	59.68
Ash, %	1.11	1.00	1.27	0.04	3.89
Crude protein, %	24.58	23.09	26.31	0.58	2.37
Cholesterol, mg/100g	56.35	50.45	70.07	3.20	5.68
Collagen, mg/100g	18.43	9.02	36.81	5.29	28.74

Table 2 summarizes the results obtained for FA content. The CV for the FA ranged from 33 to 89%.

The predominant saturated fatty acids (SFA) was C14:0 (myristic acid), C16:0 (palmitic acid) and C18:0 (stearic). Of the total SFA, 48 % were represented by palmitic acid (16:0), 45 % were represented by stearic acid (18:0) and 4 % were represented by myristic acid (14:0). SFA represented 47 % of the total fatty acid (TFA).

They are recognized to influence plasma cholesterol, though stearic acid (18:0) is regarded as neutral in this regard and palmitic (16:0) is not hypercholesterolemic if the diet contains high levels of linoleic acid (18:2n-6; Clandinin *et al.* 2000; Yu *et al.* 1995). Myristic acid (14:0) is regarded as more potent than palmitic acid (16:0) in raising plasma lipids (Zock *et al.* 1994).

The main monounsaturated fatty acid (MUFA) was oleic acid (C18:1) and accounted for 93 % of total MUFA. With the remainder of the MUFA occurring mainly as *cis* (C18:1n9ct) and *trans* (C18:1n11tr) isomers of oleic acid. MUFA represented 37 % of the total fatty acid (TFA).

Linoleic acid (C18:2n-6) was the main polyunsaturated fatty acid (PUFA), and accounted for 81 % against the arachidonic acid (C20:4n-6) which accounted for 11 % of the total PUFA. PUFA represented 16 % of the total fatty acid (TFA).

The PUFA and MUFA are generally regarded as beneficial for human health. There is much interest in CLA. Recent studies have confirmed that the main CLA isomer in beef is *cis*-9, *trans*-11 and is mainly associated with the neutral lipid fraction (typically representing 72-90 % of total CLA isomers in muscle lipid).

It is also established that the majority of CLA found in muscle is synthesized from C18:1-n11 *trans* (vaccenic acid) via delta-9 desaturase in the tissue rather than directly from the rumen (Corl *et al.* 2003).

Dannenberger et al. (2004) reported 10 isomers of CLA in beef with *cis*-9, *trans*-11 CLA representing approximately 70% of total CLA isomers.

Biological effects of two of these isomers, *cis*-9 and *trans*-11 CLA, have been extensively investigated and anticarcinogenic and antiatherogenic effects of *cis*-9, *trans*-11 have been documented.

This study was less successful in improving the MUFA+PUFA:SFA ratio. This relates to the competition between them for deposition in muscle lipids (in particular in phospholipids).

As the content of SFA increase faster with increasing fatness than does the content of PUFA, the relative proportion of PUFA and the PUFA:SFA ratio decrease with increasing fatness.

The reason is that the Piemontese beef breed is characterized by less fat deposition, and we know that there is a strong negative relationship between fatness and this ratio.

Table 2. Summary statistics for the fatty acids composition of fresh *Longissimus Thoracis* muscle (n=148).

Trait	Mean[4]	Min	Max	S.D.	C.V (%)	% TFA[5]
C14:0 (myristic)	3.62	0.16	20.56	2.95	81.31	1.75
C16:0 (palmitic)	45.09	5.49	226.7	31.16	69.11	22.71
C18:0 (stearic)	40.58	5.31	137.21	24.03	59.21	21.16
SFA[1]	91.68	12.07	394.03	58.52	63.83	46.90
C16:1	3.59	0.17	23.79	3.17	88.17	1.70
C18:1n-9ct (*cis*-oleic)	63.96	5.81	333.09	47.55	74.34	31.40
C18:1n-11tr (*vaccenic*)	6.42	0.76	25.37	4.08	63.5	3.37
MUFA[2]	75.47	6.97	387.27	55.23	73.18	37.27
C18:2n-6 (linoleic)	11.8	4.1	27.3	4.7	39.9	12.75
C20:4n-6 (arachidonic)	2.39	0.04	10.8	1.09	45.70	1.67
PUFA[3]	25.17	5.92	80.1	8.65	34.37	15.82
ω 3	0.82	0.06	3.61	0.44	53.73	0.47
ω 6	23.4	5.48	76.9	7.93	33.91	14.85
(MUFA+PUFA)/SFA	2.29	0.48	9.6	1.35	58.97	1.24

[1] Total saturated fatty acids.

[2] Total Monounsaturated fatty acids.

[3] Total Polyunsaturated fatty acids.

[4] mg/1000 g of fresh meat.

[5] Percentage of total FA.

Generally, the data on fatty acid compositions were more variable, as suggested by their higher CV, and thus appear better suited for the calibration procedure.

Table 3 provides descriptive statistics for L*, a*, b*, Hue*, Chroma*, cooking loss, drip loss and shear force of fresh samples. The physical traits had CV ranging from 9 to 45 %. Drip loss percentage appeared higher (3.86 %) in this study than that (2.41 %) found by Russo et al. (2002).

Table 3. Summary statistics for physical traits of fresh *Longissimus Thoracis* muscle (n=148).

Trait[1]	Mean	Min	Max	S.D.[2]	C.V (%)[3]
L^*	33.57	25.82	44.54	3.45	10.29
a^*	16.53	11.11	22.80	2.43	14.72
b^*	14.61	9.36	19.91	2.25	15.38
H^*	41.42	29.63	53.19	3.86	9.33
C^*	22.12	15.52	30.23	2.98	13.47
CL, %	23.80	15.45	31.25	3.56	14.95
DL, %	3.86	1.39	16.45	1.72	44.54
SF, kg	2.69	1.32	4.90	0.56	21.61

[1] Color parameters: L* : lightness; a* : redness; b* : yellowness; H* : Hue angle, arctangent (a*/b*); C* : saturation index (chroma), √(a*2+b*2). CL, cooking loss; DL, drip loss; SF, shear force.

[2] Standard deviation.

[3] Coefficient of variation expressed in percentage.

3.3.2 NIRS calibration results

Calibration and validation statistics results for the best NIRS calibrations developed for predicting Piemontese beef chemical composition are shown in Table 4. Even the indexes of certainty (R^2_{cv}) and uncertainty (SECV) for the cross validation purposes, the standard error of calibration (SEC) and coefficient of determination in calibration (R^2) are presented.

The values of these statistics are indicators of the relative merit of the best equations generated.

For chemical composition the best calibration, the highest R^2 and R^2_{cv} and lowest SEC and SECV, was obtained with a second order derivative.

Table 4. Statistics results for the best NIRS calibrations developed for predicting Piemontese beef chemical composition.

Trait	N[a]	SEC[b]	R^{2c}	SECV[d]	R^2_{cv} [e]
Chemical composition					
pH	135	0.04	0.23	0.04	0.01
Dry matter, %	140	0.24	0.96	0.35	0.91
Ether extract, %	139	0.10	0.99	0.13	0.99
Ash, %	142	0.03	0.44	0.03	0.38
Crude protein, %	142	0.22	0.85	0.33	0.64
Cholesterol mg/100g	145	2.61	0.18	2.90	0.01
Collagen mg/100g	139	2.70	0.56	3.05	0.44

[a] Number of samples in calibration (after outlier elimination).

[b] SEC = standard error of calibration.

[c] R^2 = coefficient of determination in calibration.

[d] SECV = standard error of cross validation.

[e] R^2_{CV} = coefficient of determination of cross validation.

Chemical composition showed an R^2 ± SEC ranging from 0.18 ± 2.61 for cholesterol to 0.99 ± 0.10 for ether extract (%), and R^2_{cv} ± SECV ranging from 0.01 ± 0.04 for pH and 0.01 ± 2.90 for cholesterol (%) to 0.64 ± 0.33 for crude protein (%).With the exception of ether extract and dry matter (%) which presented higher values of R^2 ± SEC (0.99 ± 0.10 and 0.96 ± 0.24, respectively) and higher values of R^2_{cv} ± SECV (0.99 ± 0.13 and 0.91 ± 0.35, respectively). Prediction equations for dry matter and ether extract were well calibrated.

Calibration equations for ash had poor performance (R^2 ± SEC of 0.44 ± 0.03 and R^2_{cv} ± SECV of 0.38 ± 0.03) because near-infrared radiations do not interact with pure minerals or inorganic compounds as ionic forms and salts (Shenk and Westerhaus, 1995).

Likewise, here was no satisfying calibration equation for pH (R^2 ± SEC of 0.23 ± 0.04 and R^2_{cv} ± SECV of 0.01 ± 0.04), which is likely due to the very low variability for this trait (less than 1 % of CV).

Furthermore, no useful regression equation was obtained for collagen (mg/100g) content (R^2 ± SEC of 0.56 ± 2.7 and R^2_{cv} ± SECV of 0.44 ± 3.05); this was in agreement with results of Calvo et al. (1997), Alomar et al. (2003), and Prieto et al. (2006).

Calibration equation for cholesterol was also not sufficient (R^2 ± SEC of 0.18 ± 2.61 and R^2_{cv} ± SECV of 0.01 ± 2.9) to obtain an accurate prediction.

Calibration and validation statistics results for the best NIRS calibrations developed for predicting Piemontese beef fatty acid profiles are shown in Table 5. Even the indexes of certainty (R^2_{cv}) and uncertainty (SECV) for the cross validation purposes, the standard error of calibration (SEC) and coefficient of determination in calibration (R^2) are presented.

For fatty acid compositions the best calibrations, the highest R^2 and R^2_{cv} and lowest SEC and SEC, was obtained applying the first derivative.

