

### 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 S4.** Partitioning systems (including sequences of predicted partitioning sites – *parS*) identified within the ANT plasmids.

Plasmid name	<i>par</i> genes (coordinates)	Sequences and coordinates of putative direct repeats (DR) of <i>parS</i> site <sup>a</sup>	Homologous PAR system (found based on the best BLASTp hit to the ParA protein)
pA2H2	<i>pA2H2_49-50</i> (51,902 – 52,672)	DR.1: 51851-ATGCAA-51856 DR.2: 51871-ATGAAA-51876 DR.3: 51879-ATGAAA-51884 DR.4: 51902-ATGCAA-51907  Consensus: ATGMAA	<i>Arthrobacter</i> sp. MA-N2 [GenBank: WP_028268205 and WP_028268206]
pA8H1	<i>pA8H1_01-02</i> (78 – 961)	DR.1: 5-CACTTACTCATCTACT-20 DR.2: 46-CATTACTCACCTCT-61  Consensus: CAYTTACTCAYCYWCT	<i>Glutamicibacter</i> sp. BW77 [GenBank: WP_096253931 and WP_096253932]
pA19BH1	<i>pA19BH1_01-02</i> (300 – 1,633)	DR.1: 198-CAGTAAAAGCAGCA-211 DR.2: 216-CAGCAAAAAGCAGCA-229 DR.3: 252-CAGCATTAGCTGTA-265  Consensus: CAGYAWWAGCWGYA	<i>Cryobacterium arcticum</i> plasmid pP27867_2 [GenBank: ANP74904 and ANP74905]
pA40H1	<i>pA40H1_01-02</i> (90 – 1,138)	DR.1: 27-AATCTTTC-34 DR.2: 39-AATCTTTC-46 DR.3: 63-AATCTTTC-70  Consensus: AATCTTTC	<i>Arthrobacter</i> sp. MA-N2 [GenBank: WP_028268205 and WP_028268206]
pA40H2	<i>pA40H2_01-02</i> (241 – 1,397)	DR.1: 174-CAAGTAATGC-183 DR.2: 201-CAAGTAATAC-210 DR.3: 219-CAAGTACTAC-228  Consensus: CAAGTAMTRC	<i>Kocuria marina</i> [GenBank: KHE74185 and KHE74186]
pA44BH1	<i>pA44BH1_01-02</i> (453 – 1,689)	DR.1: 383-GTGAATGTC-392 DR.2: 393-GTGAATTGC-402  Consensus: GTGAATKGC	<i>Arthrobacter</i> sp. 31.31 [GenBank: WP_015061701 and WP_015061702]
pA48BH1	<i>pA48BH1_01-02</i> (441 – 1,677)	DR.1: 371-GTGAATGTC-380 DR.2: 381-GTGAATTGC-390  Consensus: GTGAATKGC	<i>Arthrobacter</i> sp. 31.31 [GenBank: WP_015061701 and WP_015061702]
pA58H1	<i>pA58H1_01-02</i> (172 – 1,622)	DR.1: 127-AATCAGCA-134 DR.2: 146-AATCACCA-153  Consensus: AATCASCA	<i>Microbacterium esteraromaticum</i> [GenBank: WP_087130340 and WP_087130341]
pA58H2	<i>pA58H2_01-02</i> (276 – 1,046)	DR2.1: 181-CTTGACGTC-189 DR2.2: 208-CTTACTTTC-216 DR2.2: 240-CTTGCTATC-248  Consensus: CTRMYDTC	<i>Kocuria polaris</i> [GenBank: KHD96206 and KHD96206]
pA58H3	<i>pA58H3_01-02</i> (248 – 1,404)	DR.1: 174-CAAGTAATGC-183 DR.2: 208-CAAGTAATAC-217 DR.3: 226-CAAGTACTAC-235  Consensus: CAAGTAMTRC	<i>Kocuria marina</i> [GenBank: KHE74185 and KHE74186]

<sup>a</sup> Sequences shown in the 5' to 3' orientation.