Data Article

Proteomic and functional data sets on synaptic mitochondria from rats with genetic ablation of Parkin

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A B S T R A C T

In this paper, we provide proteomic and functional data for synaptic mitochondria from the striatum of rats with Parkin ablation. The quantitative proteomic data was obtained using SWATH-MS methodology and mitochondrial function was assessed through measurement of oxygen consumption rate using the Seahorse XF Analyzer. This data facilitates comparisons with previous proteomic and functional data obtained using the exact same methods. A complete set of proteomic data is contained in Supplementary Table 1.

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Specifications Table

| Subject area        | Biology |
|---------------------|---------|
| More specific subject area | Neurobiology |
| Type of data        | Table, Graph |
| How data was acquired | SWATH-MS: TripleTOF 5600 (SCIEX), Respiration: Seahorse XF24 Extracellular Flux Analyzer |
| Data format         | Analyzed |

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Experimental factors: Genetic ablation of Park2 (Parkin).

Experimental features: Striatal synaptic mitochondria were isolated from 3-month-old male Parkin KO rats and age-matched controls and used for respiration studies or proteins were processed for mass spectrometry.

Data source location: Omaha, NE.

Data accessibility: The Seahorse data are included in this article. The complete SWATH-MS data can be accessed in Supplementary Table 1.

Value of the data:

- These data sets provide a useful resource to identify different synaptic mitochondrial processes that are affected due to loss of Parkin.
- This data will aid in comparisons of synaptic mitochondrial changes in Parkin KO rats with other PD animal models.

1. Data

Bioenergetic data generated using the Seahorse XF®96 Extracellular Flux Analyzer is provided. No significant alteration of either the respiratory state (Fig. 1A) or the electron transport chain function (Fig. 1B) for striatal synaptic mitochondria from 3-month-old male Parkin KO rats was found. Furthermore, no significant alteration was present in either the amount of proton leak (Fig. 1C) or the respiratory control ratio (RCR, Fig. 1D), which is an overall measure of mitochondrial health.

SWATH-MS-based proteomic data is presented for striatal synaptic mitochondria from 3-month-old Parkin KO rats, compared to control animals. The list of 131 differentially expressed proteins is provided in Supplementary Table 1. Consistently changed proteins found from the comparison of the striatal synaptic and non-synaptic mitochondria [1] isolated from Parkin KO rats are shown in Table 1. Furthermore, common differentially expressed proteins in striatal synaptic mitochondria from Parkin KO and PINK1 KO rats [2] are shown in Table 2.

2. Experimental design, materials and methods

2.1. Animals

Male Long Evans Hooded (LEH) (RRID:RGD_2308852) control and Parkin KO rats [3] were used at 3 months of age (three rats from each strain for respiration studies, n = 3; and four rats from each strain for proteomic experiments, n = 4). All protocols were conducted within NIH-approved guidelines for the Care and Use of Laboratory Animals with the approval and oversight of the University of Nebraska Medical Center Institutional Animal Care and Use Committee.

2.2. Isolation of synaptic mitochondria and respiration analysis

Brains were rapidly isolated from the animals, and the striatum (identified as per [4]) was removed by an investigator blinded to rat genotype and immediately rinsed with ice-cold 1x Phosphate Buffered Saline (Sigma, 806552) to remove blood. Tissue was chopped and homogenized using 10 strokes with a Dounce homogenizer (abcam, ab110169). Striatal synaptic mitochondria were isolated as previously described [5] with slight modifications [6] and oxygen consumption rates were measured using 3–4 technical replicate wells (7.5 μg of striatal synaptic mitochondria per well) for each biological replicate with a Seahorse XFe24 Analyzer (Agilent) for the previously described coupling and electron flow assays [7]. For data calculation the Seahorse Wave software (v2.2.0) was
used. Prism (GraphPad) was used for graphs and statistical analyses (ANOVA and Sidak's multiple comparisons post-hoc testing).

2.3. Sample preparation for mass spectrometry

Synaptic mitochondria were lysed in 4% sodium dodecyl sulfate (Gibco, 15553), protein concentration was determined using a Pierce 660 nm Protein Assay (Thermo Fisher Scientific, 22660), and the filter aided sample preparation method [8] was used to prepare the synaptic mitochondrial peptides for mass spectrometry as described previously [9].
2.4. Data-independent SWATH-MS analysis

Striatal synaptic mitochondrial peptides were analyzed using SWATH data-independent analysis (DIA) mode on a TripleTOF 5600 (SCIEX) followed by targeted data extraction as described previously [10] with the PeakView software (v2.1, SCIEX, RRID:SCR_015786) using our published reference spectral library [2,9,11]. CyberT (http://cybert.ics.uci.edu/) [12] was used with a sliding window of 61 and a Bayesian confidence coefficient of 12 and proteins were denoted as significantly altered following multiple-hypothesis testing correction if Benjamini & Hochberg (BH) q-values < 0.05.

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.08.053.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.08.053.

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