Table 5. Statistics results for the best NIRS calibrations developed for predicting fatty acid profiles in Piemontese beef cattle.

Trait	N[a]	SEC[b]	R^{2c}	SECV[d]	R^2_{cv} [e]
Fatty acids					
C14:0 (myristic)	130	0.53	0.92	0.57	0.89
C16:0 (palmitic)	134	3.91	0.97	4.77	0.96
C18:0 (stearic)	137	4.29	0.96	5.13	0.94
SFA[1]	134	6.97	0.98	8.15	0.97
C16:1	140	0.58	0.93	0.73	0.89
C18:1n-9ct (*cis*-oleic)	134	4.89	0.98	6.06	0.97
C18:1n-11tr (*trans*-oleic)	135	1.02	0.89	1.05	0.88
MUFA[2]	132	4.50	0.99	5.87	0.98
C18:2n-6 (linoleic)	144	3.15	0.69	3.27	0.67
C20:4n-6 (arachidonic)	143	0.73	0.02	0.73	0.01
PUFA[3]	140	3.55	0.71	3.73	0.68
Ω 3	140	0.19	0.74	0.19	0.72
Ω 6	140	3.43	0.66	3.63	0.62
(MUFA+PUFA)/SFA	136	0.16	0.98	0.20	0.96

[a]Number of samples in calibration (after outlier elimination).

[b]SEC = standard error of calibration.

[c]R^2 = coefficient of determination in calibration.

[d]SECV = standard error of cross validation.

[e] R^2_{CV} = coefficient of determination of cross validation.

Fatty acid profiles showed an R^2 ± SEC ranging from 0.02 ± 0.73 for arachidonic acid (C20:4n-6) to 0.99 ± 4.5 for MUFA, and R^2_{cv} ± SECV ranging from 0.01 ± 0.73 for arachidonic acid to 0.98 ± 5.87 for MUFA.

The calibrations were most accurate for the major fatty acids, in such cases, there appear to be a strong relationship between spectra and analytical data, which indicates accurate predictive ability, with the exception of linoleic acid (C18:2n-6ct), arachidonic acid (C20:4n-6), PUFA, ω3 and ω6 where R^2 values were 0.69, 0.02, 0.71, 0.74 and 0.66, respectively. Maybe it is due to the low number of samples used in the calibration.

Calibration and validation statistics results for the best NIRS calibrations developed for predicting Piemontese beef physical properties are shown in Table 6. For physical traits the best calibrations, the highest R^2 and R^2_{cv} , and lowest SEC and SECV, was obtained applying the first derivative.

Table 6. Statistics results for the best NIRS calibrations developed for predicting Piemontese beef physical properties.

Trait	N[a]	SEC[b]	R^{2c}	SECV[d]	R^2_{cv} [e]
Physical properties					
L*	137	2.08	0.62	2.35	0.51
a*	145	1.82	0.48	1.98	0.40
b*	138	1.88	0.30	1.99	0.23
Hue*	148	2.33	0.39	2.51	0.31
Chroma*	146	1.53	0.83	2.18	0.66
Cooking loss, %	144	3.31	0.10	3.50	0.01
Drip loss, %	145	1.20	0.19	1.27	0.10
Shear force, kg	142	5.09	0.08	5.21	0.03

[a] Number of samples in calibration (after outlier elimination).

[b] SEC = standard error of calibration.

[c] R^2 = coefficient of determination in calibration.

[d]SECV = standard error of cross validation.

[e] R^2_{CV} = coefficient of determination of cross validation.

Calibration equations for physical traits had much poorer performances; $R^2 \pm$ SEC ranging from 0.08 ± 5.09 for shear force (kg) to 0.83 ± 1.53 for chroma, and $R^2_{cv} \pm$ SECV ranging from 0.01 ± 3.5 for cooking loss (%) to 0.66 ± 2.18 for chroma.

These unsatisfied results were also the case in the study of Savenije et al. (2006).

Then no useful regression could be obtained for predicting physical traits of Piemontese beef cattle; other studies have shown that NIR spectroscopy can be used to predict beef shear force (Mitsumoto et al., 1991; Hildrum et al., 1994, 1995; Byrne et al., 1998; Park et al., 1998; Venel et al., 2001; Yongliang et al., 2003) but our results were in contrast with these, where no relation was found between shear force and spectra, with R^2 of 0.20 and R^2_{cv} of 0.12.

These results are probably linked to the insufficient variability for physical traits in our dataset (CV ranging from 10 to 45%), and maybe to the low number of samples used in this study.

3.4 IMPLICATIONS

This chapter demonstrates that NIR spectroscopy is a useful tool to predict, with high accuracy, the composition of fatty acids, dry matter, ether extract in Piemontese beef cattle. Furthermore, this study has shown that NIR spectroscopy could not be used to predict physical properties, cholesterol and collagen contents in Piemontese beef cattle, which has been attributed to low analytical data variations used in calibrations.

Further investigations:

- NIRS technique will be applied to a larger dataset for predicting fatty acids and ether extract compositions of Piemontese beef cattle.
- Estimations of genetic components and heritabilities of fatty acids and ether extract predicted by NIRS methodology will be defined.

LITTERATURE CITED

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CHAPTER 4

Estimation of heritability and additive genetic variations of beef quality traits for Piemontese young bulls

ABSTRACT

The chapter aimed to estimate heritability for meat quality traits of Piedmontese young bulls. A total of 1,080 young bulls, offspring of 139 AI sires, were sampled from 167 fattening farms. Animals were slaughtered at different times at the same commercial abattoir. Carcasses were weighed and scored for fleshiness using the EU grading system. Bulls were 525 ± 44 d old and average carcass weight was 428 ± 43 kg. Individual samples of *Longissimus Thoracis* were collected 24 h after slaughter and held refrigerated at 4 °C for quality analyses. The pH at ageing (8 ± 2 d), beef color parameters (L*, a*, b*, H* and C*), shear force, drip and cooking losses were determined. Pedigree information was provided by the Italian Association of Piedmontese Cattle and included 11,701 animals. Estimation of variance components was based on an univariate linear animal model and was accomplished using Bayesian methodology and the Gibbs sampling integrations. The linear animal model included the non-genetic effects of fattening farms, slaughter age, week of analysis, and hot carcass weight in classes; and included the additive genetic effect of the bull. Marginal posterior distributions of probabilities of additive genetic standard deviations and heritabilities for all traits were obtained. The median of marginal posterior densities was used as a point estimate of heritabilities and additive genetic standard deviations of beef traits. Estimation of heritabilities of meat quality traits for Piemontese beef cattle were relevant ranging from 13 (for redness parameter) to 58 % (for hue angle parameter) .

Key words : Genetic parameters, Bayesian inference, Piemontese beef cattle, Meat quality

4.1 INTRODUCTION

4.1.1 Eating meat quality

Eating meat quality is becoming an increasingly important issue for meat scientists, breeders, consumers, and the meat industry in richer countries. Therefore, in animal breeding extensive interest has been renewed in the carcass characteristics of the double muscled beef cattle, especially due to the fact that consumer demand is moving toward leaner meat.

The double muscling condition in beef cattle was originally considered to be undesirable (Kieffer and Cartwright, 1980), but over time it became accepted and even desirable.

4.1.2 Piemontese breed

The Piemontese breed is highly specialized for beef production due to double muscling (**DM**) inherited condition induced by a specific mutation of Myostatin gene (*mh*) located on Chromosome 2 (Grobet et al., 1998). This phenotype is characterized by greater muscle mass with less fat deposition (Menissier, 1982; Shahin and Berg, 1985), reduced weight of the skeleton (Vissac, 1968), reduced feed intake, and improved feed conversion (Hanset et al., 1987; Arthur, 1995; Cundiff et al., 1996; Wheeler et al., 1996, 1997).

These characteristics in cattle have led to the selection of this phenotype in Europe despite its association with reduced female fertility, susceptibility to respiratory illness, and the need for Caesarian section due to high incidence of dystocia (Hanset, 1991).

Menissier et al., 1982, reported that the Piemontese breed showed less fat and more muscle than the Limousine, Charolaise and Belgian Blue breeds. In a comparison with the Limousine, Simmental, and Belgian Blue the Piemontese breed had a progeny with better carcass grades (Hoving-Bolink et al., 1999; Grundy et al., 2000).

Some researches were achieved on the determination of genetic parameters of carcass and beef quality traits (Mohiuddin, 1993 and Koots et al. 1994a, 1994b). However, few investigations have been conduced on double-muscled cattle breed.

The current Piemontese breeding goals include daily gain, live fleshiness, bone thinness, and direct and maternal calving performance (Albera *et al.*, 2001). No investigations have been conducted for this breed on genetic aspects of beef quality and no information is currently available on the amount of genetic variation exhibited by these traits.

The aim of this study was to estimate additive genetic standard deviations and heritabilities of beef quality traits in Piemontese beef cattle using Bayesian inference.

4.1.3 Bayesian approach

Meat quality analyses are usually performed with small data, mainly because it is expensive to measure a large amount of variables, some of them involving a lot of lab work. Until now, classical statistics has been the usual way of expressing uncertainty in meat quality analysis whereas Bayesian analyses have been mainly applied by animal breeders to complicated genetic problems (Blasco, 2001, a review).

Bayesian inference is based in probabilities, which gives a great flexibility to construct all types of confidence intervals. The generalized use of Bayesian statistics in many fields of science is relatively new. Although Bayesian methods were theorically powerful, they usually led to formulas in which multiple integrals had to be solved in order to perform Bayesian inference.

In a Bayesian context, the objective is to describe the uncertainty about the true value of some parameter using probability as a measure of this uncertainty.

