



Metabolomics 👄

PLOS Genetics

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Cage Studies



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EXT ERNAL LINK

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THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Aw WC, Towarnicki SG, Melvin RG, Youngson NA, Garvin MR, Hu Y, Nielsen S, Thomas T, Pickford R, Bustamante S, Vila-Sanjurjo A, Smyth GK, Ballard JWO (2018) Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. PLoS Genet 14(11): e1007735. doi: 10.1371/journal.pgen.1007735

PROTOCOL STATUS

Working

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- Metabolites were extracted using an ultrasonic probe (30 s), 1 h incubation at 4° C and then centrifugation to remove particulates
- 100 Âul aliquots of the supernatant were derivatised [200] before mass spectrometric interrogation with an Agilent GC/MSD system 3 (Agilent Technologies, CA, USA) controlled by Chemstation software.
- The GC inlet temperature was set to 230° C. 1.0 µl of derivatised sample was injected in splitless mode, using helium as a carrier gas at constant-flow of 1.0 ml/ min.
- Chromatographic separation was performed on a 30 m SH-RXi-5Sil MS column (Shimadzu, NSW, Australia) with 0.25 mm internal 5 diameter and 0.25 µm film thickness.
- The oven temperature was programmed at 70Ű C for 2 min, then ramped at 15Ű C/ min to 320Ű C, and held 8 min.
- Electron ionisation mass spectra were recorded at 1.4 scans/ s over the range m/z 50â€"700. The MSD auxiliary temperature, source temperature, and quadrupole temperature were set to 280° C, 230° C, and 150° C, respectively.
- Analytes were identified using the NIST 2011-Wiley Mass Spectra Library. GC peaks containing mass spectra with a match quality (spectral purity) of more than 70% were considered to be tentatively identified.
- No internal standard was employed. Normalisation was performed by maintaining a constant sample mass per volume.



10 Peak areas were log-transformed and statistical analysis used the limma package. Benjamini-Hochberg's correction was used to control the FDR.

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