

Molecular basis of differential sensitivity to MeJA in floret opening between indica and japonica rice

ZHIQIANG YAN, RUYUE DENG, HUIHUI TANG, HONGWEI ZHANG, SUSONG ZHU

Guizhou Provincial Academy of Agricultural Sciences, Guiyang, P.R. China

Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Sample information

Cultivar name	Variety name abbreviation	Subsp.	Heading date
Hefengsimiao	Ind	indica	August 12, 2023
Jindao104	Jap	japonica	August 9, 2023

Table S2. RNA integrity number (RIN) and sequencing data

Sample	RIN	Raw data (reads)	Base	Valid data (reads)	Base	Valid ratio (reads)	Q20%	Q30%
Ind (CK) 1h_1	8.62	37 485 404	5.62G	36 574 524	5.49G	97.57	99.97	97.47
Ind (CK) 1h_2	8.58	52 183 322	7.83G	50 920 336	7.64G	97.58	99.97	97.47
Ind (CK) 1h_3	8.47	36 380 150	5.46G	35 532 414	5.33G	97.67	99.97	97.33
Ind (T) 1h_1	8.50	41 281 568	6.19G	40 260 836	6.04G	97.53	99.97	97.35
Ind (T) 1h_2	8.45	43 134 658	6.47G	42 180 992	6.33G	97.79	99.97	97.64
Ind (T) 1h_3	8.52	38 102 064	5.72G	37 154 096	5.57G	97.51	99.97	97.48
Jap (CK) 1h_1	8.31	44 738 884	6.71G	43 579 080	6.54G	97.41	99.97	97.39
Jap (CK) 1h_2	8.23	39 421 492	5.91G	38 437 700	5.77G	97.50	99.97	97.33
Jap (CK) 1h_3	7.76	36 823 256	5.52G	35 687 652	5.35G	96.92	99.77	96.90
Jap (T) 1h_1	8.68	52 639 742	7.90G	51 434 464	7.72G	97.71	99.97	97.16
Jap (T) 1h_2	8.70	44 899 002	6.73G	43 859 578	6.58G	97.68	99.96	97.07
Jap (T) 1h_3	8.71	44 645 282	6.70G	43 650 042	6.55G	97.77	99.96	97.14

<https://doi.org/10.17221/43/2024-CJGPB>

Table S3. Primers information

Gene ID	Gene	Primer	Primer sequence
<i>Os10g0392400</i>	<i>OsJAZ12</i>	OsJAZ12-QF OsJAZ12-QR	GACTATGCAGCTCTTCCCCC ACCATCCTCCCGTCGTAGAA
<i>Os03g0181100</i>	<i>OsJAZ10</i>	OsJAZ10-QF OsJAZ10-QR	CTGAGCCTGATGCCTGGG CCGTAGAAGATGGTCAGCGG
<i>Os03g0402800</i>	<i>OsJAZ6</i>	OsJAZ6-QF OsJAZ6-QR	ATCTTCCGCTACTGCAACCG GCAGCATTTGGACGAACAGG
<i>Os03g0180900</i>	<i>OsJAZ11</i>	OsJAZ11-QF OsJAZ11-QR	GACGCTGAAAGACACGCAAG GGGGAAATCGTCGAACACCA
<i>Os04g0653000</i>	<i>OsJAZ1</i>	OsJAZ1-QF OsJAZ1-QR	GGAGGAGAAGAGCCATCAGC GGAGGGCTCGACATTGGAAA
<i>Os03g0180800</i>	<i>OsJAZ9</i>	OsJAZ9-QF OsJAZ9-QR	TCAAGGTGTGAGTGGCCTCA AAGATCGTGAACGTCTGCC
<i>Os04g0395800</i>	<i>OsJAZ5</i>	OsJAZ5-QF OsJAZ5-QR	TCTACAACGGTTCAGTCGCC ACGAGCGAGTCCTTTTGCTT
<i>Os03g0438100</i>	<i>OsAOC</i>	OsAOC-QF OsAOC-QR	TGTACGAGATCAACGAGCGC TTGTTGGTGAAGGGGACGAG
<i>Os03g0767000</i>	<i>AOS1</i>	OsAOS1-QF OsAOS1-QR	TTCTACCTCCTCTCCCACCG CGAGGTCGTTCTCCATGAGG
<i>Os02g0218700</i>	<i>AOS3</i>	OsAOS3-QF OsAOS3-QR	CTTTGCCGCCATGTTTCGAC GCAGGTGAAGTCGAGCATGT
<i>Os02g0218800</i>	<i>AOS4</i>	OsAOS4-QF OsAOS4-QR	GACGAGCTCCTCCACAACC CGAGCCACTTGACGATGTGT
<i>Os02g0117700</i>	<i>OsUGP2</i>	OsUGP2-QF OsUGP2-QR	TCAATGTTCCAAGTCCCGG CCGGGTTGCGTGTAACAAAG
<i>Os01g0851700</i>	<i>Pho2</i>	Pho2-QF Pho2-QR	ACAGGCCCAGGTTGATGAAG CGCTGCTGAATTTGCCACTT
<i>Os07g0243200</i>	<i>OsAGPL4</i>	OsAGPL4-QF OsAGPL4-QR	ACAGGGGAATCAGGAAAGCG ATGCGTTTGAGCCTTGCATC
<i>Os02g0528200</i>	<i>OsBEI1b</i>	OsBEI1b -QF OsBEI1b -QR	AGCACTTCACTGCCGATTGT TCCGCTGGAGCATAGACAAC
<i>Os07g0627000</i>	<i>DPE1</i>	DPE1-QF DPE1-QR	TCAGTTTGCTTTTGCGGGTG TCATTGTCGTGTGTTCCGGT
<i>Os09g0469400</i>	<i>OsISA3</i>	OsISA3-QF OsISA3-QR	CCCCACCACCACACCATAAA TGGTCCTGTAAATGGCACCC
<i>Os04g0413500</i>	<i>GIF1</i>	GIF1-QF GIF1-QR	ACATGTACCAGCCGACGTTT AGCTCTCAACAACCGACCTG
<i>Os06g0133000</i>	<i>WX1</i>	WX1-QF WX1-QR	GACAACATCATGCGGCTCAC TGGCGGTGATGTACTTGTCC
<i>Os05g0375100</i>	<i>OsHXK10</i>	OsHXK10-QF OsHXK10-QR	GAGGAGATTGCAGCCACTGT GGAGTTCTTCTGCCTAGCCG
	<i>GAPDH</i> (internal reference)	GAPDH-QF GAPDH-QR	AAGCCAGCATCCTATGATCAGATT CGTAACCCAGAATACCCTTGAGTTT

