Table S1. KEGG enrichment analysis of DEGs in the library pair comparison of DCPTA vs. the control.

Pathway **(id)**	**DEGs with Pathway Annotation** **(123)**	***P*-Value**	**Gene Ids**
Sesquiterpenoid and triterpenoid biosynthesis (ko00909)	5 (4.07%)	9.46E-09	XM_008664083.1, XM_008664550.1, NM_001158449.1, XM_008650427.1, XM_008650428.1
Valine, leucine and isoleucine biosynthesis (ko00290)	4 (3.25%)	3.12E-04	NM_001138804.1, XM_008678367.1, NM_001157694.1, XM_008678369.1
Pathogenic Escherichia coli infection (ko05130)	4 (3.25%)	3.73E-03	NM_001155135.1,XM_008675206.1,NM_001111986.1,NM_001174192.1
Starch and sucrose metabolism (ko00500)	13 (10.57%)	8.80E-05	XM_008649866.1,NM_001111443.1,XM_008646898.1,NM_001154527.1,XM_008666556.1,XM_008667214.1,NM_001134283.1,NM_001136824.1,NM_001157472.1,XM_008646897.1,XM_008650730.1,NM_001153213.1,XM_008679443.1
Degradation of aromatic compounds (ko01220)	1 (0.81%)	5.81E-03	NM_001176213.1
Carotenoid biosynthesis (ko00906)	4 (3.25%)	7.19E-04	XR_559803.1, XM_008664126.1, XR_559802.1, XR_555316.1
C5-Branched dibasic acid metabolism (ko00660)	4 (3.25%)	5.02E-07	NM_001138804.1, XM_008678367.1, NM_001157694.1, XM_008678369.1
Gap junction (ko04540)	3 (2.44%)	2.75E-03	XM_008675206.1, NM_001111986.1, NM_001174192.1
Nitrogen metabolism (ko00910)	5 (4.07%)	1.70E-03	XM_008658536.1, NM_001149554.1, **XM_008648080.1**, XM_008658537.1, **XM_008680224.1**
Phenylpropanoid biosynthesis (ko00940)	9 (7.32%)	1.47E-04	NM_001111864.1, XM_008649866.1, NM_001111443.1, NM_001153744.1, XM_008666556.1, NM_001134283.1, NM_001136824.1, XM_008680606.1, NM_001174615.1

Naphthalene degradation (ko00626)	1 (0.81%)	2.28E-03	NM_001176213.1
Tyrosine metabolism (ko00350)	3 (2.44%)	2.75E-03	NM_001148740.1, NM_001176213.1, XM_008659837.1
Alanine, aspartate and glutamate metabolism (ko00250)	5 (4.07%)	3.41E-03	XM_008677536.1, XM_008658536.1, XM_008677530.1, NM_001138219.1, XM_008658537.1
Cutin, suberine and wax biosynthesis (ko00073)	2 (1.62%)	1.79E-03	NM_001147243.1, XM_008678619.1
Transcriptional misregulation in cancer (ko05202)	4 (3.25%)	3.41E-03	XM_008658363.1, XM_008656581.1, XM_008651906.1, XM_008651911.1
Cyanoamino acid metabolism (ko00460)	6 (4.88%)	1.30E-05	XM_008649866.1, NM_001111443.1, XM_008666556.1, NM_001134283.1, NM_001136824.1, XM_008646063.1

Table S2. KEGG enrichment analysis of DEGs in the library pair comparison of PEG vs. the control.

