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Data Article

Proteomics data in support of the quantification of the changes of bovine milk proteins during mammary gland involution

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ABSTRACT

Here we provide data from three proteomics techniques; two-dimensional electrophoresis (2-DE) followed by identification of selected spots using PSD MALDI-TOF MS/MS, one-dimensional gel electrophoresis followed by LC-MS/MS analysis of gel slices (GeLC) and dimethyl isotopic labelling of tryptic peptides followed by Orbitrap MS/MS (DML), to quantify the changes in the repertoire of bovine milk proteins that occurs after drying off. We analysed skim milk and whey sampled at day 0 and either day 3 or day 8 after drying off. These analyses identified 45 spots by MALDI-TOF, 51 proteins by GeLC and 161 proteins by DML, for which the detailed data work-up is presented as three Excel files. The data supplied in this article supports the accompanying publication "Changes in the repertoire of bovine milk proteins during mammary involution" (Boggs et al., 2015) [1]. Data are available via ProteomeXchange with identifiers ProteomeXchange: PXD003110 and ProteomeXchange: PXD003011.

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Specifications Table

Subject area	Biology
More specific subject area	Mammary gland physiology
Type of data	Excel files
How data was acquired	Two-dimensional electrophoresis followed by PSD MALDI-TOF (LIFT) mass spectrometry of selected spots using a Bruker Ultraflex instrument. One-dimensional gel electrophoresis followed by LC-tandem MS of peptides excised from gel slices (GeLC) using a QStar instrument. Dimethyl labelling followed by LC tandem MS mass spectrometry (DML) using an Oribtrap intrument.
Data format	Raw
Experimental factors	Skim milk and whey from day 0 and day 3 or day 8 after drying off
Experimental features	Pooled skim milk and whey samples were separated using 2-DE and gel spots that were altered in abundance were excised, digested with trypsin and identified by MALDI-TOF. The pooled samples were also analysed by 1D electrophoresis, slices of each lane were subjected to trypsin digestion, and the extracted peptides were analysed by LC-MS/MS. Peptide abundance was estimated by peptide count and EMPAI value. The pooled samples were also digested, isotope labelled and subjected to LC-MS/MS. Isotope ratios were determined for each peptide.
Data source location	Waikato region of New Zealand
Data accessibility	Data is available within this article and through ProteomeXchange accession numbers ProteomeXchange: PXD003110 and ProteomeXchange: PXD003011.

1. Value of the data

- This data characterizes the physiological responses occurring in milk during mammary involution in dairy cows.
- Many host defence related proteins were increased in abundance after drying off.
- These data could be used for developing improved milking strategies to maximise production efficiency and yield of milk bioactives.

2. Data

Three Excel files are presented. File 1 contains the MALDI-TOF tandem MS data of the 2-DE gel spots which were successfully identified, File 2 contains the raw data excised from ProteinScape, the processed data, and a detailed description of the contents of each of the sheets, along with the workflow used. File 3 contains a single sheet containing collated data listing all the distinct proteins that were identified, along with the number of peptides detected, their isotope ratios, and biological function as determined by querying the GO database. A complete description of the data and methods is presented elsewhere [1].