



## Article

# Rice Momilactones and Phenolics: Expression of Relevant Bio-synthetic Genes in Response to UV and Chilling Stresses

## Supplementary Materials:

**Table S1.** Primer sequences of the tested genes

Gene	Gene description	Primer sequence
PAL	Phenylalanine ammonia-lyase	Forward: GAGGATCTCGAACCGGATGC Reverse: GTGGATCCTCAACTGCATCGC
OsCPS4	Syn-copalyl diphosphate synthase-like	Forward: TGGAGGACGGCATGTTTGA Reverse: CCGTACTTCCCCATTCTGG
OsKSL4	Syn-pimara-7,15-diene synthase-like	Forward: AAGAGGCTAAAGAGGCCA Reverse: TCAGTGGCTCAAAGATTACTC
CYP99A3	9-Beta-pimara-7,15-diene oxidase-like	Forward: CGTCAAGGCAATTATACTGGAT Reverse: CATGAGCCACTCGGTGGTAG
OsMAS	Momilactone A synthase-like	Forward: AGCACTTCTCGGACAGCAAAT Reverse: CTTGCCACCAGCTTCCTT
OsMAS2	Momilactone A synthase-like	Forward: GAAAGAGACCCATCGTCGTCGT Reverse: CCACGCCAACATTGGAAACCA
Actin	Housekeeping gene	Forward: CTCCCCATGCTATCCTTCG Reverse: TGAATGAGTAACCACGCTCCG
eIF-4A	Housekeeping gene	Forward: TTGTGCTGGATGAAGCTGATG Reverse: GGAAGGAGCTGGAAGATATCATAGA

**Table S2.** Expression (Ct value) of candidate housekeeping genes (*eIF-4A* and *actin*) in rice under UV and chilling stresses

Treatment	Sample	Ct value	
		<i>eIF-4A</i>	<i>Actin</i>
UV	UVC	31.35 ± 0.07	28.72 ± 0.15
	UV2	28.23 ± 0.33	29.16 ± 0.10
	UV4	28.24 ± 0.15	29.05 ± 0.17
Chilling	ChiC	27.46 ± 0.07	26.95 ± 0.25
	Chi4	31.64 ± 0.28	26.74 ± 0.28
	Chi8	29.40 ± 0.12	23.46 ± 0.16

Data express mean ± standard deviation (SD). UVC, control rice seedlings without UV treatments; UV2, UV-treated rice seedlings for 2 h per day; UV4, UV-treated rice seedlings for 4 h per day; ChiC, control rice seedlings without chilling treatments; Chi4, chill-treated rice seedlings for 4 h per day; Chi8, chill-treated rice seedlings for 8 h per day.

**Table S3.** Relative quantification (RQ) of relevant genes to the biosynthesis of phenolics and momilactones in rice response to UV and chilling stresses

Gene	UV treatment			Chilling treatment		
	UVC	UV2	UV4	ChiC	Chi4	Chi8
<i>PAL</i>	1.000 ± 0.000 <sup>c</sup>	2.047 ± 0.233 <sup>b</sup>	2.582 ± 0.105 <sup>a</sup>	1.000 ± 0.000 <sup>a</sup>	0.230 ± 0.062 <sup>b</sup>	0.021 ± 0.002 <sup>c</sup>
<i>OsCPS4</i>	1.000 ± 0.000 <sup>b</sup>	3.710 ± 0.884 <sup>a</sup>	3.852 ± 0.520 <sup>a</sup>	1.000 ± 0.000 <sup>a</sup>	0.026 ± 0.006 <sup>b</sup>	0.008 ± 0.001 <sup>c</sup>
<i>OsKSL4</i>	1.000 ± 0.000 <sup>c</sup>	5.851 ± 1.110 <sup>b</sup>	17.887 ± 0.765 <sup>a</sup>	1.000 ± 0.000 <sup>a</sup>	0.054 ± 0.136 <sup>b</sup>	0.004 ± 0.000 <sup>c</sup>
<i>CYP99A3</i>	1.000 ± 0.000 <sup>b</sup>	48.217 ± 26.324 <sup>a</sup>	58.781 ± 35.049 <sup>a</sup>	1.000 ± 0.000 <sup>a</sup>	0.012 ± 0.005 <sup>b</sup>	0.002 ± 0.000 <sup>c</sup>
<i>OsMAS</i>	1.000 ± 0.000 <sup>b</sup>	54.932 ± 19.724 <sup>a</sup>	48.148 ± 22.926 <sup>a</sup>	1.000 ± 0.000 <sup>a</sup>	0.010 ± 0.004 <sup>b</sup>	0.006 ± 0.002 <sup>b</sup>
<i>OsMAS2</i>	1.000 ± 0.000 <sup>b</sup>	33.265 ± 4.426 <sup>a</sup>	42.267 ± 9.562 <sup>a</sup>	1.000 ± 0.000 <sup>a</sup>	0.061 ± 0.016 <sup>b</sup>	0.007 ± 0.001 <sup>c</sup>

