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Data Article

Data from proteomic characterization and comparison of mammalian milk fat globule proteomes by iTRAQ analysis

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ABSTRACT

Milk fat globules memebrane (MFGM)-enriched proteomes from Holstein, Jersey, yak, buffalo, goat, camel, horse, and human were extracted and identified by an iTRAQ quantification proteomic approach. Proteomes data were analyzed by bioinformatic and multivariate statistical analysis and used to present the characteristic traits of the MFGM proteins among the studied mammals. The data of this study are also related to the research article "Proteomic characterization and comparison of mammalian milk fat globule proteomes by iTRAQ analysis" in the Journal of Proteomics [1].

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Specifications table

Subject area	*Biology*
More specific subject area	*Milk proteomics*
Type of data	*Table, excel file*
How data was acquired	*iTRAQ labeling (Applied Biosystems)* *SCX chromatography and AKTA Purifier system (GE Healthcare)* *EASY-nLC 1000 system coupled with Q-Exactive mass spectrometery (Thermo FisherScientific)* *Proteome Discoverer 1.4 and MASCOT search engine (Matrix Science, London, UK; version 2.2)* *uniprot database (86 803 bovidae, 20 368 camelus, 28 583 horse, and 136 615 human entries, released in May 2014)*
Data format	*Analyzed*
Experimental factors	*Milk samples from Chinese Holstein cows, Jersey cattle, goats, Bactrian camels, horses, yak, buffalo and human were collected and used to systematically characterize the protein components of milk fat globules memebrane-enriched fractions.*
Experimental features	*Isobaric tags for relative and absolute quantification (iTRAQ)*
Data source location	*Beijing, China*
Data accessibility	*Analyzed datasets are directly provided with this article.*

Value of the data

- The data provide insight into the protein composition of milk fat globules memebrane-enriched fractions in parallel from the studied mammals.
- The bioinformatics data provide the potential physiological functions of the identified proteins.
- The data of multivariate analysis highlight the significance differences in the milk fat globules memebrane-enriched fractions among mammalian species.
- The data point out the breed-markers for identification of species specific milk fat globules.

1. Data, experimental design, materials and methods

1.1. Sample preparation

Milk samples were collected from 60 Chinese Holstein cows (*Bos taurus*) on a farm in Beijing, 21 Jersey cattles (*Bos taurus*) on a farm in Hebei, 27 goats (*Capra hircus*) on a farm in Shanxi, 21 Bactrian camels (*Camelus bactrianus*) and 18 horses (*Equus ferus caballus*) on a farm in Xinjiang, 24 yaks (*Bos grunniens*) on a farm in Qinghai, and 21 buffalo (*Bubalus bubalis*) on a farm in Yunnan. Ten human (*Homo sapiens*) milk samples were donated by healthy mothers between 3 and 8 months lactation and pooled.

The raw milk from each species was randomly pooled into three groups. Each group was treated as follows. Whole milk was centrifuged at 3000*g* at 4 °C for 15 min to recover the fat layer. The fat layer was incubated with PBS for 20 min at 37 °C and then centrifuged at 3000*g* for 30 min to obtain the floating fat layer. This procedure was repeated three times to recover the fat globules and remove residual caseins and whey proteins.

To analyze the fat globules, they were incubated with a lysis buffer containing 50 mM Tris–HCl, pH 7.4, and 4% (w/v) SDS for 1 h with periodic vortexing. Samples were then incubated in water for 5 min at 95 °C and centrifuged at 12 000*g* for 15 min. The floating cream layer was removed, the lysates were centrifuged again, and the supernatant was collected. Then, 200- μL aliquots of the protein mixtures were mixed with 1 mL acetone and stored at −20 °C for 20 h. Samples were then centrifuged at