

Supplementary material

Creation of Zinc (II)-Complexed Green Tea and Its Effects on Gut Microbiota by Daily Green Tea Consumption

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Table S1. Each catechin content of GTE.

	g/100 g GTE
EC	3.49
EGC	10.24
ECg	1.48
EGCg	12.47
(+)C	0.70
GC	2.58
Cg	0.41
GCg	1.40
Gallate catechins (ECg+EGCg+Cg+GCg)	15.78
Free catechins (EC+EGC+C+GC)	17.00
Total catechins	32.78

Table S2. The log2 fold change (log2FC) values of Metabolic Pathways From all Domains of Life (MetaCyc) pathways that are significantly different between groups ($p < 0.05$).

Pairs		Entry	Function	log2FC
WD/ND	Sig_up	P261-PWY	coenzyme M biosynthesis I	4.18
		GOLPDLAT-PWY	superpathway of glycerol degradation to 1,3-propane- diol	3.74
		PWY-5677	succinate fermentation to butanoate	2.60
		P163-PWY	L-lysine fermentation to acetate and butanoate	2.42
		PWY-6628	superpathway of L-phenylalanine biosynthesis	2.21
		PWY-6630	superpathway of L-tyrosine biosynthesis	2.19
		PWY-1541	superpathway of taurine degradation	1.78
		PWY-7003	glycerol degradation to butanol	1.74
		PWY-6749	CMP-legionaminic acid biosynthesis I	1.33
		PWY-7090	UDP-2,3-diacetamido-2,3-dideoxy- α -D-mannuronate biosynthesis	1.13
		PWY-7332	superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis	1.03
	Sig_down	PWY-7315	dTDP-N-acetylthiosamine biosynthesis	-1.10
		PWY-3781	aerobic respiration I (cytochrome c)	-1.29
		PWY-5920	heme biosynthesis	-1.35
		P23-PWY	reductive TCA cycle I	-1.54
		TYRFUMCAT-PWY	tyrosine degradation	-1.87
GTE/WD	Sig_up	PWY-6876	isopropanol biosynthesis (engineered)	-4.11
		P261-PWY	coenzyme M biosynthesis I	1.74
	Sig_down	RUMP-PWY	formaldehyde oxidation I	-1.24
		HEMESYN2-PWY	heme b biosynthesis II (anaerobic)	-1.25
		PWY-7237	myo-, chiro- and scyllo-inositol degradation	-1.26
		PWY-1861	formaldehyde assimilation II (assimilatory RuMP Cy- cle)	-1.30
		PWY-6630	superpathway of L-tyrosine biosynthesis	-1.52
		PWY-6628	superpathway of L-phenylalanine biosynthesis	-1.54
		PWY0-1261	anhydromuropeptides recycling I	-1.72
		PWY-5177	glutaryl-CoA degradation	-1.75
		PWY-7234	inosine-5'-phosphate biosynthesis III	-1.92
		PWY-5920	superpathway of b heme biosynthesis from glycine	-2.59
		PWY-1541	superpathway of taurine degradation	-2.83
		P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	-3.37
		GOLPDLAT-PWY	superpathway of glycerol degradation to 1,3-propane- diol	-4.56
Zn-GTE/GTE	Sig_up	TYRFUMCAT-PWY	L-tyrosine degradation I	3.14
		PWY-5920	superpathway of heme b biosynthesis from glycine	2.29
		REDCITCYC	TCA cycle VI (Helicobacter)	1.58
		PWY-3781	aerobic respiration I (cytochrome c)	1.41
		FAO-PWY	fatty acid β -oxidation I (generic)	1.40
		CENTFERM-PWY	pyruvate fermentation to butanoate	1.36
		PWY-5177	glutaryl-CoA degradation	1.34
		PWY-6590	superpathway of Clostridium acetobutylicum acido- genic fermentation	1.34

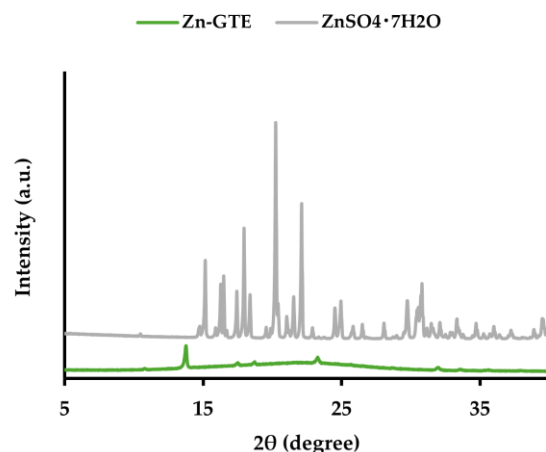


Figure S1. PXRD patterns of Zn-GTE and ZnSO₄·7H₂O.

