Data in Brief 1 (2014) 37–41

Contents lists available at ScienceDirect

Data in Brief

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

Data Article

Data for chicken semen proteome and label free quantitative analyses displaying sperm quality biomarkers

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ARTICLE INFO

Article history:
Received in revised form
22 August 2014
Accepted 22 August 2014
Available online 21 September 2014

Keywords:
Chicken (*Gallus gallus*)
Spermatozoa
Seminal plasma
Proteome
Fertility

ABSTRACT

Understanding of biology of the avian male gamete is essential to improve the conservation of genetic resources and performances in farming. In this study, the semen proteome of the main domestic avian species (*Gallus gallus*) and evaluation of the molecular phenotype related to sperm quality were investigated using GeLC–MS/MS approach and label-free quantitative proteomic based on Spectral Counting (SC) and extracted ion chromatograms (XIC) methods. Here we describe in details the peptide/protein inventory of chicken ejaculated spermatozoa (SPZ) and seminal plasma (SP). We also show differential analyses of chicken semen (SPZ and corresponding SP) from 11 males demonstrating different levels of fertilizing capacity and sperm motility. The interpretation and description of these data can be found in a research article published by Labas and colleagues in

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DOI of original article: http://dx.doi.org/10.1016/j.jprot.2014.07.024

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http://dx.doi.org/10.1016/j.dib.2014.08.008

the Journal of Proteomics in 2014 [1]. This is a new resource for exploring the molecular mechanisms involved in fertilizing capacity and to reveal new sets of fertility biomarkers.

Specifications table

Subject area	*Male gamete proteins and reproductive capacity*
More specific subject area	*Chicken (Gallus gallus) ejaculated spermatozoa and seminal plasma protein content and semen quality*
Type of data	Raw and processed/analyzed mass spectrometry data obtained by nanoliquid chromatography combined to high resolution tandem mass spectrometry,.xls tables with identified/validated and quantified proteins
How data was acquired	Experiments performed on a LTQ Orbitrap Velos Mass Spectrometer (Thermo Fisher Scientific, Bremen, Germany) coupled to an Ultimate® 3000 RSLC Ultra High Pressure Liquid Chromatographer (Dionex, Amsterdam, The Netherlands)
Data format	Raw data: raw.mzml Processed and analyzed data using Mascot Search engine:.dat
Experimental factors	Sub/infertile and fertile chickens
Experimental features	Ejaculated spermatozoa and seminal plasma proteome (*Gallus gallus*) of experimental lines D+/D− and evaluation of the molecular phenotype related to sperm quality
Data source location	N/A
Data accessibility	Data are present here with this paper and the MS proteomics data were deposited to the ProteomeXchange Consortium (http://proteomecentral.proteomexchange.org) via the PRIDE partner repository with the dataset identifiers PXD000287 and PXD001254. ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2014/08/PXD000287 ftp://ftp.pride.ebi.ac.uk/pride/data/archive/2014/08/PXD001254

Value of the data

- First description of peptidome/proteome of chicken ejaculated spermatozoa.
- First description of peptidome/proteome of chicken seminal plasma.
- Semen proteomic phenotyping at an individual level from 11 males.
- First proteome comparisons of sub/infertile and fertile chickens to characterize biomarkers related to fertility.

1. Data, experimental design, materials and methods

We describe here a unique dataset composed of qualitative proteomic analysis of chicken spermatozoa and seminal plasma and quantitative proteomic analyses related to semen quality. The present study identified a large number of proteins that have never previously been described in *Gallus gallus*. Furthermore, label free quantitative proteomic analyses combined with physiological tests allowed phenotyping semen at the individual level and characterization of new peptides and proteins that are biomarker candidates of fertility.