Data on endogenous chicken sperm peptides and small proteins obtained through Top-Down High Resolution Mass Spectrometry

Laura Soler, Valérie Labas, Aurore Thelie, Ana Paula Teixeira Gomes, Isabelle Grasseau, Laura Bouguereau, Elisabeth Blesbois

To cite this version:
Laura Soler, Valérie Labas, Aurore Thelie, Ana Paula Teixeira Gomes, Isabelle Grasseau, et al.. Data on endogenous chicken sperm peptides and small proteins obtained through Top-Down High Resolution Mass Spectrometry. Data in Brief, Elsevier, 2016, 8, pp.1421-1425. 10.1016/j.dib.2016.07.050. hal-02630224

HAL Id: hal-02630224
https://hal.inrae.fr/hal-02630224
Submitted on 27 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution - NonCommercial 4.0 International License
Data Article

Data on endogenous chicken sperm peptides and small proteins obtained through Top-Down High Resolution Mass Spectrometry

L. Soler, V. Labasa, A. Thélie, A.P. Teixeira-Gomes, I. Grasseau, L. Bouguereau, E. Blesbois

PRC, INRA, CNRS, Université de Tours, IFCE, 37380 Nouzilly, France
ISP, INRA, Université de Tours, 37380 Nouzilly, France
INRA, Plateforme d’Analyse Intégrative des Biomolécules, Laboratoire de Spectrométrie de Masse, 37380 Nouzilly, France

Article history:
Received 27 May 2016
Received in revised form 21 July 2016
Accepted 26 July 2016
Available online 16 August 2016

Keywords:
Chicken
Sperm
Top-Down HRMS
Peptidome

Abstract

The endogenous peptides and small proteins present in chicken sperm were identified in the context of the characterization of a fertility-diagnostic method based on the use of ICM-MS (Intact Cell Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry). The interpretation and description of these data can be found in a research article, “Intact cell MALDI-TOF MS on sperm: a molecular test for male fertility diagnosis” (Soler et al., 2016) [1], and raw data derived from this analysis have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PRIDE: PXD002768.

Here, we describe the inventory of all the molecular species identified, along with their biochemical features and functional analysis. This peptide/protein catalogue can be further employed as reference for other studies and reveal that the use of proteomics allows for a global evaluation of sperm cells functions.

© 2016 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).
### Value of the data

- Here we make available for the scientific community the first repository of chicken sperm endogenous peptides and small proteins.
- This data describes Top-Down mass spectrometry protein identification results using two different pre-fractionation strategies: gel filtration and reverse phase chromatography, which can be useful when designing future identification strategies using the same technique.
- Data presented here include a description of the biochemical properties of the abovementioned identified sperm cells biomolecules as well as the molecular functions, biological processes and cellular components in which they are implicated.
- This information can be valuable in male fertility research studies.

### 1. Data

This dataset consists of a compendium of peptidoforms and small proteoforms extracted from chicken ejaculated sperm, that were pre-fractionated using gel filtration or reverse phase chromatography and identified through a Top-Down mass spectrometry analysis. Hence, this set includes data regarding the identity of chicken sperm intact peptides and proteins as well as some structural biologically relevant information like N-terminal amino acids or post-translational modifications. See Figs. 1 and 2 and Supplementary Table S1.

### 2. Experimental design, materials and methods

#### 2.1. Experimental design and sample collection

This dataset was produced with the objective of identifying by Top-Down mass spectrometry the peptides and small proteins contained in chicken sperm cells [1]. Sperm cells (200 μL) protein extraction was performed by sonication in 400 μL of 6 M Urea 50 mM Tris–HCl pH 8.8 buffer.
containing protease inhibitor cocktail (Roche, Switzerland). Samples were centrifuged (45 min at 13,000 rpm and 4 °C) and supernatants containing the extracted proteins were kept for further analysis. The protein content was determined using a Bradford assay (BioRad, Marnes-la-Coquette, France).