<https://doi.org/10.17221/43/2024-CJGPB>

Table S4. Genes on plant hormone signal transduction

Serial No.	Gene ID	Gene name	Description	KEGG annotation
1	<i>Os04g0662400</i>	uncloned	indole-3-acetic acid-induced protein ARG7(LOC4337295)	plant hormone signal transduction
2	<i>Os03g0180800</i>	<i>OsJAZ9</i>	protein TIFY 11a-like(LOC4331832)	plant hormone signal transduction
3	<i>Os02g0551100</i>	<i>OsSAPK6</i>	serine/threonine-protein kinase SAPK6-like(LOC4329630)	plant hormone signal transduction
4	<i>Os10g0392400</i>	<i>OsJAZ12</i>	protein TIFY 11d-like(LOC4348533)	plant hormone signal transduction
5	<i>Os03g0180900</i>	<i>OsJAZ11</i>	protein TIFY 11c-like(LOC4331833)	plant hormone signal transduction
6	<i>Os09g0439200</i>	<i>OsJAZ8</i>	protein TIFY 10c-like(LOC4347164)	plant hormone signal transduction
7	<i>Os03g0297600</i>	<i>OsPYL4</i>	abscisic acid receptor PYL4(LOC4332548)	plant hormone signal transduction
8	<i>Os02g0574800</i>	uncloned	putative ETHYLENE INSENSITIVE 3-like 4 protein(LOC4329746)	plant hormone signal transduction
9	<i>Os10g0391400</i>	<i>OsJAZ13</i>	protein TIFY 11e-like(LOC4348531)	plant hormone signal transduction
10	<i>Os02g0805100</i>	uncloned	auxin-responsive protein IAA9-like (LOC4331061)	plant hormone signal transduction
11	<i>Os04g0653000</i>	<i>OsJAZ1</i>	protein TIFY 3-like(LOC4337240)	plant hormone signal transduction
12	<i>Os03g0402800</i>	<i>OsJAZ6</i>	protein TIFY 10a-like(LOC4333065)	plant hormone signal transduction
13	<i>Os02g0766700</i>	<i>OsZIP23</i>	bZIP transcription factor 23-like (LOC4330838)	plant hormone signal transduction
14	<i>Os03g0181100</i>	<i>OsJAZ10</i> (uncloned)	protein TIFY 11b-like(LOC4331834)	plant hormone signal transduction
15	<i>Os04g0395800</i>	<i>OsJAZ5</i>	protein TIFY 9-like(LOC4335698)	plant hormone signal transduction
16	<i>Os02g0643800</i>	uncloned	auxin-responsive protein SAUR36 (LOC4330132)	plant hormone signal transduction
17	<i>Os07g0685700</i>	<i>OsEIL2</i>	ETHYLENE INSENSITIVE 3-like 1 protein(LOC4344331)	plant hormone signal transduction

<https://doi.org/10.17221/43/2024-CJGPB>

Table S5. Genes on alpha-linolenic acid metabolism

Serial No.	Gene ID	Gene name	Description	KEGG annotation
1	<i>Os03g0438100</i>	<i>AOC</i>	allene oxide cyclase, biosynthesis of jasmonic acid, defence respons	alpha-linolenic acid metabolism
2	<i>Os03g0767000</i>	<i>AOS1</i>	allene oxide synthase (CYP74A1), biosynthesis of jasmonic acid (JA)	alpha-linolenic acid metabolism
3	<i>Os03g0179900</i>	<i>OsLOX2</i> (uncloned)	similar to Avr9/Cf-9 rapidly elicited protein 44 (fragment)	alpha-linolenic acid metabolism
4	<i>Os04g0447100</i>	<i>OsLOX2</i> (uncloned)	similar to lipoxygenase	alpha-linolenic acid metabolism
5	<i>Os06g0215900</i>	uncloned	similar to oxo-phytodienoic acid reductase	alpha-linolenic acid metabolism
6	<i>Os10g0457600</i>	uncloned	similar to acetyl-CoA C-acyltransferase (3-ketoacyl-coa thiolase b) (EC 2.3.1.16) (fragment)	alpha-linolenic acid metabolism
7	<i>Os04g0372700</i>	uncloned	similar to quinone-oxidoreductase QR1 (fragment)	alpha-linolenic acid metabolism
8	<i>Os11g0146600</i>	uncloned	similar to lipase family protein	alpha-linolenic acid metabolism
9	<i>Os02g0218700</i>	<i>AOS3</i>	allene oxide synthase (CYP74A3), fatty acid 9-/13-hydroperoxide lyase (CYP74C), biosynthesis of jasmonic acid (JA), plant defens	alpha-linolenic acid metabolism
10	<i>Os02g0218800</i>	<i>AOS4</i>	allene oxide synthase (CYP74A4), fatty acid 9-/13-hydroperoxide lyase (CYP74C), biosynthesis of jasmonic acid (JA), plant defens	alpha-linolenic acid metabolism

