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Data Article

Data in support of metabolic reprogramming in transformed mouse cortical astrocytes: A proteomic study

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ABSTRACT

2D-DIGE analysis coupled with mass spectrometry is a global, without a priori, comparative proteomic approach particularly suited to identify and quantify enzymes isoforms and structural proteins, thus making it an efficient tool for the characterization of the changes in cell phenotypes that occur in physiological and pathological conditions. In this data article in support of the research article entitled "Metabolic reprogramming in transformed mouse cortical astrocytes: a proteomic study" [1] we illustrate the changes in protein profile that occur during the metabolic reprogramming undergone by cultured mouse astrocytes in a model of in-vitro cancerous transformation [2].

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Specifications table

Subject area	Biology
More specific subject area	Cancer biology, Neurobiology
Type of data	Table, figures
How data was acquired	Fluorescence scanning of bi-dimensional electrophoretic separations of pre-labeled protein samples, using a Typhoon 9400 scanner. Mass spectrometry of peptides generated from proteins in 2D gel plugs, using an UltraFlex II spectrometer (Brüker Daltonics).
Data format	Analyzed using DeCyder 7.0 program
Experimental factors	Proteins extracted from treated and control cultures in a detergent and urea containing buffer, then labeled with CyDyes.
Experimental features	2D electrophoresis (1st dimension pH 3–10 gradient; 2nd dimension 12.5% PAGE). Spot picking with EtanDalt Spotpicker. Trypsin digestion of proteins and MALDI-TOF/TOF analysis of the peptides.
Data source location	N/A
Data accessibility	Data is provided in Supplementary materials directly with this article.

Value of the data

- Quantitative proteomics study exploring the changes in cellular protein abundance that result from metabolic reprogramming following astrocyte transformation.
- Multiple changes occur with similar amplitude for enzymes catalyzing successive steps in canonical metabolic pathways.
- Illustration of the power of 2D-DIGE to reveal (and quantify) changes in abundance of multiple isoforms of enzymes and cellular proteins.

1. Data, experimental design, materials and methods

Using the 2D-DIGE approach we have obtained relevant information on the changes in abundance of most enzymes implicated in major canonical metabolic pathways [1]. Supplementary Table 1 lists all the identified proteins whose abundance differs by at least 1.5-fold ($p < 0.05$, student t-test) between normal astrocytes (NA) and transformed astrocytes (TA).

Our results suggest that transformation causes major losses of astrocyte-specific proteins and functions and the acquisition of metabolic adaptations that favor intermediate metabolites production for increased macromolecule biosynthesis. We also observe a loss of some enzymes implicated in the oxidative stress defense. This is illustrated in Supplementary materials showing zoomed-in 2D gels regions where the spots containing the proteins/enzymes that underwent these changes (e.g. Pyruvate kinase, Lactate dehydrogenase, Glutamate dehydrogenase, Glutamine synthetase, Transaldolase, Peroxiredoxin 1 and 6, Glutathione S-transferase Mu1…) are visible, together with a graphical representation of the quantitative data.

1.1. Cell culture preparation

Cultures of mouse normal astrocytes were prepared from cortices of 1-to-2-day-old C57Bl6/J mice according to protocols described by Sharif in 2007 [3] and Prevot in 2005 [4] with slight adaptations.