

Supplementary file

Manuscript title: A novel biological agent Cytosinpeptidemycin inhibited the pathogenesis of tobacco mosaic virus by inducing host resistance and stress response

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Supplementary figures

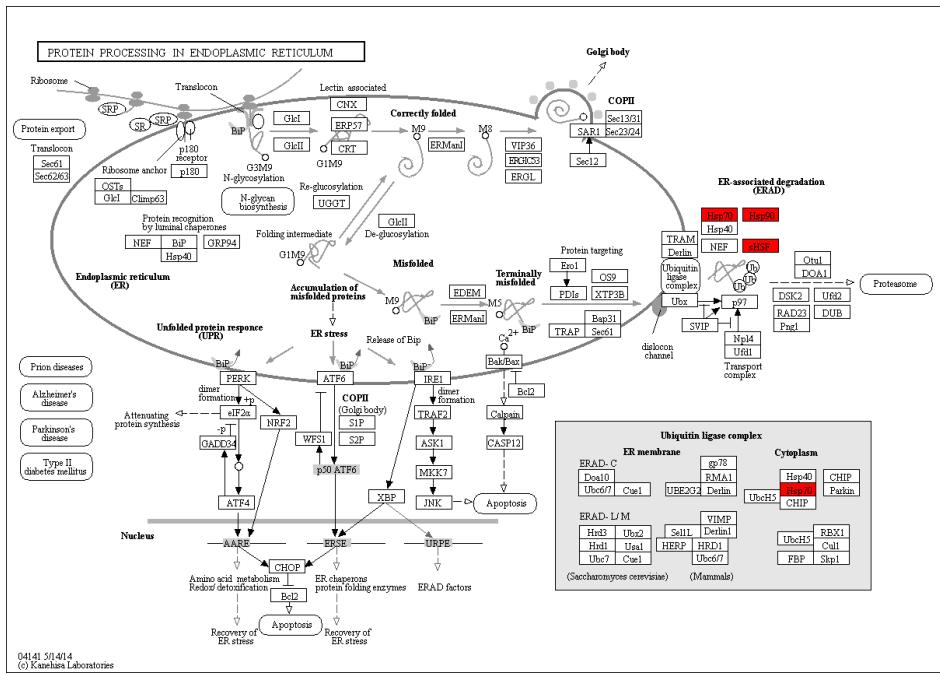


Figure S1. CytPM induced KEGG pathway involved in protein processing in endoplasmic reticulum

Supplementary tables

Table S1. Total genes of CytPM-responsive tobacco BY-2 transcriptome. (PDF)

Table S2. Total Annotation of KEGGs in tobacco BY-2 transcriptome. (PDF)

Table S3. Annotation of DEGs of CytPM-responsive tobacco BY-2 transcriptome. (PDF)

Table S4. List of DEGs involved in the KEGG pathways. (PDF)

