fortune Journals

Research Article

JOURNAL OF BIOINFORMATICS AND SYSTEMS BIOLOGY

ISSN: 2688-5107

Theoretical 2D protein gel of Helicobacter pylori

Wenfa Ng

Abstract

Two-dimensional (2D) gel electrophoresis affords us a qualitative view of the proteome of an organism, which offers a rich understanding of the molecular weight and isoelectric points of proteins expressed under given environmental and nutritional conditions. But, clustering of proteins of similar molecular weight or isoelectric point or both makes separation of proteins difficult. To this end, a theoretical 2D protein gel calculated based on experimental proteome of an organism would provide important clues to the ability of 2D gel electrophoresis to separate two target proteins. More importantly, a theoretical 2D gel is a visualisation of the distribution of isoelectric points and molecular weights of all proteins in the species, which is important to gaining an approximate but high-level understanding of the physiological properties of the organism. This work presents the theoretical 2D protein gel of Helicobacter pylori.

Keywords: *Helicobacter pylori*; 2D gel electrophoresis; Isoelectric point; Molecular weight; Cellular proteome.

Subject areas: Biochemistry; Bioinformatics; Computational Biology.

Introduction

Proteomics is our windows to the ensemble of proteins that participates in varied processes in the cell. While the current go-to technique for understanding intracellular proteomics is liquid chromatography mass spectrometry (LC-MS) [1] [2], the standard 2-D gel electrophoresis technique is still useful in lending a qualitative understanding of the quintessential characteristics of the microbial species' proteome, particularly, in the dimension of distribution of isoelectric point and molecular weight [3].

In a standard 2D gel electrophoresis experiment interrogating the proteome of a species, not all proteins can be fully resolved as separate entities on the gel as they may not be separated in one or both dimensions of the gel. Thus, this study aims to provide a qualitative readout of the theoretical proteome of a species through a x-y scatter plot of the molecular weight and isoelectric point of all theoretical proteins of the cell. Theoretical proteins, in this case, refers to the encoded proteins corresponding to genes on the genome of the species. Hence, a theoretical 2D-gel of the species captures all the proteins of the organism, while a real-life 2D gel electrophoresis is constrained by variance of gene expression pattern given environmental and nutritional conditions as not all genes are expressed at any given time. At the minimum, a theoretical 2D gel will give us an understanding of the relative difficulty of separating target proteins on a real 2D gel electrophoresis experiment. In addition, it will also provide a visual readout of the distribution of proteins in the cell according to molecular weight and isoelectric point. This work attempts to calculate the theoretical 2D gel of the gastric pathogen, *Helicobacter pylori*.

Affiliation:

Department of Biomedical Engineering, National University of Singapore, Singapore

***Corresponding author:**
Wenfa Ng, Department of Biomedical Engineering, National University of Singapore, Singapore.

Citation: Wenfa Ng. Theoretical 2D protein gel of Helicobacter pylori. Journal of Bioinformatics and Systems Biology. 8 (2025): 36-37.

Received: February 21, 2025
Accepted: February 27, 2025
Published: March 07, 2025

Wenfa Ng., J Bioinform Syst Biol 2025
DOI:10.26502/jbsb.5107100

Materials and Methods

Proteome of *Helicobacter pylori* was downloaded from UniProt and processed with an in-house MATLAB proteome analysis software that parses the original FASTA file, and also calculated new variables such as number of residues, molecular weight of protein, isoelectric point of protein, and nucleotide sequence of protein. The ensemble of molecular weight and their corresponding isoelectric point were plotted in Excel to yield the theoretical 2D gel presented in this work.

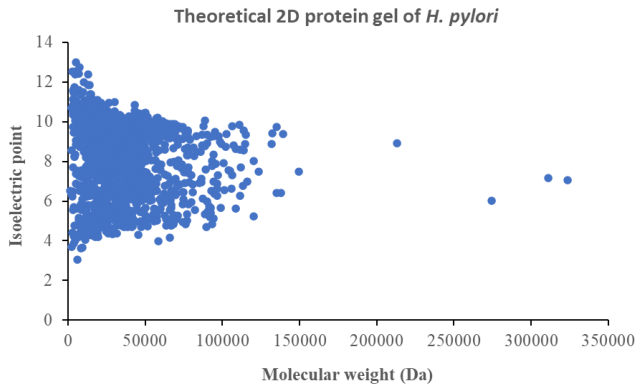

Figure 1: Theoretical 2D protein gel of *Helicobacter pylori*

Figure 1 shows the theoretical 2D gel visualisation for *H. pylori*. It can be seen from the plot that there is a big cluster of proteins of molecular weight under 75 kDa and isoelectric point between 4 and 10. This means that there is a paucity of large marcomolecular complex in *H. pylori* given the few large proteins in the proteome. In addition, isoelectric points of proteins in the species span a relatively large range between 4 and 10, which means that *H. pylori* has the protein machinery to handle a relatively large range of environmental conditions and changes to its cytoplasm. This latter property augments *H. pylori's* ability to survive harsher environments such as that in the human stomach.

Conclusion

Despite the advent and increasing popularity of liquid chromatography mass spectrometry (LC-MS) methods for interrogating proteome of organisms, 2D gel electrophoresis remain useful as a quick, easy to setup, first experiment looking into the distribution of cellular proteins along the principal component dimensions of isoelectric point and molecular weight. Theoretical calculations based on an experimental proteome of H. pylori done in this work reveals that the theoretical 2D-gel visualisation of the organism reveals a heavy clustering of proteins under 75 kDa and with isoelectric point between 4 and 10. Prevalence of smaller proteins and ability to function within a larger pH range suggests that H. pylori may have unique adaptations, at the protein level, to survive and thrive under extreme environments such as in the human stomach.

Conflicts of interest

The author declares no conflicts of interest.

Funding

No funding was used in this work.

References

1. Karpievitch YV, Polpitiya AD, Anderson GA, et al. Liquid chromatography mass spectrometry-based proteomics: Biological and technological aspects. Ann Appl Stat 4 (2010): 1797–1823.
2. Xiang P, Zhu Y, Yang Y, et al. Picoflow Liquid Chromatography–Mass Spectrometry for Ultrasensitive Bottom-Up Proteomics Using 2-µm-i.d. Open Tubular Columns. Anal Chem 92 (2010): 4711–4715.
3. Marcus K, Lelong C, Rabilloud T. What Room for Two-Dimensional Gel-Based Proteomics in a Shotgun Proteomics World?. Proteomes 8 (2020).