<https://doi.org/10.17221/43/2024-CJGPB>

Table S6. Genes on starch and sucrose metabolism

Serial No.	Gene ID	Gene name	Description	KEGG annotation
1	<i>Os02g0117700</i>	<i>OsUGP2</i>	UDPas	starch and sucrose metabolism
2	<i>Os01g0851700</i>	<i>Pho2</i>	similar to cytosolic starch phosphorylase (fragment)	starch and sucrose metabolism
3	<i>Os07g0243200</i>	<i>OsAGPL4</i>	plastidic large subunit of ADP-glucose pyrophosphorylase (AGP), starch synthesis in rice polle	starch and sucrose metabolism
4	<i>Os01g0715400</i>	<i>OsSTA30</i> (uncloned)	hypothetical conserved gene	starch and sucrose metabolism
5	<i>Os03g0141200</i>	<i>OsBamy4</i> (uncloned)	similar to beta-amylase PCT-BMYI (EC 3.2.1.2)	starch and sucrose metabolism
6	<i>Os09g0569200</i>	uncloned	similar to beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase)	starch and sucrose metabolism
7	<i>Os02g0778600</i>	uncloned	similar to CEL5=CELLULASE 5 (fragment)	starch and sucrose metabolism
8	<i>Os02g0528200</i>	<i>OsBEIIb</i>	starch branching enzyme 3, starch synthesis	starch and sucrose metabolism
9	<i>Os07g0627000</i>	<i>DPE1</i>	plastidial disproportionating enzyme1, alpha-1,4-D-glucanotransferase, storage starch synthesis in rice endosperm	starch and sucrose metabolism
10	<i>Os09g0469400</i>	<i>OsISA3</i>	similar to isoamylase-type starch debranching enzyme ISO3	starch and sucrose metabolism
11	<i>Os04g0413500</i>	<i>GIF1</i>	cell-wall invertase, carbon partitioning during early grain filling	starch and sucrose metabolism
12	<i>Os06g0133000</i>	<i>WX</i>	granule-bound starch synthase, synthesis of amylose in endosperm	starch and sucrose metabolism
13	<i>Os05g0375100</i>	<i>OsHXK10</i>	similar to hexokinase-10	starch and sucrose metabolism
14	<i>Os01g0813800</i>	uncloned	similar to beta-glucosidase 3	starch and sucrose metabolism
15	<i>Os02g0765400</i>	uncloned	similar to alpha-amylase	starch and sucrose metabolism
16	<i>Os04g0554000</i>	uncloned	similar to OSIGBa0143N19.11 protein	starch and sucrose metabolism

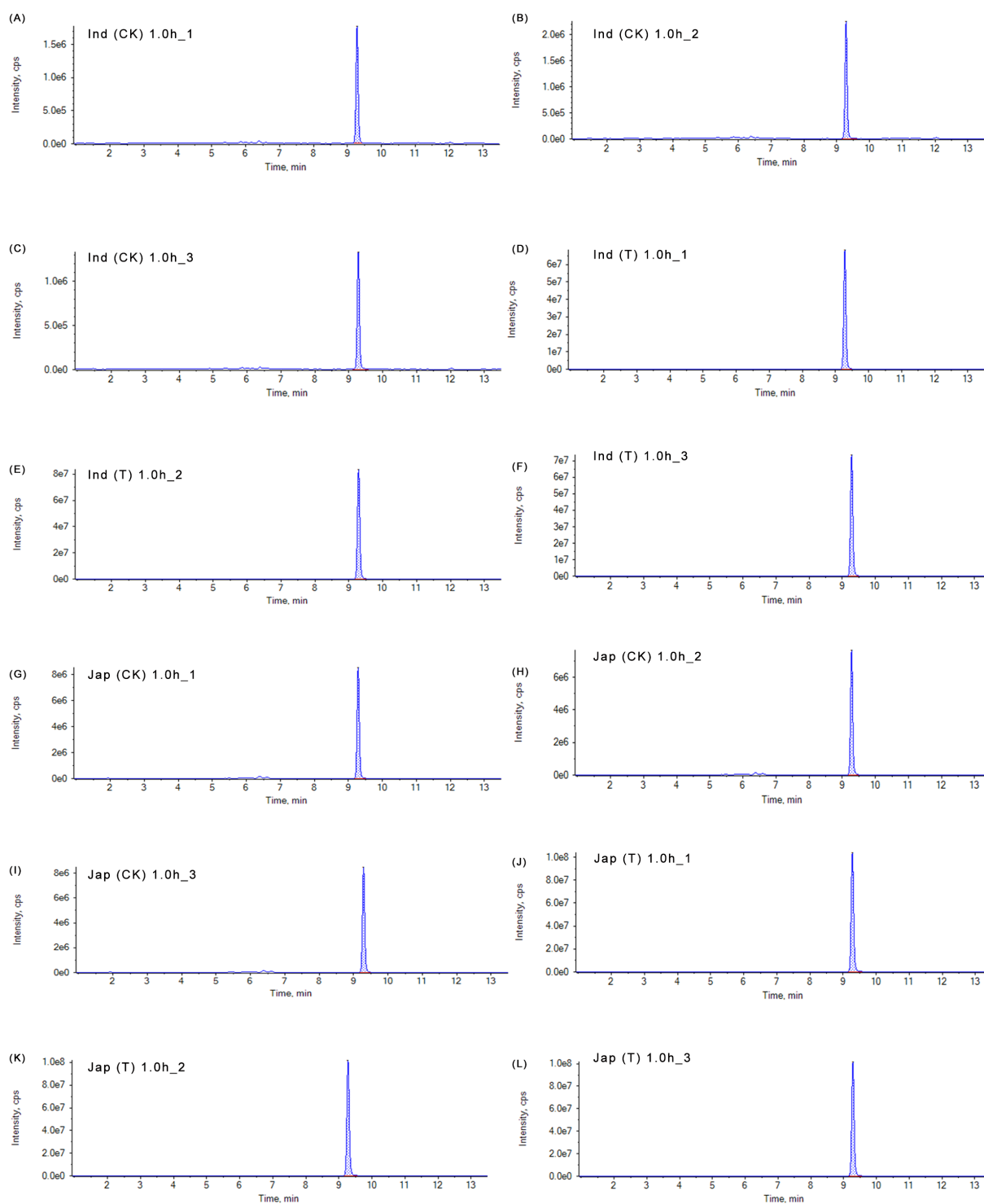


Figure S1. HPLC analysis of MeJA: three replicate chromatograms for CK of Ind (Hefengsimiao) (A–C), three replicate chromatograms for treatment (4 mmol/L MeJA) of Ind (Hefengsimiao) (D–F), three replicate chromatograms for CK of Jap (Jindao104) (G–I), three replicate chromatograms for treatment (4 mmol/L MeJA) of Jap (Jindao104) (J–L)