Gene symbol	Gene description	Regulate	logFC	p-value	Major reported functions	References
LOC107763443	leucine-rich repeat receptor protein kinase EMS1-like	Up	4.35	1.2E-10	LRR-RLK, development and differentiation	S20
LOC107819168	protein LYK5-like	Up	3.99	2.3E-08	unknown function, PRR like protein	S21
LOC107801313	LRR receptor-like serine/threonine-protein kinase RPK2	Up	3.04	1.6E-05	PRR protein, enhanced resistance to nematodes	S22
LOC107767708	probable L-type lectin-domain containing receptor kinase S.7	Up	2.66	2.6E-05	unknown function, PRR protein?	
LOC107779438	G-type lectin S-receptor-like serine/threonine-protein kinase	Down	-1.94	2.6E-05	unknown function, PRR protein?	
LOC107762392	receptor-like protein kinase	Up	2.59	2.2E-04	unknown function, PRR protein?	
LOC107816125	G-type lectin S-receptor-like serine/threonine-protein kinase RLK1	Up	1.74	2.9E-04	receptor-like protein kinase, PRR in PTI pathway	29
LOC107789370	wall-associated receptor kinase 5-like	Up	2.33	7.3E-05	unknown function	
LOC107761617	serine/threonine-protein kinase WAG1-like	Up	1.71	2.4E-04	negatively regulate root waving	S23
LOC107779812	toll-like receptor 13	Down	-1.9	2.2E-04	unknown function	
LOC107779134	probable glutathione S-transferase	Up	4.31	1.4E-16	induced by plant pathogen interaction	S7
LOC107789895	probable glutathione S-transferase	Down	-2.42	1.1E-06	induced by plant pathogen interaction	S7
LOC107816122	proteinase inhibitor type-2	Down	-2.28	1.1E-06	wound induced responses, defense against pathogen	S15
LOC107794263	wound-induced protein WIN1-like	Down	-1.86	5.6E-05	wound induced responses, anti-fungal activity	45
LOC107812674	125 kDa kinesin-related protein-like	Down	-1.91	9.0E-05	motor protein on microtubule	
LOC107780076	polyubiquitin-like	Up	2.21	3.9E-06	unknown function, basal host resistance?	S24
LOC107798618	basis form of pathogenesis-related protein 1-like	Down	-2.65	1.0E-06	response to pathogen infection?	S25
LOC107811874	thaumatin-like protein	Up	3.39	1.2E-08	PR proteins, in response to viroid	
LOC107815427	defensin-like protein 19	Down	-2.64	3.8E-08	unknown function, antibiotics?	S26
LOC107831203	putative calcium-transporting ATPase 13, plasma membrane-type	Up	2.84	3.9E-08	plant immunity	S27
LOC107824186	defensin-like protein 1	Down	-2.16	7.9E-05	unknown function, antibiotics?	S26
LOC107803876	pleiotropic drug resistance protein 1-like	Up	2.96	3.7E-06	resistance to pathogens?	S28
LOC107775267	cytochrome P450 78A7-like	Up	2.95	4.8E-05	secondary metabolite biosynthesis, toxin resistance	S29
LOC107794082	SKP1-like protein 11	Up	1.97	4.0E-05	involved in RNA silencing or autophagy?	S30
LOC107792571	calmodulin-like	Up	1.88	7.5E-05	unknown function, RNA silencing or autophagy?	S31

Table S5. defense responsive and signal transduction genes induced by CytPM.

Gene symbol	Gene description	Regulate	logFC	p-value	Major reported functions	References
LOC107798260	16.9 kDa class I heat shock protein 1-like	Up	2.84	1.4E-07		
LOC107802502	17.3 kDa class II heat shock protein-like	Up	4.37	6.8E-17		
LOC107762094	17.4 kDa class III heat shock protein	Up	4.18	8.0E-14		
LOC107802394	17.6 kDa class I heat shock protein	Up	3.15	1.4E-09	multiple stress response	S1
LOC107787546	17.8 kDa class I heat shock protein-like	Up	3.26	3.2E-11		S2
LOC107769078	18.2 kDa class I heat shock protein-like	Up	3.00	1.2E-09		S6
LOC107760429	18.8 kDa class II heat shock protein-like	Up	2.68	2.3E-08		
LOC107775020	22.0 kDa heat shock protein-like	Up	3.84	9.3E-14		
LOC107764596	small heat shock protein, chloroplastic-like	Up	3.57	5.2E-12		
LOC107796657	heat shock 70 kDa protein	Up	3.39	4.4E-11	biotic and abiotic stress response	S3, S4
LOC107779564	heat shock cognate 70 kDa protein 2-like	Up	3.51	2.0E-11	signal transduction, apoptosis	39
LOC107807848	heat shock protein 82	Up	2.74	1.5E-05	unknown function, stress response?	
LOC107784191	hsp70-Hsp90 organizing protein 3-like	Up	1.99	2.0E-05	stress response, thermotolerance	S5
LOC107818463	heat shock protein 83-like	Up	2.05	1.0E-04	unknown function, stress response?	
LOC107763527	chaperone protein ClpB1 (Hsp100 family)	Up	2.13	7.1E-06	stress response	S6
LOC107779134	probable glutathione S-transferase	Up	4.31	1.4E-16	biotic stress response	S7
LOC107789895	probable glutathione S-transferase	Down	-2.41	1.1E-06	biotic stress response	S7
LOC107791128	zinc finger protein ZAT12-like	Up	2.16	3.8E-06	stress response	41
LOC107810147	transcription factor bHLH12-like	Up	4.83	4.5E-14	abiotic and salt stress response	S8, S9
LOC107793215	late embryogenesis abundant protein Dc3-like	Up	3.16	1.8E-10	stress regulated	S10
LOC107819695	pyridoxal 5'-phosphate synthase-like subunit PDX1.2	Up	3.02	1.6E-09	heat shock tolerance	S11
LOC107794006	galactinol synthase 1-like	Up	2.82	1.0E-07	drought tolerance	S12
LOC107825532	multiprotein-bridging factor 1c-like	Down	-3.01	2.0E-07	osmotic stress regulation	S13, S14
LOC107811676	ethylene-responsive transcription factor ERF109-like	Up	2.09	7.2E-06	retards PCD, improves salt tolerance	43
LOC107816122	proteinase inhibitor type-2	Down	-2.28	1.1E-06	wound induced responses	S15
LOC107803197	cysteine proteinase COT44-like	Down	-2.46	7.3E-07	hypersensitive response regulation	S16
LOC107782101	CBL-interacting serine/threonine-protein kinase 14	Up	1.94	3.2E-05	drought tolerance	S17
LOC107820880	potassium channel AKT1-like	Up	2.15	9.7E-05	salt stress adaption	
LOC107829507	BAG family molecular chaperone regulator 6-like	Up	2.03	1.9E-05	unknown function, chaperon protein	
LOC107794263	wound-induced protein WIN1-like	Down	-1.86	5.6E-05	wound induced responses	45
LOC107764180	universal stress protein A-like protein	Up	2.49	6.4E-05	unknown function, stress response?	
LOC107783248	dnaJ homolog subfamily B member 13-like	Up	2.33	7.7E-07	unknown function, chaperon protein	
LOC107831045	CBS domain-containing protein CBSX5-like	Up	2.16	8.0E-05	ER localization, regulate H ₂ O ₂	S18
LOC107821202	galactinol synthase 2	Up	2.17	9.8E-06	drought tolerance	S12
LOC107776258	NAC transcription factor 29-like	Down	-4.26	2.0E-04	cold stress response	S19

