Supporting information for Liu *et al.* (2003) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.0630387100

Table 3. Selected genes and operons of DEIRA with a *recA*-like expression pattern

Gene ID*	Function group†	Protein description and comments	Relative basal level	Maximum induction level, fold	STD	CV	Maximum induction time, h
DR0003	-	Uncharacterized protein	1.32	14.03	5.53	39.39	1.5
DR0046	-	Leucine-rich repeat protein	0.18	2.14	0.35	16.21	3
DR0047	-	Uncharacterized protein	0.11	2.48	1.40	56.42	3
DR0048	S	Uncharacterized membrane protein, YcaP ortholog	0.33	3.90	0.55	14.01	3
DR0050	L	DinB/YfiT family protein	0.53	3.84	0.93	24.23	3
DR0051	S	Small cysteine-rich protein of the HesB family	0.70	5.93	3.32	55.97	3
DR0052	-	Uncharacterized conserved protein	0.34	6.50	2.15	33.14	1.5
DR0053	L	DinB/YfiT family protein	0.44	10.25	2.36	23.00	3
DR0070	ST?	Uncharacterized protein	0.08	3.89	1.72	44.18	9
DR0103	R	Predicted metal-binding protein	0.57	6.46	4.02	62.22	1.5
DR0140	-	Uncharacterized protein	0.97	6.44	2.87	44.60	1.5
DR0160	-	Conserved membrane protein	0.42	3.90	0.86	22.09	1.5
DR0161	S	AmsJ/WcaK related protein, possibly involved in exopolysaccharide biosynthesis	0.97	8.12	4.07	50.14	1.5
DR0203	R	Uncharacterized membrane protein	0.28	3.82	0.86	22.43	1.5
DR0204	-	Uncharacterized membrane protein	0.51	6.01	1.35	22.52	3
DR0205	Q	ABC transporter ATPase	0.49	4.10	2.45	59.75	3
DR0206	-	Uncharacterized protein	0.19	5.45	2.65	48.56	3
DR0207	L	ComEA related protein, secreted	0.26	15.47	10.31	66.66	3
DR0324	E	Predicted glutamate formiminotransferase	0.31	3.30	1.47	44.50	0.5
DR0363	E	ABC-type dipeptide transporter	2.79	4.09	1.75	42.74	24

Gene ID*	Function group†	Protein description and comments	Relative basal level	Maximum induction level, fold	STD	CV	Maximum induction time, h
		periplasmic binding protein, DppA					
DR0365	E	ABC-type dipeptide transporter, permease ,DppC	2.11	1.48	0.84	56.88	5
DR0394	ST	Predicted kinase antibiotic/homoserine kinase homolog	0.29	7.51	2.76	36.69	1.5
DR0395	G	MDR-type permease	1.09	4.40	2.12	48.16	1.5
DR0396	-	Uncharacterized protein	1.15	5.57	2.39	42.78	1.5
DR0421	-	Uncharacterized protein	0.68	4.94	2.30	46.60	1.5
DR0422	Q	Trans-aconitate methylase	0.68	18.85	7.46	39.59	1.5
DR0477	E	Membrane permease, DhlC homolog	0.56	4.63	1.71	36.85	1.5
DR0478	E	Aminopeptidase P	0.77	2.86	0.55	19.36	0.5
DR0479	M	Penicillin-binding protein 1	0.77	7.07	2.42	34.21	1.5
DR0599	ST	Aminoglycoside N3'-acetyltransferase family	1.31	4.24	1.41	33.31	1.5
DR0609	R	Predicted kinase, adenylate kinase homolog	0.47	2.43	1.14	46.95	3
DR0610	-	Uncharacterized protein	0.25	6.10	4.51	73.93	3
DR0665	-	Uncharacterized protein	0.54	11.66	5.74	49.24	3
DR0694	C	Phage protein homolog	0.60	5.57	2.02	36.28	1.5
DR0812	O	Extracellular alkaline serine protease	0.59	3.32	1.24	37.52	3
DR0841	L	DinB/YfiT family protein	0.48	5.93	1.47	24.84	1.5
DR0842	ST	NimC-like (5-nitroimidazole antibiotics resistance) protein	2.62	1.89	0.69	36.67	24
DR0911	K	DNA-directed RNA polymerase beta' subunit	1.62	1.99	1.37	68.70	0.5
DR0912	K	DNA-directed RNA polymerase beta subunit	0.54	3.19	0.80	24.90	0.5
DR1143	-	Uncharacterized protein	0.49	8.85	4.26	48.13	1.5
DR1144	-	Uncharacterized conserved protein	1.10	2.69	1.31	48.82	1.5