For example, if the parameter of interest is heritability (h^2) of a meat quality trait, the aim of Bayesian inference is to find a probability density function (*or* marginal posterior distribution) of this parameter f ($h^2/\mathbf{y}$), where **y** is the vector of observations.

Once this distribution is obtained, we can give several values of h^2 calculated from the distribution f ($h^2/\mathbf{y}$). We can give the *mode,* which is the maximum of the distribution, or the most probable value of h^2 that we can infer with our data. We can also give the *median,* which has the property that the probability of the true value of h^2 being greater than the median is the same as being smaller. We can give also the mean of the distribution, which has the property of minimizing the risk of the estimation when the loss function is a quadratic one, which is the most common loss function used in statistics (figure 1).

Posterior distributions tend to be normal when the number of data increases. When the distribution is symmetrical, the three values are coincident.

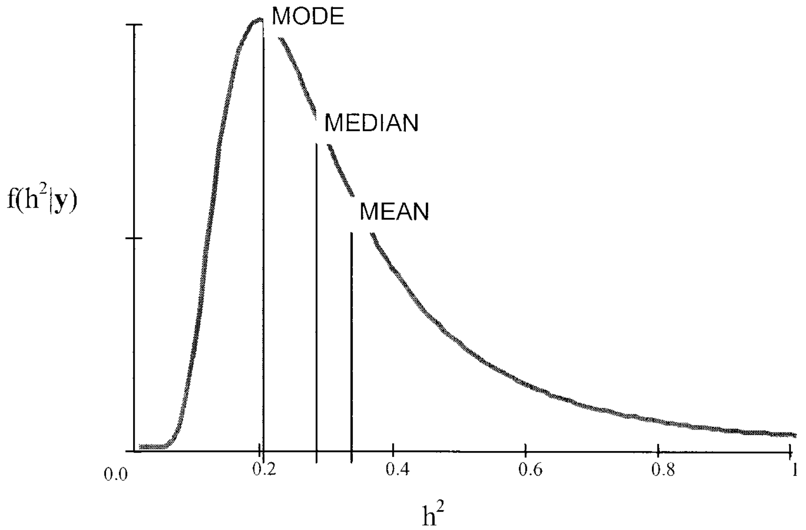

Figure 1. example of a probability density for heritability (h^2) given the data (**y**) and estimates from posterior distribution.

4.2 MATERIALS AND METHODS

4.2.1 Animals

Data used in this study were from 1080 Piemontese young bulls which were randomly selected within the progeny of 139 AI sires. Young bulls were fattened in 167 different fattening farms and slaughtered at the same commercial abattoir from March 2005 to September 2007 (211 slaughter groups, mean ± SD: 6 ± 3 bulls per group). At slaughter animals were 525 ± 44 d old.

After slaughtering, carcasses were graded for fleshiness using the EU grading system (Commission of European Communities, 1982), and weighed: average hot carcass weight ± SD was 428 ± 43 kg. (S)EUROP classification was rearranged into scores for statistical analyses (EUS: S+ = 6.33, S = 6, S- = 5.66, E+ = 5.33, E = 5, E- = 4.66, U+ = 4.33, U = 4, U- = 3.66).

4.2.2 Meat quality traits

Individual samples of *Longissimus Thoracis* muscle were collected 24 h after slaughtering, and were taken between the 5th and 6th thoracic vertebra. After collection, each sample was immediately weighed and vacuum-packaged.

For beef quality assessment, all samples were transferred to the meat laboratory in the Department of Animal Sciences of the University of Padova using a portable chilling device at 4 °C. At arrival, the samples were stored in a chilling room at 4 °C for 8 ± 2 days.

pH, Drip loss, cooking loss, Meat color parameters (L*, a*, b*, C*, and H*), and shear force were determined (see Chapter 2).

4.2.3 Pedigree information

Pedigree file was provided by the Italian Association of Piemontese Cattle (ANABORAPI), and included animals with phenotypic records and all their known ancestors (*11,701* animals).

4.2.4 Mixed linear model

Preliminary analyses, using GLM procedure of SAS package (1990), were carried out aimed to identify non-genetic effects to be included in the univariate mixed linear models for estimating genetic variations and heritabilities of meat quality traits.

For lightness (L*) and redness (a*) the non-genetic effects included in the model were the fattening farm (167 levels), age at slaughter into classes (5 levels), week of the analysis, and hot carcass weight into classes (6 levels). The additive genetic effect of young bull was included.

For cooking loss (CL), drip loss (DL), ph, and shear force (SF) the non-genetic effects included in the model were the fattening farm (167 levels), and the week of the analysis. The additive genetic effect of young bull was included. For Europ classification trait the model used included the non genetic effects of fattening farms (167 levels) and hot carcass weight into classes (6 levels), and The additive genetic effect of young bull was included.

A genetic group, for unknown male and female parents, were adopted in every analysis.

4.2.5 Univariate Bayesian analysis

Estimation of variance components and heritabilities was performed through univariate Bayesian analyses performing numerical integration using the Gibbs sampler tool.

Flat prior distributions were considered for all non-genetic effects, excepted for fattening farm effect. Normal prior distributions were adopted for additive genetic effects and for fattening farm effect. Prior scaled inverted chi-square distributions were assumed for residual, additive genetic variances and for fattening farm effect.

Univariate Bayesian analyses were based on conditional densities and on the scalar form of the Gibbs sampler presented by Wang et al. (1994). Each Bayesian analysis has been carried out generating three Gibbs chains, using iBay software version 1.1.

iBay stands for '*iterative Bayes*', referring to the MCMC (Monte Carlo Markov Chain) algorithms applied to obtain Bayesian inferences.

Size of the chains and burn-in length were chosen by comparing results obtained for two randomly selected sites with chain and burn-in period of different sizes and by subjective inspection of plots of values from the Gibbs chains. The length of the generated chains was 500.000 iterations (*or* samples), and the burn-in period used was 100.000. Samples were saved every 10 iterations.

4.2.6 Assessment of Gibbs chains convergence

Convergence diagnostics were assessed for all variance components and heritabilities of each beef quality trait.

Three separate Gibbs chains of 500,000 cycles each one were generated. Based on the trace plots and running mean plots of samples obtained from 500,000 cycles for the three chains, it was determined that 100,000 cycles was a sufficiently long burn-in period. The length of the burn-in chosen was enough to eliminate the effect of the different starting values.

After discarding the first 100,000 cycles within each chain as 'burn-in' , each set of the remaining 400,000 cycles within each chain were subsequently saved every 10 cycles to determine the marginal posterior density of each variance component and to determine the posterior medians and standard deviations of each parameter.

It was important to check the convergence of the Gibbs Sampler iterations and to get the following plots using R and BOA:

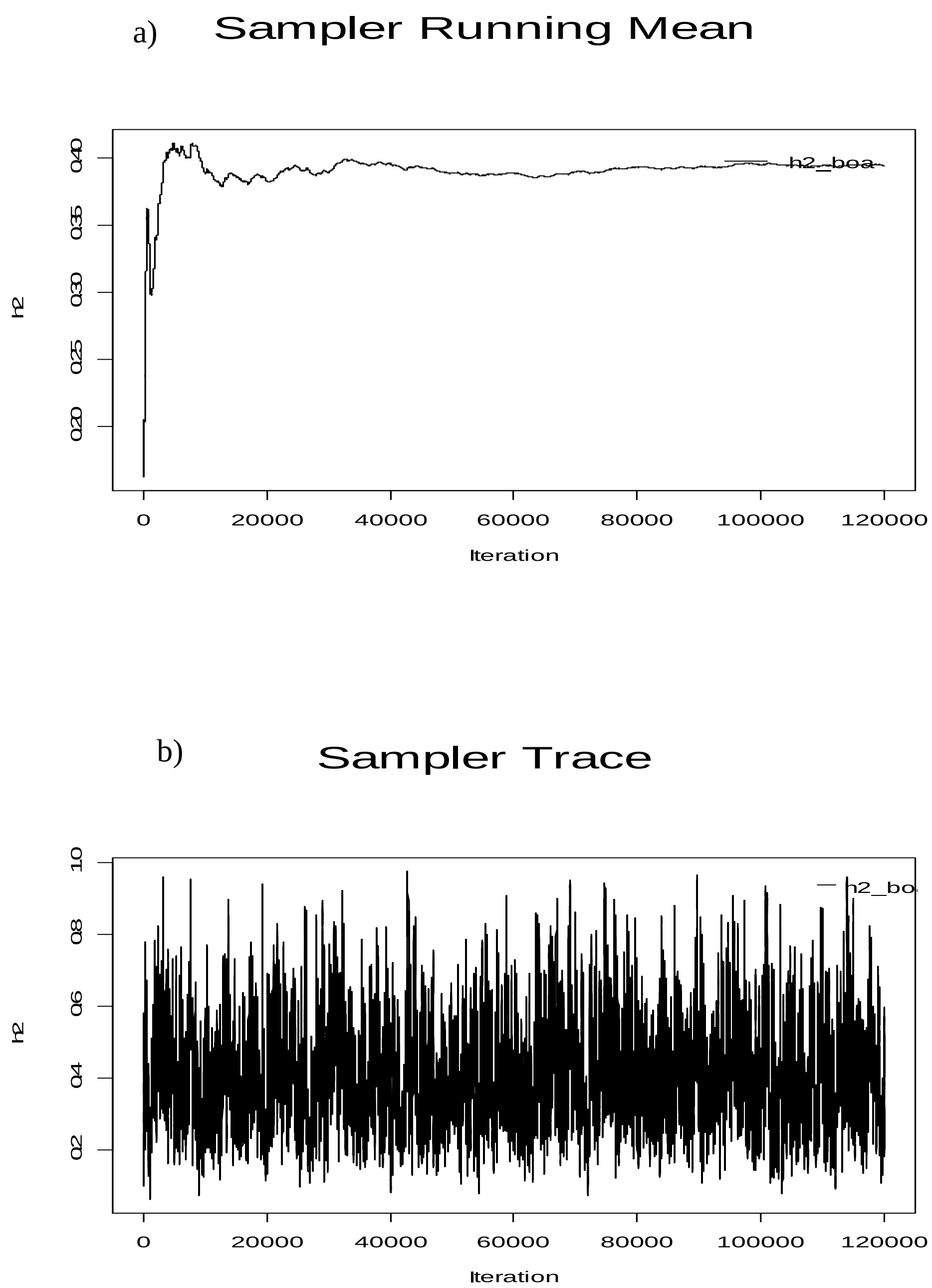

Figure 2. a) Running mean, explains the convergence of cycles; b) sampler trace. the parameter used in this example is h^2 of drip loss trait.

