Electronic Supplementary Material (ESI) for Food & Function.
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Supplemental Materials

Figure S1. MMP.

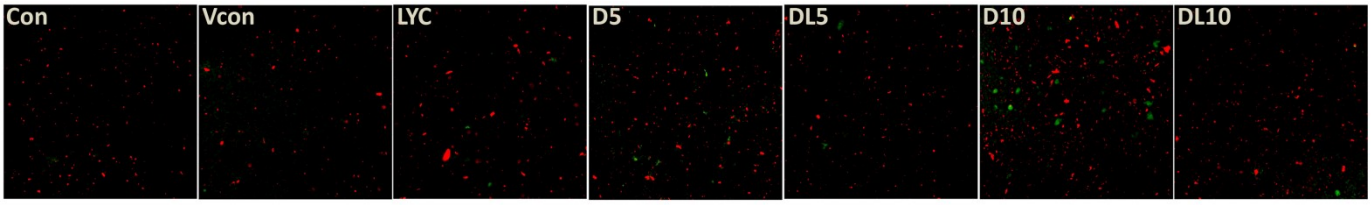

Table S1. Animal groups.

Groups	Number	Treatment	Concentration
Con	20	Pure water	
Vcon	20	Corn oil	
LYC	20	LYC	5 mg/kg/day
D5	20	DEHP	500 mg/kg/day
DL5	20	DEHP + LYC	DEHP: 500 mg/kg/day LYC: 5 mg/kg/day
D10	20	DEHP	1000 mg/kg/day
DL10	20	DEHP + LYC	DEHP: 1000 mg/kg/day LYC: 5 mg/kg/day

Table S2. Sequences of oligonucleotide primers for QRT-PCR.

Gene Names	Sequence (5' → 3')	NCBI Reference Sequence	Amplicon size (bp)
GAPDH1	AAGGTCGGTGTGAACGGATT CAACAATCTCCACTTTGCCACT	NM_001289726.1	82
GAPDH2	GCGACTTCAACAGCAACTCC ACCCTGTTGCTGTAGCCGTA	NM_008084.3	121
HSF1	ATGACACCGAGTTCCAGCATC CACGCTGGTCACTTTCCTCT	NM_001331152.1	83
HSP10	TGCTGCCGAAACTGTAACCA CCACAGCCACGACCGTTG	NM_008303.4	86
HSP25	CAGTCAGCGGAGATCACCAT TGTTCAGACTTCCCAGCTTC	NM_013560.2	80
HSP32	AGGTACACATCCAAGCCGAGA TACAAGGAAGCCATCACCAG	NM_013560.2	80
HSP47	GCCCCAAGCTGTTCTATGCC TCTCGCATCTTGTCTCCCT	NM_009825.2	115
HSP60	CCACTGTTCTGGCACGAT ATCCACAGCCAACATCACACC	NM_010477.4	101
HSP70	CCCGCCTACTTCAACGACT TCGTTGATGATCCGCAGCAC	NM_010479.2	86
HSP90	TGACATCATCCCCAACCCTC TTCGTGCCAGACTTAGCAA	NM_008302.3	114
HSP110	CAGAAGAAAGCAAAACCCCAG GCAGCTCAACATTTACCACCT	NM_013559.2	105
Nrf2	TCACACGAGATGAGCTTAGGGCAA TACAGTTCTGGGCGGCGACTTTAT	NM_010902.4	183
NQO1	GGTGAGCTGAAGGACTCGAA ACCACTGCAATGGGAACTGAA	NM_008706.5	148
HO-1	ACATCCAAGCCGAGAATGCTG CCAGTGAGGCCCATACCAGA	NM_010442.2	230
TXN-1	AAGCCCTTCTTCCATTCCCT ACATCCTGGCAGTCATCCAC	NM_011660.3	80
GCLM	GCCACCAGATTTGACTGCCTTT CAGGGATGCTTTCTTGAAGAGCTT	NM_008129.4	119