Gene ID*	Function group[†]	Protein description and comments	Relative basal level	Maximum induction level, fold	STD	CV	Maximum induction time, h
DR1356	R	ABC transporter, ATPase subunit	0.40	9.85	5.98	60.68	3
DR1357	R	ABC transporter, permease subunit	0.31	6.79	2.56	37.67	1.5
DR1358	M	ABC transporter, periplasmic subunit	0.38	22.73	13.73	60.39	1.5
DR1359	M	ABC transporter, periplasmic subunit	0.50	24.83	11.13	44.82	1.5
DR1398	-	Uncharacterized protein	0.24	4.17	1.04	24.83	1.5
DR1548	T	Bacillus ykwD ortholog, Divergent member of the secreted PRP1, plant pathogenesis related protein superfamily	0.48	5.62	2.34	41.32	3
DR1556	-	Membrane-associated sensor histidine kinase	2.27	3.61	1.71	47.23	1.5
DR1557	T	Uncharacterized protein	1.37	5.06	1.57	31.04	1.5
DR1558	-	Receiver domain (flavodoxin, CheY family) of a two component system, contains a C- terminal helix-turn-helix (HTH) DNA-binding domain	1.12	5.64	1.49	26.43	1.5
DR1559	E	Uncharacterized protein	0.87	4.39	1.60	36.47	1.5
DR1639	L	Uncharacterized protein	1.15	4.41	1.84	41.73	1.5
DR1641	L	DinB/YfiT family protein	2.52	1.88	0.78	41.24	5
DR1642	-	DinB/YfiT family protein	0.27	3.71	1.30	35.02	1.5
DR1643	-	Uncharacterized protein	0.61	4.06	2.21	54.45	1.5
DR1644	Q	Uncharacterized protein	0.77	2.45	0.56	22.82	1.5
DR1672	-	SAM-dependent methyltransferase	0.41	1.24	0.73	59.15	12
DR1673	-	Predicted dehydrogenase	1.05	4.53	1.29	28.54	1.5
DR1744	L	Uncharacterized protein	1.47	5.02	1.64	32.69	1.5
DR1776	-	Nudix/MutT family pyrophosphatase	0.84	4.70	2.83	60.18	1.5
DR1850	L	Uncharacterized protein	0.62	4.36	1.13	26.00	1.5
DR1899	-	DinB/YfiT family protein	0.35	1.60	0.65	40.30	1.5