The median of marginal posterior densities was used as a point estimate of additive genetic standard deviations and heritabilities of all traits.

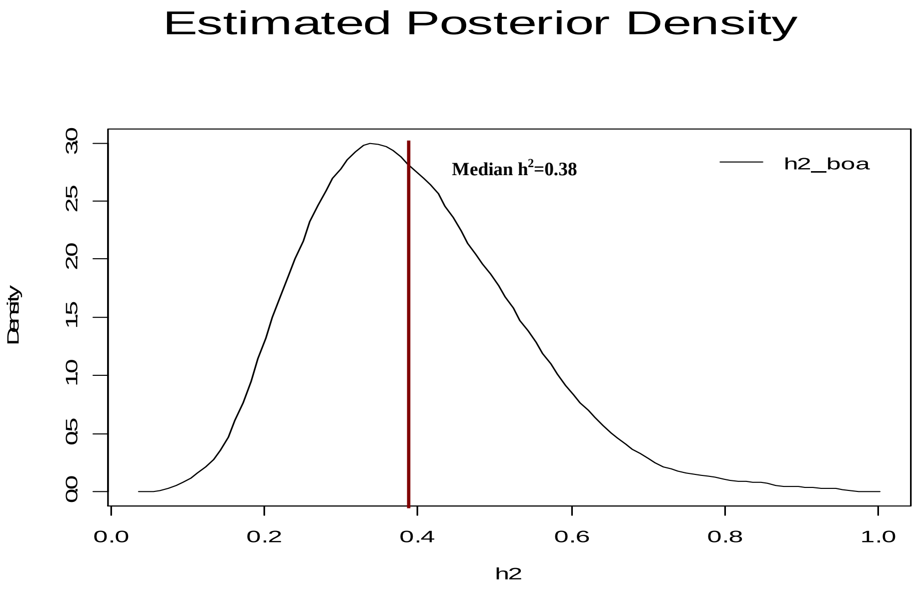

Figure 3. Median of marginal posterior distribution of heritability (h^2), for drip loss (%) trait.

Other statistics were obtained from the estimated marginal densities, and considered in the discussion:

- fixing h^2 to a value of 10 %, we obtained the posterior probability for values of h^2 greater than 10 % : P(h^2 >10%).
- fixing the posterior probability to a value of 90 %, we obtained the minimum values of h^2 for 90 % of samples : (min $h^2_{P90\%}$).
- additive genetic coefficient of variation CV_a (σ_a /mean) was calculated.

4.3 RESULTS AND DISCUSSION

Summary statistics for beef and carcass traits (n=1080) are shown in Table 1. A very low variation in pH, SA, HCW, L*, and H* (C.V. from 1 to 12%) was observed. Variation of SF, DL, CL, a*, b*, C* and EUS was higher (C.V. from 14 to 34%).

Table 1. Summary statistics for investigated beef quality and carcass traits (n = 1,080).

Trait[a]	Mean	Min	Max	SD	CV%
pH	5.49	5.31	5.81	0.05	1
L*	34.27	25.26	47.95	3.41	10
a*	16.15	7.51	24.14	2.58	16
b*	14.81	5.73	22.54	2.16	15
H*	42.55	29.63	57.72	3.94	9
C*	21.97	9.49	33.01	3.03	14
SF, kg	2.65	1.18	2.28	0.57	21
CL, %	23.93	11.36	36.26	3.62	34
DL, %	4.21	0.96	16.45	1.50	15
HCW, kg	427.66	277.00	576.00	44.57	10
EUS, scores	3.89	2.66	5.00	0.66	17

[a] SF, shear force; CL, cooking loss; DL, drip loss; HCW, hot carcass weight; EUS, Seurop classification into scores.

Color parameters: L* : lightness; a* : redness; b* : yellowness; H* : Hue angle, arctangent (a*/b*); C* : saturation index (chroma), √(a*2+b*2).

Because of the quite different technique used in this study to assess DL, average DL was higher than that reported by Destefanis *et al.* (2003). Also average CL was higher in our data than in that study.

Meat color traits exhibited average values that indicate a darker and more pigmented meat in comparison to results reported by Russo *et al.* (2002).

The low mean value of shear force (2.65 kg) is a good indicator of a complete proteolysis of myofibrillar proteins in muscles from Piemontese breed, which confirm this characteristic in DM beef cattle.

The Piemontese breed, with higher beef aptitude, is characterized by having a low pH of meat after 10 days of ageing, lower drip losses.

4.3.1 Animal model

Preliminary analyses were carried out through general linear model procedure of SAS package (1990) to investigate the effects to be fitted in the models for genetic parameter estimation. Significance of non-genetic effects considered in the analysis of traits and R^2 of models are presented in Table 2.

Table 2. Significance of non-genetic effects considered in the analysis of traits, and R^2 of the model (n=1080)

Trait[a]	Effect[b]				$R^{2,c}$
	FF	SA	HCW	WA	
pH	$P < 0.001$	n.s.	n.s.	$P < 0.001$	0.66
L*	$P < 0.05$	$P < 0.001$	$P < 0.001$	$P < 0.001$	0.47
a*	$P < 0.001$	$P < 0.001$	$P < 0.001$	$P < 0.001$	0.58
B*	$P < 0.001$	n.s.	$P < 0.001$	$P < 0.001$	0.58
H*	$P < 0.001$	$P < 0.001$	n.s.	$P < 0.001$	0.57
C*	$P < 0.001$	$P < 0.01$	$P < 0.001$	$P < 0.001$	0.58
CL, %	$P < 0.05$	n.s.	n.s.	$P < 0.001$	0.55
DL, %	$P < 0.05$	n.s.	n.s.	$P < 0.001$	0.48
SF, kg	$P < 0.05$	n.s.	n.s.	$P < 0.001$	0.48
EUS, scores	$P < 0.05$	n.s.	$P < 0.001$	Not consid	0.37

[a]: SF, shear force; CL, cooking loss; DL, drip loss; HCW, hot carcass weight; EUS, Seurop classification into scores.

Color parameters: L* : lightness; a* : redness; b* : yellowness; H* : Hue angle, arctangent (a*/b*); C* : saturation index (chroma), √(a*2+b*2).

[b]: FF, fattening farm; SA, slaughter age; HCW, hot carcass weight; WA, period or week of meat analysis

[c]: coefficient of determination

All beef quality and carcass traits were significantly affected by the fattening farm (FF) effect, $P<0.05$, and the week of meat analysis (WA) effect, $P<0.001$. The correlation between age at slaughter (SA) and hot carcass weight (HCW) was low (r = 26 %) in this sample. Hence, it was possible to include, when needed, both them in the linear model of analysis.

The SA and HCW effects influenced variation of some traits. The non-genetic effects accounted for proportions of the total variation (R^2) of traits ranging from 37 to 66 %.

The median of marginal posterior densities for h^2, the posterior probability of h^2 greater than 10%, $P(h^2 > 10\%)$, the minimum values of h^2 for 90 % of samples, min $h^2_{P90\%}$, and the additive genetic coefficient of variation, CV_{ga} calculated by the ratios of additive genetic standard deviation and the mean of the trait (σ_a /mean), obtained from Univariate Bayesian analyses are reported in Table 3.

Table 3. Features of the marginal posterior densities of h^2 and additive genetic standard deviations

Trait[a]	h^2 (%)			CV_{ga}, (%)[e]
	Median[b]	P(h^2 >10%)[c]	min $h^2_{P90\%}$[d]	
pH	50	99	29	0.05
L*	29	99	18	5
a*	33	99	19	8
b*	13	64	4	4
H*	58	99	42	5
C*	14	67	4	4
CL, %	8	39	2	3
DL, %	38	99	23	19
SF, kg	14	71	6	7
EUS, points	23	92	11	8

[a] SF, shear force; CL, cooking loss; DL, drip loss; HCW, hot carcass weight; EUS, Seurop classification into scores; Color parameters: L* : lightness; a* : redness; b* : yellowness; H* : Hue angle, arctangent (a*/b*); C* : saturation index (chroma), $\sqrt{(a^{*2}+b^{*2})}$.

[b] median of the posterior density of h^2

[c] posterior probability for values of h^2 greater than 10 %

[d] minimum values of h^2 for 90 % of samples

[e] additive genetic coefficient of variation (σ_a /mean)

Estimated heritabilities obtained in the present study, *median of estimated posterior densities* (Table 3) which was used as the point estimate of h^2, were heterogeneous ranging from 8 (for CL%) to 58 % (for H*).

