

Genetic upregulation of activated protein C mitigates delayed effects of acute radiation exposure in the mouse plasma

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LC gradient and MS instrument parameters

Untargeted metabolomics

For untargeted metabolomics data acquisition, each sample (1 μ L) was injected to a 1.7 μ m, 2.1 mm \times 50 mm Acquity BEH C18 column (Waters Corporation, MA, USA) using an Acquity UPLC system connected to an electrospray ion source coupled with a quadrupole time-of-flight mass spectrometer (ESI-Q-TOF, Xevo-G2S, Waters Corporation, MA, USA) operating in positive and negative ionization mode. The gradient mobile phases consisted of 100% water with 0.1% formic acid (solvent A), 100% acetonitrile with 0.1% formic acid (solvent B), 100% isopropanol with 0.1% formic acid (solvent C). Each sample injection was run for 13 minutes at a flow rate for 500 μ L/min. The LC gradient conditions with a ramp curve of 6 at each step were as follows: Initial – 98% A, 2% B till 0.5 minutes; 4.0 minutes – 40% A, 60% B; 8.0 minutes – 2% A, 98% B till 9.0 minutes; 9.5 minutes – 11.8% B, 88.2% C till 11 minutes; 11.5 minutes – 50% A, 50% B, 12.0 minutes – 98% A, 2% B till 13 minutes. Positive mode had a capillary voltage of 2.75 kV, a sampling cone voltage of 30 V, and a source offset of 80 V. Negative mode had a capillary voltage of 2.75 kV, a sampling cone voltage of 20 V, and a source offset of 80 V. The desolvation gas flow was 600 L/h. and the temperature was set to 500 $^{\circ}$ C. The cone gas flow was 25 L/h, and the source temperature was 100 $^{\circ}$ C. The data were acquired in the sensitivity MS Mode with a scan time of 1.000 seconds, and inter-scan delay at 0.014 seconds. Real-time mass correction was applied using a solution of Leucine-Enkephalin (1.0 ng/ml) [M+H]⁺ (m/z 556.2771), [M–H][–] (m/z 554.2615) in 500 ml of a mixture containing acetonitrile: water (50:50) and 250 μ L formic acid at an infusion rate of 20 μ L/min utilizing the Waters Lockspray® interface. Before and after samples run, a mixture of six standards (acetaminophen: m/z 152.0712 [M+H]⁺/150.0555 [M–H][–], sulfaguanidine: m/z 215.0603 [M+H]⁺/213.0446 [M–H][–], sulfadimethoxine: m/z 311.0814 [M+H]⁺/309.0658 [M–H][–], Val-Tyr-Val: m/z 380.2185 [M+H]⁺/378.2029 [M–H][–], terfenadine: m/z 472.3216 [M+H]⁺ and leucine-enkephalin: m/z 556.2771 [M+H]⁺/554.2615 [M–H][–]) were run to ensure mass accuracy during data acquisition (Supplementary Figure 3 and 4).

Targeted metabolomics

A binary solvent comprising of water with 0.1% formic acid (solvent A) and acetonitrile with 0.1% formic acid (solvent B) was used. The extracted metabolites were resolved at 0.2 mL/min flow rate starting with 100% of solvent A and hold for 2.1 minutes and moving to 5% of solvent A over a time period of 12 minutes and hold for 1 minute and equilibrating to initial conditions over a time period of 7 minutes using auto sampler temperature 15 $^{\circ}$ C and oven temperature 30 $^{\circ}$ C. Source and gas setting for the method were as follow: curtain gas = 35, CAD gas = medium, ion spray voltage = 2500 V in positive mode and –4500 V in negative mode, temperature = 400 $^{\circ}$ C, nebulizing gas = 60 and heater gas = 70.

Targeted Lipidomics

A binary solvent comprising of acetonitrile/water 95/5 with 10 mM ammonium acetate as solvent A and acetonitrile/water 50/50 with 10 mM ammonium acetate as solvent B was used for the resolution. Lipids were resolved at 0.7 mL/min flow rate, initial gradient conditions started with 100% of solvent A, shifting towards 99.9% of solvent A over a duration of 3 minutes, 94% of solvent A over a time period of 3 minutes and 25% of solvent A over a period of 4 minutes. Finally, washing with 100% of B for 6 minutes and equilibrating to initial conditions (100% of solvent A) over a time period of 6 minutes using auto sampler

temperature 15 °C and oven temperature 35 °C. Source and gas setting were as follow: curtain gas = 30, CAD gas = medium, ion spray voltage = 5.5 kV in positive mode and -4.5 kV in negative mode, temperature = 550 °C, nebulizing gas = 50 and heater gas = 60.

Data processing and statistical analysis

The quality and reproducibility of LC-MS data was ensured using several measures. The column was conditioned using a pooled QC sample that was prepared as a pooled aliquot of all samples in the study set. The QC sample was injected periodically (after every 10 sample injections) to monitor shifts in signal intensities and retention time as measures of reproducibility and ensure high quality data acquisition. A solvent blank sample was also run periodically to monitor and minimize the sample-to-sample carry-over. For targeted data, the detected metabolites were filtered using a signal/noise ratio >20:1 and retention time (RT) tolerance of 5 seconds criteria, to identify the reliable features. The details on LC gradient and mass spectrometry instrument parameters have been provided in the Supplementary information. Data pre-processing include normalization of the raw LC-MS data initially using internal standards. The detected metabolites/features (m/z_rt pairs) with more than 20% missing value were filtered out and with less than 20% of missing value were imputed by half of the minimum positive value in the original data. The features with more than 15% of coefficient of variance (CV) were also filtered out. The remaining high-quality features were normalized by Quality Control-Robust LOESS Signal Correction (QC-RLSC) followed by statistical analyses using R (version 4.0.1). For the 67 samples in the study set, the level of differential expression for each metabolite was calculated using an unpaired t-test, comparing sham versus irradiated plasma samples, constrained by p-value<0.05. We also compared gender and genotype based metabolic differences post irradiation in mice plasma. The identities of significantly dysregulated metabolites were confirmed using tandem mass spectrometry. Raw files from untargeted data were converted into MSP format with an in-house developed R package “msmsr” (Li et al., unpublished) and the NIST 2017 MS/MS spectra database. Mummichog v2.0, a Python package specifically designed for untargeted metabolomics was used for pathway analysis [12]. Mummichog v2.0 tests pathway enrichment patterns using permutations and computes the probability for involvement in each pathway. Figures were created using R and BioRender (www.BioRender.com).

[illegible]

Supplementary Table S2. List of dysregulated metabolites following exposure to 0.5 Gy of gamma-radiation, 6 months' post irradiation