<https://doi.org/10.17221/43/2024-CJGPB>

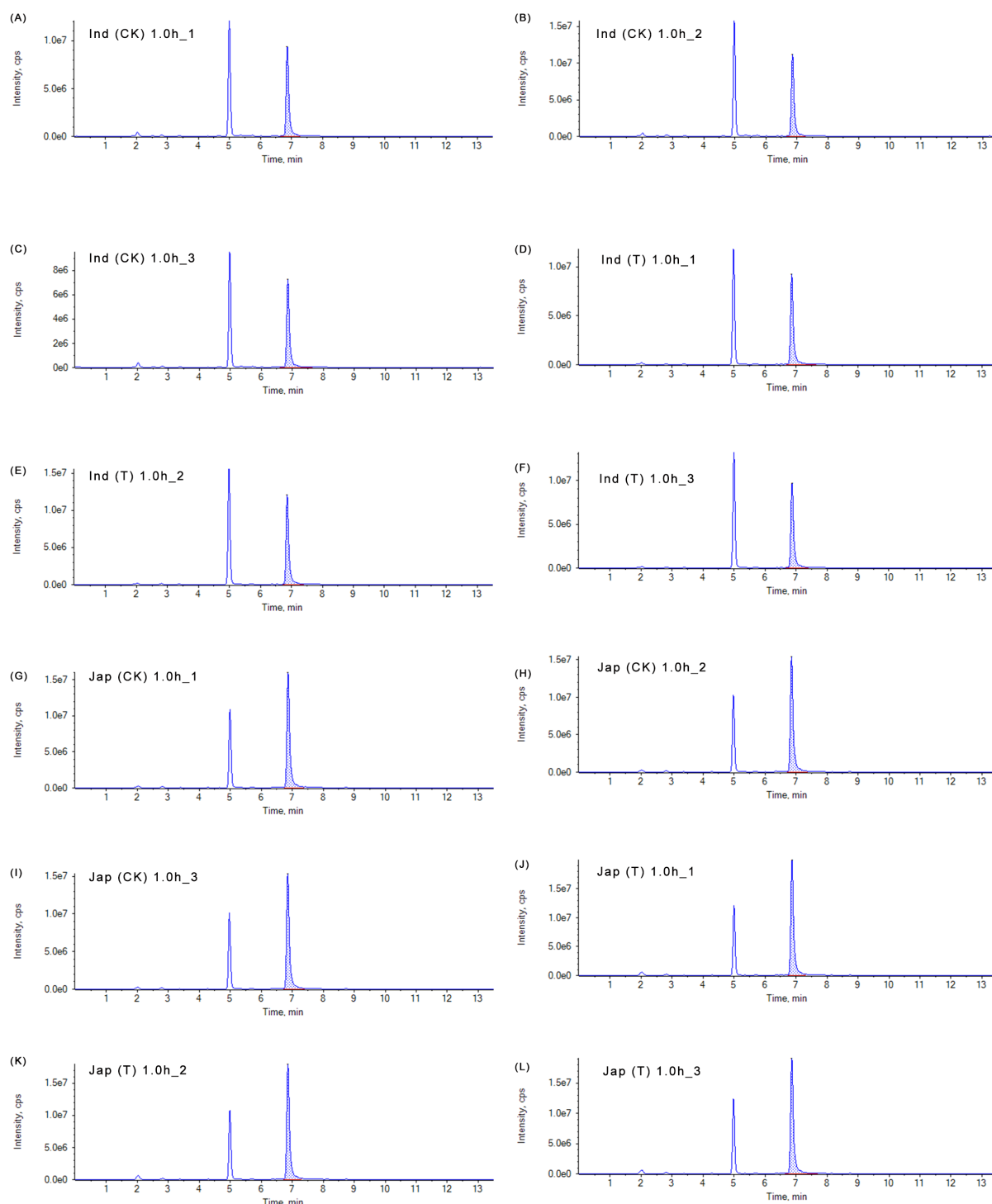


Figure S2. HPLC analysis of SA: three replicate chromatograms for CK of Ind (Hefengsimiao) (A–C), three replicate chromatograms for treatment (4 mmol/L MeJA) of Ind (Hefengsimiao) (D–F), three replicate chromatograms for CK of Jap (Jindao104) (G–I), three replicate chromatograms for treatment (4 mmol/L MeJA) of Jap (Jindao104) (J–L)

