

The Combination of Epigallocatechin Gallate and *Lactiplantibacillus plantarum* P101 alleviated Carbon Tetrachloride-Induced Liver Injury in Mice by Regulating Gut Microbiota

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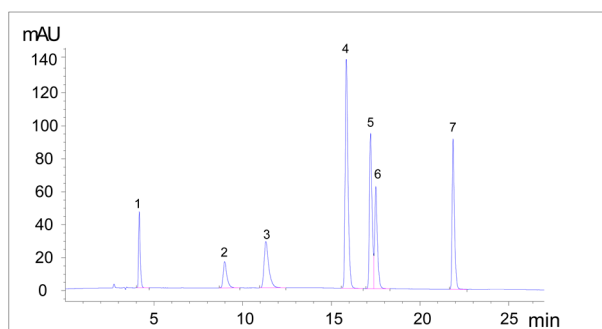


Figure S1. The chromatogram of catechins standard.

Table S1. The retention time and peak area of catechins standard.

Peak	Retention time (min)	Peak area (mAU*s)
1	4.170	294.29129
2	8.986	227.97755
3	11.311	510.29016
4	15.844	1532.63416
5	17.209	964.60785
6	17.507	649.75330
7	21.861	820.93536

Table S2. The retention time and peak area of catechins sample.

Peak	Retention time (min)	Peak area (mAU*s)
1	2.935	481.80072
2	3.716	929.43695
3	6.137	397.52637
4	10.430	807.30261
5	15.847	3367.54736
6	17.176	3397.59619
7	18.702	526.64307
8	21.834	1157.81091

Table S3. Primers used in this study

Gene	Forward	Reverse	Accession number
<i>β-actin</i>	GCTCCTCCTGAGCGCAAGTA	CAGCTCAGTAACAGTCCGCC	NM_007393
<i>TLR-4</i>	CTGTATTCCCTCAGCACTCTTGATT	TGCTTCTGTTCCTTGACCCACT	NM_021297
<i>NF-κB</i>	ACACTGGAAGCACGGATGAC	TGTCTGTGAGTTGCCGGTCT	NM_008689
<i>TNF-α</i>	CTGAACTTCGGGGTGATCGG	GGCTTGTCACCTCGAATTTTGAGA	NM_013693
<i>IL-10</i>	TAACTGCACCCACTTCCCAG	AAGGCTTGGCAACCCAAGTA	NM_010548
<i>Nrf2</i>	TTCCATTTACGGAGACCCACC	GGATTCACGCATAGGAGCACTG	NM_010902
<i>Keap1</i>	GAAGAGGCGGCAGAAGAAG	GCTCCAGGGCTATGACAGAT	NM_001110 307
<i>NQO1</i>	AGGATGGGAGGTACTCGAATC	TGCTAGAGATGACTCGGAAGG	NM_008706
<i>SOD1</i>	TAACTGAAGGCCAGCATGGGT	GGTCTCCAACATGCCTCTCTTC	NM_011434
<i>SOD2</i>	CAGACCTGCCTTACGACTATGG	GCTGAAGAGCGACCTGAGTTGT	NM_013671
<i>CAT</i>	TTGTTCAGTGACCGAGGGATT	TTCCTGAGCAAGCCTTCCTG	NM_009804
<i>GCLC</i>	ATGTGGACACCCGATGCAGTATT	TGTCTTGCTTGTAAGTCAGGATGGTTT	NM_010295

Table S4. The activities of liver antioxidant enzymes.

	CAT (U/mg prot)	SOD (U/mg prot)
Control	66.07 ± 1.06 ^{ab}	288.67 ± 17.93 ^a
Model	84.16 ± 4.95 ^c	378.72 ± 24.19 ^b
P101	100.88 ± 5.97 ^d	362.93 ± 35.56 ^b
EGCG	72.74 ± 3.02 ^b	353.02 ± 18.69 ^b
P+E	56.52 ± 6.05 ^a	289.55 ± 3.65 ^a

Data was expressed as mean ± SD. Different letters represented significant differences, $p < 0.05$.

Table S5. The α diversity index of gut microbiota.

	<i>Shannon</i>	<i>Simpson</i>	<i>Ace</i>	<i>Chao</i>
Control	6.35 ± 0.36	0.96 ± 0.01	481.76 ± 12.42	482.68 ± 13.26
Model	6.44 ± 0.22	0.96 ± 0.01	483.52 ± 3.74	491.32 ± 8.63
P+E	6.5 ± 0.15	0.96 ± 0.01	494.83 ± 7.31	497.85 ± 7.24

Data was expressed as mean ± SD.