Data in Brief 4 (2015) 468–473

Contents lists available at ScienceDirect

Data in Brief

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

Data for comparative proteomics analysis of the antitumor effect of CIGB-552 peptide in HT-29 colon adenocarcinoma cells

Teresa Núñez de Villavicencio-Díaz [a], Yassel Ramos Gómez [a], Brizaida Oliva Argüelles [b], Julio R. Fernández Masso [a], Arielis Rodríguez-Ulloa [a], Yiliam Cruz García [c], Osmany Guirola-Cruz [a], Yasset Perez-Riverol [d], Luis Javier González [a], Inés Tiscornia [e], Sabina Victoria [e], Mariela Bollati-Fogolín [e], Vladimir Besada Pérez [a], Maribel Guerra Vallespi [b]

[a] *Department of Systems Biology, Center for Genetic Engineering and Biotechnology, Cuba*
[b] *Pharmaceuticals Department, Center for Genetic Engineering and Biotechnology, Cuba*
[c] *Department of Preclinical Studies, National Institute of Oncology and Radiobiology of Cuba, Cuba*
[d] *European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Trust Genome Campus, Hinxton, Cambridge, UK*
[e] *Cell Biology Unit, Institut Pasteur of Montevideo, Uruguay*

ARTICLE INFO

Article history:
Received 11 June 2015
Received in revised form
23 June 2015
Accepted 24 June 2015
Available online 8 July 2015

Keywords:
Colorectal cancer
Apoptosis
Inflammation
CIGB-552 synthetic peptide
Enrichment analysis
Text mining

ABSTRACT

CIGB-552 is a second generation antitumor peptide that displays potent cytotoxicity in lung and colon cancer cells. The nuclear subproteome of HT-29 colon adenocarcinoma cells treated with CIGB-552 peptide was identified and analyzed [1]. This data article provides supporting evidence for the above analysis.

© 2015 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

DOI of original article: http://dx.doi.org/10.1016/j.jprot.2015.05.024
E-mail address: teresa.nunez@biocomp.cigb.edu.cu (T. Núñez de Villavicencio-Díaz).

http://dx.doi.org/10.1016/j.dib.2015.06.024
2352-3409/© 2015 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

Specifications Table

Subject area	Biology
More specific subject area	Pharmacology, Proteomics
Type of data	Figure, table, methods
How data was acquired	Mass spectrometry: hybrid quadrupole orthogonal acceleration tandem mass spectrometer QTof-2 (Micromass, Manchester, U.K.)
Data format	Analyzed
Experimental factors	Isolation of the Nuclear Proteins Enriched Fraction, trypsin digestion and isotope labeling of peptides
Experimental features	Subcellular fractionation, protein and peptide fractionation by DF-PAGE and LC-MS/MS peptide identification
Data source location	Havana, Cuba
Data accessibility	The data are provided in this article.

Value of the data

- The data details the DF-PAGE separation method used in the proteomics analysis of GIGB-552 peptide effect.
- The data details the bioinformatics-driven approach used for the functional classification of the identified and differentially modulated proteins.
- The data provides an overview of the nuclear proteins differentially modulated in HT-29 colon adenocarcinoma cells treated with the antitumor peptide CIGB-552 and their functional classification.

1. Data, experimental design, materials and methods

We performed a comparative proteomics experiment in duplicate focusing on the quantification of the nuclear subproteome of the human HT-29 colon adenocarcinoma cells via a dual-fractionation by polyacrylamide gel electrophoresis (DF-PAGE) approach. The differentially modulated proteins were functionally analyzed using a systems biology workflow that integrates the information obtained from two main groups of bioinformatics tools [1].

2. Dual fractionation by polyacrylamide gel electrophoresis (DF-PAGE)

The DF-PAGE method combines sequentially, protein fractionation by SDS-PAGE, in-gel tryptic digestion and peptide fractionation by SDS-free PAGE [2,3]. In the first fractionation step (SDS-PAGE), proteins are solubilized in a SDS containing solution and separated according to their size. The presence of SDS ensures the solubilization of virtually all the proteins including highly hydrophobic proteins [2]. After the in-gel tryptic digestion, the peptide mixture is transferred to a second SDS-free gel. In the absence of SDS, peptides migrate according to their charge and size which is orthogonal to the peptide separation in RP-C18 during the LC-MS/MS analysis [2]. For quantitative DF-PAGE, isotope labeling of peptides is introduced with normal- or deuterated N-acetoxysuccinimide just before peptide fractionation by SDS-free PAGE. Fig. 1 shows a SDS-PAGE analysis of soluble and nuclear fractions for CIGB-552 peptide treated and control samples of two independent experiments. Fig. 2 represents a schematic representation of the DF-PAGE method [3]. Finally, Fig. 3 shows same data as Fig. 1 but for the nuclear fractions obtained from control and treated samples.

Download English Version:

https://daneshyari.com/en/article/175094

Download Persian Version:

https://daneshyari.com/article/175094

Daneshyari.com