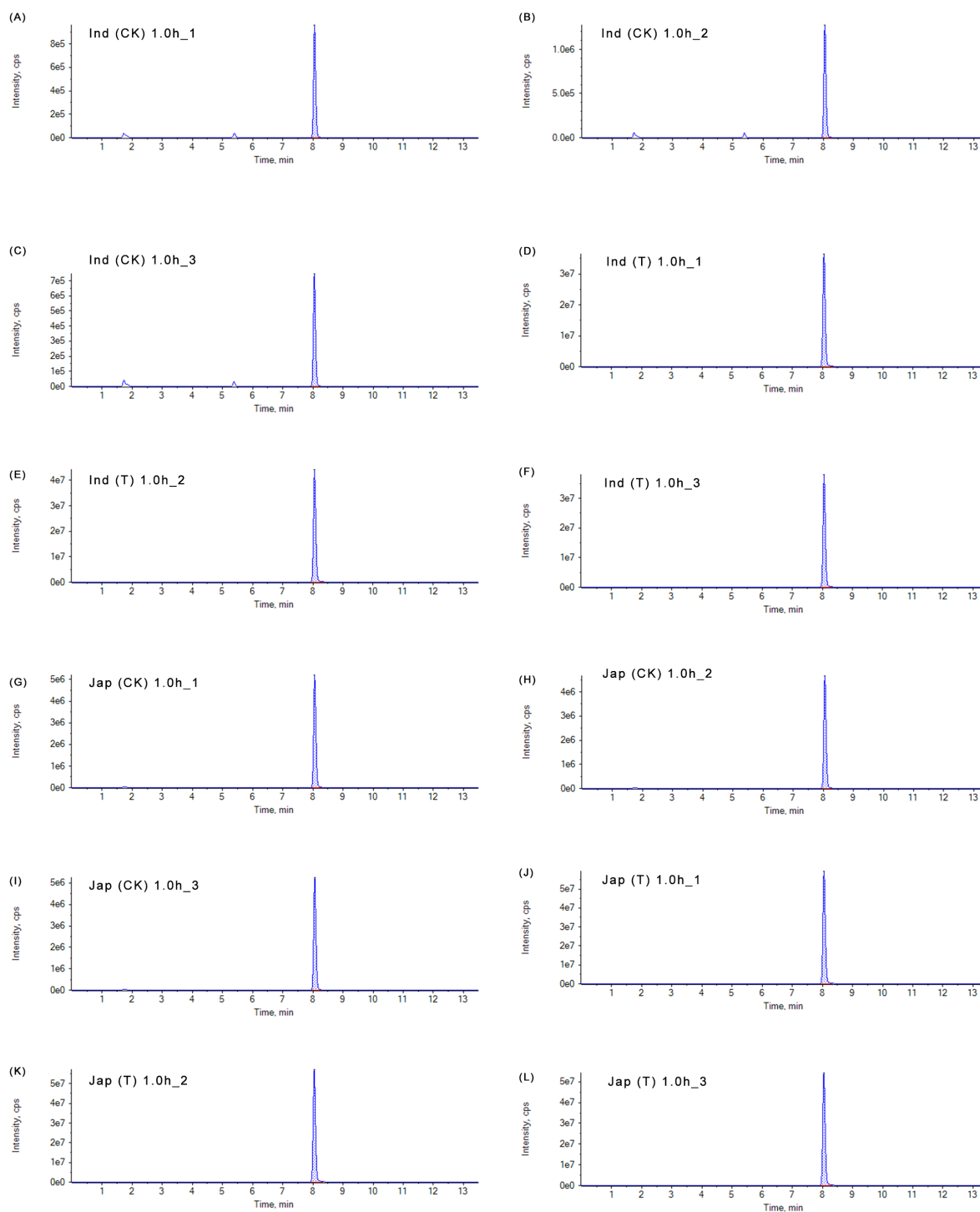


Figure S3. HPLC Analysis of JA: three replicate chromatograms for CK of Ind (Hefengsimiao) (A–C), three replicate chromatograms for treatment (4 mmol/L MeJA) of Ind (Hefengsimiao) (D–F), three replicate chromatograms for CK of Jap (Jindao104) (G–I), three replicate chromatograms for treatment (4 mmol/L MeJA) of Jap (Jindao104) (J–L)

<https://doi.org/10.17221/43/2024-CJGPB>

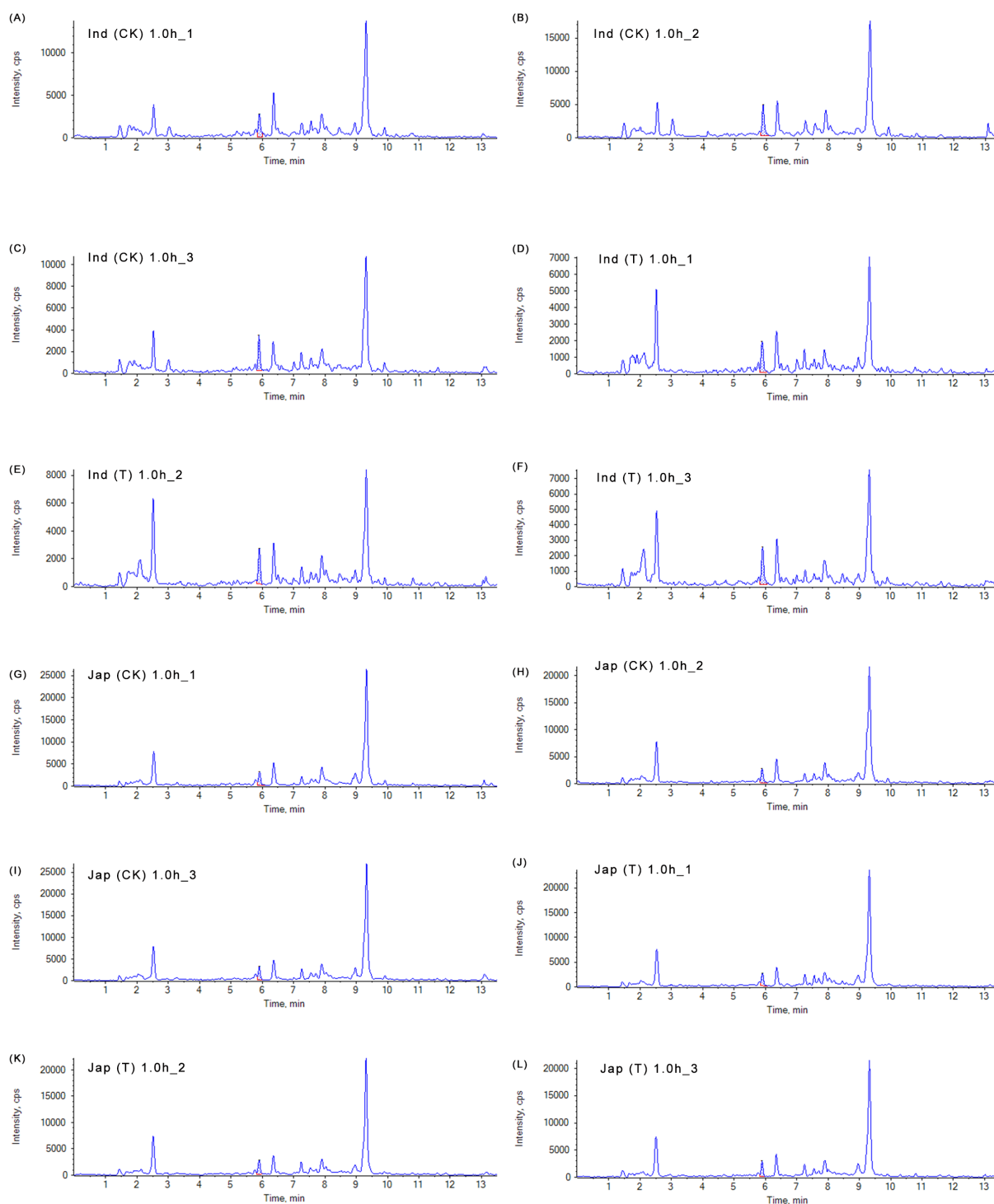


Figure S4. HPLC Analysis of GA3: three replicate chromatograms for CK of Ind (Hefengsimiao) (A–C), three replicate chromatograms for treatment (4 mmol/L MeJA) of Ind (Hefengsimiao) (D–F), three replicate chromatograms for CK of Jap (Jindao104) (G–I), three replicate chromatograms for treatment (4 mmol/L MeJA) of Jap (Jindao104) (J–L)

