Supplementary Materials

PARP-1 inhibitor alleviates liver lipid accumulation of

atherosclerosis via modulating bile acid metabolism and gut

microbes

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Supplementary Tables

Supplementary Table S1. The multiple reaction monitoring (MRM) scanning method

Bile	Formula	Parent	Cone	Daughters	Collision	Ion
acids		,	Voltag		Energy	Mode
		m/z	e			
CA	$C_{24}H_{40}O_5$	407.19	78	342.60	28	ES-
α-MCA	$C_{24}H_{40}O_5$	407.26	86	407.73	30	ES-
β-ΜCΑ	$C_{24}H_{40}O_5$	407.26	92	371.32	32	ES-
DCA	$C_{24}H_{40}O_4$	391.26	62	345.39	34	ES-
UDCA	$C_{24}H_{40}O_4$	393.20	10	376.25	16	ES-
CDCA	$C_{24}H_{40}O_4$	393.20	2	376.25	16	ES-
TUDCA	$C_{26}H_{45}NO_6S$	498.20	100	80.14	60	ES-
TCDCA	C ₂₆ H ₄₅ NO ₆ S	498.20	86	80.14	66	ES-
Τ-β-ΜCΑ	$C_{26}H_{45}NO_7S$	514.26	100	80.14	66	ES-
TCA	C ₂₆ H ₄₅ NO ₇ S	514.32	78	80.14	62	ES-

TUDCA, Tauroursodeoxycholic acid; UDCA, Ursodeoxycholic acid; TCA, Taurocholic acid; CDCA, Chenodeoxychilic acid; TCDCA, Taurochenodeoxycholic acid; CA, Choilic acid; DCA, Deoxycholic acid; β -MCA, β -Muricholic acid; α -MCA, α -Muricholic acid; T- β -MCA, Tauro- β -Muricholic acid.

Supplementary Table S2. The linearity tests of liver bile acids of *apoE-/-* mice

Bile acids	Linear equation	Correlation coefficient
СА	Y=274.9X+1457	0.9992
TCA	Y=644.5X+4986	0.9994
UDCA	Y=59.02X+14.26	0.9920
CDCA	Y=70.24X-169.7	0.9991
α-ΜCΑ	Y=93.11X+515.5	0.9996
β-ΜCΑ	Y=15.22X-70.99	0.9991
TUDCA	Y=295.7X+331.4	0.9996
TCDCA	Y=579.3X-7119	0.9937
Τ-β-ΜCΑ	Y=527.4X+3921	0.9994

TUDCA, Tauroursodeoxycholic acid; UDCA, Ursodeoxycholic acid; TCA, Taurocholic acid; CDCA, Chenodeoxychilic acid; TCDCA, Taurochenodeoxycholic acid; CA, Choilic acid; DCA, Deoxycholic acid; β-MCA, β-Muricholic acid; α -MCA, α -Muricholic acid; T-β-MCA, Tauro-β-Muricholic acid.

Bile acids	Linear equation	Correlation coefficient
СА	Y=274.2X+1634	0.9992
DCA	Y=748.5X+2110	0.9999
TCA	Y=644.5X+4986	0.9994
UDCA	Y=59.00X+16.20	0.9914
CDCA	Y=70.24X-253.4	0.9977
α-MCA	Y=93.11X+515.5	0.9996
β-ΜCΑ	Y=15.09X+5.294	0.9970
TUDCA	Y=295.6X+250.5	0.9994
TCDCA	Y=211.2X+991.2	0.9974
Τ-β-ΜCΑ	Y=527.4X+3921	0.9994

Supplementary Table S3. The linearity tests of ileum bile acids of SD rats.

TUDCA, Tauroursodeoxycholic acid; UDCA, Ursodeoxycholic acid; TCA, Taurocholic acid; CDCA, Chenodeoxychilic acid; TCDCA, Taurochenodeoxycholic acid; CA, Choilic acid; DCA, Deoxycholic acid; β -MCA, β -Muricholic acid; α -MCA, α -Muricholic acid; T- β -MCA, Tauro- β -Muricholic acid.

Supplementary Figures



Supplementary Figure S1. Food intake of Apoe-/- mice. *ns* represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.



Supplementary Figure S2. Alpha diversity analysis of the gut microbes in feces of apoE-/mice. *ns* represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.



Supplementary Figure S3. Composition analysis of the gut microbes in feces of $apoE^{-/-}$ mice. (A) Composition of the gut microbes in feces of $apoE^{-/-}$ mice at the phylum level. (B) Statistical results of the majority of the microbial composition at the phylum level. (C) Composition of the gut microbes in $apoE^{-/-}$ mice fecal at the genus level. (D) Statistical results of the majority of the microbial composition at the genus level. (D) Statistical results of the majority of the microbial composition at the genus level. (D) Statistical results of the majority of the microbial composition at the genus level. ns represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.



Supplementary Figure S4. The relative abundance of 10 bile salt hydrolase-related gut microbes in feces of *apoE*^{-/-} mice. *ns* represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.



Supplementary Figure S5. Food intake of SD rats. *ns* represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.



Supplementary Figure S6. The protein levels of PARP1 in liver and ileum of SD rats. (A) Expression level of PARP1 in liver in SD rats. (B) Expression level of PARP1 in ileum of SD rats. Three repeats shows the whole blot after cutting membrane at molecular weight 100 kDa, 75 kDa, 35 kDa for PARP1 (89 kDa), GAPDH (36 kDa). (C) Statistical results of PARP1 expression in the liver of SD rats. (D) Statistical results of PARP1 expression in the ileum of SD rats. *ns* represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.



Supplementary Figure S7. Alpha diversity analysis of the gut microbes in feces of SD rats. *ns* represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.



Supplementary Figure S8. Composition analysis of the gut microbes in feces of SD rats. (A) Composition of the gut microbes in SD rats fecal at the phylum level. (B) Statistical results of the majority of the microbial composition at the phylum level. (C) Composition of the gut microbes in SD rats fecalat the genus level. (D) Statistical results of the majority of the microbial composition at the genus level. (D) Statistical results of the majority of the microbial composition at the genus level. (D) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the microbial composition at the genus level. (n_s) Statistical results of the majority of the micro



Supplementary Figure S9. The relative abundance of 10 bile salt hydrolase-related gut microbes in feces of SD rats. *ns* represents no significant, *P < 0.05, **P < 0.01, ***P < 0.001.