Data Article

Dataset supporting the proteomic differences found between excretion/secretion products from two isolates of *Fasciola hepatica* newly excysted juveniles (NEJ) derived from different snail hosts

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** Abstract

Here we present the proteomic profile datasets of two *Fasciola hepatica* NEJ isolates derived from different snail hosts: *Lymnaea viatrix* and *Pseudosuccinea columella*. The data used in the analysis are related to the article ‘A proteomic comparison of excretion/secretion products in *Fasciola hepatica* newly excysted juveniles (NEJ) derived from *Lymnaea viatrix* or *Pseudosuccinea columella*’ (Di Maggio et al., 2019)

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1. Data

Here we report the proteomic analysis of excretion/secretion products (ESP) from two isolates of *Fasciola hepatica* NEJ (Rubino strain and US Pacific North West wild strain), contrasting their similarities and differences in protein composition and abundance. The complete list of identified proteins and their corresponding peptides have been provided in Supplementary Table 1 (*F. hepatica*-derived proteins) and Supplementary Table 2 (*B. taurus*-derived proteins). Also, provide a comparison between *B. taurus*-derived proteins identified in *Pseudosuccinea columella* and *Lymnea viatrix* NEJ ESP samples (Table 1).

2. Experimental design, materials and methods

2.1. Biological material

The biological materials, metacercariae, were purchased from the laboratory DILAVE “Miguel C. Rubino” in Montevideo, Uruguay (Rubino strain) and from Baldwin Aquatics Inc. in Oregon, USA (US Pacific North West wild strain). The Rubino strain derived from cercariae developed in *Lymnaea viatrix*, and the US Pacific North West wild strain derived from cercariae developed in *Pseudosuccinea columella*. NEJ in vitro excystation proceeded at the same time and laboratory conditions for both strains. In brief, metacercariae (n = 500–1000) were activated in vitro and NEJ were allowed to excyst as previously described [4]. The emerging NEJ (n = 200–600) were washed with sterile phosphate-buffered saline (PBS, pH 7.4), and maintained at 37 °C, 5% CO₂ in 1 mL of sterile culture medium.
The ESP-containing supernatants were collected after incubation for 12 h. All ESP supernatant samples were syringe-filtered (0.22 μm), and concentrated using centrifugal filter of 3 kDa molecular weight cut-off. The protein concentrates were quantified by absorbance at 280 nm in a Nanodrop 1000 spectrophotometer (Thermo Fisher Scientific, USA), lyophilized, and stored at -80 °C.

2.2. LC-MS-MS sample preparation

Lyophilized ESP samples were diluted in a buffer containing 8 M urea/0.1 M Tris, pH 8.5, reduced with 5 mM Tris (2-carboxyethyl) phosphine hydrochloride, and alkylated with 25 mM iodoaceamide. The ESP samples were hydrolyzed overnight at 37 °C in 2 M urea/0.1M Tris pH 8.5, 1 mM CaCl₂ buffer with trypsin (final ratio 1:20, enzyme: substrate). Formic acid (5% final concentration) was added to stop the reaction, and samples were centrifuged at 17,000 g for 5 min at 4 °C for debris removal. Pre-columns were packed in-house with 2 cm of a reversed-phase resin (5-μm ODS-AQ C18) particle slurry stored in methanol. Analytical reversed-phase columns were prepared by pulling a 100 μm ID/360 μm OD silica capillary into a 5-μm ID tip. Reversed-phase resin (20 cm) was packed directly onto the pulled column. Pre-columns and analytical columns were connected using a zero-dead volume union.

2.3. LC-MS/MS

Nanoflow LC-MS/MS with an Easy NanoLC II coupled to a Q Exactive mass spectrometer (Thermo Fisher Scientific, USA) was used to analyze the peptide mixtures. Mobile phases were solution A (5% acetonitrile/0.1% formic acid) and solution B (80% acetonitrile/0.1% formic acid), at a flow rate of 400 nL/min. Sample material (1.5 μg per injection) was applied into the column. LC-MS/MS was performed in 155-min chromatographic runs as follows: 1—10% B for 10 minutes, 10—40% B for 100 minutes, 40—50% B for 10 minutes, and 50—90% B in 10 minutes. The column was flushed with 90% B for 10 minutes, then brought back to 1% B, and re-equilibrated prior to the next injection. Peptides eluted from the analytical column were electrosprayed directly into the mass spectrometer.