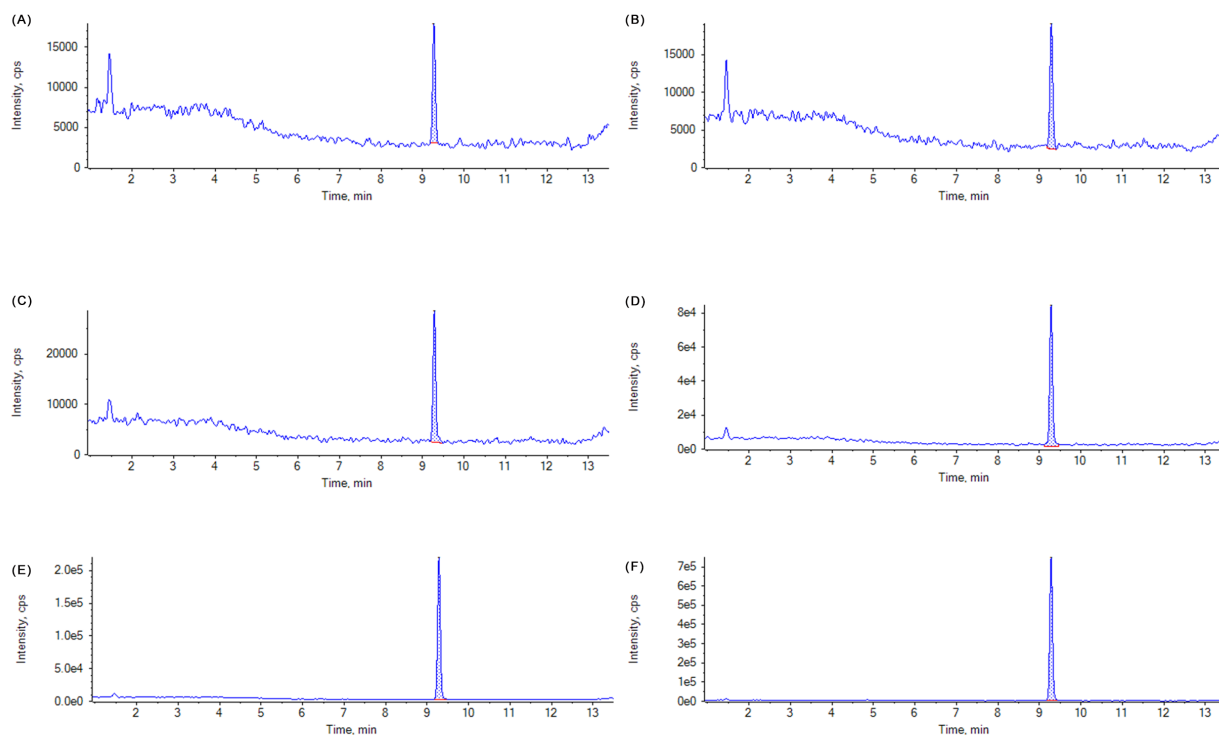


Figure S5. HPLC analysis of MeJA standard: MeJA standard at 0.1 ng/mL (A), MeJA standard at 0.2 ng/mL (B), MeJA standard at 0.5 ng/mL (C), MeJA standard at 2 ng/mL (D), MeJA standard at 5 ng/mL (E), MeJA standard at 50 ng/mL (F)

