

Data description for data files associated with Gangloff et al. 2020, "Mitochondria as central characters in a complex narrative: Linking genomics, energetics, pace-of-life, and aging in natural populations of garter snakes" published in *Experimental Gerontology*. <https://doi.org/10.1016/j.exger.2020.110967>

"Gangloffetal2020_CellularOCRData.csv"

Provides data on measures of cellular oxygen consumption rate and white blood cell counts in garter snakes (*Thamnophis elegans*).

ID: Identification number of each snake

Ecotype: Life-history ecotype of snake (genetic background): Slow-aging (SA) or Fast-aging (FA)

Population: Abbreviation for population of origin

CollectDate: Date on which the snake was collected

Sex: Male (M) or Female (F)

Mass: Mass (g)

SVL: Snout-to-vent length (mm)

Basal_OCR: Basal cellular oxygen consumption rate of peripheral blood mononuclear cells (picomoles per minute)

ATPProd_OCR: ATP-production associated cellular oxygen consumption rate of peripheral blood mononuclear cells (picomoles per minute)

Max_OCR: Maximum cellular oxygen consumption rate of peripheral blood mononuclear cells (picomoles per minute)

RBC_Contamination: Indicates evidence of red blood cell contamination of peripheral blood mononuclear cell sample (Y/N)

Lymphocytes: Number of lymphocytes counted in blood smear

Heterophils: Number of heterophils counted in blood smear

Basophils: Number of basophils counted in blood smear

Monocyte: Number of monocytes counted in blood smear

TotalWBC: Total number of white blood cells counted in blood smear

"Gangloffetal2020_RMRHaplogroupData.csv"

Provides data on whole-organism resting metabolic rate (oxygen consumption rate) and haplogroups in garter snakes (*Thamnophis elegans*).

ID: Identification number of each snake

Litter: Identification number for each litter born (2010 captive snake Cohort)

Temp: Temperature at which measurement was made (°C)

Sex: Male (M) or Female (F)

Mass: Mass (g)

SVL: Snout-to-vent length (mm)

Ecotype: Life-history ecotype of snake (genetic background): Slow-aging (SA) or Fast-aging (FA)

Population: Abbreviation for population of origin

VO2: Whole-organism resting oxygen consumption rate (mL O₂ per hour)

MassSpec_VO2: Mass-specific whole-organism resting oxygen consumption rate (mL O₂ per hour per gram)

CytB_SNP: Nucleotide in cytochrome B SNP position: cytosine (C) or thymine (T)

HaploGroup: Haplogroup assignment (A, B, or C)

AHaplotype: If within "A" haplogroup, A1 and A2 mitocluster

"Gangloffetal2020_RMRCytBSNP.csv"

Provides data on whole-organism resting metabolic rate (oxygen consumption rate) and haplogroups in garter snakes (*Thamnophis elegans*).

Experiment: Source of data: Gangloff et al. 2015 *Physiol Biochem Zool* (2015Gangloffetal) or newly collected data (2016Measures)

ID: Identification number of each snake

Litter: Identification number for each litter born (2010 captive snake Cohort)

Temp: Temperature at which measurement was made (°C)
Sex: Male (M) or Female (F)
Mass: Mass (g)
SVL: Snout-to-vent length (mm)
Ecotype: Life-history ecotype of snake (genetic background): Slow-aging (SA) or Fast-aging (FA)
Population: Abbreviation for population of origin
VO2: Whole-organism resting oxygen consumption rate (mL O₂ per hour)
MassSpec_VO2: Mass-specific whole-organism resting oxygen consumption rate (mL O₂ per hour per gram)
CytB_SNP: Nucleotide in cytochrome B SNP position: cytosine (C) or thymine (T)

“Gangloffetal2020_MtGenomeHaplotypes_AnnotatedAlignment.geneious”

This file can be imported into the program Geneious (14-day free trial available at www.geneious.com). It contains an annotated alignment of the protein-coding genes for the 127 mitochondrial haplotypes used in this study with the *T. elegans* mitochondrial reference genome. The naming convention of the samples is as follows:

PopulationCode_SampleID_Locality_Haplogroup_MitoCluster_Haplotype_CytB-SNP
Example: L4_5171-02_ELF_A_A2_A6_T

“Gangloffetal2020_Telegans_MitoGenomes_PhylogenyAlignment.nex”

This is a NEWICK file of the alignment of 127 unrelated *T. elegans* mitochondrial genomes (protein-coding regions), that was used for the phylogenetic analyses.

The naming convention of the samples is as follows:

PopulationCode_SampleID_Locality_Haplogroup_MitoCluster_Haplotype_CytB-SNP
Example: L4_5171-02_ELF_A_A2_A6_T

“Gangloffetal2020_Telegans_MitoGenomes_Phylogeny.nex.treefile”

This is a NEWICK file of the maximum-likelihood phylogeny estimated from protein-coding genes of 127 *T. elegans* mitochondrial genomes used in this study. This file can be imported into tree-reading programs such as FigTree, iTOL, or into phylogenetics packages such as the *r* package APE.

The naming convention of the samples is as follows:

PopulationCode_SampleID_Locality_Haplogroup_MitoCluster_Haplotype_CytB-SNP
Example: L4_5171-02_ELF_A_A2_A6_T

“Gangloffetal2020_StorageEffectsOCR.csv”

Provides data on measures of cellular oxygen consumption rate in garter snakes (*Thamnophis elegans*) measured repeatedly in samples held for a variable number of days in cell medium. Data from captive-born and wild animals.

RunDate: Date on which cellular OCR measurements were made

ID: Identification number of each snake

Nights: Number of nights isolated PBMCs held on growth medium before measurement

Basal_OCR: Basal cellular oxygen consumption rate of peripheral blood mononuclear cells (picomoles per minute)

ATPPProd_OCR: ATP-production associated cellular oxygen consumption rate of peripheral blood mononuclear cells (picomoles per minute)

Max_OCR: Maximum cellular oxygen consumption rate of peripheral blood mononuclear cells (picomoles per minute)