The relative quantification (RQ) value is expressed as mean ± standard deviation (SD). Different superscript letters in a row within a treatment indicate significant differences at  $p < 0.05$ . UVC, control rice seedlings without UV treatments; UV2, UV-treated rice seedlings for 2 h per day; UV4, UV-treated rice seedlings for 4 h per day; ChiC, control rice seedlings without chilling treatments; Chi4, chill-treated rice seedlings for 4 h per day; Chi8, chill-treated rice seedlings for 8 h per day; *PAL*, gene encoding phenylalanine ammonia-lyase; *OsCPS4*, gene encoding syn-copalyl diphosphate synthase-like; *OsKSL4*, gene encoding syn-pimara-7,15-diene synthase-like; *CYP99A3*, gene encoding 9-beta-pimara-7,15-diene oxidase-like; *OsMAS*, gene encoding momilactone A synthase-like; *OsMAS2*, gene encoding momilactone A synthase-like.

**Table S4.** Pearson's correlation coefficients between antioxidant activity, chemical profiles, and relevant gene expressions of rice seedlings under UV stress

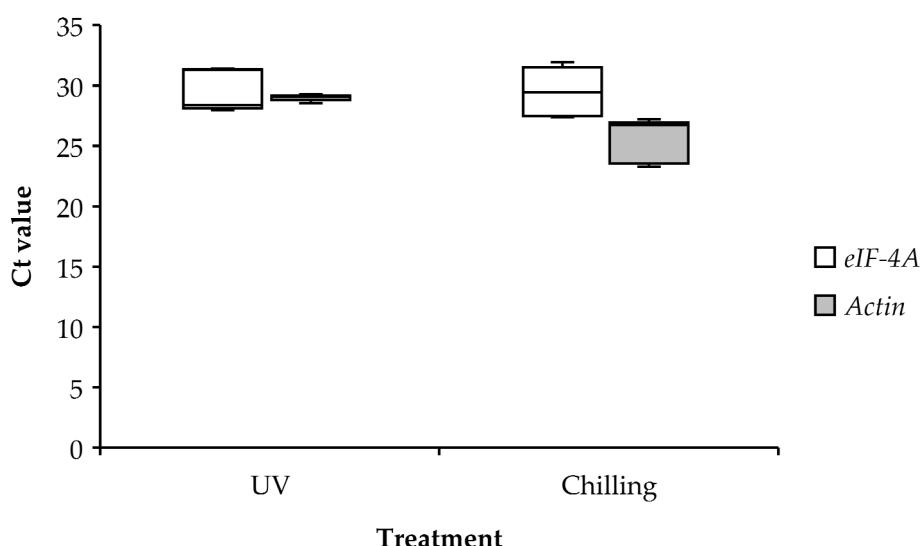
	DPPH	ABTS	PAL	Cat	ChA	HyA	SaA	Esc	Rut	Fis	CPS	KSL	CYP	MAS	MAS2	MA
ABTS	0.24	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PAL	-0.95	-0.21	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Cat	-0.28	-0.38	0.19	-	-	-	-	-	-	-	-	-	-	-	-	-
ChA	-0.64	-0.33	0.58*	0.90*	-	-	-	-	-	-	-	-	-	-	-	-
HyA	-0.27	-0.39	0.20	1.00*	0.90*	-	-	-	-	-	-	-	-	-	-	-
SaA	-0.95	-0.23	0.93*	0.50*	0.81*	0.50*	-	-	-	-	-	-	-	-	-	-
Esc	-0.81	-0.28	0.74*	0.78*	0.96*	0.76*	0.93*	-	-	-	-	-	-	-	-	-