<https://doi.org/10.17221/43/2024-CJGPB>

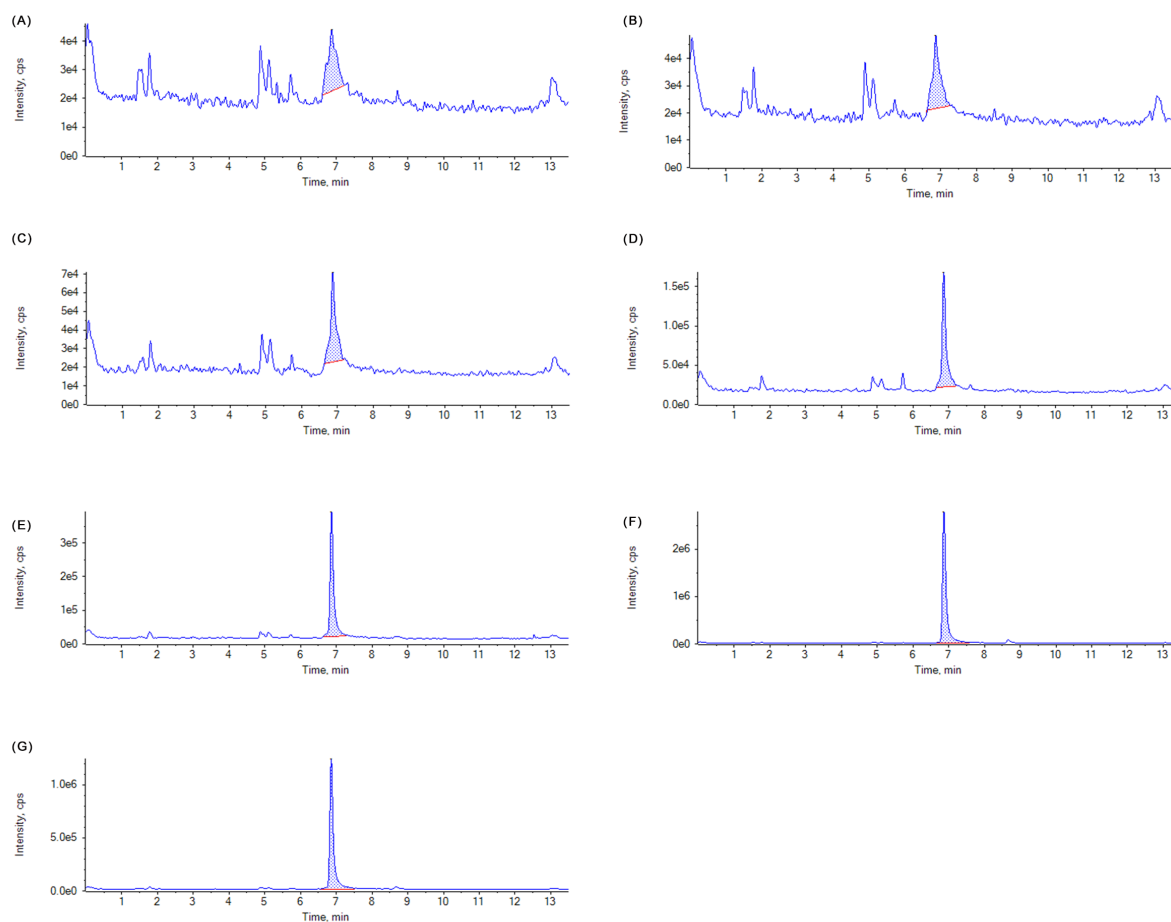


Figure S6. HPLC analysis of SA standard: SA standard at 0.1 ng/mL (A), SA standard at 0.2 ng/mL (B), SA standard at 0.5 ng/mL (C), SA standard at 2 ng/mL (D), SA standard at 5 ng/mL (E), SA standard at 20 ng/mL (F), SA standard at 50 ng/mL (G)

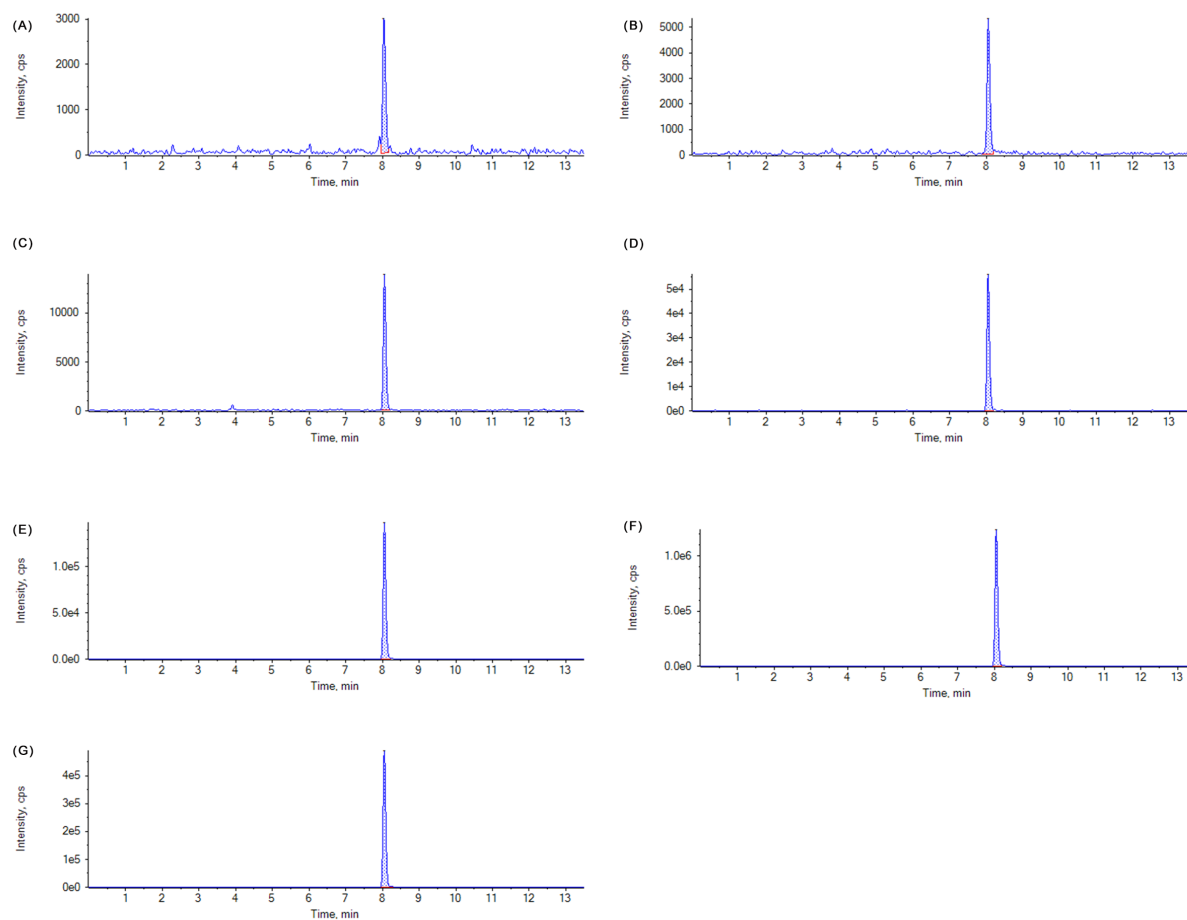


Figure S7. HPLC analysis of JA standard: JA standard at 0.1 ng/mL (A), JA standard at 0.2 ng/mL (B), JA standard at 0.5 ng/mL (C), JA standard at 2 ng/mL (D), JA standard at 5 ng/mL (E), JA standard at 20 ng/mL (F), JA standard at 50 ng/mL (G)

