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Data in Brief





Data Article

Dataset for the proteomic and transcriptomic analyses of perivitelline fluid proteins in *Pomacea* snail eggs



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ABSTRACT

This article describes how the proteomic and transcriptomic data were produced during a study of the reproductive proteins of Pomacea maculata, an aquatic apple snail laying colorful aerial eggs, and provides public access to the data. The data are related to a research article titled 'An integrated proteomic and transcriptomic analysis of perivitelline fluid proteins in a freshwater gastropod laying aerial eggs' (Mu et al., 2017) [1]. RNA was extracted from the albumen gland and other tissues and sequenced on an Illumina Hiseq. 2000. The assembled transcriptome was translated into protein sequences and then used for protein identification. Proteins from the perivitelline fluid of P. maculata were separated in SDS-PAGE and analyzed by LTQ-Orbitrap Elite coupled to an Easy-nLC. The translated transcriptome data are provided in this article. Proteomic data (.raw file format) are available via ProteomeXchange with the identifier PXD006718. © 2017 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license

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Specifications Table

Subject area	Biology
More specific sub- ject area	Apple snail proteomics and transcriptomics
Type of data	Table and.raw file
How data was acquired	SDS-PAGE, strong cation exchange (SCX) chromatography, and LTQ-Orbitrap Elite coupled to an Easy-nLC were used to acquire the proteomic data; Illumina Hiseq. 2000 sequencing was applied to acquire the transcriptomic data.
Data format	Analyzed
Experimental factors	Perivitelline fluid of snail eggs laid within 12 h.
Experimental features	Mass spectrometry was applied to determine the proteome profile of the egg perivitelline fluid, and transcriptome sequencing was used to determine differential gene expression in different tissues.
Data source location	Department of Biology, Hong Kong Baptist University, Hong Kong, China
Data accessibility	Data are available via ProteomeXchange with the identifier PXD006718
Related research article	An integrated proteomic and transcriptomic analysis of perivitelline fluid proteins in a freshwater gastropod laying aerial eggs [1]

Value of the data

- This dataset provides a comprehensive proteomic profile of perivitelline fluid of the apple snail *Pomacea maculata*. The proteomic data which were obtained from state-of-the-art mass spectrometry analysis can be used for protein identification, especially for reproductive proteins in gastropods.
- This dataset also provides translated transcriptomic profiles of the albumen gland and other tissues of *Pomacea maculata*. The translated transcriptome can be used as the database to support protein identification in gastropods.
- The data presented here can be used for studies of protein function and evolution in gastropods.

1. Data

Pomacea maculata is a freshwater snail native to South America that has invaded many regions of the world [2]. There is considerable interest in the reproductive biology of this species [3,4], but a lack of genomic resources has hindered such studies at the molecular level. We extracted the RNA from the albumen gland and other tissues, and sequenced them on Illumina Hiseq. 2000 to generate a database to support protein identification. Table 1 shows the number of contigs and unigenes in the assembled transcriptome, as well as the quality of the data. Table S2 contains 44,350 protein sequences which were translated from the transcriptome. These sequences were used for protein identification as described below. Proteins were extracted from the perivitelline fluid of newly laid eggs, fractionated using SDS-PAGE and analyzed with LTQ-Orbitrap Elite coupled to an Easy-nLC. The data files (.raw) generated by mass spectrometry was converted into.mgf files using Proteome Discovery 1.3.0.339 and searched against the protein database in Mascot 2.3.2 and they were deposited in ProteomeXchange.

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