
High glucose-induced cardiomyocyte death may be linked to unbalanced branched-chain amino acids and energy metabolism

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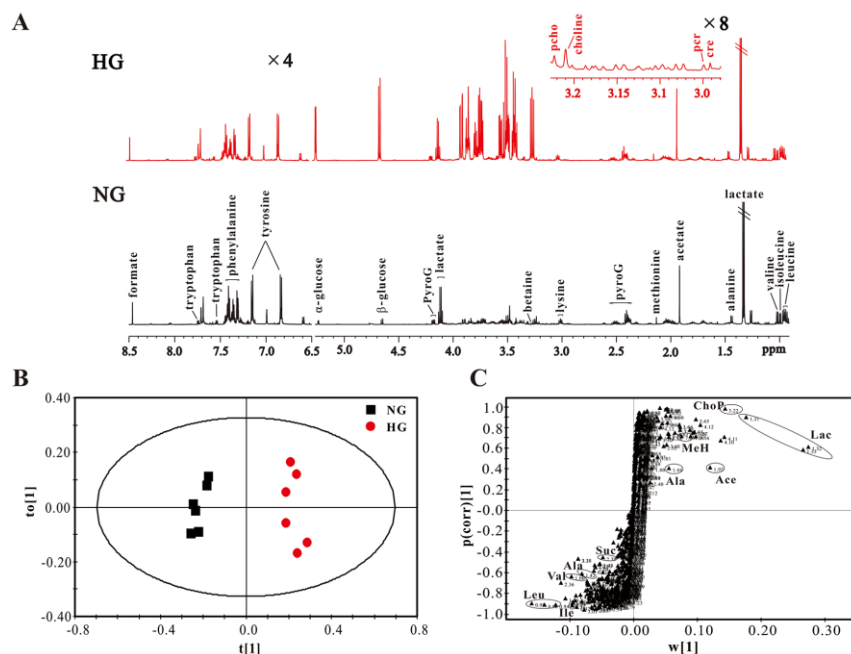


Fig. S1. NMR-based metabolomic analysis: (A) Typical 600 MHz ^1H NMR spectra obtained from the extracellular extracts under high glucose (HG, 33 mM) and normal glucose (NG, 5.5 mM) conditions; OPLS-DA scores plot (B) and its corresponding S-plot (C) based on the metabolomic data of the extracellular extracts. Metabolite: Leu, leucine; Val, valine; Ala, alanine; Suc, succinate; ChoP, choline phosphate; Lac, lactate; MeH, methionine; Ace, acetate.

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Table S1. Changes in metabolite levels from the extracellular extracts under normal glucose (NG) and high glucose (HG) conditions.

$\delta^1\text{H}(\text{ppm})$	Metabolite	NG	HG	P value
0.96	leucine	22.76 $\pm$ 0.92 ^a	20.52 $\pm$ 0.90	0.0017
0.94, 1.01	isoleucine	17.06 $\pm$ 0.66	14.97 $\pm$ 0.74	0.0004
0.99, 1.04	valine	18.35 $\pm$ 0.57	16.58 $\pm$ 0.47	0.0002
1.33, 4.12	lactate	200.76 $\pm$ 15.18	232.29 $\pm$ 19.9	0.0117
1.48	alanine	18.60 $\pm$ 0.60	17.89 $\pm$ 0.53	0.0538
1.91	acetate	34.83 $\pm$ 4.18	38.04 $\pm$ 3.26	0.1693
2.14	methionine	4.07 $\pm$ 0.14	3.57 $\pm$ 0.13	0.0001
3.03, 3.92	creatine	0.80 $\pm$ 0.02	0.76 $\pm$ 0.08	0.2013
3.05, 3.95	creatine phosphate	0.82 $\pm$ 0.04	0.67 $\pm$ 0.04	0.0001
3.21	choline	3.01 $\pm$ 0.18	2.97 $\pm$ 0.17	0.6917
3.22	choline phosphate	1.82 $\pm$ 0.07	2.11 $\pm$ 0.13	0.0008
3.30	betaine	1.38 $\pm$ 0.08	1.89 $\pm$ 0.07	0.0000
6.91	tyrosine	0.53 $\pm$ 0.02	0.48 $\pm$ 0.03	0.0029
7.38	phenylalanine	7.04 $\pm$ 0.19	6.56 $\pm$ 0.10	0.0002
7.55	tryptophan	0.54 $\pm$ 0.02	0.53 $\pm$ 0.02	0.8043
8.46	formate	0.61 $\pm$ 0.05	0.60 $\pm$ 0.07	0.8282

^a Metabolite level was calculated in accordance with the peak area by reference to the internal TSP concentration and expressed as Means $\pm$ SE (n = 6).