Rut	-0.73	-0.23	0.67*	0.79*	0.93*	0.78*	0.87*	0.97*	-	-	-	-	-	-	-	-
Fis	-0.32	-0.36	0.20	1.00*	0.90*	0.99*	0.52*	0.79*	0.81*	-	-	-	-	-	-	-
CPS	-0.95	-0.24	0.88*	0.44	0.72*	0.42	0.94*	0.87*	0.78*	0.47	-	-	-	-	-	-
KSL	-0.81	-0.16	0.80*	-0.11	0.25	-0.12	0.68*	0.43	0.26	-0.09	0.79*	-	-	-	-	-
CYP	-0.85	-0.27	0.72*	0.26	0.52*	0.23	0.76*	0.67*	0.50*	0.30	0.91*	0.89*	-	-	-	-
MAS	-0.83	0.02	0.78*	0.56*	0.82*	0.55*	0.93*	0.92*	0.87*	0.59*	0.86*	0.54*	0.68*	-	-	-
MAS2	-0.90	0.01	0.94*	0.30	0.66*	0.31	0.94*	0.81*	0.79*	0.32	0.84*	0.63*	0.60*	0.91*	-	-
MA	-0.92	0.03	0.94*	-0.01	0.40	-0.01	0.85*	0.61*	0.52*	0.01	0.84*	0.88*	0.76*	0.77*	0.90*	-
MB	-0.95	-0.06	0.97*	-0.20	0.59*	0.20	0.94*	0.76*	0.67*	0.22	0.91*	0.84*	0.79*	0.86*	0.95*	0.98*

\* , a significance at  $p < 0.05$ ; DPPH, 2,2-diphenyl-1-picrylhydrazyl; ABTS, 2,2'-azinobis-(3-ethylbenzothiazoline-6-sulfonic acid); PAL, gene encoding phenylalanine ammonia-lyase; Cat, catechol; ChA, chlorogenic acid; HyA,  $\rho$ -hydroxybenzoic acid; SaA, salicylic acid; Esc, esculetin; Rut, rutin; Fis, fisetin; CPS, gene encoding syn-coparyl diphosphate synthase-like (*OsCPS4*); KSL, gene encoding syn-pimara-7,15-diene synthase-like (*OsKSL4*); CYP, gene encoding 9-beta-pimara-7,15-diene oxidase-like (*CYP99A3*); MAS, gene encoding momilactone A synthase-like (*OsMAS*); MAS2, gene encoding momilactone A synthase-like (*OsMAS2*); MA, momilactone A; MB, momilactone B.

**Table S5.** Pearson's correlation coefficients between antioxidant activity, chemical profiles, and relevant gene expressions of rice seedlings under chilling stress