Low estimated heritabilities were obtained for b*, C*, CL, and SF (ranging from 8 to 14 %) albeit these traits presented C.V. of magnitude comparable to that of traits exhibiting higher heritability estimates. The heritability for SF (14 %) was lower than the average estimate reported by Koots *et al.* (1994) who reviewed literature estimates of genetic parameters for beef traits. That could be due to the different effects included in the model in the two studies.

L*, a*, and EUS exhibited an intermediate estimated heritability values ranging from 23 to 29 %. The estimated heritability for EUS was similar to the estimate reported by Sarti *et al.* (2005), for the Chianina population. Despite the double muscling condition, EUS exhibited exploitable additive genetic variation. The highest heritability estimates were for H^* (58 %), pH (50 %), and DL (38 %).

The posterior probabilities for values of h^2 greater than 10 % were very high for the traits pH, L*, a*, H*, DL, and EUS (from 92 to 99 %). This is in correspondence with the traits with high and intermediate heritabilities.
The $P(h^2 > 10\%)$ were intermediate for b*, SF, and C* (from 64 to 71 %). The lowest probability for value of h^2 greater than 10 % was obtained for CL (39 %).

Few research studies (on small dataset) have been conducted on the genetic variability of color measurement (Aass, 1996; Johnston et al., 2003), but our results were higher than those, h^2 value of L* was 0.29 Vs 0.22 %, and h^2 value of a* was 0.33 Vs 0.15.

The minimum values of heritability for 90 % of samples, min $h^2_{P90\%}$, were very heterogeneous ranging from 4 to 42 %, naturally the high values were in correspondence with the high heritabilities.

The additive genetic coefficient of variation, CV_{ga}, ranged from 0.05 to 19 %, this statistic gives an idea in relation to the weight of the additive genetic variations on the mean of the trait.

These results permits to have an idea about the confidence intervals to take into account for an eventual selection for the meat quality traits of Piemontese breed.

4.4 IMPLICATIONS

Univariate animal models used for estimating the genetic parameters for meat quality traits have been obtained for the Piemontese population taking into account non-genetic effects of fattening farm, age at slaughter, hot carcass weight and week of meat analysis, and the additive genetic effect of young bull.

Estimation of heritabilities of meat quality traits for Piemontese beef cattle were relevant, exploitable for an indirect selection of Piemontese population.

Further investigations aiming:

- to estimate genetic (co)variances among beef quality traits in Piemontese breed and evaluate the genetic and phenotypic correlations among them.
- to evaluate the relationship between these traits and the performance traits currently included in the breeding goal of Piemontese population.

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CHAPTER 5

Estimation of heritabilities for fatty acid profiles predicted by NIRS technique

ABSTRACT

The aims of this chapter were to Predict the fatty acid profiles on a dataset of 733 fresh samples of *Longissimus thoracis* muscle of Piemontese young bulls using the same regression developed by the calibration curve obtained with near infrared reflectance Spectroscopy (NIRS) technique, and to estimate heritabilities and additive genetic variations for NIRS-predicted traits. Young bulls were progeny of 84 AI sires, and were sampled from 137 fattening farms. Animals were slaughtered at different times at the same commercial abattoir. Carcasses were weighed and scored for fleshiness using the EU grading system. Young Bulls were 520 ± 63 d old and average carcass weight was 424 ± 44 kg. Measurements of the NIR spectra were obtained using a FOSS NIR Systems model 5000 with small ring cup cells. Absorption spectra of fatty acids and ether extract were made in reflectance mode between 1,100 and 2,498 nm of the near-infrared region at intervals of 2 nm. All spectra were collected in duplicate and the average spectrum was used for NIR analysis. The resulting spectra were stored as absorbance, *log (1/R)* where R is reflectance, on WINISI II version 1.02 software. Estimation of variance components and heritabilities of fatty acids and ether extract was based on a Univariate mixed animal model and was performed throughout Bayesian methodology and the Gibbs sampling. The linear animal model included the non-genetic effects of fattening farms (FF, 152 levels), slaughter age (SA, 5 classes), and hot carcass weight (HCW, 6 classes); and the additive genetic effect of the bull. Marginal posterior probabilities of additive genetic standard deviations and heritabilities of all traits were obtained. The median of marginal posterior densities was used as a point estimate of heritabilities and additive genetic standard deviations of fatty acids and ether extract. Pedigree file was provided by ANABORAPI and included animals with phenotypic records and all their ancestors; 9,087 animals. Estimate heritabilities obtained in the present study, *median of estimated posterior densities*, were homogeneous ranging from 10 for C14:0 to 23 % for C20:4n-6. This homogeneity in the estimation

of heritabilities maybe could be due to the use of the same equation of calibration for all fatty acids composition.

Key Words: NIRS-predicted traits, fatty acids profile, genetic components, heritabilities, Piemontese beef cattle.

5.1 INTRODUCTION

The fatty acid composition of meat products has become increasingly important in recent years, because of the association between the fatty acid composition of dietary fat (in particular saturated fats) and cardiovascular and other lifestyle diseases humans. Fat content and fatty acid compositions are important issues for consumers. The fatty acid composition of beef is influenced, also, by genetic factors.

It is known that double muscled animals are very lean (<1% of intramuscular fat). Lean beef has an intramuscular fat content of around 5 % or less with approximately 47, 42 and 4% of total fatty acids as saturated fatty acids (SFA), monounsaturated fatty acids (MUFA) and polyunsaturated fatty acids (PUFA), respectively. The polyunsaturated: saturated ratio for beef is typically low at around 0.1 (Scollan *et al.*, 2001), except for DM animals where the ratio is 0.5-0.7 (Raes *et al.*, 2004).

Existing techniques in meat quality assessment, either instrumental or sensory evaluation can provide reliable information about meat quality. However, these techniques are destructive, time consuming, and unsuitable for on-line application. The development of fast, non-destructive, accurate, and on-line techniques is desired. Near infrared (NIR) spectroscopy could form the basis for such techniques due to the speed, ease of use, and less interferences from moisture or color of meat samples. Over the years, NIR spectroscopy has been developed and applied considerably in quality management of beef meat products (Mitsumoto, Maeda, Mitsuhashi, & Ozawa, 1991). NIRS method is a good tool in order to estimate fatty acid compositions with acceptable accuracy.

Consequently, the objective of this work was to predict the fatty acids composition on a large dataset of Piemontese young bulls using a calibration curve developed in the third chapter of this thesis. As a secondary objective, estimation of heritabilities and additive genetic variations of fatty acids profile for Piemontese young bulls.

5.2 MATERIALS AND METHODS

5.2.1 Dataset

Data used in this study were the fatty acid profiles and ether extract component of meat samples collected from 733 Piemontese young bulls. These bulls were progeny of 84 sires selected randomly from a pool of 1080 animals. Animals were sampled from 137 fattening farms feeding an *ad libitum* diet based on corn meal, soybean meal, barley meal, sugar beet pulp, wheat bran, molasses, mineral and vitamin supplements, and hay. Animals were slaughtered at a single commercial abattoir from March 2005 to September 2007.

5.2.2 Tissue samples

Individual samples of *Longissimus thoracis* muscle were collected 24 h after slaughter between the 5th and 6th thoracic vertebra. Samples were weighed, vacuum-packaged and sent to the meat laboratory of the department of Animal Sciences at the University of Padova. And were refrigerated for a period of 8 ± 2 d at 4 °C, and then analyzed for meat quality characteristics in the meat laboratory of the department of Animal Sciences at the University of Padova.

5.2.3 NIRS-fatty acids determination

Minced fresh samples were used for NIR spectroscopy analyses. Measurements of the NIR spectra were obtained using a FOSS NIR Systems model 5000 with small ring cup cells. Measurements were made in reflectance mode between 1,100 and 2,498 nm of the near-infrared region at intervals of 2 nm.

All spectra were collected in duplicate and the average spectrum was used for NIR analysis. The resulting spectra were stored as absorbance, *log (1/R)* where R is reflectance, on WINISI II version 1.02 software (InfraSoft International, Port Matilda, PA, USA). In order to identify each fatty acid type, regression equations were computed (software WinISI II) using a partial least squares (PLS) regression technique.

5.2.4 Pedigree information

Pedigree file was provided by the Italian Association of Piemontese Cattle (ANABORAPI), and included animals with phenotypic records and all their known ancestors (*9,087* animals).

5.2.5 Mixed linear model

Preliminary analyses, using GLM procedure of SAS package (1990), were carried out aimed to identify non-genetic effects to be included in the univariate mixed linear models for estimating genetic variations and heritabilities of meat quality traits.

The non-genetic effects included in the mixed model were the fattening farm (137 levels),**FF**, age at slaughter into 5 classes, **SA**, and hot carcass weight into 6 classes, **HCW**. The additive genetic effect of young bull was included.

5.2.6 Univariate Bayesian analysis

Estimation of variance components and heritabilities was performed through univariate Bayesian analyses performing numerical integration using the Gibbs sampler tool.

Flat prior distributions were considered for all non-genetic effects , excepted for fattening farm effect. Normal prior distributions were adopted for additive genetic effects and for fattening farm effect. Prior scaled inverted chi-square distributions were assumed for residual, additive genetic variances and for fattening farm effect.

Univariate Bayesian analyses were based on conditional densities and on the scalar form of the Gibbs sampler presented by Wang et al. (1994). Each Bayesian analysis has been carried out generating three Gibbs chains, using iBay software version 1.1.

iBay stands for '*iterative Bayes*', referring to the MCMC (Monte Carlo Markov Chain) algorithms applied to obtain Bayesian inferences.

Size of the chains and burn-in length were chosen by comparing results obtained for two randomly selected sites with chain and burn-in period of different sizes and by subjective inspection of plots of values from the Gibbs chains. The length of the generated chains was 500.000 iterations (*or* samples), and the burn-in period used was 100.000. Samples were saved every 10 iterations.

