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Supplementary data

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Supplementary Methods

1. HPLC analysis and polymerization degree identification of PCO

The HPLC analysis of PCO was performed on the Waters 1525 HPLC system coupled with RID. X-Amide column (5 μm, 4.6 mm × 150 mm, ACCHROM, China) maintained at 35 °C. The mobile phase contained acetonitrile (A) and water (B) at a flow rate of 1 mL/min, and separation was achieved using the following gradient: 0−30 min, 82% to 60% A; 30−35 min, 60% A; 35−40 min, 60% to 82% A; 40−50 min, 82% A.

To identify the polymerization degree of PCO, we performed HPLC-MS analysis on an ultra-high performance liquid chromatography system (SCIEX, Framingham, MA, USA) with an Agilent Poroshell Hilic column (2.1 × 100 mm, 2.7 μm) (Santa Clara, CA, USA) fitted with a Triple TOF 4600 high-resolution mass spectrometry system (SCIEX, Framingham, MA, USA). The mobile phase was composed of 0.1% aqueous formic acid (A) and acetonitrile (B). The gradient elution was performed as follows: 0−1 min, 100% B; 1−2 min, 100% to 85% B; 2−32 min, 85% to 50% B; 32−33 min, 50% to 20% B; 33−37 min, 20% to 85% B; 37−44 min, 85% B. The injection volume was 10 μL, and the flow rate was 0.03 mL/min. The ESI source in positive ion mode was used with resolving power 30,000 and a scan range of m/z 100-1000. The parameters were set as follows: capillary temperature, 600 °C; ion spray voltage, 5.5 kV in positive ion mode; sheath and auxiliary gas flow rate, 55 psi; collision energy, 35 eV.

2. Methylation analysis of PCO by GC-MS

The methylated PCO was analyzed by Agilent GC/MS 5975 (Agilent, CA, USA) equipped with a DB-5MS capillary column (30 m × 0.32 mm × 0.5 μm) (Agilent, CA, USA) with He as the carrier gas (1 mL/min). The oven temperature of column was programmed as follows: 0−16 min, 100 °C to 180 °C at 5 °C/min; 16−17 min, 180 °C; 17−27 min, 180 °C to 190 °C at 1 °C/min; 27−29 min, 190 °C; 29−30 min, 190 °C to 220 °C at 30 °C/min; 30−32 min, 220 °C; 32−42 min, 220 °C to 230 °C at 1 °C/min;

42−44 min, 230 °C; 44−46.5 min, 230 °C to 280 °C at 20 °C/min; 46.5−56.5 min, 280 °C. The mass spectrometer was operated with an electron impact (EI) source in full scan mode. The electron energy was 70 eV, and the transfer line temperature was set at 250 °C. The data were collected in the range of m/z 50 to m/z 1500.