<https://doi.org/10.17221/43/2024-CJGPB>

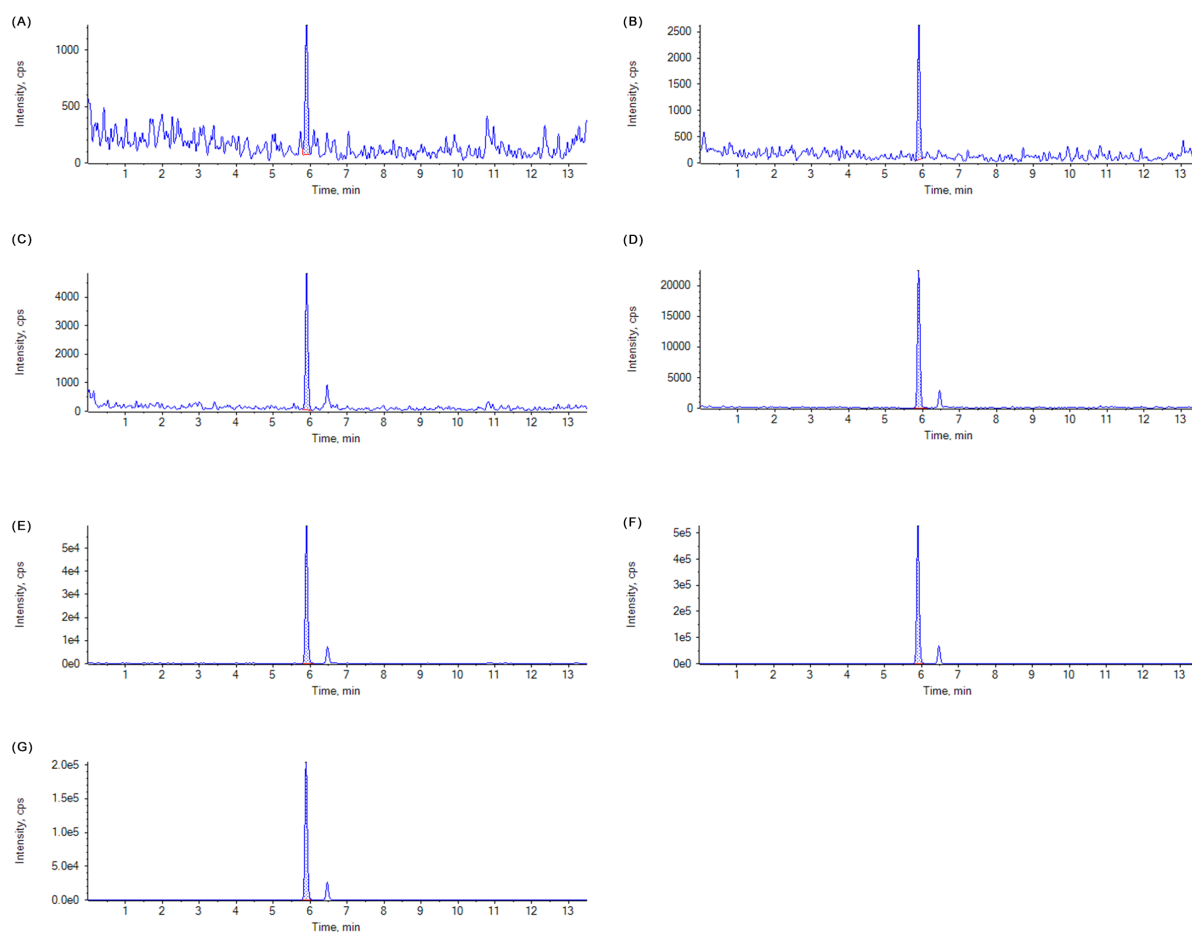


Figure S8. HPLC analysis of GA3 standard: GA3 standard at 0.1 ng/mL (A), GA3 standard at 0.2 ng/mL (B), GA3 standard at 0.5 ng/mL (C), GA3 standard at 2 ng/mL (D), GA3 standard at 5 ng/mL (E), GA3 standard at 20 ng/mL (F), GA3 standard at 50 ng/mL (G)

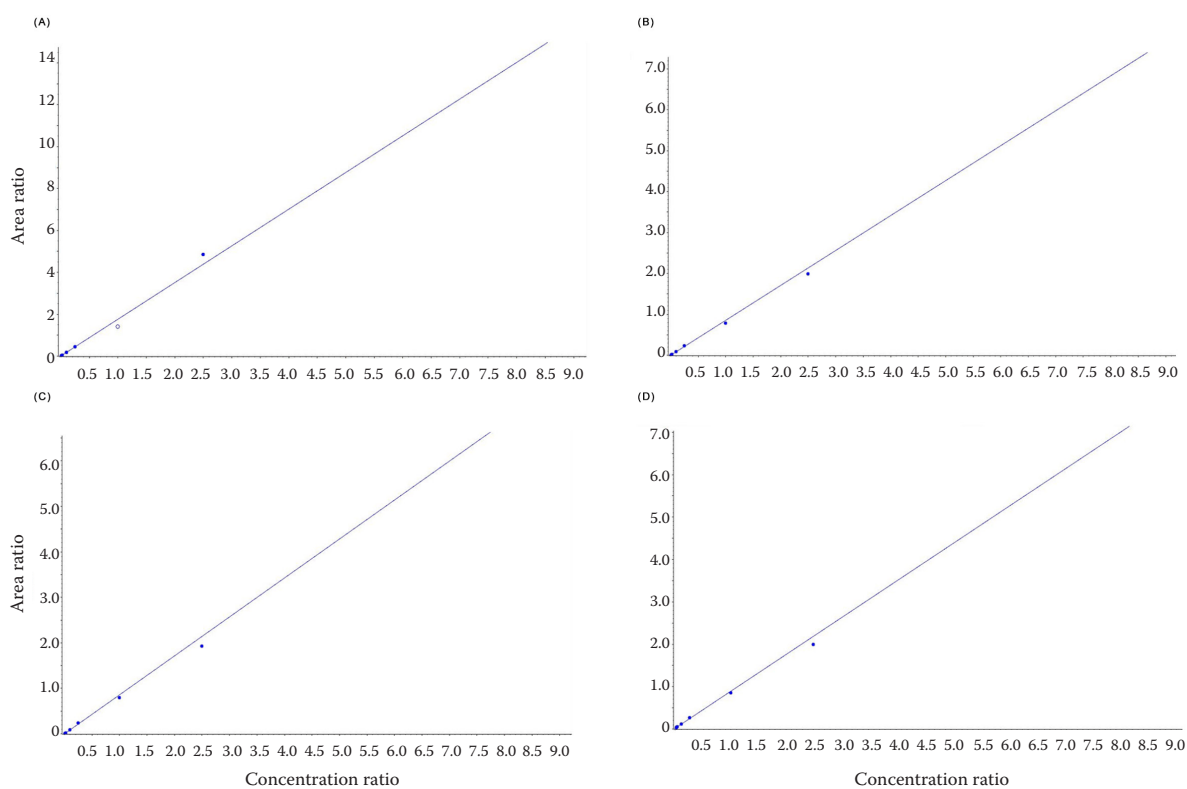


Figure S9. Standard curve of endogenous hormones: standard curve of MeJA (A), standard curve of SA (B), standard curve of JA (C), standard curve of GA3 (D)