

Supplementary Materials

Metabolic Profile of C-Prenyl Coumarins Using Mass Spectrometry-Based Metabolomics

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Figure S1. Metabolic profiling of MH, ISM and MER *in vitro*. **(A)** Scores plot of OPLS-DA and S-plot analysis from control and MH incubated with MLM. **(B)** Scores plot of OPLS-DA and S-plot analysis from control and ISM incubated with MLM. **(C)** Scores plot of OPLS-DA and S-plot analysis from control and MER incubated with MLM.

Figure S2. Role of MH, ISM and MER in RAW 264.7. **(A)** Cell viability test of MH, ISM and MER in RAW 264.7. **(B)** Correlation of NO production and inflammatory cytokines transcription level.

Figure S3. Metabolic map of MH and ISM. **(A)** Metabolic map of MH. **(B)** Metabolic map of ISM.

Fig S1

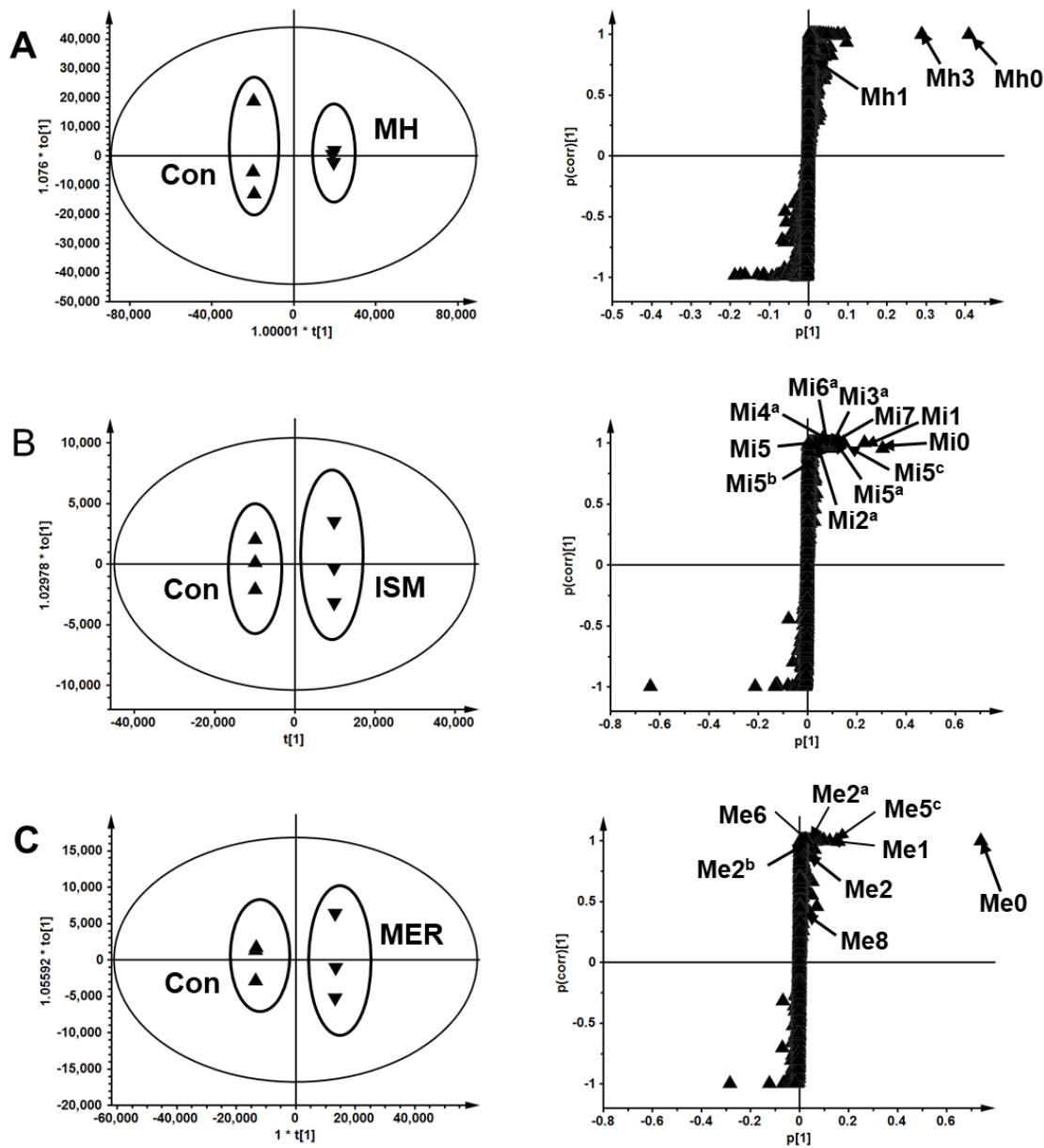


Fig S2

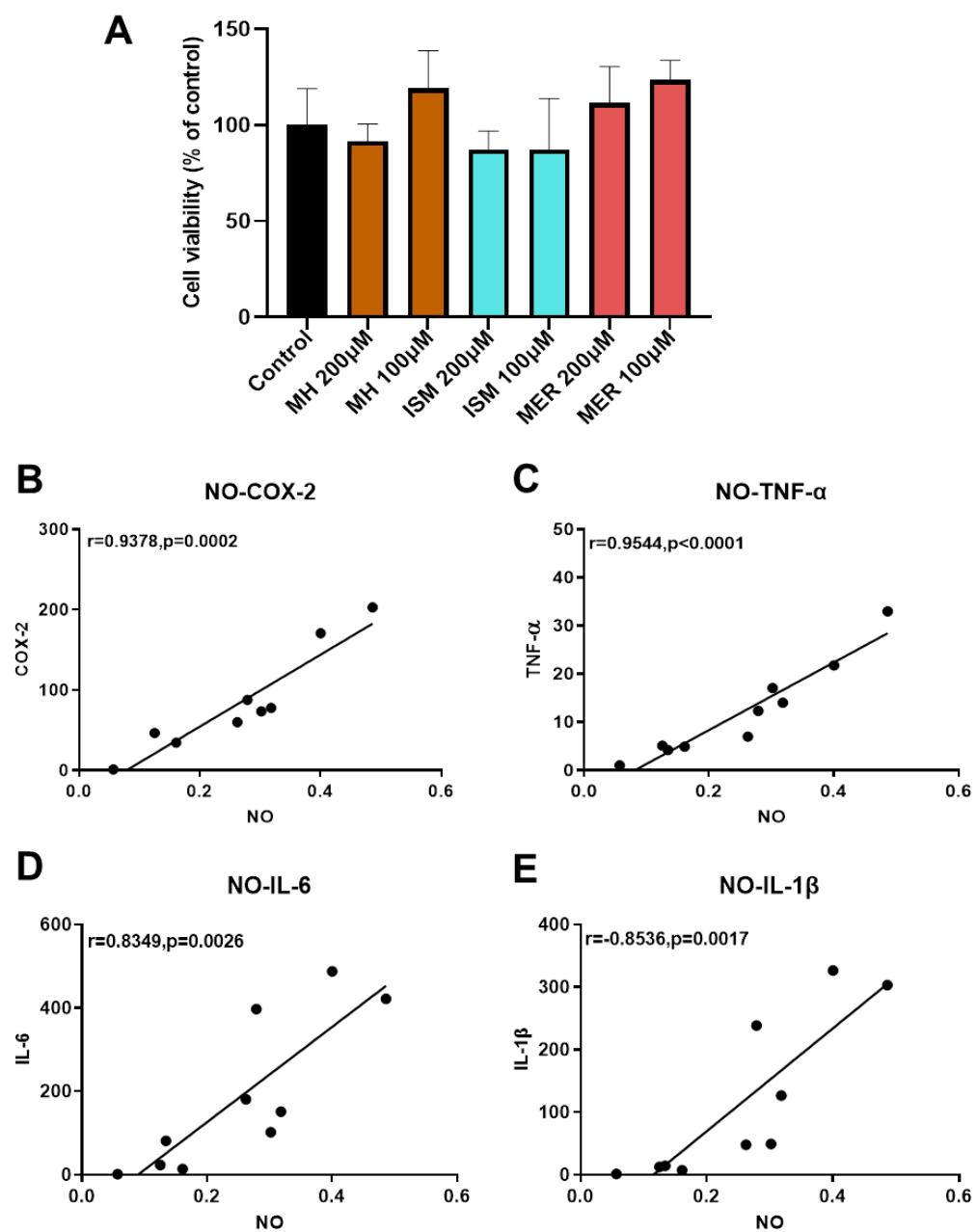


Fig S3

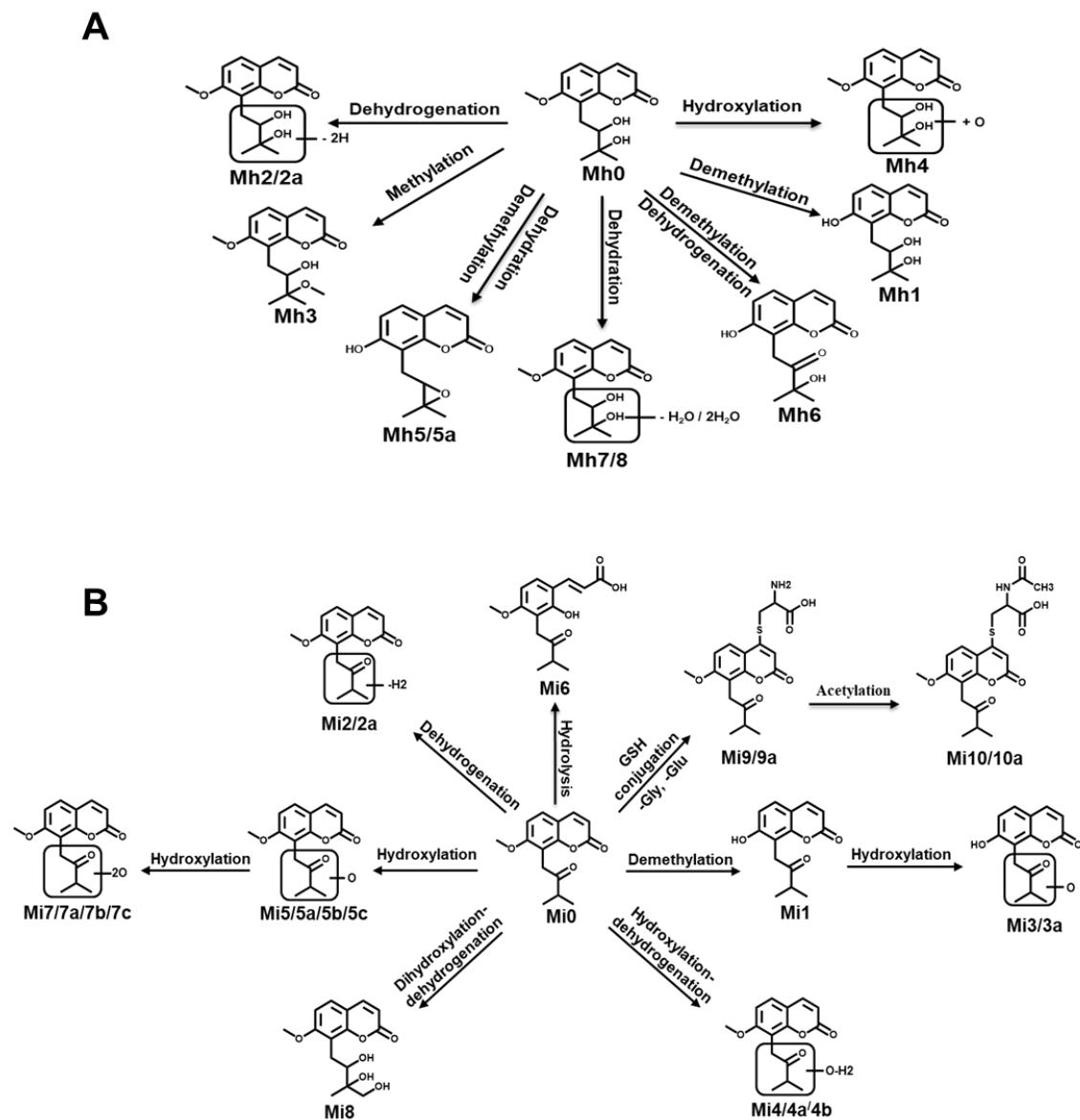


Table S1. Summary of MH metabolites produced *in vivo* and *in vitro* metabolism

Metabolite ID	Molecular formula	RT (min)	m/z[M+H] ⁺	Mass error (ppm)	MS/MS fragments	Identification	Source
Mh0	C ₁₅ H ₁₈ O ₅	6.32	279.1227	2.53	261, 243, 189, 175, 159	Meranzin hydrate	C, H, M
Mh1*	C ₁₄ H ₁₆ O ₅	5.57	265.1070	1.64	247, 229, 223, 177	Mh-CH ₂	C, M
Mh2*	C ₁₅ H ₁₆ O ₅	5.40	277.1070	3.81	259, 249, 235, 227, 219	Mh-2H	C, M, U
