



ELSEVIER

Contents lists available at ScienceDirect

## Data in Brief

journal homepage: [www.elsevier.com/locate/dib](http://www.elsevier.com/locate/dib)

## Data Article

Data from salivary gland proteome analysis of female *Aedes aegypti* Linn

Rakhi Dhawan<sup>a,b,c</sup>, Ajeet Kumar Mohanty<sup>b</sup>, Manish Kumar<sup>d,e</sup>,  
Gourav Dey<sup>d,e</sup>, Jayshree Advani<sup>d,e</sup>, T.S. Keshava Prasad<sup>d,f,g,\*</sup>,  
Ashwani Kumar<sup>b,\*\*</sup>

<sup>a</sup> Department of Community Medicine, Armed Forces Medical College, Pune 411040, India

<sup>b</sup> National Institute of Malaria Research, Field Station, Goa 403001, India

<sup>c</sup> Department of Zoology, Goa University, Taleigao Plateau, Goa 403206, India

<sup>d</sup> Institute of Bioinformatics, International Technology Park, Bangalore 560066, India

<sup>e</sup> Manipal University, Madhav Nagar, Manipal, Karnataka 576104, India

<sup>f</sup> YU-IOB Center for Systems Biology and Molecular Medicine, Yenepoya University, Mangalore 575018, India

<sup>g</sup> NIMHANS-IOB Proteomics and Bioinformatics Laboratory, Neurobiology Research Centre,

National Institute of Mental Health and Neurosciences, Bangalore 560029, India

## ARTICLE INFO

## Article history:

Received 20 March 2017

Received in revised form

13 May 2017

Accepted 18 May 2017

Available online 25 May 2017

## Keywords:

Proteomics

Salivary gland

Immunogenic

Vectorborne Diseases

*Aedes aegypti*

Protein–protein interactions

## ABSTRACT

Salivary gland proteins from female *Aedes aegypti* mosquito were extracted and analyzed on high-resolution mass spectrometry. Proteomic data was analysed using two search algorithms SEQUEST and Mascot, which results in acquisition of 83,836 spectra which were assigned to 5417 peptides belonging to 1208 proteins. These proteins were then assigned molecular functions and further analysis revealed biological processes they are involved in using Gene Ontology annotations. Several immunity related pathways were found to be enriched in salivary gland. The data of this study are also related to the research article “Mosquito–Borne Diseases and Omics: Salivary gland proteome of the female *Aedes aegypti* mosquito” (Dhawan et al., 2017) [1]. These data are deposited in ProteomeXchange in the public dataset PXD002468. In addition, a scientific interpretation of this dataset by Dhawan et al. [1] is available at <http://dx.doi.org/10.1089/journal.omi.2016.0160>.

© 2017 Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

\* Corresponding author at: Institute of Bioinformatics, International Tech Park, Bangalore 560066, India.

\*\* Corresponding author.

E-mail addresses: [keshava@ibioinformatics.com](mailto:keshava@ibioinformatics.com) (T.S.K. Prasad), [ashwani07@gmail.com](mailto:ashwani07@gmail.com) (A. Kumar).

## Specifications Table

Subject area	Biology
More specific subject area	Mosquito proteomics
Type of data	Mass spectrometry raw files, Excel tables, Graph, Figure
How data was acquired	LTQ-OrbitrapVelos ETD mass spectrometer (Thermo Scientific, Bremen, Germany) Proteome Discoverer 1.4 and MASCOT search engine (Matrix Science, London, UK; version 2.2) Protein database <i>Aedes aegypti</i> ( <a href="http://www.VectorBase.org">www.VectorBase.org</a> , release date 21 Oct 2014)
Data format	Analyzed output data
Experimental factors	Salivary gland tissues were obtained from the female <i>Aedes aegypti</i> mosquitoes
Experimental features	Qualitative protein analysis of salivary gland tissue of <i>Aedes aegypti</i>
Data source location	Goa and Bangalore, India
Data accessibility	Data are available here and via a web application (ProteomeXchange) Consortium ( <a href="http://proteomecentral.proteomexchange.org">http://proteomecentral.proteomexchange.org</a> ) via the PRIDE partner repository with the dataset identifier PXD002468.

## Value of the data

- To the best of our knowledge this data set is the largest catalogue so far providing insight into the proteome composition of salivary gland of female *Aedes aegypti*.
- Data provides information on roles identified proteins play in biological and functional categories, protein–protein interactions in metabolic pathways, secretory and immunogenic salivary proteins. Overall it enables better understanding of host-vector interaction and disease transmission.
- The data set is a useful resource of proteins expressed in salivary gland of *Aedes aegypti* female mosquitoes and will aid in biomedical research focused on development of transmission blocking vaccine.

## 1. Data

The core of this dataset is the raw and processed data of the LC-MS/MS analysis of salivary gland proteins of female *Aedes aegypti*. The processed data set contains 83,836 MS/MS spectra, which led to identification of 5417 peptides and 1208 proteins. All the peptides and proteins identified in this study are listed in [Supplementary Tables S1](#) and [S2](#). Twenty nine proteins were involved in immunity related pathways. Another 15 proteins with signal cleavage site were found to be secretory in nature and thus possibly playing critical roles in blood meal ingestion. To assign molecular functions to these proteins, we used VectorBase resource to assign Gene Ontology (GO) terms [2]. Dhawan et al. [1] performed a scientific interpretation of this dataset with the goal to identify salivary gland proteins that can be the attractive candidates for the transmission blocking vaccines.

## 2. Experimental design

### 2.1. Sample preparation

The freshly emerged five hundred female *Aedes aegypti* mosquitoes from laboratory maintained culture were dissected to obtain the salivary gland. The proteins were extracted using 0.5%SDS

Download English Version:

<https://daneshyari.com/en/article/4765027>

Download Persian Version:

<https://daneshyari.com/article/4765027>

[Daneshyari.com](https://daneshyari.com)