

University of Groningen

Metabolic engineering of beta-oxidation in *Penicillium chrysogenum* for improved semi-synthetic cephalosporin biosynthesis

Veiga, Tânia; Gombert, Andreas K; Landes, Nils; Verhoeven, Maarten D; Kiel, Jan; Krikken, Arjen; Nijland, Jeroen; Touw, Hesselien; Luttik, Marijke A H; van der Toorn, John C

Published in:
Metabolic Engineering

DOI:
[10.1016/j.ymben.2012.02.004](https://doi.org/10.1016/j.ymben.2012.02.004)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2012

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Veiga, T., Gombert, A. K., Landes, N., Verhoeven, M. D., Kiel, J. A. K. W., Krikken, A. M., ... Daran, J-M. (2012). Metabolic engineering of beta-oxidation in *Penicillium chrysogenum* for improved semi-synthetic cephalosporin biosynthesis. *Metabolic Engineering*, 14(4), 437-448. DOI: 10.1016/j.ymben.2012.02.004

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Supplemental Table 2 – Transcript levels of the 52 genes consistently up-regulated in the strains DS17690, DS49834 and DS50661 in the presence of adipic acid (ADA). Genes marked with * contained the cis regulatory motif (5'-CCKSGGB-3') within their 1-kb upstream sequence.

The genes underlined correspond to the six putative acyl-CoA oxidases and dehydrogenases analysed in the study.

Gene ID	Similar to	DS17690		DS49834		DS50661	
		-ADA	+ADA	-ADA	+ADA	-ADA	+ADA
Pc12g07430*	mitochondrial dicarboxylate transport protein like protein An02g01730 – <i>A. niger</i>	34±8	88±12	28±6	115±26	29±7	187±19
Pc13g02710*	multifunctional beta-oxidation protein – <i>N. crassa</i>	460±15	1688±131	450±36	1267±152	325±45	2223±210
Pc13g02780*	subunit of succinyl-CoA:benzylsuccinate CoA-transferase like protein An18g05120 – <i>A. niger</i>	122±26	917±150	111±5	799±133	102±37	1379±124
Pc13g03380*	peroxisomal transporter Ant1 – <i>S. cerevisiae</i>	93±4	228±23	87±2	248±35	79±17	347±85
Pc13g06830	3-hydroxybutyryl-CoA dehydrogenase like protein An14g00430 – <i>A. niger</i>	138±8	277±14	126±15	274±36	83±12	299±23
Pc13g10320*	hypothetical protein contig_1_84_scaffold_5.tfa_720wg – <i>A. nidulans</i>	376±55	1960±185	286±54	1531±241	171±54	2527±11
Pc13g11270	hypothetical protein YER182w – <i>S. cerevisiae</i>	27±7	151±7	26±8	162±41	20±1	271±45
Pc13g11580*	hypothetical protein contig46_part_1.tfa_3280wg – <i>A. fumigatus</i>	112±16	242±23	81±4	219±35	69±11	350±70
Pc13g12930*	peroxisomal acetyl-CoA C-acyltransferase POT1 – <i>Y. lipolytica</i>	447±123	1030±210	334±38	883±100	275±77	1419±421
<u>Pc13g14410</u>	hypothetical protein contig42.tfa_690wg – <i>A. fumigatus</i>	12±0	438±34	12±0	346±96	12±0	1049±136
Pc13g14420	malonyl CoA synthase matB – <i>R. trifolii</i>	12±0	259±24	14±2	319±82	13±7	587±140
Pc13g14430	hypothetical protein contig_1_112_scaffold_8.tfa_680cg – <i>A. nidulans</i>	12±0	367±69	12±0	31879	12±0	616±112
Pc14g00500	D-amino acid hydantoin hydrolase huA - <i>Pseudomonas sp.</i>	12±0	35±9	12±0	28±5	13±2	60±6
Pc15g00110*	subunit 13 of glutathione S-transferase GTK1 – <i>R. norvegicus</i>	38±1	394±63	37±3	342±71	25±4	735±134
Pc15g00410*	peroxisomal acetyl-CoA C-acyltransferase POT1 – <i>Y. lipolytica</i>	164±17	431±43	117±24	386±64	105±13	630±87
Pc15g00630*	hypothetical protein SPBC31F10.02 – <i>S. pombe</i>	172±24	356±29	143±32	401±38	143±52	450±60
Pc16g03120*	hypothetical protein An07g02450 – <i>A. niger</i>	99±12	230±16	105±7	219±30	78±21	306±31
Pc16g12360*	glutathione-dependent formaldehyde dehydrogenase FDH – <i>M. marinus</i>	25±4	123±10	23±8	122±19	17±5	204±7
Pc16g14230	beta-ketoacyl reductase rhlG – <i>P. aeruginosa</i>	139±11	507±21	140±18	575±123	49±16	585±100
Pc16g14240*	acetamidase amdS – <i>A. oryzae</i>	228±41	539±58	195±39	424±67	150±44	767±102
Pc16g15270*	hypothetical protein YBR096w – <i>S. cerevisiae</i>	12±0	67±6	12±0	109±24	12±0	161±52
Pc19g00540	membrane steroid hormone-binding protein MSBP – <i>B. taurus</i>	12±0	30±2	12±0	30±8	12±0	35±7
<u>Pc20g01800*</u>	hypothetical protein contig42.tfa_690wg – <i>A. fumigatus</i>	125±13	339±40	113±11	291±50	63±14	378±73