The median of marginal posterior densities was used as a point estimate of additive genetic standard deviations and heritabilities of all traits.

Other statistics were obtained from the estimated marginal densities, and considered in the discussion:

- fixing h^2 to a value of 10 %, we obtained the posterior probability for values of h^2 greater than 10 % : $P(h^2 > 10\%)$.
- fixing the posterior probability to a value of 90 %, we obtained the minimum values of h^2 for 90 % of samples : (min $h^2_{P90\%}$).
- additive genetic coefficient of variation CV_a (σ_a /mean) was calculated.

5.3 RESULTS AND DISCUSSION

Descriptive statistics for the fatty acids composition of *Longissimus thoracis* muscles are presented in Table 1. Summary statistics in this study correspond to those obtained on a smaller dataset (n=148, see Chapter 3), which confirm that the small sample was selected randomly and was representative to the entire pool of Piemontese population.

Table 1. Summary statistics for the fatty acids composition of fresh *Longissimus Thoracis* muscle (n=733).

Trait	Mean[4]	Min	Max	S.D.	C.V (%)	% TFA[5]
C14:0 (myristic)	3.62	0.16	20.56	2.95	81.31	1.75
C16:0 (palmitic)	45.09	5.49	226.7	31.16	69.11	22.71
C18:0 (stearic)	40.58	5.31	137.21	24.03	59.21	21.16
SFA[1]	91.68	12.07	394.03	58.52	63.83	46.90
C16:1	3.59	0.17	23.79	3.17	88.17	1.70
C18:1n-9ct (*cis*-oleic)	63.96	5.81	333.09	47.55	74.34	31.40
C18:1n-11tr (*trans*-oleic)	6.42	0.76	25.37	4.08	63.5	3.37
MUFA[2]	75.47	6.97	387.27	55.23	73.18	37.27
C18:2n-6 (linoleic)	11.8	4.1	27.3	4.7	39.9	12.75
C20:4n-6 (arachidonic)	2.39	0.04	10.8	1.09	45.70	1.67
PUFA[3]	25.17	5.92	80.1	8.65	34.37	15.82
ω 3	0.82	0.06	3.61	0.44	53.73	0.47
ω 6	23.4	5.48	76.9	7.93	33.91	14.85
(MUFA+PUFA)/SFA	2.29	0.48	9.6	1.35	58.97	1.24

[1] Total saturated fatty acids.

[2] Total Monounsaturated fatty acids.

[3] Total Polyunsaturated fatty acids.

[4] mg/1000 g of fresh meat.

[5] Percentage of total FA.

In the Table 2, they are reported the median of marginal posterior densities for h^2, the posterior probability of h^2 greater than 10%, $P(h^2 > 10\%)$, the minimum values of h^2 for 90 % of samples, min $h^2_{P90\%}$, and the additive genetic coefficient of variation, CV_{ga} calculated by the ratios of additive genetic standard deviation and the mean of the trait (σ_a /mean), obtained from Univariate Bayesian analyses.

Table 2. Features of the marginal posterior densities of h^2 and additive genetic standard deviation of fatty acid composition of Piemontese beef cattle.

Trait	h^2 (%)			CV_{ga}, (%)[d]
	Median[a]	$P(h^2 > 10\%)$[b]	min $h^2_{P90\%}$[c]	
C14:0 (myristic)	10	52	2	11
C16:0 (palmitic)	12	61	4	12
C18:0 (stearic)	10	52	4	11
SFA[1]	12	59	3	12
C16:1	13	65	4	13
C18:1n-9ct (*cis*-oleic)	14	66	4	15
C18:1n-11tr (*trans*-oleic)	14	67	5	11
MUFA[2]	15	73	6	16
C18:2n-6 (linoleic)	15	74	6	9
C20:4n-6 (arachidonic)	23	89	9	2
PUFA[3]	13	67	5	5
ω 3	14	71	5	9
ω 6	13	64	4	5

[a] median of the posterior density of h^2

[b] posterior probability for values of h^2 greater than 10 %

[c] minimum values of h^2 for 90 % of samples

[d] additive genetic coefficient of variation (σ_a /mean)

Estimate heritabilities obtained in the present study, *median of estimated posterior densities* (Table 2), were homogeneous ranging from 10 for C14:0 to 23 % for C20:4n-6. This homogeneity in the estimation of heritabilities maybe could be due to the use of the same equation of calibration for all fatty acids composition.

IMPLICATIONS

Estimate heritabilities obtained in the present study were homogeneous. This homogeneity in the estimation of heritabilities maybe could be due to the use of the same equation of calibration for all fatty acids composition.

DM cattle is thus a very interesting model to study the effect of one major gene in interaction with other genes, and to understand how an increased muscular mass may be associated with lower intramuscular fat.

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CHAPTER 6

Estimation of genetic and phenotypic correlations for beef quality traits

ABSTRACT

The objectives of this study were to determine variance and covariance components and corresponding genetic parameter estimates, and to estimate genetic and phenotypic correlations among meat quality traits in Piemontese beef cattle. (Co)variance components were estimated using a bivariate mixed animal model and was accomplished using Bayesian methodology and the Gibbs sampling integrations. The linear animal model included the non-genetic effects of fattening farms, slaughter age, week of analysis (when was possible), and hot carcass weight in classes; and included the additive genetic effect of the bull. Marginal posterior distributions of probabilities of (co)variances for additive genetic effect, permanent environmental effect (fattening farm) and residual of all meat quality traits were obtained. The median of marginal posterior densities was used as a point estimate of heritabilities and additive genetic standard deviations of beef traits. Pedigree file was provided by ANABORAPI and included animals with phenotypic records and all their ancestors; 11,170 animals. Generally, genetic correlations among meat quality traits were very heterogeneous and ranged from -0.55 to 0.68. Phenotypic correlations were low and ranged from -0.09 to 0.47.

Key words: estimates genetic and phenotypic correlations, beef quality traits, Piemontese young bulls.

6.1 INTRODUCTION

Breeding objectives for beef cattle have evolved over the years to meet production standards, resources, consumer demands, and marketing practices. Because the current trend in the beef industry is to focus not only on growth and maternal traits, but also on carcass and meat composition, reliable estimates of genetic correlations are needed to determine whether improvement in one or more traits would compromise improvement in the others.

The current breeding goal of the Piemontese population includes traits related to quantitative beef production such growth potential, muscularity and maternal calving performance of animals which are selected by performance testing on station of young bulls (Albera et al., 2001). Then meat quality traits are currently not included in the Piemontese breeding goal.

The objectives of this study were to determine variance and covariance components and corresponding genetic parameter estimates, and to estimate genetic and phenotypic correlations among meat quality traits in Piemontese beef cattle.

6.2 MATERIALS AND METHODS

6.2.1 Animals

Data used in this study were from 1080 Piemontese young bulls which were randomly selected within the progeny of 139 AI sires. After slaughtering, carcasses were graded for fleshiness using the EU grading system (Commission of European Communities, 1982), and weighed: average hot carcass weight ± SD was 428 ± 43 kg. (S)EUROP classification was rearranged into scores for statistical analyses (EUS: S+ = 6.33, S = 6, S- = 5.66, E+ = 5.33, E = 5, E- = 4.66, U+ = 4.33, U = 4, U- = 3.66).

6.2.2 Meat quality traits

Individual samples of *Longissimus Thoracis* muscle were collected 24 h after slaughtering, and were taken between the 5th and 6th thoracic vertebra. For beef quality assessment, all samples were transferred to the meat laboratory in the Department of Animal Sciences of the University of Padova using a portable chilling device at 4 °C. At arrival, the samples were stored in a chilling room at 4 °C for 8 ± 2 days.

pH, Drip loss, cooking loss, Meat color (L*, a*, b*, H*, C*), and shear force were determined (see Chapter 2).

6.2.3 Pedigree information

Pedigree file was provided by the Italian Association of Piemontese Cattle (ANABORAPI), and included animals with phenotypic records and all their known ancestors (*11,701* animals).

6.2.4 Mixed linear model

Preliminary analyses, using GLM procedure of SAS package (1990), were carried out aimed to identify non-genetic effects to be included in the bivariate mixed animal models for estimating genetic covariances and variances of meat quality traits.

For lightness (L*) and redness (a*) the non-genetic effects included in the model were the fattening farm (167 levels), age at slaughter into classes (5 levels), week of the analysis, and hot carcass weight into classes (6 levels). The additive genetic effect of young bull was included. For cooking loss (CL), drip loss (DL), ph, and shear force (SF) the non-genetic effects included in the model were the fattening farm (167 levels), and the week of the analysis. The additive genetic effect of young bull was included. For Europ classification trait the model used included the non genetic effects of fattening farms (167 levels) and hot carcass weight into classes (6 levels), and The additive genetic effect of young bull was included.

A genetic group, for unknown male and female parents, were adopted in every analysis.

6.2.5 Bivariate Bayesian analysis

Estimation of variance and covariance components and heritabilities was performed through bivariate Bayesian analyses performing numerical integration using the Gibbs sampler tool.

Flat prior distributions were considered for all non-genetic effects, excepted for fattening farm effect. Normal prior distributions were adopted for additive genetic effects and for fattening farm effect. Prior scaled inverted chi-square distributions were assumed for residual, additive genetic variances and for fattening farm effect.

Each Bayesian analysis has been carried out generating three Gibbs chains, using TM (threshold model) software.

Three separate Gibbs chains were generated. Based on the trace plots and running mean plots of samples obtained from 500,000 cycles for the three chains, it was determined that 200,000 cycles was a sufficiently long burn-in period. The length of the burn-in chosen was enough to eliminate the effect of the different starting values.

