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Data Article

Quantification of proteome changes in bovine muscle from two-dimensional electrophoresis data

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ABSTRACT

Proteome changes in the *longissimus thoracis* bovine muscle in response to pre-slaughter stress were assessed on the basis of two-dimensional electrophoresis (2-DE) data. In this study, the bootstrap resampling statistical technique and a new measure of relative change of the volume of 2-DE protein spots are shown to be more efficient than commonly used statistics to reliably quantify changes in protein abundance in stress response. The data are supplied in this article and are related to "Tackling proteome changes in the *longissimus thoracis* bovine muscle in response to pre-slaughter stress" by Franco et al. [1].

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Specifications table

Subject area	Biology
More specific subject area	Meat science, bovine muscle proteome
Type of data	Table, figure
How data was acquired	2-DE gel images stained for total protein with SYPRO Ruby stain were acquired using a Gel Doc XR+system. Image analysis of digitalized gels was performed through PDQuest Advanced software
Data format	Analyzed output data
Experimental factors	2-DE was performed using total protein extracts from normal meat and DFD meat of animals affected by pre-slaughter stress
Experimental features	2-DE gels (1st dimension pH 4-7 gradient; 2nd dimension 12% SDS-PAGE) were obtained, protein spots were excised and peptides were analyzed after trypsin digestion by LC-MS/MS and MALDI-TOF/TOF MS
Data source location	Lugo, Spain
Data accessibility	Data are with this article and provided in Supplementary materials directly with this article

Value of the data

- Proteome changes in bovine muscle in response to pre-slaughter stress using 2-DE data.
- Application of the bootstrap statistical technique for testing proteome changes in cattle.
- Illustration of the efficiency of "relative change" as a new measure in quantitative proteomics.

1. Experimental design

Valuable information about the proteome changes in the *longissimus thoracis* (LT) bovine muscle in response to pre-slaughter stress (PSS) was obtained from 2-DE data. The occurrence of Dark, Firm and Dry (DFD) meat was used as indicator of animals affected by PSS. A total of four biological replicates of control (normal or non-DFD) and DFD meats from male calves of the Rubia Gallega breed (Spain) were used in this study. DFD and control samples were selected from 76 male calves after evaluation of meat quality parameters that differentiate both types of meat [1]. 2-DE protein spots with statistically significant changes in protein abundance between control and DFD samples were identified by mass spectrometry (MS).

2. Materials and methods

2.1. Meat sample preparation, protein extraction and quantification

Meat samples from the LT bovine muscle were excised from the left half of each carcass at 24 h post-mortem. A 2.5 cm thick steak was taken at the fifth rib and packed under vacuum conditions at the abattoir and subsequently transported to laboratory under refrigerated conditions. Meat samples were then lyophilized under optimal conditions [2] and frozen at −80 °C until proteome analysis. Lyophilization is a cheap, practical and safe alternative for the storage of samples prior to protein extraction, separation and quantification by 2-DE [2].

Lyophilized beef powder (50 mg) was resuspended in 1.5 mL of lysis buffer (7 M urea; 2 M thiourea; 4% CHAPS; 10 mM DTT; and 2% pharmalyte pH 3-10, GE Healthcare) for 2 h at 25 °C. An aliquot of 250 μL was lysed using a Sonifier 250 (Branson) by cycling. Protein purification and extraction from crude cell lysates were carried out with the Clean-Up kit (GE Healthcare) as described in manufacturer's indications. The proteins were then resuspended in 250 μL of lysis buffer. Protein quantification was assessed for each extraction using the CB-X protein assay kit (G-Biosciences) according to manufacturer's recommendations. The BSA protein standard was used to get a calibration curve.