The mass spectrometer was operated in a data-dependent mode, collecting a full MS scan from 400 to 1,200 m/z at 70,000 resolution and AGC target of $1 \times 10^5$. The 10 most abundant ions in each MS scan were selected for MS/MS with AGC target of $2 \times 10^5$, and an underfill ratio of 0.1%. Normalized collision Table 1

Bos taurus-derived proteins identified by LC-MS/MS in Pseudosuccinea columella and Lymnea viatrix NEJ ESP samples.

| Accession number | Description | L.viatrix | L. columella |
|------------------|-------------|-----------|-------------|
| sp/Al1595/K1C17_BOVIN | Keratin, type II cytoskeletal 80 | * | * |
| sp/P08728/K1C19_BOVIN | Keratin, type I cytoskeletal 19 | * | * |
| tr/E1BG5/E1BG5_BOVIN | Complement component C1q receptor | * | * |
| tr/E1BJB1/E1BJB1_BOVIN | Tubulin | * | * |
| tr/F1MC11/F1MC11_BOVIN | Keratin | * | * |
| tr/F1MIH7/F1MIH7_BOVIN | Small GTPase mediated signal transduction | * | * |
| sp/P68138/ACTS_BOVIN | Actin, alpha skeletal muscle | * | * |
| sp/Q5XQ5/K2C5_BOVIN | Keratin, type II cytoskeletal 5 | * | * |
| sp/P00760/TRY1_BOVIN | Cationic trypsin | * | * |
| sp/P06394/K1C10_BOVIN | Keratin | * | * |
| sp/P0CH28/UBC_BOVIN | Polyubiquitin-C | * | * |
| sp/Q29521/K2C7_BOVIN | Keratin type II cytoskeletal 7 | * | * |
| tr/F1MF9/F1MF9_BOVIN | Keratin | * | * |
| tr/F1MU2/F1MU2_BOVIN | Keratin | * | * |
| tr/F2Z4I6/F2Z4I6_BOVIN | Histone H2A | * | * |
| tr/G3N0V2/G3N0V2_BOVIN | Keratin | * | * |
| tr/M0QVY0/M0QVY0_BOVIN | Keratin | * | * |
| tr/Q17QG8/Q17QG8_BOVIN | Histone H2A | * | * |

(RPMI 1640, 30 mM HEPES pH 7.2, 2% glucose and 10% penicillin/streptomycin/amphotericin B mix).
energy was set to 25 and maximum fill times were 20 ms and 120 ms for MS and MS/MS scans, respectively, with dynamic exclusion of 15 s. Peptide and protein identification was done with Integrated Proteomics Pipeline–IP2 (Integrated Proteomics Applications, http://www.integratedproteomics.com). Tandem mass spectra were extracted from Thermo RAW files using RawExtract 1.9.9.2 [5], and searched with ProLuCID [6] against a non-redundant database comprising coding sequences from Fasciola hepatica genome [2] concatenated with a Bos taurus UniProt reference database, in addition to reverse sequences of all entries. The search space included all fully-tryptic and half-tryptic peptide candidates with no missed cleavage restrictions. Carbamidomethylation on cysteine residues was used as a static modification. Data was searched with 50 ppm precursor ion tolerance and 20 ppm fragment ion tolerance. Identified proteins were filtered using DTASelect. Filtering required a minimum of 2 peptides per protein, at least one tryptic terminus for each peptide identification, and less than 1% FDR (false discovery rate). Normalized spectral abundance factor (NSAF) of the different samples was calculated according to Zybailev et al. [7]. A volcano plot was generated by pairwise comparison between ESP derived from NEJ from L. viatrix and from P. columella snails, using the PaternLab’s TFold module [8].

2.4. Functional annotation

The functional annotation and classification of the matched proteins by BLASTP searches against several databases were performed using a program developed and provided by Dr. José M. C. Ribeiro [9]. After annotation, proteins for each dataset were manually curated or annotated, and results were compiled in hyperlinked Excel spreadsheets (Supplementary Table 1 and Supplementary Table 2), as well as a table comparing B. taurus proteins found in both samples (Table 1). Proteomic profiles were compared between samples as functional categories or individual proteins. For data comparison, we used 90 proteins identified in our previously published study with ESP from F. hepatica NEJ derived from P. columella metacercaria [10]. Both F. hepatica metacercariae batches were obtained, processed and analyzed at the same time.

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Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dib.2019.104272.

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