	DPPH	ABTS	PAL	TPC	TFC	SyA	SaA	BeA	CiA	CoA	Que	Tri	CPS	KSL	CYP	MAS	MAS2	MA
<b>ABTS</b>	0.92*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<b>PAL</b>	0.20	0.31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<b>TPC</b>	0.85*	0.79*	-0.25	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<b>TFC</b>	0.91*	0.94*	0.45	0.75*	-	-	-	-	-	-	-	-	-	-	-	-	-	-
<b>SyA</b>	0.79*	0.79*	-0.25	0.96*	0.72*	-	-	-	-	-	-	-	-	-	-	-	-	-
<b>SaA</b>	0.93*	0.88*	-0.03	0.94*	0.84*	0.92*	-	-	-	-	-	-	-	-	-	-	-	-
<b>BeA</b>	0.63*	0.74*	0.85*	0.27	0.83*	0.26	0.46	-	-	-	-	-	-	-	-	-	-	-
<b>CiA</b>	0.47	0.57*	0.95*	0.05	0.70*	0.04	0.25	0.96*	-	-	-	-	-	-	-	-	-	-
<b>CoA</b>	0.64*	0.74*	0.85*	0.29	0.85*	0.28	0.46	0.99*	0.97*	-	-	-	-	-	-	-	-	-
<b>Que</b>	0.60*	0.68*	0.89*	0.19	0.78*	0.19	0.38	0.96*	0.98*	0.98*	-	-	-	-	-	-	-	-
<b>Tri</b>	0.68*	0.76*	0.83*	0.33	0.87*	0.32	0.50*	0.98*	0.96*	0.99*	0.98*	-	-	-	-	-	-	-
<b>CPS</b>	0.37	0.48	0.98*	-0.06	0.61*	-0.07	0.14	0.93*	0.99*	0.94*	0.96*	0.92*	-	-	-	-	-	-
<b>KSL</b>	0.35	0.46	0.98*	-0.09	0.59*	-0.10	0.11	0.92*	0.99*	0.93*	0.95*	0.91*	1.00*	-	-	-	-	-
<b>CYP</b>	0.38	0.49	0.98*	-0.05	0.62*	-0.06	0.15	0.93*	0.99*	0.94*	0.96*	0.92*	1.00*	1.00*	-	-	-	-
<b>MAS</b>	0.39	0.49	0.98*	-0.05	0.62*	-0.06	0.16	0.94*	1.00*	0.94*	0.96*	0.92*	1.00*	1.00*	1.00*	-	-	-
<b>MAS2</b>	0.35	0.46	0.99*	-0.09	0.59*	-0.10	0.11	0.92*	0.99*	0.93*	0.95*	0.91*	1.00*	1.00*	1.00*	1.00*	-	-
<b>MA</b>	0.34	0.43	0.99*	-0.12	0.56*	-0.13	0.09	0.90*	0.98*	0.91*	0.95*	0.90*	1.00*	1.00*	1.00*	1.00*	1.00*	-
<b>MB</b>	0.67*	0.77*	0.84*	0.29	0.84*	0.27	0.48	0.99*	0.96*	0.99*	0.97*	0.98*	0.93*	0.91*	0.93*	0.93*	0.91*	0.90*

\*, a significance at  $p < 0.05$ ; DPPH, 2,2-diphenyl-1-picrylhydrazyl; ABTS, 2,2'-azinobis-(3-ethylbenzothiazoline-6-sulfonic acid); PAL, gene encoding phenylalanine ammonia-lyase; TPC, total phenolic content; TFC, total flavonoid content; SyA, syringic acid; SaA, salicylic acid; BeA, benzoic acid; CiA, cinnamic acid; CoA,  $\rho$ -coumaric acid; Que, quercitin; Tri, tricin; CPS, gene encoding syn-coparyl diphosphate synthase-like (*OsCPS4*); KSL, gene encoding syn-pimara-7,15-diene synthase-like (*OsKSL4*); CYP, gene encoding 9-beta-pimara-7,15-diene oxidase-like (*CYP99A3*); MAS, gene encoding momilactone A synthase-like (*OsMAS*); MAS2, gene encoding momilactone A synthase-like (*OsMAS2*); MA, momilactone A; MB, momilactone B.

**Figure S1.** A boxplot for the Ct values of candidate housekeeping genes (*eIF-4A* and *actin*) in rice under UV and chilling conditions. The line inside the box indicates the median. The top and bottom lines of the box display the first and third quartiles, respectively. Whiskers present the minimum and maximum Ct values.