Supplementary Figures

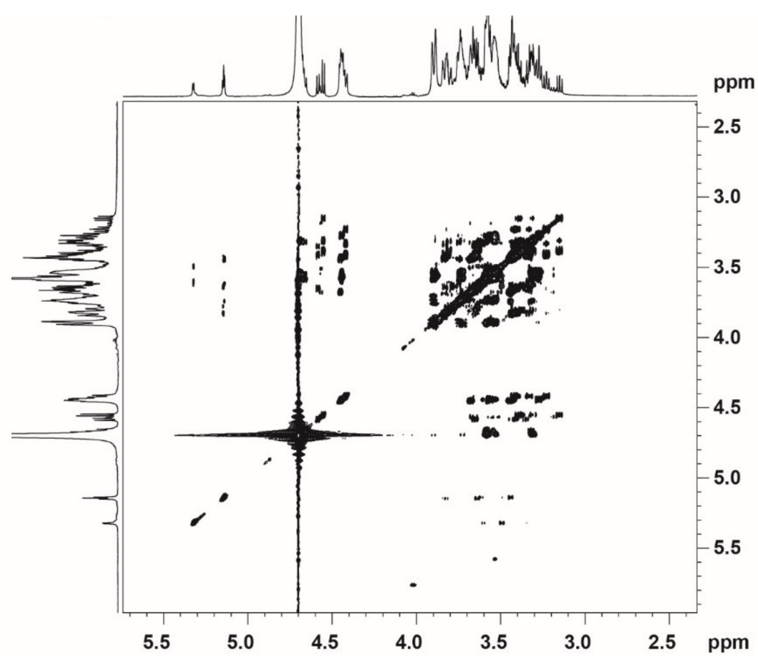

Fig. 1. ^1H-^1H TCOSY NMR spectrum of PCO.

