

Method of Cu Analysis

Water samples were collected for Cu analysis at the beginning of the experiment, daily updates of the treatment solution and the end of the experiment. The sample was acidified (65 % HNO₃) and stored at 4 °C until analysis. The Cu content in the water and in the digested samples was quantified using electrothermal atomic absorption spectrometry (Unicam 939 Spectrometer, GF90 furnace). All samples were analyzed repeatedly. The concentration of Cu in water was expressed as mean ± standard deviation (SD).

Table S1 Primers used for mtDNA copy number analysis from zebrafish

Gene	Primer (5'-3')	Amplicon size (bp)	Accession No.
<i>beta-2-microglobulin (b2m)</i>	F- CTGCTGTTGTCCTGAATGC T	131	ENSDART00000075127
	R- GAGTGGAGACTTTCCCCTG T		
<i>NADH dehydrogenase 1, mitochondrial (mt-nd1)</i>	F- ACAGCTCAGGAAGACACA TGAC	93	ENSDART00000093596
	R- CGGTGCTCGGTTTGTCT G		

Table S2 Primers used for RT-qPCR analysis from zebrafish

Gene	Primer (5'-3')	Amplicon size (bp)	Accession No.
<i>peroxisome proliferator activated receptor γ coactivator-1a (pgc1a)</i>	F- AGATGAGGAAAATGAGGC CAA	137	XM_017357140 .2
	R- GACAGCTCTGATCACTGGC A		
<i>mitofusin 1a (mfn1a)</i>	F- AGACTCGGAGGAGAGGAA GG	106	NM_200647.1
	R- AGGCCAAAACACTCGAACC A		
<i>mitofusin 1b (mfn1b)</i>	F- CTGTCAGTCAGTCGGTGTG T	146	XM_017358379 .2
	R- GCGCTTTAACGGAGAGGGA T		
<i>mitofusin 2 (mfn2)</i>	F- TGGCAGGGATTGGTGAAGT C	73	NM_001128254 .2
	R- TTCCGTTACTGGTCCTGCC		
<i>dynamin-related protein 1 (drp1)</i>	F- CGATCCTCTTGGCGGACTT A	123	NM_200922.1
	R- TTCACCTGCCTCTTCACCA G		
<i>ATP synthase δ, mitochondria 1 (mt-atp8)</i>	F- TCAGCTTAATCCAAAACCC TGA	114	ENSDARG0000 0063910
	R- ACTTGAGTTGGGTCATTAG GTTGA		
<i>cytochrome c oxidase I, mitochondria 1 (mt-co1)</i>	F- ATTCCACATCCAACCCCTG C	104	ENSDART0000 0093606
	R- TTGATGGCAGCTCTAGTTG GG		

<i>cytochrome b, mitochondria l (mt-cyb)</i>	F- GGCCTAAACCCCAACATGG A	158	ENSDART0000 0093625
	R- AGAGGGTTAGCAGGGGTG AA		
<i>NADH dehydrogenase 2, mitochondria l (mt-nd2)</i>	F- TGGAGGGTGAAGCGGACTT A	116	ENSDART0000 0093600
	R- TCAGAGTAAGTTGCGGAGC G		
<i>NADH dehydrogenase 4l, mitochondria l (mt-nd4l)</i>	F- GACACCCACGCACTTTAGT C	250	ENSDART0000 0093617
	R- GGTTCGAGCTGTGGCTACT A		
<i>NADH dehydrogenase 5, mitochondria l (mt-nd5)</i>	F- ACCACCTCCCATCTTAACG C	111	ENSDART0000 0093622
	R- TCGGGGGCTTCCTAACAG A		
<i>NADH dehydrogenase 6, mitochondria l (mt-nd6)</i>	F- AGCACGAAGCACACCATA ACT	136	ENSDART0000 0093623
	R- AGCTGATGTAAGCGGGGTT G		
<i>fatty acid binding protein 1b (fabp1b)</i>	F- AAGCTGAAGGTGGTGCTGA A	153	DQ062096.1
	R- GTCTTGCGTGTGTTTGCTCA		
<i>fatty acid binding protein 2 (fabp2)</i>	F- GCCCATGACAACCTGAAGA T	199	AY266452.1
	R- TGCCTTGCGTGTGAAAGT C		
<i>fatty acid binding protein 3</i>	F- TGGTAAAATGGTTATGACC TTGA	248	NM_152961.3

<i>(fabp3)</i>	R- CCCACCACCATCCATCATT		
<i>fatty acid binding protein 6 (fabp6)</i>	F- GCTGACCATAAGCTTCCCC A	70	NM_001002076 .2
	R- GGAGGTCTCCACCAGC TTTC		
<i>fatty acid binding protein 7a (fabp7a)</i>	F- ATGGTAAAATGGTTATGAC CTTGA	245	NM_131605.2
	R- CCACCATCCATCATTGACA TTCT		
<i>fatty acid binding protein 10a (fabp10a)</i>	F- TCTCCAGAAAGCATGGCCT	269	NM_152960.1
	R- TCCAGCTTGACGATGCACT T		
<i>apolipoprotein A-Ib (apoA1b)</i>	F- CAGCCACATCCACAGATCC A	177	NM_001100144 .2
	R- TGAGTGAGGGACTTGTGTG C		
<i>adipose triglyceride lipase (atgl)</i>	F- GCGTGACGGATGGAGAAA	102	XM_005174256 .4
	R- AGGCCACAGTAAACAGGA ATAT		
<i>carnitine palmitoyltransferase 1 (cpt1)</i>	F- CATCCTTAGGCCTGCTCTTC AAA	94	NM_001044854 .1
	R- ACCATGACACCCCCAACTA ACAT		
<i>peroxisome proliferator-activated receptor alpha (ppara)</i>	F- ACAGTGCGCTGTTCGTCAG	153	NM_001102567 .1
	R- CAGGGGTCAGAGCATCCAG		
<i>peroxisome proliferator-</i>	F- AATTCGCCAAGAGCATCCC	109	NM_131467.1

<i>activated receptor gamma (ppary)</i>	G		
	R- ATGAGCGGAGAAATCATG ATGATC		
<i>sterol regulatory element binding proteins1c (srebp1)</i>	F- CTAATGGCAGGAGCCAGTC C	161	NM_001105129 .1
	R- GATGGAGGCAGAAACCGA CA		
<i>β-actin</i>	F- CGAGCTGTCTTCCCATCCA	86	AF025305.1
	R- TCACCAACGTAGCTGTCTT TCTG		