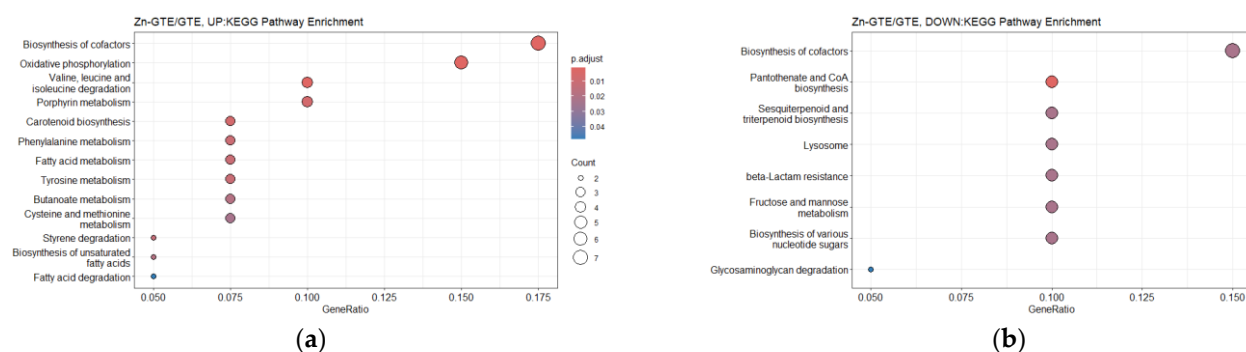


Figure S2. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of upregulated (a) and downregulated (b) pathways in Zn-GTE group compared to GTE group.

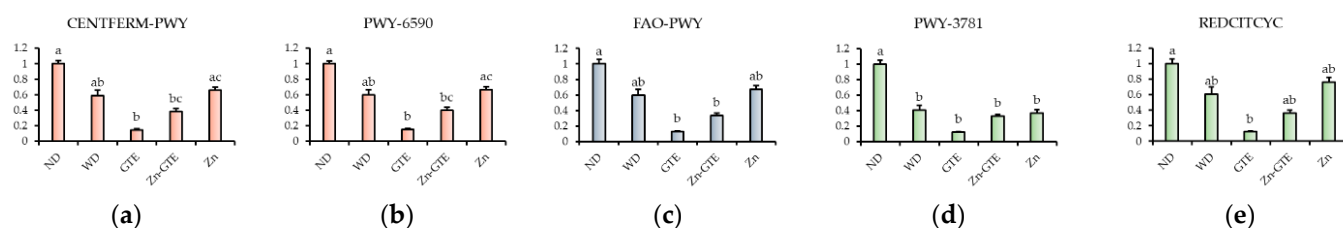


Figure S3. Effect of samples on gut microbial metabolic pathway detected in volcano plot between GTE and Zn-GTE based on Metabolic Pathways From all Domains of Life (MetaCyc) database. The relative abundance of (a) CENTFERM-PWY, (b) PWY-6590, (c) FAO-PWY, (d) PWY-3781, and (e) REDCITCYC. ND group was set as control value 1. The data represent mean $\pm$ SE and different letters in the same column indicate significant differences ($p < 0.05$).

Table S3. Effect of samples on final body weight, liver weight, hepatic triglyceride (TG) content, and serum biochemical indexes. The numerical values with different letters significantly differ ($p < 0.05$) in the same row.

	ND	WD	GTE	Zn-GTE	Zn
Final body weight (g)	39.3 $\pm$ 0.69a	46.1 $\pm$ 1.29b	46.2 $\pm$ 1.80b	43.0 $\pm$ 1.36ab	46.1 $\pm$ 0.80b
Liver weight (g)	1.48 $\pm$ 0.12a	2.39 $\pm$ 0.18a	2.35 $\pm$ 0.29a	2.05 $\pm$ 0.30a	2.00 $\pm$ 0.18a
Hepatic TG (mg/g liver)	155.1 $\pm$ 11.8a	292.9 $\pm$ 4.9b	306.3 $\pm$ 5.9bb	300.5 $\pm$ 10.6b	250.4 $\pm$ 9.5b
AST (IU/L)	309.0 $\pm$ 26.6a	218.2 $\pm$ 18ab	175.8 $\pm$ 7.3b	211.8 $\pm$ 23.4ab	229 $\pm$ 33.8ab
ALT (IU/L)	147.8 $\pm$ 35.1a	173.2 $\pm$ 23.3a	151.8 $\pm$ 32.3a	152.0 $\pm$ 48.6a	184.0 $\pm$ 44.8a
ALT/AST	0.5 $\pm$ 0.1a	0.8 $\pm$ 0.1a	0.9 $\pm$ 0.2a	0.7 $\pm$ 0.2a	0.8 $\pm$ 0.1a
Total cholesterol (mg/dL)	180.4 $\pm$ 18.2a	276.0 $\pm$ 14.3ab	281.5 $\pm$ 35.8ab	283.8 $\pm$ 21.6b	243.5 $\pm$ 8.4ab
HDL-Cholesterol (mg/dL)	85.8 $\pm$ 6.4a	153.0 $\pm$ 6.5b	165.3 $\pm$ 14.1b	150.0 $\pm$ 8.3b	137.8 $\pm$ 3.8b

Non-HDL-Cholesterol (mg/dL)	94.6±12.6a	123.0±9.5a	116.3±26.5a	133.8±14.3a	105.8±5.6a
Triglyceride (mg/dL)	91.4±6a	76.2±4.3a	71.5±4.3a	75.8±8.4a	63.3±4a
Glucose (mg/dL)	169.0±12.2ab	146.0±9.4b	216.8±14.7a	160.0±10ab	131.5±9.8b
Insulin (ng/mL)	2.5±0.4a	3.2±1.5a	3±1.2a	1.3±0.6a	2.0±1.2a
HOMA-IR	1.1±0.3a	1.2±0.6a	1.5±0.4a	0.6±0.3a	0.6±0.3a
