



ELSEVIER

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib



Data article

Comparative proteomics dataset of skimmed milk samples from Holstein and Jersey dairy cattle



Rinske Tacoma^a, Julia Fields^b, David B. Ebenstein^a,
Ying-Wai Lam^b, Sabrina L. Greenwood^{a,*}

^a The University of Vermont, Department of Animal & Veterinary Sciences, 570 Main Street, Burlington, VT 05405, United States

^b The University of Vermont, Vermont Genetics Network Proteomics Facility, 109 Carrigan Drive, Burlington, VT 05405, United States

ARTICLE INFO

Article history:

Received 30 October 2015

Received in revised form

11 December 2015

Accepted 20 January 2016

Available online 30 January 2016

Keywords:

Bovine

Proteome

Milk

ABSTRACT

Milk samples were collected from Holstein and Jersey breeds of dairy cattle maintained under the same management practices and environmental conditions over a seven-day period. Milk samples were collected twice daily from six cows of each breed as previously described (Tacoma et al., 2016) [1]. Samples were composited within individual cow over the experimental period and skimmed to remove the fat layer. Skimmed milk samples were fractionated using CaCl_2 precipitation, ultracentrifugation and ProteoMiner treatment to remove the high abundance milk proteins. Separation of the low abundance proteins was achieved using SDS-PAGE. Differential protein abundances were analyzed by mass spectrometry-based proteomic approaches followed by statistical analyses of the peptide count data. The complete list of low-abundance proteins identified in both breeds is provided in the dataset as well as the total number of distinct sequenced peptides and gene ontology functions for each protein. The relative abundance of a select few proteins is depicted using the SIEVE software.

Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

DOI of original article: <http://dx.doi.org/10.1016/j.jprot.2015.09.024>

* Corresponding author. Tel.: +1 802 656 0145; fax: +1 802 656 8196.

<http://dx.doi.org/10.1016/j.dib.2016.01.038>

2352-3409/Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Specifications Table

Subject area	<i>Biology</i>
More specific subject area	<i>Milk proteomics</i>
Type of data	<i>Table, figure</i>
How data was acquired	<i>Acquired by Linear ion trap (LTQ)-Orbitrap Discovery mass spectrometer coupled to a Surveyor MS Pump Plus (Thermo Fisher Scientific, Waltham, MA, USA). Raw data searched using the SEQUEST search engine on Proteome Discoverer 1.4 (Thermo Fisher Scientific, Waltham, MA, USA) against a curated Bovine Uniprot (-Bos taurus database (24,206 entries) downloaded July 9, 2014-)</i>
Data format	<i>Analyzed</i>
Experimental factors	<i>Milk samples were collected from Holstein and Jersey dairy cattle, frozen in a dry-ice ethanol bath and stored at -80°C until they were thawed and pooled within cow according to yield. A protease inhibitor was added to each sample before the fat layer was skimmed and removed.</i>
Experimental features	<i>Skimmed milk samples were fractionated using CaCl_2 for casein precipitation, ultracentrifugation, and ProteoMiner treatment. Proteins were separated on SDS-PAGE followed by in-gel tryptic digestion. Protein abundances were analyzed using nano LC-MS/MS. A subset of differentially expressed proteins were analyzed using SIEVE software, which plots the ion elution profile on the chromatographic time scale (extracted ion chromatograms) of the identified target peptides.</i>
Data source location	<i>Paul R. Miller Research and Educational Center, University of Vermont, Burlington, VT and The Vermont Genetics Network Proteomics Facility, University of Vermont, Burlington, VT</i>
Data accessibility	<i>Analyzed datasets are directly provided with this article</i>

Value of the data

- Compares the diversity of the bovine milk proteome from two prominent North American dairy breeds maintained under the same diet, environment and management conditions in order to better assess true breed differences.
- Allows for more direct comparison between research being performed using different breeds of dairy cattle, and can allow for general extrapolation and application of results seen in one breed to another.
- Expands the bovine milk proteome and provides a platform for future research investigating milk proteomics.

1. Experimental design, materials and methods

1.1. Sample collection

Milk samples were collected from six Jersey cows (80 ± 49 days in milk (DIM)) and six Holstein cows (75 ± 21 DIM) maintained under the same management practices and environmental conditions over a period of seven days as previously described [1]. Cows were milked twice daily at 0400 and 1600 h. Milk yield was recorded at each milking and milk samples were collected during the morning and afternoon milking throughout the 7-day experiment. Milk subsamples collected for low abundance protein analysis were immediately frozen in a dry-ice ethanol bath after collection and stored at -80°C until further analysis.

Download English Version:

<https://daneshyari.com/en/article/175024>

Download Persian Version:

<https://daneshyari.com/article/175024>

[Daneshyari.com](https://daneshyari.com)