2.2. Protein/peptide fractionation strategies, Top-Down mass spectrometry identification protocol and results

One mg of the extracted peptides/proteins were subjected to fractionation through chromatographic separation on an UltiMate 3000 RSLC system controlled by Chromeleon version 6.80 SR13 software (Thermo Scientific Dionex, Sunnyvale, USA) using reversed phase (RP) and gel filtration (GF) chromatography as described elsewhere [1]. A total of 35 and 65 fractions were obtained after RP and GF chromatography, respectively. All fractions obtained after fractionation were then analyzed by on-line micro-liquid chromatography tandem mass spectrometry (μLC-MS/MS) on a dual linear ion trap Fourier Transform Mass Spectrometer (FT-MS) LTQ Orbitrap Velos (Thermo Fisher Scientific, Darmstadt, Germany) coupled to an Ultimate® 3000 RSLC Ultra High Pressure Liquid Chromatographer (Thermo Scientific Dionex, Sunnyvale, USA) controlled by Chromeleon Software (version 6.8 SR11; Thermo Scientific Dionex, Sunnyvale, USA). Proteo/peptidoform identification and structural
characterization were performed using ProSight PC software v 3.0 SP1 (Thermo Fisher Scientific, Darmstadt, Germany). The detailed procedure followed for this analysis is described elsewhere [1]. Raw data derived from Top-Down analysis have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PRIDE: PXD002768.

In total, 1038 intact or fragment protein masses were detected by Top-Down mass spectrometry (Supplementary data Table S1). A total of 447 biomolecules were detected in RP-derived fractions and 591 biomolecules in GF-derived fractions. From all the identified biomolecules, 65 were identified using both fractionation methods, while the rest was identified uniquely after RP or GF chromatography separation. The distribution of molecular weight and isoelectric point of the identified masses after each pre-fractionation method is represented in Fig. 1A and B, respectively.

3. Functional analysis

In order to identify which cell compartments/functions/pathways were mainly represented by the data set, a systems biology analysis was performed. In brief, the UniProtKB accession numbers from all m/z masses that were confidently identified through Top-Down analysis were recovered and listed. From these, the official human gene symbols (HuGO Gene Nomenclature Committee) were retrieved from Gallus gallus annotated proteins, whereas uncharacterized proteins were mapped to the corresponding Homo sapiens orthologs by identifying the reciprocal-best-BLAST hits. When manual annotation was needed (i.e. for deleted entries), this was performed by BLASTp (E value ≤ e−04), together with Gene Ontology (GO) functional annotation. Because far more human genes are annotated and more information in databases is available for humans than for chicken, the human background was employed when possible. The functional classification tool from the Database for Annotation, Visualization and Integrated Discovery (DAVID version 6.7) website (https://david.ncifcrf.gov/home.jsp) was employed to group proteins contained in our dataset based on functional similarity (Supplementary Data Table S2). Functional analysis was also performed using the Panther Functional Classification System (http://pantherdb.org/) to evidence the most represented molecular functions (Fig. 2A) and biological processes (Fig. 2B). The functional analysis was completed using the “Set Distiller” module of GeneDecks (http://genecards.weizmann.ac.il/v3/index.php?path=GeneDecks; Supplementary Data Table S3).

The data presented here consist in a list of intact and unmodified (by chemical treatment) endogenous low molecular weight biomolecules (< 15 kDa) present in chicken sperm. This dataset can be further employed as reference for other studies focused on the research of sperm cells.

Acknowledgments

This work was supported by the French National Infrastructure of Research CRB anim funded by “Investissements d’avenir”, ANR-11-INBS-0003 and from the French National Institute of Agronomic Research. The high resolution mass spectrometer was financed (SMHART project no. 3569) by the European Regional Development Fund (ERDF), the Conseil Régional du Centre, the French National Institute for Agricultural Research (INRA) and the French National Institute of Health and Medical Research (Inserm). Laura Soler has received the support of the EU in the framework of the Marie-Curie FP7 COFUND People Programme, through the award of an AgreenSkills fellowship (under Grant agreement no. 267196).

Transparency document. Supplementary material

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.07.050.
Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.07.050.

Reference

[1] L. Soler, V. Labas, A. Thelie, I. Grasseau, A.P. Teixeira-Gomes, E. Blesbois, Intact cell MALDI-TOF MS on sperm: a molecular test for male fertility diagnosis, Mol. Cell. Proteom. (2016), pii: mcp.M116.058289.