Data in Brief 5 (2015) 560–563

Contents lists available at ScienceDirect

Data in Brief

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

Data Article

Supporting data for analysis of the *Helicobacter pylori* exoproteome

Christina A. Snider [a], Bradley J. Voss [b], W. Hayes McDonald [c,d], Timothy L. Cover [a,b,e,*]

[a] *Department of Medicine, Nashville, TN, USA*
[b] *Department of Pathology, Microbiology and Immunology, Nashville, TN, USA*
[c] *Proteomics Laboratory, Mass Spectrometry Research Center, Nashville, TN, USA*
[d] *Department of Biochemistry, Nashville, TN, USA*
[e] *Vanderbilt University School of Medicine; Veterans Affairs Tennessee Valley Healthcare System, Nashville, TN, USA*

ARTICLE INFO

Article history:
Received 16 September 2015
Received in revised form
6 October 2015
Accepted 6 October 2015
Available online 17 October 2015

Keywords:
Mass spectrometry
Proteomics
Bacterial protein secretion
Secretome
Exoproteome
Gastric cancer
Peptic ulcer disease

ABSTRACT

The goal of this research was to analyze the composition of the *Helicobacter pylori* exoproteome at multiple phases of bacterial growth (Snider et al., 2015) [1]. *H. pylori* was grown in a serum-free medium and at serial time points, aliquots were centrifuged and fractionated to yield culture supernatant, a soluble cellular fraction, and a membrane fraction. Samples were analyzed by single dimensional LC-MS/MS analyses and multidimensional protein identification technology (MudPIT). Here we present data showing the numbers of assigned spectra and proportional abundance of individual proteins in each of the samples analyzed, along with a calculation of the level of enrichment of individual proteins in the supernatant compared to the soluble cellular fraction.

DOI of original article: http://dx.doi.org/10.1016/j.jprot.2015.08.025
* Correspondence to: Division of Infectious Diseases, Vanderbilt University School of Medicine, A2200 Medical Center North, Nashville, TN 37232, USA.
E-mail address: timothy.l.cover@vanderbilt.edu (T.L. Cover).

http://dx.doi.org/10.1016/j.dib.2015.10.008

Specifications Table

Subject area	Biology
More specific subject area	Microbiology
Type of data	Tables
How data was acquired	Mass spectrometry using a ThermoFisher LTQ equipped with a nano-electrospray source and attached to a Nanoacuity (Waters) HPLC unit.
Data format	Filtered and analyzed
Experimental factors	Bacteria were grown in broth culture, and at serial time points, aliquots were removed, centrifuged and fractionated, to yield culture supernatant, a soluble cellular fraction, and a membrane fraction.
Experimental features	Concentrated *H. pylori* broth culture supernatants, soluble cellular fractions, and membrane preparations were analyzed by single- dimensional LC-MS/MS or multidimensional protein identification technology.
Data source location	Nashville, Tennessee, USA
Data accessibility	Data are provided in the supplementary materials accompanying this article.

1. Value of the data

- Comparative analyses of the proteins present in *H. pylori* broth culture supernatants, soluble bacterial fractions, and membrane fractions allow the identification of *H. pylori* proteins that are selectively released into the extracellular space.
- Analysis at multiple time points allows the identification of growth phase-dependent changes in the composition of the exoproteome.
- Further analysis of the data should allow new insights into mechanisms by which *H. pylori* proteins are released into the extracellular space.
- Further analysis of the data may allow the identification of selectively released *H. pylori* proteins that cause alterations in host cells.

2. Data

H. pylori broth culture supernatants, soluble cellular fractions, and membrane fractions were analyzed by one dimensional LC-MS/MS (1D) or multidimensional protein identification technology (MudPIT). The numbers of assigned spectra were analyzed to calculate the proportional abundance of individual proteins in samples, the enrichment of proteins in the supernatant compared to soluble bacterial fraction, and the distribution of proteins between soluble and membrane fractions (membrane localization).

Supplemental Table S1 shows all assigned spectra detected by single-dimensional LC-MS/MS analysis of supernatant and cellular fractions from five time points, collected in three independent experiments.

Supplemental Table S2 shows an analysis of merged single-dimensional LC-MS/MS data from Supplemental Table S1 to calculate enrichment of individual proteins in the supernatant compared to the soluble cellular fraction.

Supplemental Table S3 shows an analysis of merged single-dimensional LC-MS/MS data from Supplemental Table S1 for 74 putative secreted proteins (identified as described in [1]). The table