GCLC	ATCTACCACGCAGTCAAG GTCTCAAGAACATCGCCT	NM_010295.2	134
GSS	CAAAGCAGGCCATAGACAGGG AAAAGCGTGAATGGGGCATAC	NM_008180.2	103
GSTA4	AGTGCAGCGTGCTTTAAGGT GGGCAGAGTGGTTTTGTTGT	NM_010357.3	135
CAT	ATGGCTATGGATCACACACCT CCTTCCTGCCTCTCCAAC	NM_009804.2	119
SOD-1	GCCCGGCGGATGAAG CCTTTCCAGCAGTCACATTGC	NM_011434.2	57
SOD-2	GCCACACATTAACGCGCAGA GAGCCTCGTGGTACTTCTCC	NM_013671.3	101
ATF5	CTTGCCCACCTTTGACCTCC GGTTGACAAGCCTGAATCCC	NM_030693.2	106
Clpp	TCATTGCCCAGCTGTTGT CAGGCCCGCAGTTACCAC	NM_017393.2	95
Lonp	GGTCGTATCATCAATGGCTT TTCCCCAGCTTGTCAACCTC	NM_025827.3	80
YME1L1	TCCTCTTTGTTTTGCTCCTGT TACCGCAGAATCAAGTCCTGT	NM_013771.5	98
Sirt7	CGCCATCTCAGAGCTCCA CGCTCAGTCACATCAAACACT	NM_153056.3	96
ATF5	CTTGCCCACCTTTGACCTCC GGTTGACAAGCCTGAATCCC	NM_030693.2	106

Supplementary 1. Details of Materials and Methods

Supplementary 1.1 Western Blotting

The total protein were extracted from the heart tissues and quantified by commercially available kits (Beyotime institute of biotechnology, P.R. China). Protein extracts from the samples were separated by SDS-PAGE and transferred to a nitrocellulose membrane (Biosharp, P.R. China). Non-specific binding sites were then incubated with PBST which contained 5% fat-free milk. Furthermore, GAPDH (1:1500, Beijing Biosynthesis Biotechnology Co., Ltd) was used as a protein loading control respectively (Zhang et al., 2017a,b). Afterwards, the incubated membranes further incubated in the Secondary antibody against rabbit IgG (1:3000; Santa Cruz, CA) at 37 ℃ for around 1.5 h. Then the membranes were washed with PBST three times after 1.5 h. The protein bands were quantified by Amersham Imager 600 (GE, Switzerland). Densitometry analysis of specific bands was performed by Image J (National Institute of Health, USA).

Supplementary 1.2 The measurement of the number of myocardial fibers disordered and measurement of mitochondria volume.

1.2.1 The measurement of the number of myocardial fibers disordered.

Under the (400X) microscope, randomly select five visual fields in the middle ring muscle layer, analyze the disorder of myocardial fiber arrangement in the visual field, and count the number of observed disorder of myocardial fiber arrangement. And the data were analysed by GraphPad Prism 5.1 SPSS 19.0 software. Statistical significance was indicated by the value of $P < 0.05$.

1.2.2 The measurement of mitochondria volume.

Randomly select 5 electron microscope pictures, place the selected pictures in the grid, divide the grid into 81 grids, a total of 100 crossing points, and count how many crossing points fall on mitochondria.And the data were analysed by GraphPad Prism 5.1 SPSS 19.0 software. Statistical significance was indicated by the

value of $P < 0.05$.

Supplementary 1.3 MMP

Mitochondria were isolated from liver tissue by using the commercial kit (Beyotime, Shanghai, China). Briefly, 100 mg heart tissue was obtained from the mice in all 7 groups after deep anaesthesia. The tissue was cut in 1ml PBS solution, and remove supernatant (600×g for 20 sec at 4° C). Add 0.8ml trypsin digestive solution, ice bath for 20 minutes, and discard the (600×g for 20 sec at 4° C) . After that add the isolation reagent A(0.2 ml), then resuspend and discard the (600×g for 20 sec at 4° C). Then the isolation reagent A (1 ml) was mixed with the tissue and both were made into homogenates, which were centrifuged (600×g for 5 min at 4° C) to collect the supernatants. The supernatant was collected for a second centrifuge (11000×g for 10 min at 4° C) to settle mitochondria. Finally, the mitochondria were resuspended and preserved in a preserving solution (supplied by the kit). All of the procedures were accomplished in iced bath. The mitochondrial protein concentrations were determined by a BCA Protein. JC-1 staining working solution was diluted with the prepared with JC-1 staining buffer (1X) 5 times. The 0.1 ml purified mitochondria extracted from liver tissues with a total protein content of 10-100μg was added to 0.9ml of the 5-fold diluted JC-1 staining working solution. The emission wavelength is 590nm, the excitation wavelength is 485nm, respectively.