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Data Article

Data for mitochondrial proteomic alterations in the developing rat brain

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ABSTRACT

Mitochondria are a critical organelle involved in many cellular processes, and due to the nature of the brain, neuronal cells are almost completely reliant on these organelles for energy generation. Due to the fact that biomedical research tends to investigate disease state pathogenesis, one area of mitochondrial research commonly overlooked is homeostatic responses to energy demands. Therefore, to elucidate mitochondrial alterations occurring during the developmentally important phase of E18 to P7 in the brain, we quantified the proteins in the mitochondrial proteome as well as proteins interacting with the mitochondria. We identified a large number of significantly altered proteins involved in a variety of pathways including glycolysis, mitochondrial trafficking, mitophagy, and the unfolded protein response. These results are important because we identified alterations thought to be homeostatic in nature occurring within mitochondria, and these results may be used to identify any abnormal deviations in the mitochondrial proteome occurring during this period of brain development. A more comprehensive analysis of this data may be obtained from the article "Proteomic analysis of mitochondria from embryonic and postnatal rat brains reveals response to developmental changes in energy demands" in the Journal of Proteomics.

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Specifications table

Subject area	Biology
More specific subject area	Development
Type of data	Protein Expression Table
How data was acquired	SWATH Mass spectrometry; AB SCIEX Triple-TOF 5600
Data format	Normalized data
Experimental factors	Age
Experimental features	Brains were harvested from male E18 and P7 rats ($n=4$). Mitochondria were isolated by a dual, sequential isolation, and the resulting protein was used for mass spectrometry analysis
Consent	Data was obtained with approval for animal experiments provided by the University of Nebraska Medical Center IACUC
Data source location	Omaha, NE
Data accessibility	Data is provided in the paper

Value of the data

- These data demonstrate the ability to perform a mass spectrometry experiment with low biological variability.
- Proteins involved in many key mitochondrial processes including the electron transport chain, glycolysis, trafficking, mitophagy and the unfolded protein response were found to be differentially expressed.
- Altered mitochondrial localization can be inferred by the change in cytoplasmic proteins interacting with the mitochondria.
- Extensive proteomic alterations occur between E18 and P7 rat brain mitochondria.

1. Experimental design, materials and methods

Sprague-Dawley rats from Charles River were used for experiments (Wilmington, MA). Four male animals were used in the E18 and P7 groups. All protocols were conducted within NIH-approved guidelines with the approval and oversight of the University of Nebraska Medical Center IACUC.

1.1. Isolation of whole brain mitochondria

Brains were isolated using a previously established protocol [1] from E18 or P7 Sprague-Dawley rats (Charles River). Brains were rinsed, chopped and mitochondria were isolated as previously published using a dual sequential isolation consisting of differential centrifugation and an affinity purification with TOM22 [1,2]. Protein amount was quantified using Scopes method in conjunction with a Nanodrop (Thermo Fisher Scientific).

1.2. Sample preparation for mass spectrometry

Protein was treated as stated previously for mass spectrometry. In short, proteins were digesting with trypsin using FASP, and the resultant peptides were cleaned with an Oasis mixed-mode weak cation exchange cartridge (Waters, Milford, MA). A Savant ISS 110 SpeedVac Concentrator was used to concentrate samples (Thermo Fisher Scientific). A Nanodrop (Thermo Fisher Scientific) in conjunction with Scopes method was used for peptide quantification [3]. Peptides from each sample were resuspended in 6 μL of 0.1% formic acid for LC–MS/MS analysis.