

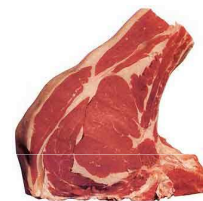


# BUILD UP A SYNTHETIC REFERENCE MAP OF BOVINE MUSCLE PROTEINS

Paola Roncada<sup>1\*</sup>, Alessandro Gaviraghi<sup>2</sup>, Francesca Deriu<sup>2</sup>, Gian Franco Greppi<sup>3</sup>, Luigi Bonizzi<sup>2</sup>

<sup>1</sup>Istituto Sperimentale Italiano L. Spallanzani, Milano; <sup>2</sup>DIPAV, Facoltà di Medicina Veterinaria, Università Degli Studi di Milano; <sup>3</sup>Dipartimento di Scienze Zootecniche, Università Degli Studi di Sassari.

Variability of meat quality is a major concern for industry and consumers. Sensory properties of meat have an important influence on the purchasing behavior of consumers. Many factors can affect final meat quality, such as breeding, animal welfare, feeding and transport conditions, slaughtering conditions, electrical stimulation, and chilling conditions. The current agricultural policy of the European Union considers a new reorientation of meat bovine market, fomenting diversification of agricultural production and promotion of specific products. The traceability of the meat from the farmer to the consumer guarantees the meat quality. Creation of meat quality labels, normally under a geographical situation and with a specific genotype and production system, has been the symbol of this guarantee, since all these factors can affect meat quality. The importance of different breeds on meat property were tested using a proteomic approach.



Aim of this work is to evaluate protein expression profiles in different bovine breeds towards the building up of an informative synthetic map of bovine muscle proteins.

**Material and Methods:** Fifty bulls and cows from 5 different cattle breeds reared in Italy were used in the present study: Chianina, Piemontese, Limousine, Charolaise and Italian Holstein. All animals were reared under local production systems and slaughtered in their areas of origin in commercial slaughterhouse. *Longissimus Thoracis* muscle from the 9th thoracic ribs was collected 2 hours after slaughtering and stored at -80°C. Amounts of 100 mg for each muscle sample have been suspended in 1ml of OMNIZOL with addition of protease inhibitor and 20µl of 0.25M EDTA. After homogenization on ice, protein samples have been extracted using OMNIZOL Extraction protocol (EuroClone). Protein pellets were suspended in 8M Urea, 4% CHAPS, 1% DTT, 15mM Tris, 2% Ampholine 3.5-10. First dimension was performed using IPG strips pH 3-10 NL 18cm and second dimension in 10% polyacrilamide gels. Gels were stained with standard silver nitrate staining protocol. Image analysis was performed with Image Master 2D Platinum (GE) and Progenesis SameSpots software (Nonlinear Dynamics).

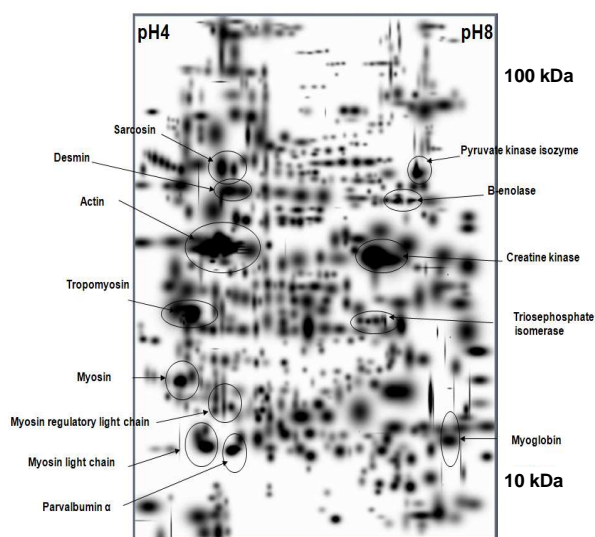


Fig.1: synthetic map of bovine muscle

**Results:** Identification of muscle proteome changes related to different breed was based on a comparison of muscle samples taken immediately from animals after slaughter. Approximately 500 spots were detected in each gel. We have identified a few proteins that are significantly changing in meat of different breeds. The identified proteins could be divided into 3 groups: energy metabolism, defense and stress, myofibrillar filaments. The dairy breeds differ in their muscle characteristics, in particular fiber composition and enzyme activity, compared with the beef breeds.

A synthetic map of bovine muscle proteins was created from an artificial gel combining all of the spots presenting in different gels into one image, as shown in Figure 1. A synthetic gel consists of a representative set of spots generated from several registered gel images.

**Conclusions:** Skeletal muscle fibers are important factors influencing meat quality. Breed probably accounts for most of the genetic factors affecting the muscle fiber composition of a certain muscle. Differences in muscle characteristics between breeds are likely to be a consequence of metabolic and physiological differences in the breeds that have evolved in response to production purposes.

2-DE-based proteome analysis is a useful tool for characterizing expression and metabolism of muscle protein in relationship to different breed. Besides, analysis of expression profiles could be a key to find protein markers for meat quality and give deep understanding of characteristics of different breeding, welfare, feeding, transport conditions and slaughtering conditions.