Mh2a*	C ₁₅ H ₁₆ O ₅	6.07	277.1070	-1.24	259, 231, 205, 189, 175	Mh-2H	H, M
Mh3*	C ₁₆ H ₂₀ O ₅	6.12	293.1383	-4.92	275, 261, 247, 229, 217	Mh+CH ₂	H, M, U
Mh4*	C ₁₅ H ₁₈ O ₆	6.05	295.1176	-1.08	277, 259, 247, 219, 205	Mh+O	M
Mh5*	C ₁₄ H ₁₄ O ₄	3.98	247.0960	3.64	265, 229, 201, 187, 175	Mh-CH ₂ -H ₂ O	U
Mh5a*	C ₁₄ H ₁₄ O ₄	5.05	247.0960	3.64	263, 229, 201, 187, 175	Mh-CH ₂ -H ₂ O	U
Mh6*	C ₁₄ H ₁₄ O ₅	4.51	263.0910	-2.66	245, 277, 191, 163, 116	Mh-CH ₂ -2H	U
Mh7*	C ₁₅ H ₁₄ O ₃	5.84	243.1010	4.93	228, 203, 189, 175, 159	Mh-2H ₂ O	U
Mh8*	C ₁₅ H ₁₆ O ₄	5.81	261.1110	-4.59	243, 189, 177, 159, 131	Mh-H ₂ O	P

a/b/c/d, isomer metabolite; *, undescribed metabolite. P, plasma; U, urine; C, cell; H, HLM; M, MLM;

