

## Population Cage studies including four mitotype 👄

PLOS Genetics

Wen Aw1

<sup>1</sup>z3314717@unsw.edu.au

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Cage Studies



Wen Aw



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

1	1	Placing about 210	eggs from each fly	y line onto instant <i>Dro</i>	sophila media	(Carolina Biological S	นทท	ly Company	. NC	.USA	in bottles

- Bottles, each with a different mitotype, were placed into population cages (22 cm x 21 cm x 36 cm) such that there were ~850 flies/ cage.
- To establish a homogeneous gut flora each generation, four males from each mitotype, raised on instant food unless otherwise 3 stated, were ground in distilled water and 130 µL of the homogenate aliquoted into each bottle.
- On the first day of eclosion (adult emerging from a pupal case), plugs were removed from bottles and flies were released into population cages for 3 d.
- Bottles were removed and oviposition resources (yeast placed on top of the solidified agar-based medium containing 4% agar and 5 10% treacle) were put in cages and eggs were collected from 3-5 d old adult females.
- Surface sterilisation of eggs was achieved by washing in dilute bleach, and ~200 eggs were then placed on each diet.
- This protocol was then repeated for each generation. Following oviposition, adult flies were frozen.Â
- The frequency of adult females harbouring the distinct mitotypes was individually determined by sequencing and allele-specific PCR of 95 individual females from each cage.
- For the initial studies, DNA was extracted, and a ~900bp region of mtDNA amplified using the ND4L forward 5'-TAAACAAACTAATCTAACTAATA-3' and reverse 3'-GGTTGTGATATTATCTTATGG-5' primer and Sanger sequenced.



10 Chromatograms were imported into Sequencher 4.5 (Gene Codes, MI, USA) and the proportion of each mitotype/diet/generation determined.

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