

## Supplementary Material

Simultaneous extraction of total polyphenols and triterpenes from leaves of *Celtis sinensis* by deep eutectic solvent multiple system combined with response surface methodology

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Figure S1. Schematic representation of *Celtis sinensis* leaves.



Figure S2. The structure of main compounds about polyphenols and triterpenes in *Celtis* leaves. (A) 2, 4-Dihydroxybenzaldehyde, (B) 2, 4-Dihydroxybenzoic acid, (C)  $\beta$ -Sitosterol, (D) 3-Hydroxy-12-ursen-28-oic acid

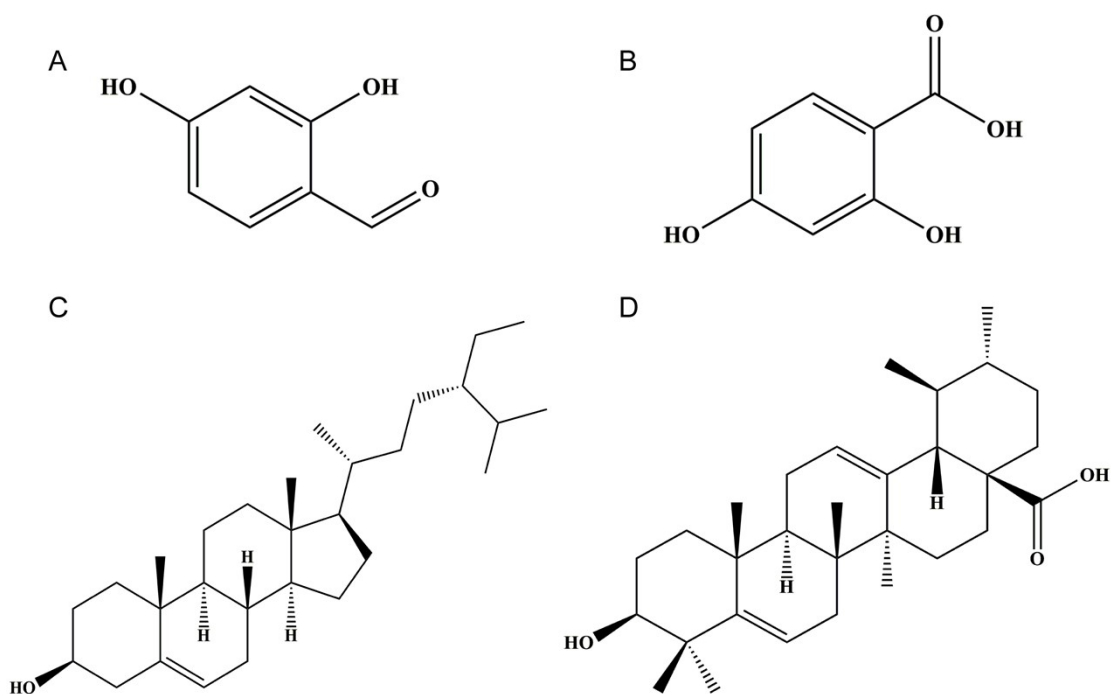


Figure S3. Gallic acid was used as the standard substance to establish curve to measure total polyphenol. (X is the concentration (mg/mL) of gallic acid, Y is absorbance of

gallic acid)

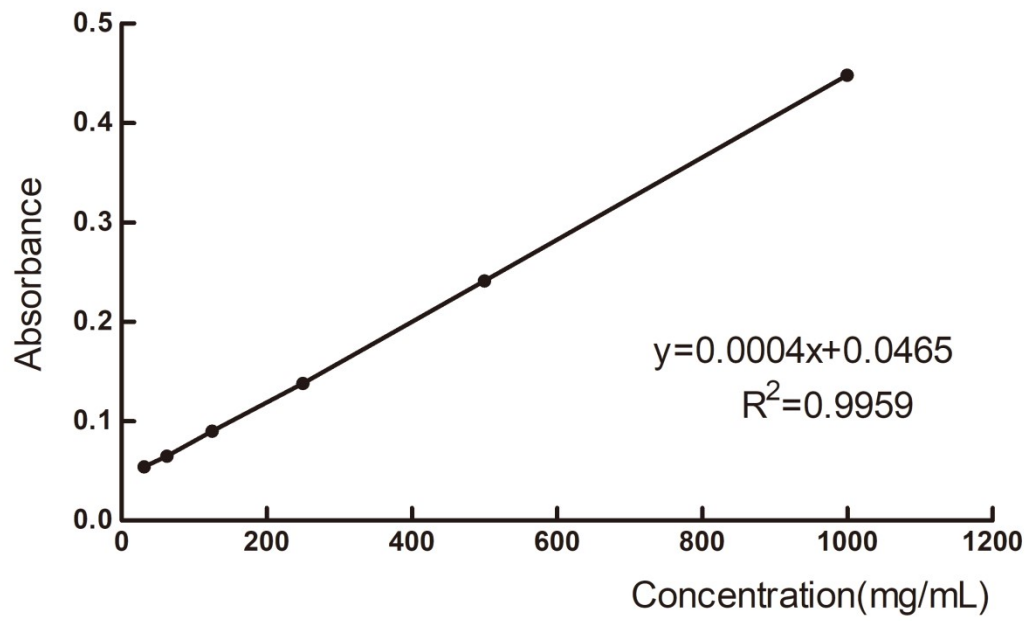


Figure S4. Oleanolic acid was used as the standard substance to establish curve to measure total triterpene. (X is the concentration (mg/mL) of oleanolic acid, Y is absorbance of oleanolic acid)