Table S2. Summary of ISM metabolites produced *in vivo* and *in vitro* metabolism

Metabolite ID	Molecular formula	RT (min)	m/z[M+H] ⁺	Mass error (ppm)	MS/MS fragments	Identification	Source
Mi0	C ₁₅ H ₁₆ O ₄	8.41	261.1121	1.80	243, 231, 201, 189	Isomeranzin	P, F, U, H, M
Mi1*	C ₁₄ H ₁₄ O ₄	6.94	247.0965	3.32	229, 201, 187, 175	Ism-CH ₂	P, F, U, H, M
Mi2*	C ₁₅ H ₁₄ O ₄	7.11	259.0965	-6.10	243, 231, 213, 189	Ism-2H	H, M
Mi2a*	C ₁₅ H ₁₄ O ₄	8.19	259.0965	-1.85	241, 231, 205, 189	Ism-2H	F, U, H, M
Mi3*	C ₁₄ H ₁₄ O ₅	5.54	263.0914	1.54	245, 233, 221, 187	Ism+O-CH ₂	F, M
Mi3a*	C ₁₄ H ₁₄ O ₅	6.39	263.0914	3.06	245, 217, 203, 191, 175	Ism+O-CH ₂	H, M
Mi4*	C ₁₅ H ₁₄ O ₅	6.08	275.0914	-8.70	231, 215, 203, 189	Ism+O-2H	H
Mi4a*	C ₁₅ H ₁₄ O ₅	6.79	275.0914	1.47	259, 247, 231, 217, 205	Ism+O-2H	H
Mi4b*	C ₁₅ H ₁₄ O ₅	7.58	275.0914	2.56	259, 247, 243, 217	Ism+O-2H	M
Mi5*	C ₁₅ H ₁₆ O ₅	6.33	277.107	0.56	263, 247, 231, 221	Ism+O	U, H, M
Mi5a*	C ₁₅ H ₁₆ O ₅	6.67	277.107	3.45	259, 231, 217, 205, 189	Ism+O	H, M
Mi5b*	C ₁₅ H ₁₆ O ₅	7.12	277.107	-0.88	259, 249, 243, 233, 227	Ism+O	F, H, M
Mi5c*	C ₁₅ H ₁₆ O ₅	7.95	277.107	3.56	259, 243, 221, 205,	Ism+O	F, U, H, M
Mi6*	C ₁₅ H ₁₈ O ₅	6.99	279.1227	5.03	261, 233, 249, 219	Ism+H ₂ O	U
Mi7*	C ₁₅ H ₁₆ O ₆	5.71	293.102	2.18	275, 263, 245, 231, 217	Ism+2O	H, M
Mi7a*	C ₁₅ H ₁₆ O ₆	6.08	293.102	10.37	279, 263, 219, 203, 189	Ism+2O	H
Mi7b*	C ₁₅ H ₁₆ O ₆	6.36	293.102	15.83	275, 261, 247, 233, 207	Ism+2O	M
Mi7c*	C ₁₅ H ₁₆ O ₆	6.63	293.102	4.23	277, 259, 231, 217, 205	Ism+2O	M
Mi8*	C ₁₅ H ₁₈ O ₆	6.24	295.1176	0.99	277, 259, 233, 221, 203	Ism+2O+2H	H, M
Mi9*	C ₁₈ H ₂₁ NO ₆ S	5.36	380.1162	-0.08	334, 291, 259	Ism+Cysteine	P, F, U
Mi9a*	C ₁₈ H ₂₁ NO ₆ S	6.04	380.1162	2.56	362, 334, 291, 259	Ism+Cysteine	P, F, U
Mi10*	C ₂₀ H ₂₃ NO ₇ S	6.56	422.1268	0.72	376, 334, 291, 259	Ism+N-acetylCysteine	F, U
Mi10a*	C ₂₀ H ₂₃ NO ₇ S	7.36	422.1268	2.15	404, 380, 376, 362, 334	Ism+N-acetylCysteine	F, U

a/b/c/d, isomer metabolite; *, undescribed metabolite. P, plasma; F, feces; U, urine; H, HLM; M, MLM