Supplementary Material

Insight into the Diversity and Possible Role of Plasmids in the Adaptation of Psychrotolerant and Metalotolerant *Arthrobacter* spp. to Extreme Antarctic Environments

Krzysztof Romaniuk, Piotr Golec, Lukasz Dziewit*

*** Correspondence:** Dr. Lukasz Dziewit: ldziewit@biol.uw.edu.pl

TABLE S5. Summary of phenotypic modules found within the ANT plasmids.

Plasmid name	Protein	Predicted protein function [Enzyme commission number]
Protection against UV radiation		
pA2H2	pA2H2_p51,	DNA-directed DNA polymerase subunit UmuD, COG1974
	pA2H2_p59	DNA-directed DNA polymerase subunit UmuC, COG0389 [EC: 2.7.7.7]
pA8H1	pA8H1_p03,	DNA-directed DNA polymerase subunit UmuD, COG1974
	pA8H1_p21	DNA-directed DNA polymerase subunit UmuC, COG0389 [EC: 2.7.7.7]
pA40H2	pA40H2_p03	DNA-directed DNA polymerase subunit UmuD, COG1974
	pA40H2_p11	DNA-directed DNA polymerase subunit UmuC, COG0389 [EC: 2.7.7.7]
pA58H3	pA58H3_p03	DNA-directed DNA polymerase subunit UmuD, COG1974
	pA58H3_p04	DNA-directed DNA polymerase subunit UmuC, COG0389 [EC: 2.7.7.7]
Uptake and utilisation of various organic compounds		
pA2H2	pA2H2_p16	ABC-type lipoprotein export system, ATPase component, COG1136 [EC: 3.6.3.28]
	pA2H2_p17	ABC-type antimicrobial peptide transport system, permease component, COG0577
	pA2H2_p18	TetR family transcriptional regulator
pA2H2	pA2H2_p20	MMPL family transporter
	pA2H2_p21	TetR/AcrR family transcriptional regulator, COG1309
	pA2H2_p22	drug resistance transporter, EmrB/QacA subfamily
	pA2H2_p23	TetR family transcriptional regulator
pA8H1	pA8H1_p12	laminarinase, glycoside hydrolase, COG2273
pA58H3	pA58H3_p13	tripartite tricarboxylate transporter substrate binding protein, COG3181
	pA58H3_p14	tripartite tricarboxylate transporter TctB
	pA58H3_p15	tripartite tricarboxylate transporter permease, TctA, COG3333
	pA58H3_p16	LysR family transcriptional regulator, COG0583
pA58H3	pA58H3_p17	major facilitator superfamily transporter
	pA58H3_p18	MurR/RpiR family transcriptional regulator, COG1737
pA58H3	pA58H3_p19	NAD(P)-dependent dehydrogenase, COG1028 [EC: 1.1.1.-]
	pA58H3_p20	aldehyde dehydrogenase, COG1022, [EC: 1.2.1.3]
	pA58H3_p21	major facilitator superfamily transporter, COG2814
	pA58H3_p22	IclR family transcriptional regulator, COG1414
	pA58H3_p23	IclR family transcriptional regulator, COG1414
	pA58H3_p24	Phthalate 4,5-dioxygenase, COG1018 [EC: 1.14.12.7]
	pA58H3_p25	hypothetical protein
	pA58H3_p26	L-threonine 3-dehydrogenase, COG1063 [EC: 1.1.1.103]
	pA58H3_p27	aromatic ring-hydroxylating dioxygenase subunit alpha, COG4638 [EC: 1.14.12.7]
pA58H3	pA58H3_p32	taurine transporter substrate binding subunit TauA, COG0715
	pA58H3_p33	taurine ABC transporter permease TauC, COG0600 [EC: 3.6.3.31]
	pA58H3_p34	taurine transporter TauB, COG:1116
	pA58H3_p35	arabinose ABC transporter permease