After discarding the first 200,000 cycles within each chain as 'burn-in' , each set of the remaining 300,000 cycles within each chain were subsequently saved every 10 cycles to determine the marginal posterior density of each variance and covariance components and to determine the posterior medians and standard deviations of each parameter.

6.3 RESULTS AND DISCUSSION

Estimates of heritabilities (diagonal), genetic (above diagonal) and phenotypic (below diagonal)correlations for meat quality traits with bivariate analysis of Piemontese young bulls are presented in Table 1.

Table 1. estimates of heritabilities (diagonal), genetic (above diagonal) and phenotypic (below diagonal)correlations for meat quality traits with bivariate analysis of Piemontese young bulls

Trait[a]	pH	L*	a*	CL, %	DL, %	SF	EUS
pH	0.50	-0.23	0.40	0.10	-0.55	0.19	-0.08
L*	-0.08	0.19	No convergence	0.10	0.48	-0.25	0.25
A*	-0.08	-0.09	0.26	-0.54	0.22	0.37	0.68
CL,	0.02	0.10	0.01	0.07	0.46	0.27	-0.20
DL,	-0.09	0.30	-0.04	0.12	0.32	0.18	-0.001
SF	0.18	0.07	0.03	0.47	-0.005	0.15	-0.29
EUS	0	0.10	0.05	-0.06	-0.005	0.08	0.23

[a] SF, shear force; CL, cooking loss; DL, drip loss; EUS, Seurop classification into scores; Color parameters: L* : lightness; a* : redness.

Estimation of heritabilities by bivariate analyses ranged from 0.07 to 0.50, and were a bit lower than the univariate analyses estimations. At exception of pH, shear force and EUS where the estimates heritabilities were equal.

There were no estimations of genetic correlations between yellowness (b*) parameter and the other traits because there were no convergenge for covariance matrices, then genetic covariances could not be estimated.

For chroma and hue angle traits we did not estimate the genetic and phenotypic correlations because they are two traits calculated by a* and b*, then highly correlated with them.

Estimated genetic correlations between pH and the other traits ranged from -0.55 to 0.40, negative values were presented for L*, DL and EUS, -0.23, -0.55 and -0.08, respectively. Phenotypic correlations were very low ranged from -0.08 to 0.18. Genetic correlations between lightness and the other traits ranged from -0.25 to 0.48, at exception of the correlation with a* where there was no convergence in the genetic covariance matrix. Phenotypic correlations were low also in this case and ranged from -0.09 to 0.30.

Redness (a*) parameter has shown values of genetic correlations with the other meat quality traits ranging from -0.54 to 0.68. Estimates genetic correlations between cooking loss and meat quality traits ranged from -0.54 to 0.46.

Generally, genetic correlations among meat quality traits were very heterogeneous and ranged from -0.55 to 0.68. Phenotypic correlations were low and ranged from -0.09 to 0.47.

6.4 IMPLICATIONS

The results of this study demonstrate that the genetic correlations among beef quality traits obtained are very interesting and could be exploited for a indirect selective program for these traits.

Further investigations aiming to evaluate the relationships between these traits and the performance traits currently included in the breeding goal of Piemontese population.

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CHAPTER 7

Genetic correlations among beef quality traits and performance traits included in the current breeding goal of the Piemontese population

ABSTRACT

The aim of this chapter was to estimate genetic correlations among beef quality traits and performance traits for Piemontese beef cattle, and to evaluate the possibility to include, indirectly, meat quality traits in the selection objective. Meat quality data used in this study were from 1,080 Piemontese young bulls. After slaughtering meat quality assessment were performed on *Longissimus Thoracis*. The traits analyzed in the meat laboratory in the department of Animal Science of the University of Padova were pH, Drip loss (DL), cooking loss (CL), meat color parameters (L*, a*, b*, C*, and H*), and shear force (SF). Performance data used in this study was from a total of 2,432 animals which were evaluated for performance testing. Performance traits considered were daily gain (DG), live fleshiness (LF), withers width (WW), shoulder muscularity (SM), loins thickness (LT), thigh muscularity (TM), limbs thickness (LT), limbs width (LW), and bone score (BS). Performance traits were determined by scores (9 levels) assigned by three classifiers at the genetic station located in Carrù owned by ANABORAPI. (Co)variance components were estimated using a bivariate Animal model with Restricted maximum Likelihood procedures (REML) using VCE package.

For meat quality traits we used the mixed linear animal models included the non-genetic effects of fattening farms (FF), slaughter age (SA), week of analysis (WA, when needed), and hot carcass weight in classes (HCW); and included the additive genetic effect of the bull. For performance traits, models used included maternal effect (parity of Dam, 4 classes) and the effect of the contemporary group on test (which included year-season effect and age of the bulls, from 1 to 234). The model used for fleshiness trait was the same in addition to the effect of the weight at evaluation. Pedigree file was provided by ANABORAPI and included animals with meat quality records, animals with performance records and all their ancestors; 19,407 animals. Genetics correlation values among beef quality traits and performance traits in Piemontese populations obtained in this study were very interesting, ranged from 0.01 to 0.85 for positive values, and ranged from -

0.60 to -0.15 for negative values. And, that could be useful for an indirect selection for meat quality traits.

Key words: meat quality traits, performance traits, genetic correlations, REML.

7.1 INTRODUCTION

The Piemontese is an important breed specialized in beef production in Italy. The high specialization in beef production exploited by this breed is related to the muscular hypertrophy due to a specific mutation in the myostatin gene (Grobet et al., 1998).

The current breeding goal of Piemontese population includes daily gain, live fleshiness, bone thinness, direct and maternal calving performance (Carnier et al., 2000; Albera et al., 2001), and beef production traits (Albera et al., 2004), but covariances between these traits and meat quality traits, treated in this thesis, are unknown.

Therefore, knowledge of genetic relationships between performance traits, included currently in the breeding goal of Piemontese populations, and meat quality traits, treated in this thesis, would be needed to improve more efficiently both productive traits (related to meat production) and meat quality traits (related to the composition of meat). It is, then, necessary to evaluate the genetic relationships between performance traits of Piemontese sire bulls and beef traits of their progeny.

Since beef quality traits are difficult and expensive to measure, a reliable indirect method to select for them would be welcomed by the beef industry.

The objective of this study was to estimate the genetic correlations between traits associated with performance measured on sires, and beef quality traits measured on their progeny in Piemontese populations, and to evaluate the possibility to include, indirectly, some meat quality trait in the selection objective.

7.2 MATERIALS AND METHODS

7.2.1 Performance data

A total of 2,432 animals were evaluated for performance testing. Selection is organised in two stages: young bulls are station-tested on own performance for beef production traits and selected animals are then progeny tested for direct and maternal calving ease (Carnier *et al*, 2000). The objective of performance testing in the Piemontese breed is the evaluation of young bulls for growth rate and live fleshiness. Performance traits considered in this study were daily gain (DG), live fleshiness (LF), withers width (WW), shoulder muscularity (SM), loins thickness (LT), thigh muscularity (TM), limbs thickness (LT), limbs width (LW), and bone score (BS).

Live assessments of muscularity are simple methods to evaluate carcass quality but insufficient to determine meat quality traits, unlikely we need methods requiring the slaughtering of the animals, progeny test, which it is more much expensive and require a long generation interval in breeding schemes.

7.2.2 Meat quality data

Data used in this study were from 1,080 Piemontese young bulls. After slaughtering meat quality assessment were performed on *Longissimus Thoracis* muscle taken between the 5th and 6th thoracic vertebra, and were pH, Drip loss, cooking loss, Meat color parameters (L*, a*, b*, C*, and H*), and shear force were determined (see Chapter 2).

7.2.3 Statistical analyses

The (co)variance components were estimated using the variance component estimation (VCE) computer program (Neumaier and Groeneveld, 1998) which uses restricted maximum likelihood (REML) method implementing a quasi-Newton optimization algorithm on the Cholesky factor of the covariance matrices.

7.2.4 Models of performance traits

Preliminary analyses were carried out through general linear model procedure of SAS package (1990) to investigate the effects to be fitted in the models for the bivariate analyses.

The effects of contemporary group on test, which includes year-season effect and age of the bulls, and parity of dam were tested.

Performance traits were determined by scores (9 levels) assigned by three classifiers. Data structure did not allow fitting the effect of the classifier in the model; therefore, the average of the scores given by the three classifiers was used in the model for fleshiness traits and bone score.

For all performance traits the final models included the fixed effect of the contemporary group of tested animals (1 to 234), the fixed effect of the parity of the dam (1 to 4), and the random animal effect. Parity of the dam was treated in four classes (first, second, third to seventh, higher then seventh).

At exception of live fleshiness trait where the final model included the fixed effect of the contemporary group of tested animals, the fixed effect of the parity of the dam, and the covariate of the weight of the bull at the evaluation and the random animal effect.

7.2.5 Models of meat quality traits

Preliminary analyses, using GLM procedure of SAS package (1990), were carried out aimed to identify non-genetic effects to be included in the linear models for the bivariate analyses.

For lightness (L*) and redness (a*) the non-genetic effects included in the model were the fattening farm (167 levels), age at slaughter into classes (5 levels), week of the analysis, and hot carcass weight into classes (6 levels). The additive genetic effect of young bull was included.

For cooking loss (CL), drip loss (DL), ph, and shear force (SF) the non-genetic effects included in the model were the fattening farm (167 levels), and the week of the analysis. The additive genetic effect of young bull was included. For Europ classification trait the model used included the non genetic effects of fattening farms (167 levels) and hot carcass weight into classes (6 levels).