Pathway (id)	DEGs with Pathway Annotation (130)	*p*-Value	Gene Ids
Streptomycin biosynthesis (ko00521)	2 (1.54%)	5.22E-03	NM_001137498.1, NM_001112082.1
Inositol phosphate metabolism (ko00562)	5 (3.85%)	2.75E-03	XM_008668770.1, XM_008658440.1, XM_008670908.1, NM_001112082.1, XM_008680131.1
Pathogenic Escherichia coli infection (ko05130)	4 (3.08%)	4.42E-03	NM_001155135.1, XM_008675211.1, NM_001174192.1, XR_557701.1
Fatty acid biosynthesis (ko00061)	4 (3.08%)	1.81E-03	XM_008664832.1, XM_008682945.1, XM_008682946.1, XM_008664828.1
Degradation of aromatic compounds (ko01220)	1 (0.77%)	6.28E-03	NM_001147254.1
Carotenoid biosynthesis (ko00906)	3 (2.31%)	6.45E-03	XR_559803.1, XM_008664126.1, XR_559802.1
Phenylalanine, tyrosine and tryptophan biosynthesis (ko00400)	5 (3.85%)	1.45E-03	NM_001111749.1, XR_559917.1, XM_008670310.1, NM_001157394.1, XM_008667482.1
Nitrogen metabolism (ko00910)	11 (8.46%)	2.53E-07	XM_008658536.1, XM_008676969.1, XM_008676970.1, M_001111973.1, NM_001149554.1, XM_008674335.1, XM_008674336.1, XM_008675159.1, **XM_008648080.1**, **NM_001112223.1**, **XM_008680224.1**
Diterpenoid biosynthesis (ko00904)	3 (2.31%)	9.67E-04	XM_008664610.1, XM_008670678.1, NM_001111627.1
Butirosin and neomycin biosynthesis (ko00524)	1 (0.77%)	7.48E-03	NM_001137498.1
Ras signaling pathway (ko04014)	4 (3.08%)	8.08E-03	XM_008675011.1, XM_008675225.1, XM_008670016.1, XM_008671868.1
Phagosome	6	7.01E-03	XM_008658440.1, XM_008670908.1, XM_008675211.1,

(ko04145)	(4.62%)		XM_008680131.1, NM_001174192.1, XR_557701.1
Selenocompound metabolism (ko00450)	2 (1.54%)	3.56E-03	NM_001158752.1, NM_001153955.1
Glutamatergic synapse (ko04724)	4 (3.08%)	5.70E-03	NM_001111973.1, XM_008675011.1, XM_008675225.1, XM_008671868.1
Benzoate degradation (ko00362)	2 (1.54%)	6.70E-04	NM_001148402.1, XM_008649939.1
Phenylalanine metabolism (ko00360)	5 (3.85%)	5.47E-03	NM_001174615.1, NM_001111864.1, NM_001154204.1, XM_008664867.1, NM_001147254.1
Aminoacyl-tRNA biosynthesis (ko00970)	5 (3.85%)	2.54E-03	XM_008649324.1, NM_001146882.1, XM_008649323.1, XM_008671897.1, XM_008671899.1
Propanoate metabolism (ko00640)	5 (3.85%)	2.37E-04	XM_008664832.1, XM_008682945.1, NM_001148402.1, XM_008682946.1, XM_008664828.1
Gap junction (ko04540)	3 (2.31%)	3.17E-03	XM_008675211.1, NM_001174192.1, XR_557701.1
Pyruvate metabolism (ko00620)	6 (4.62%)	8.18E-03	XM_008664832.1, XM_008665884.1, XM_008682945.1, NM_001148402.1, XM_008682946.1, XM_008664828.1
Alanine, aspartate and glutamate metabolism (ko00250)	6 (4.62%)	8.14E-04	XM_008658536.1, XM_008676969.1, XM_008676970.1, NM_001111973.1, NM_001155755.1, XM_008675159.1
Insulin signaling pathway (ko04910)	7 (5.38%)	8.09E-04	NM_001137498.1, XM_008671744.1, XM_008664832.1, XM_008667214.1, XM_008682945.1, XM_008682946.1, XM_008664828.1

Table S3. KEGG enrichment analysis of DEGs in the library pair comparison of PEG + DCPTA vs. PEG.