Gene ID*	Function group[†]	Protein description and comments	Relative basal level	Maximum induction level, fold	STD	CV	Maximum induction time, h
DR1900	-	Uncharacterized protein	0.51	3.14	1.04	33.14	1.5
DR1901	-	Uncharacterized protein	0.51	10.74	4.85	45.17	1.5
DR2097	E	Uncharacterized protein	0.14	6.95	2.08	29.93	1.5
DR2118	E	ABC-type branched amino acid transporter	0.26	3.04	1.38	45.32	5
DR2122	E	Branched amino acid periplasmic binding protein, LivBP	0.20	2.46	0.29	11.94	3
DR2128	ST	RNA polymerase alpha subunit	2.26	4.03	2.80	69.48	1.5
DR2220	ST	Tellurium resistance protein, TerB homolog	0.45	3.13	1.49	47.61	5
DR2221	ST	Tellurium resistance/cAMP-binding family protein	0.59	5.24	2.94	56.05	3
DR2223	ST	Tellurium resistance/cAMP-binding family protein	0.39	3.63	1.36	37.45	3
DR2225	-	Tellurium resistance/cAMP-binding family protein	0.58	2.14	0.41	19.30	3
DR2265	-	Large membrane protein	0.44	5.45	1.46	26.84	3
DR2337	T	Uncharacterized protein	0.11	7.41	5.71	77.05	1.5
DR2415	T	Receiver domain, CheY family and HTH	0.16	1.72	1.26	73.28	5
DR2416	-	Sensor histidine kinase	0.84	5.75	1.33	23.09	1.5
DR2481	K	Uncharacterized protein	0.39	4.66	1.27	27.17	1.5
DR2482	L	Predicted transcription regulator, HTH domain related to that of sigma factors	0.36	5.75	2.92	50.84	1.5
DR2483	R	McrA family nuclease	0.80	5.43	1.22	22.49	1.5
DR2484	L	WD40 repeat protein	0.71	5.12	2.53	49.39	1.5
DR2566	-	Homolog of HpaII repair protein, small, conserved bacterial protein	0.42	4.10	1.09	26.48	3
DR2573	E	Uncharacterized protein	0.22	3.93	2.57	65.55	0.5
DR2610	R	Periplasmic binding protein, FliY	1.01	4.13	1.67	40.46	0.5
DRA0008	T	Conserved membrane protein (possible transporter)	0.26	6.60	2.00	30.26	3

Gene ID*	Function group[†]	Protein description and comments	Relative basal level	Maximum induction level, fold	STD	CV	Maximum induction time, h
DRA0009	T	Membrane-associated sensor histidine kinase	0.19	3.03	1.25	41.30	5
DRA0010	P	CheY -like sensor regulator and HTH domain	0.28	4.66	2.12	45.44	5
DRA0013	P	Sulfite reductase	0.65	8.27	1.84	22.31	24
DRA0014	E	PAPS synthase (APS kinase domain), CysC	0.37	4.33	1.66	38.36	24
DRA0015	P	PAPS reductase	0.54	11.42	5.73	50.18	24
DRA0016	T	Sulfate adenylyltransferase	0.42	12.12	5.83	48.07	24
DRA0049	T	Response regulator CheY family, flavodoxin	0.12	3.16	1.70	53.75	9
DRA0050	-	Phytochrome-like histidine kinase and GAF domain	0.30	2.18	1.21	55.52	3
DRA0234	E	Uncharacterized protein	0.17	12.76	5.27	41.29	1.5
DRA0249	K	Metalloprotease, leishmanolysin-like	1.61	6.47	4.43	68.42	3
DRA0344	ST	LexA repressor, HTH domain and protease	0.51	1.80	1.08	59.92	1.5
DRA0345	ST	Predicted esterase, homologs of *E. coli* erythromycin esterase type II (EreB)	0.68	10.05	4.39	43.72	1.5
DRA0346	R	PprA protein, possibly involved in DNA damage resistance mechanisms	0.65	3.52	1.94	55.14	0.5
DRB0067	O	Extracellular nuclease containing fibronectin III domains	0.29	4.37	1.21	27.58	3
DRB0069	R	Subtilisin family serine protease	0.92	3.18	1.39	43.62	3
DRB0070	-	ABC-class ATPase	0.64	4.00	1.91	47.74	1.5
DRB0071	H	Uncharacterized protein	0.11	2.60	0.53	20.51	3
DRB0072	E	Salicylate 1-monooxygenase	0.37	4.91	2.31	47.04	1.5
DRB0133	E	D-alanine permease	0.46	3.51	1.39	39.61	1.5
DRB0145	-	Uncharacterized protein	0.67	4.77	1.80	37.63	1.5

*Expression profile information in two last columns is shown only for one gene in an operon. All genes selected here are significantly induced (determined by statistical analyses).

[†] Designations of functional groups (from the COG database): see the legend for Fig. 8.