A bivariate model with two traits was implemented.

The total number of animals in the pedigree file was 19,407 animals, and was provided by ANABORAPI .

7.3 RESULTS AND DISCUSSION

Summary statistics for performance traits of Piemontese cattle are reported in Table 1. Coefficient of variations of performance traits ranged from 9 to 18 %.

Table 1. Summary statistics for performance traits of Piemontese cattle (n = 2,432).

Trait[a]	Mean	Min	Max	SD	CV%
DG	1.29	0.94	1.64	0.12	9.21
WW	6.67	3.00	9.00	1.04	15.59
SM	6.53	3.00	9.00	1.01	15.51
LW	6.44	3.70	9.00	0.92	14.22
LT	6.56	3.50	9.00	0.91	13.82
TM	6.76	3.00	9.00	1.18	17.40
BS	5.73	2.70	8.70	0.81	14.16
LoT	6.48	3.00	9.00	1.11	17.20
LF	6.43	3.60	8.70	0.87	13.48

[a]DG daily gain; WW withers width; SM shoulder muscularity; LW limbs width; LT limbs thickness; TM thigh muscularity; BS bone score; LoT loins thickness; LF live fleshiness.

Descriptive statistics shown in Table 1 correspond to the results reported in the study conduced on the same traits (on a smaller dataset) by Albera et al., 2001.

Summary statistics for beef and carcass traits (n=1080) are shown in Table 2. A very low variation in pH, SA, L*, and H* (C.V. from 1 to 12%) was observed. Variation of SF, DL, CL, a*, b*, C* and EUS was higher (C.V. from 14 to 34%).

Table 2. Summary statistics for investigated beef quality and carcass traits (n = 1,080).

Trait[a]	Mean	Min	Max	SD	CV%
pH	5.49	5.31	5.81	0.05	1
L*	34.27	25.26	47.95	3.41	10
a*	16.15	7.51	24.14	2.58	16
b*	14.81	5.73	22.54	2.16	15
H*	42.55	29.63	57.72	3.94	9
C*	21.97	9.49	33.01	3.03	14
SF, kg	2.65	1.18	2.28	0.57	21
CL, %	23.93	11.36	36.26	3.62	34
DL, %	4.21	0.96	16.45	1.50	15
EUS, scores	3.89	2.66	5.00	0.66	17

[a] SF, shear force; CL, cooking loss; DL, drip loss; EUS, Seurop classification into scores.

Color parameters: L* : lightness; a* : redness; b* : yellowness; H* : Hue angle, arctangent (a*/b*); C* : saturation index (chroma), √(a*2+b*2).

7.3.1 Bivariate analyses

Estimates of genetic correlations among beef traits and performance traits in Piemontese breed obtained performing bivariate analysis are presented in Table 2.

Table 2. Estimates genetic correlations among beef traits and performance traits in Piemontese breed

Trait[a]	pH	L*	a*	CL, %	DL, %	SF	EUS
DG	0.013	0.043	0.235	0.672	0.287	0.341	0.003
WW	-0.158	0.464	-0.011	0.082	0.482	0.054	0.326
SM	-0.266	0.515	-0.095	0.566	0.492	0.213	0.342
LW	-0.038	0.277	0.033	0.499	0.475	0.254	0.533
LT	-0.277	0.316	0.077	0.474	0.253	0.107	0.254
TM	-0.414	0.342	-0.445	0.073	0.296	-0.381	0.432
BS	-0.269	-0.231	0.176	-0.215	0.056	-0.334	0.844
LoT	-0.363	0.238	-0.362	-0.317	0.051	-0.597	0.466
LF	-0.335	0.253	-0.25	-0.230	0.192	-0.364	0.605

[a] performance traits: DG, daily gain; WW, withers width; SM, shoulder muscularity; LW, limbs width; LT, limbs thickness; TM, thigh muscularity; BS, bone score; LoT, loins thickness; LF, live fleshiness.

meat quality traits: pH, at 8 days after slaughter; L*, lightness; a*, redness; CL, cooking loss; DL, drip loss; SF, shear force; EUS, europ classification into scores.

Estimated genetic correlations between pH trait and all performance traits were negative ranging from -0.414 to -0.038 that because all genetic covariances were negative. These results indicate that antagonistic relationships exist between pH as a meat quality trait and performance traits.

Estimated genetic correlations between lightness and performance traits were positive ranging from 0.043 to 0.515 at exception of bone score which were negative -0.231.

Redness (a*) parameter has shown values of genetic correlations with performance traits ranging from -0.445 to 0.235. Naturally, negative genetic correlation values were due to a negative estimates of genetic covariances.

There were no estimations of genetic correlations between yellowness (b*) parameter and performance traits because there were no convergenge for covariance matrices, then genetic covariances could not be estimated.

Estimates genetic correlations between cooking loss and performance traits ranged from -0.317 to 0.672. High positive genetic correlations between CL and DG, SM, LW and LT ranged from o.47 to 0.68. Negative genetic correlations obtained for BS, LoT and LF ranged from -0.31 to -0.21.

Estimation of genetic correlations between drip loss and performance traits were all positives and ranged from 0.05 to 0.50. A very low relationship presented with bone score and loins thickness, 0.056 and 0.051, respectively. Shear force exhibited a genetic correlations with performance traits ranged from -0.60 to 0.34. Negative values of genetic correlations mean that high muscular evaluations correspond to a low value of shear force, then high meat tenderness.

High positive values of estimates genetic correlations between Euscore carcass trait and performance traits ranged from 0.25 to 0.84, at exception of DG which had a very low genetic correlation of 0.003, due to the null genetic covariance obtained, then a genetic independence between EUS and DG.

Standard errors of estimates genetic correlations are reported in Table 3; this is a precision estimator for our correlation estimations.

Values of standard errors in this study were high for all correlations, maybe that is due to the low number of samples used for this analysis.

Table 3. Standard error of estimates genetic correlations among beef traits and performance traits in Piemontese breed

Trait[a]	pH	L*	a*	CL, %	DL, %	SF	EUS
DG	0.148	0.200	0.165	0.314	0.147	0.215	0.160
WW	0.167	0.204	0.184	0.318	0.166	0.233	0.190
SM	0.181	0.210	0.202	0.309	0.183	0.250	0.191
LW	0.185	0.289	0.085	0.335	0.178	0.264	0.200
LT	0.183	0.263	0.196	0.034	0.195	0.245	0.200
TM	0.162	0.212	0.177	0.322	16.9	0.217	0.130
BS	0.141	0.226	0.164	0.271	0.157	0.183	0.145
LoT	0.156	0.213	0.173	0.238	0.171	0.213	0.166
LF	0.157	0.208	0.186	0.355	0.169	0.229	0.184

[a] performance traits: DG, daily gain; WW, withers width; SM, shoulder muscularity; LW, limbs width; LT, limbs thickness; TM, thigh muscularity; BS, bone score; LoT, loins thickness; LF, live fleshiness.
meat quality traits: pH, at 8 days after slaughter; L*, lightness; a*, redness; CL, cooking loss; DL, drip loss; SF, shear force; EUS, europ classification into scores.

Comparing the results obtained in this study with other present in literature was difficult because different methods used for beef quality assessments on slaughtered animals, and because different definitions of traits used as evaluation of beef conformation on live animals.

7.4 IMPLICATIONS

Results of this study indicated that meat quality traits and conformation traits in Piemontese populations are well correlated, therefore these evidence can be exploited for the indirect selection for beef quality in Piemontese population.

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General conclusions

This study demonstrates that NIR spectroscopy is a useful tool to predict, with high accuracy, the composition of fatty acids, dry matter, ether extract in Piemontese beef cattle. Furthermore, this study has shown that NIR spectroscopy could not be used to predict physical properties, cholesterol and collagen contents in Piemontese beef cattle, which has been attributed to low analytical data variations used in calibrations.

Estimation of variance components was based on an univariate linear animal model and was accomplished using Bayesian methodology and the Gibbs sampling integrations. The linear animal model included the non-genetic effects of fattening farms, slaughter age, week of analysis, and hot carcass weight in classes; and included the additive genetic effect of the bull. Marginal posterior distributions of probabilities of additive genetic standard deviations and heritabilities for all traits were obtained. The median of marginal posterior densities was used as a point estimate of heritabilities and additive genetic standard deviations of beef traits.

Estimation of heritabilities of meat quality traits for Piemontese beef cattle were relevant, exploitable for an indirect selection of Piemontese population.

Estimation of variance components and heritabilities of fatty acids and ether extract was based on a Univariate mixed animal model and was performed throughout Bayesian methodology and the Gibbs sampling. The linear animal model included the non-genetic effects of fattening farms (FF, 152 levels), slaughter age (SA, 5 classes), and hot carcass weight (HCW, 6 classes); and the additive genetic effect of the bull. Marginal posterior probabilities of additive genetic standard deviations and heritabilities of all traits were obtained. The median of marginal posterior densities was used as a point estimate of heritabilities and additive genetic standard deviations of fatty acids and ether extract. Estimate heritabilities obtained in the present study, *median of estimated posterior densities*, were homogeneous ranging from 10 for C14:0 to 23 % for C20:4n-6. This homogeneity in the estimation of heritabilities maybe could be due to the use of the same equation of calibration for all fatty acids composition.

The results of the genetic correlations among beef quality traits obtained are very interesting and could be exploited for a indirect selective program for these traits. In the last Chapter genetics correlation values were estimated among beef quality traits and performance traits in Piemontese populations. The results obtained in this study were very interesting, ranged from 0.01 to 0.85 for positive values, and ranged from -0.60 to -0.15 for negative values. And, that could be useful for an indirect selection for meat quality traits.