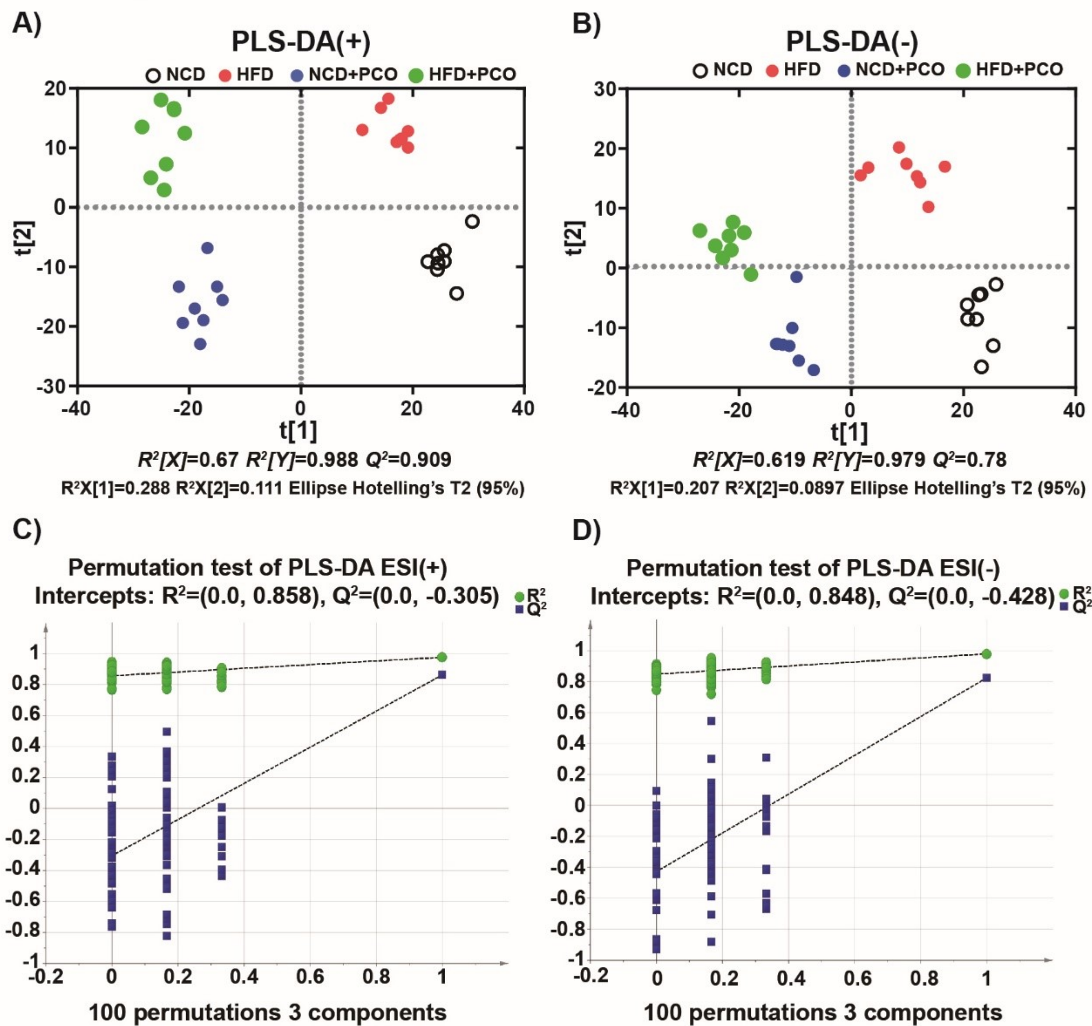

Fig. 2. PLS-DA score space and permutation test of PLS-DA models by 100 iterations. (A−B) Score plots showing group separation in PLS-DA of ESI(+) and ESI(-) ion modes. (C−D) Permutations test of PLS-DA models by 100 iterations. Q^2=(0.0, -0.305) in ESI(+) ion mode, Q^2=(0.0, -0.428) in ESI(-) ion mode. Both intercepts of Q^2 indicate a valid model.

Supplementary Tables

Table 1. Composition of normal chow diet (NCD) and high-fat diet (HFD)

Composition	Normal chow diet		High-fat diet	
	Gram	Kcal	Gram	Kcal
Casein, 80 Mesh	200	800	200	800
L-Cystine	3	12	3	12
Corn Starch	315	1260	72.8	291
Maltodextrin 10	35	140	100	400
Sucrose	350	1400	172.8	691
Cellulose, BW200	50	0	50	0
Soybean Oil	25	225	25	225
Lard	20	180	177.5	1598
Mineral Mix S10026	10	0	10	0
DiCalcium Phosphate	13	0	13	0
Calcium Carbonate	5.5	0	5.5	0
Potassium Citrate, 1	16.5	0	16.5	0
Vitamin Mix V10001	10	40	10	40
Choline Bitartrate	2	0	2	0
FD&C Red Dye #40	0.05	0	0.05	0

Table 2. List of primer sequences for RT-PCR analysis

Name	Forward primer (5'-3')	Reverse primer (5'-3')
ABCG1	GTGGATGAGGTTGAGACAGACC	CCTCGGGTACAGAGTAGGAAAG
ACC1	AAGTCCTTGGTCGGGAAGTATACA	ACTCCCTCAAAGTCATCACAAACA
CYP27A1	CACTTCCTGCTGACCAATGA	CAGTGTGTTGGATGTCGTGTC
CYP7A1	AAACTCCCTGTCATACCACAAAG	TTTCCATCACTTGGGTCTATGC
CYP8B1	CCTCTGGACAAGGGTTTTGTG	GCACCGTGAAGACATCCCC
FASN	AGGTGGTGATAGCCGGTATGT	TGGGTAATCCATAGAGCCCAG
IL-1β	GGCTGGACTGTTTCTAATGC	ATGGTTTCTTGTGACCCTGA
IL-6	GAAACCGCTATGAAGTTCCTCTCTG	TGTTGGGAGTGGTATCCTCTGTGA
Pepck	CTGCATAACGGTCTGGACTTC	CAGCAACTGCCCGTACTCC
SREBP-1	GCATGCCATGGGCAAGTAC	CCACATAGATCTCTGCCAGTGTTG
TNF-α	GGGTGTTCATCCATTCTC	GGAAAGCCCATTTGAGT
FADS1	CGCCAAACGCGCTACTTTAC	CGGTCGATCACGAGCCATC
FADS2	TCATCGGACACTATTCGGGAG	GGGCCAGCTCACCAATCAG
GAPDH	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

Table 3. List of detected metabolites in liver tissues of mice from four experimental groups by HPLC-MS/MS analysis. Please see the EXCEL file “Suppl Table 3-Lin Zhu”.

Table 4. List of efficient metabolites in liver tissues of mice from four experimental groups by HPLC-MS/MS analysis. Please see the EXCEL file “Suppl Table 4-Lin Zhu”.

Table 5. List of KEGG pathways related to metabolic changes in liver tissues of mice from four experimental groups by HPLC-MS/MS analysis. Please see the EXCEL file “Suppl Table 5-Lin Zhu”.