Pathway (**id**)	**DEGs with Pathway Annotation** (**126**)	***p*-Value**	**Gene ids**
Two-component system (ko02020)	3 (2.38%)	4.11E-03	NM_001111973.1, NM_001148402.1, NM_001279386.1
Nitrogen metabolism (ko00910)	6 (4.76%)	2.49E-04	XM_008648080.1, XM_008645823.1, NM_001111973.1, XM_008681060.1, XM_008680224.1, NM_001112223.1
Phenylpropanoid biosynthesis (ko00940)	7 (5.56%)	3.30E-03	NM_001134283.1, XM_008676178.1, XM_008659826.1, NM_001111984.1, XM_008650154.1, XM_008673799.1, NM_001154204.1
Ether lipid metabolism (ko00565)	5 (3.97%)	1.88E-04	XM_008675011.1, XM_008671868.1, XM_008675008.1, XM_008675004.1, XM_008675224.1
Ras signaling pathway (ko04014)	5 (3.97%)	1.39E-03	XM_008675011.1, XM_008671868.1, XM_008675008.1, XM_008675004.1, XM_008675224.1
Cutin, suberine and wax biosynthesis (ko00073)	2 (1.59%)	1.91E-03	NM_001147243.1, XM_008678619.1
Cyanoamino acid metabolism (ko00460)	4 (3.17%)	1.26E-03	NM_001134283.1, XM_008676178.1, XM_008646063.1, NM_001111984.1
Glutamatergic synapse (ko04724)	8 (6.35%)	1.74E-06	NM_001111973.1, XM_008675011.1, XM_008660474.1, XM_008671868.1, XM_008675008.1, XM_008682979.1, XM_008675004.1, XM_008675224.1
Benzoate degradation (ko00362)	2 (1.59%)	6.40E-04	NM_001148402.1, NM_001279386.1
Protein digestion and absorption (ko04974)	2 (1.59%)	1.68E-03	XM_008656280.1, XM_008682979.1
Lysine degradation (ko00310)	5 (3.97%)	1.16E-03	XR_557592.1, NM_001148402.1, XM_008679549.1, NM_001279386.1, NM_001147647.1
Propanoate metabolism	5 (3.97%)	2.17E-04	XM_008664831.1, XM_008670419.1, NM_001148402.1, NM_001279386.1, XM_008664828.1

(ko00640)			
GnRH signaling pathway (ko04912)	5 (3.97%)	1.51E-04	XM_008675011.1, XM_008671868.1, XM_008675008.1, XM_008675004.1, XM_008675224.1
Synthesis and degradation of ketone bodies (ko00072)	2 (1.59%)	1.68E-03	NM_001148402.1, NM_001279386.1
Glyoxylate and dicarboxylate metabolism (ko00630)	5 (3.97%)	4.13E-03	XM_008654945.1, XM_008670416.1, NM_001111973.1, NM_001148402.1, NM_001279386.1

Table S4. The data of ZmNADH-NR, ZmFd-NiR, Zm-GS2 and ZmFd-GOGAT protein abundances detected by Western blot analysis (% of control).

Protein	Treatment	Replicate 1	Replicate 2	Replicate 3	Replicate 4	Replicate 5
ZmNADH-NR	Control	100	112	97	93	97
	DCPTA	113	115	114	120	134
	PEG	30	38	36	49	22
	PEG+DCPTA	85	71	83	57	79
ZmFd-NiR	Control	100	95	113	108	94
	DCPTA	119	113	124	136	123
	PEG	52	79	58	57	51
	PEG+DCPTA	89	96	88	89	70
Zm-GS2	Control	100	89	109	90	113
	DCPTA	95	93	92	89	114
	PEG	49	55	53	34	45
	PEG+DCPTA	66	86	80	68	89
ZmFd-GOGAT	Control	100	91	118	98	103
	DCPTA	111	111	102	113	92
	PEG	53	61	39	52	48
	PEG+DCPTA	78	60	58	66	75