Pc20g06590	hypothetical protein SC1C3.21 SC1C3.21 – <i>S. coelicolor</i>	14±6	155±17	18±6	196±60	12±0	216±6
Pc20g07170	cutinase transcription factor FarB – <i>A. nidulans</i>	14±2	448±61	21±3	242±100	13±3	783±31
Pc20g07520*	hypothetical protein An01g15120 - <i>Aspergillus niger</i>	88±33	206±23	110±36	280±36	82±10	246±13
Pc20g07920*	glutaryl-CoA dehydrogenase GCHD - <i>H sapiens</i>	205±47	1713±155	195±28	1282±200	158±8	2138±577
Pc20g08300*	hypothetical protein 12F11.200 – <i>N. crassa</i>	72±3	223±22	84±8	211±37	79±22	312±61
Pc20g09870*	hypothetical protein An16g08040 – <i>A. niger</i>	54±11	111±4	50±5	115±13	66±25	167±28
Pc20g12470*	delta3-cis-delta2-trans-enoyl-CoA isomerase Eci1 – <i>S. cerevisiae</i>	153±48	786±114	111±24	591±136	74±16	1086±67
Pc20g15640	hypothetical protein – <i>B. japonicum</i>	37±6	229±20	51±8	220±34	54±18	312±53
Pc20g15650*	hypothetical protein contig_1_100_scaffold_7.tfa_390cg – <i>A. nidulans</i>	12±0	29±4	12±0	37±9	12±0	38±2
Pc20g15660	sterol carrier protein-X sterol carrier protein-2 SCP2 – <i>H. sapiens</i>	24±8	85±6	21±2	99±24	13±1	132±18
Pc21g04680*	peroxisomal acetyl-CoA C-acyltransferase POT1 – <i>Y. lipolytica</i>	44±6	149±25	57±10	117±21	39±17	217±47
Pc21g11670*	quinone reductase like protein An12g00170 – <i>A. niger</i>	102±5	274±36	88±12	207±29	83±6	327±58
Pc21g12260	alcohol dehydrogenase C ADHC – <i>M. smegmatis</i>	22±1	75±4	12±0	73±9	12±0	127±34
Pc21g17590*	acyl-CoA dehydrogenase like protein An17g01150 – <i>A. niger</i>	839±129	2143±72	699±96	1510±198	431±117	2372±364
Pc21g19470*	mitochondrial succinate-fumarate transporter Sfc1 – <i>S. cerevisiae</i>	48±46	167±15	40±17	114±20	15±7	158±16
Pc21g19590*	hypothetical protein mg00056.1 – <i>M. grisea</i>	35±8	139±21	24±3	133±31	12±0	169±28
Pc21g19600*	similarity to hypothetical protein 1329_scaffold_5.tfa_150cg – <i>F. graminearum</i>	176±5	352±32	114±6	286±55	37±9	328±19
Pc21g20650*	similarity to 4-coumarate-CoA ligase 4CL – <i>A. thaliana</i>	53±14	123±6	42±6	91±19	70±19	224±41
Pc21g21340	hypothetical protein alr1138 - <i>Nostoc sp.</i>	12±0	124±19	14±4	130±23	12±0	28±6
Pc21g22060*	hypothetical protein Rv0976c – <i>M. tuberculosis</i>	31±10	122±21	18±8	102±30	18±7	182±46
Pc22g03680*	NADPH-dependent beta-ketoacyl reductase RhlG – <i>P. aeruginosa</i>	371±84	833±98	271±162	1332±146	243±125	1348±556
Pc22g03710	hypothetical membrane protein YBR043c – <i>S. cerevisiae</i>	26±12	101±14	27±2	140±37	33±13	163±38
Pc22g03940	succinyl CoA: 3-oxoacid CoA transferase SCOT – <i>H. sapiens</i>	170±30	1006±188	205±45	708±92	177±58	1381±284
Pc22g14270*	hypothetical protein contig5_part_ii.tfa_390wg – <i>A. fumigatus</i>	319±64	798±106	226±35	627±102	197±51	1022±136
Pc22g15170*	propionyl-CoA carboxylase beta chain precursor like protein An15g02830 – <i>A. niger</i>	15±1	60±12	12±0	51±17	12±0	82±8
Pc22g15180*	pyruvate carboxylase like protein An15g02820 – <i>A. niger</i>	32±8	136±14	18±1	105±27	12±0	238±70
Pc22g20270*	4-coumarate-CoA ligase 4CL – <i>A. thaliana</i>	186±28	1317±104	181±12	1362±170	153±53	1914±190
Pc22g22390*	AK-toxin production protein Akt3-1 – <i>A. alternata</i>	51±7	681±81	48±5	510±8	31±5	991±90
Pc22g25150*	acyl CoA dehydrogenase aidB – <i>E. coli</i>	97±23	554±55	93±29	549±110	86±20	727±58