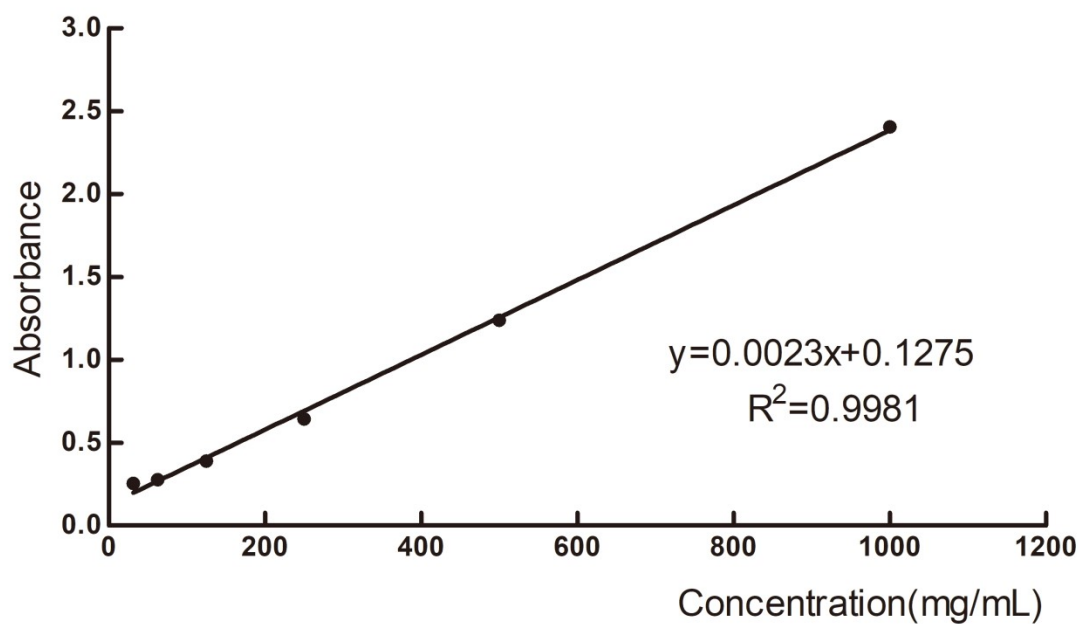


Table S1. ANOVA of the second-order polynomial equation for *Celtis* polyphenols

Source	Sum of Squares	df	Mean Square	F-Value	p-Value	Remarks
Model	1490.42	9	165.60	19.04	< 0.0001	significant
A	7.89	1	7.89	0.91	0.3634	
B	3.77	1	3.77	0.43	0.5251	
C	529.71	1	529.71	60.89	< 0.0001	
AB	22.07	1	22.07	2.54	0.1423	
AC	24.85	1	24.85	2.86	0.1218	
BC	71.99	1	71.99	8.28	0.0165	
A <sup>2</sup>	21.32	1	21.32	2.45	0.1486	
B <sup>2</sup>	3.47	1	3.47	0.40	0.5418	
C <sup>2</sup>	9.64	1	9.64	1.11	0.3172	
Residual	86.99	10	8.70			
Lack of Fit	15.88	5	3.18	0.22	0.9372	not significant
Pure Error	71.10	5	14.22			
R <sup>2</sup>	0.9449					

Table S2. ANOVA of the second-order polynomial equation for *Celtis* triterpenes

Source	Sum of Squares	df	Mean Square	F-Value	p-Value	Remarks
Model	233.89	12	19.49	7.49	0.0065	significant
A	2.46	1	2.46	0.94	0.8427	
B	8.17	1	8.17	3.14	0.0042	
C	13.41	1	13.41	5.15	0.0028	
AB	4.97	1	4.97	1.91	0.2066	
AC	5.62	1	5.62	2.16	0.1813	
BC	37.47	1	37.47	14.40	0.0040	
A <sup>2</sup>	0.37	1	0.37	0.14	0.7192	
B <sup>2</sup>	5.82	1	5.82	2.14	0.1743	
C <sup>2</sup>	1.08	1	1.08	0.40	0.5433	
A <sup>2</sup> B	2.04	1	2.04	0.78	0.4054	
A <sup>2</sup> C	4.62	1	4.62	1.78	0.2243	
AB <sup>2</sup>	2.35	1	2.35	0.90	0.3738	
Residual	18.21	7	2.72			not significant
Lack of Fit	10.21	2	5.11	3.19	0.1278	
Pure Error	8.00	5	1.60			
R <sup>2</sup>	0.9278					