Table S6. Stress responsive genes induced by CytPM.

Gene symbol	Gene description	Regulate	logFC	p-value	Major reported functions	References
LOC107811676	ethylene-responsive transcription factor ERF109-like	Up	2.09	7.2E-06	retards PCD, improves salt tolerance	43
LOC107765917	ethylene-responsive transcription factor 1B-like	Down	-2.17	5.2E-06	unknown function, ethylene response?	
LOC107765748	ethylene-responsive transcription factor 1B-like	Up	2.15	5.3E-05	unknown function, ethylene response?	
LOC107811574	ethylene-responsive transcription factor CRF4-like	Up	2.43	5.6E-05	unknown function, ethylene response?	
LOC107809368	auxin-responsive protein SAUR71-like	Down	-2.25	1.5E-06	auxin signalling	
LOC107800172	auxin-induced protein 15A-like	Down	-2.35	1.7E-05	unknown function, auxin response?	
LOC107773231	auxin-responsive protein SAUR21-like	Down	-1.86	7.7E-05	auxin response	S32
LOC107780011	auxin-responsive protein SAUR72-like	Up	2.15	1.6E-04	auxin response	S33
LOC107781392	auxin-responsive protein SAUR66-like	Down	-3.09	1.9E-04	unknown function, auxin response?	
LOC107828043	mitogen-activated protein kinase kinase kinase NPK1	Up	2.18	2.4E-05	negatively regulate auxin	27, 28
LOC107810915	probable WRKY transcription factor 40	Down	-2.00	6.6E-05	negatively regulate ABA	50
LOC107766566	protein ABA DEFICIENT 4, chloroplastic-like	Down	-2.44	6.8E-05	unknown function, ABA response?	
LOC107763169	salicylate carboxymethyltransferase-like	Down	-2.20	1.5E-04	unknown function, salicylate response?	
LOC107763786	cytokinin hydroxylase-like	Up	2.50	1.3E-05	unknown function, cytokinin response?	S34
LOC107803876	pleiotropic drug resistance protein 1-like	Up	2.96	3.7E-06	plant hormone transportation	S28

Table S7. Phytohormone responsive genes induced by CytPM.

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