pA19BH1	pA19BH1_p21	short-chain dehydrogenase, COG1028
	pA19BH1_p22	Aromatic ring-opening dioxygenase, catalytic subunit, COG3384 [EC: 1.13.11.29]
pA19BH1	pA19BH1_p24	TetR family transcriptional regulator
	pA19BH1_p25	drug resistance transporter, EmrB/QacA subfamily
	pA19BH1_p26	TetR/AcrR family transcriptional regulator, COG1309
	pA19BH1_p36	MMPL family transporter
Transport of heavy metals		
pA2H2	pA2H2_p55	tellurium resistance protein TerC, COG0861
	pA2H2_p56	putative cation transporting ATPase
pA8H1	pA8H1_p16	tellurium resistance protein TerC, COG0861,
pA8H1	pA8H1_p07	tellurium resistance protein TerC, COG0861
	pA8H1_p08	putative cation transporting ATPase
pA40H2	pA40H2_p07	tellurium resistance protein TerC, COG0861
	pA40H2_p08	putative cation transporting ATPase
pA40H1	pA40H1_p55	copper chaperone CopZ, COG2608
	pA40H1_p56	heavy metal-binding domain-containing protein
	pA40H1_p57	copper-(or silver)-translocating P-type ATPase, COG2217 [EC: 3.6.3.53]
Sulfur detoxification and energy acquisition		
pA8H1	pA8H1_p33	SulP family inorganic anion transporter, sulfate permease, COG0659
	pA8H1_p34	MerR family DNA-binding transcriptional regulator, COG0789
pA8H1	pA8H1_p35	FrmR family DNA-binding transcriptional regulator, COG1937
	pA8H1_p36	hypothetical protein
	pA8H1_p37	persulfide dioxygenase A, COG0491 [EC: 1.13.11.18]
	pA8H1_p38	rhodanese-related sulfurtransferase, COG0607
	pA8H1_p39	rhodanese-related sulfurtransferase, COG0607
	pA8H1_p40	sulfite exporter TauE/SafE, COG0730
	pA8H1_p41	major facilitator superfamily transporter
	pA8H1_p42	hypothetical protein, uncharacterized conserved protein, COG3439
pA58H2	pA58H2_p19	intracellular sulfur oxidation, DsrE/DsrF, COG1416
	pA58H2_p20	cytochrome C biogenesis protein transmembrane region, COG0785
	pA58H2_p21	thiol-disulfide oxidoreductase, COG1651
	pA58H2_p22	Cytochrome c-type biogenesis protein CcdA
	pA58H2_p23	predicted transcriptional regulator, COG3682
pA58H2	pA58H2_p24	hypothetical protein, uncharacterized conserved protein,
	pA58H2_p25	major facilitator superfamily transporter
	pA58H2_p26	sulfite exporter TauE/SafE, COG0730
	pA58H2_p27	rhodanese-related sulfurtransferase, COG0607
	pA58H2_p28	rhodanese-related sulfurtransferase, COG0607
	pA58H2_p29	persulfide dioxygenase A, COG0491 [EC: 1.13.11.18]
	pA58H2_p30	hypothetical protein
	pA58H2_p31	COG3439FrmR family DNA-binding transcriptional regulator, COG1937
pA40H2	pA40H2_p27	SulP family inorganic anion transporter, sulfate permease, COG0659
	pA40H2_p28	MerR family DNA-binding transcriptional regulator, COG0789
pA40H2	pA40H2_p29	FrmR family DNA-binding transcriptional regulator, COG1937
	pA40H2_p30	hypothetical protein
	pA40H2_p31	persulfide dioxygenase A, COG0491 [EC: 1.13.11.18]
	pA40H2_p32	rhodanese-related sulfurtransferase, COG0607
	pA40H2_p33	rhodanese-related sulfurtransferase, COG0607
	pA40H2_p34	sulfite exporter TauE/SafE, COG0730
	pA40H2_p35	major facilitator superfamily transporter
	pA40H2_p36	hypothetical protein, uncharacterized conserved protein, COG3439
pA40H2	pA58H2_p37	predicted transcriptional regulator, COG3682
	pA58H2_p38	Cytochrome c-type biogenesis protein CcdA
	pA58H2_p39	thiol-disulfide oxidoreductase, COG1651
	pA58H2_p40	cytochrome C biogenesis protein transmembrane region, COG0785
	pA58H2_p41	intracellular sulfur oxidation protein, DsrE/DsrF, COG1416