

Supplementary Information for:

Strain and substrate dependent redox mediator and electricity production by

Pseudomonas aeruginosa

Running Titel: *P. aeruginosa* strain variability of current production

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This supplementary information contains background information on the phenazine
voltametric and sequence analysis as well as a table with primers used for molecular work.

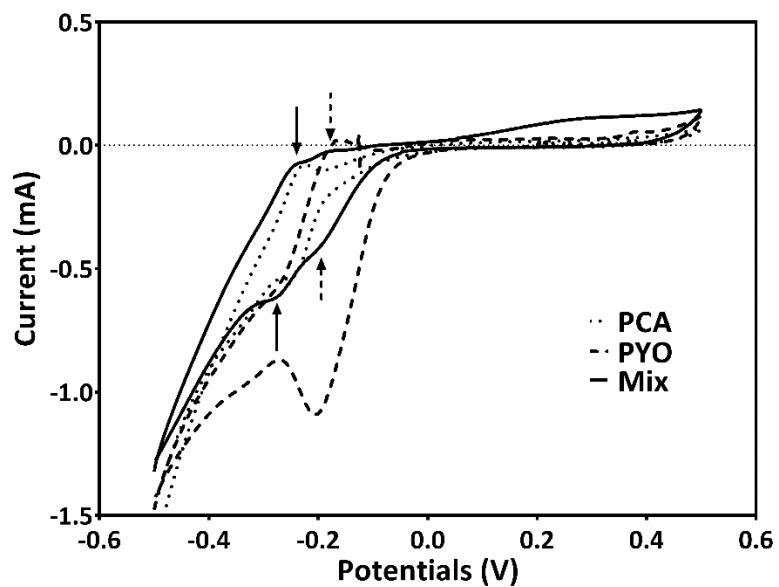


Figure S1: Cyclic voltamograms of PCA ($30 \mu\text{g mL}^{-1}$), PYO ($15 \mu\text{g mL}^{-1}$) and their mixture at the same concentrations at pH 6.9. Redox peak systems of PCA (solid arrows) and PYO (dotted arrows) in the mix are shown.

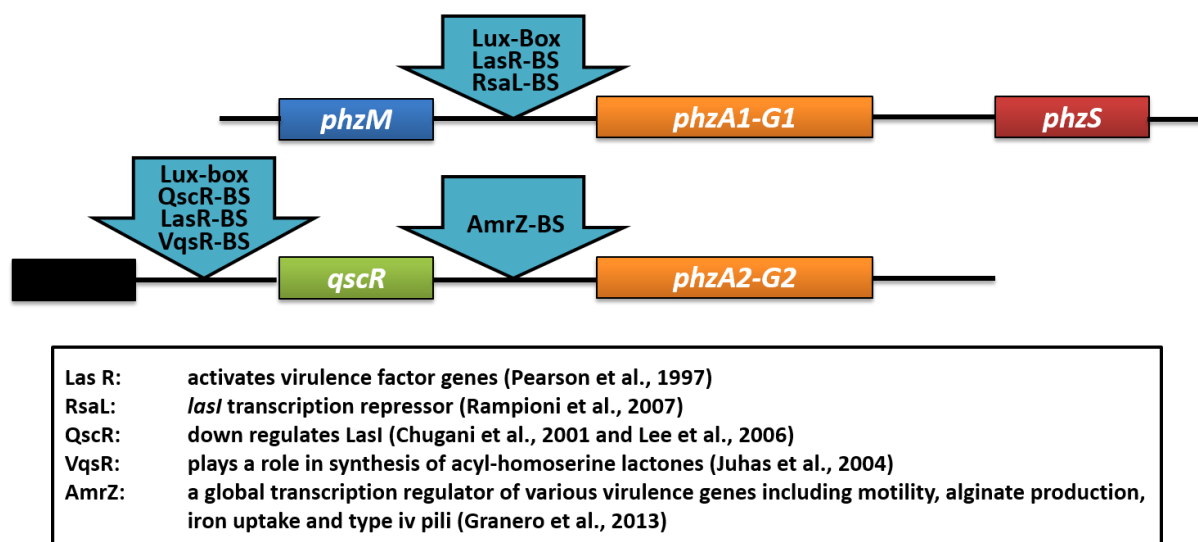


Figure S2: Analysis of transcription regulatory elements of the phenazine gene clusters. All indicated transcription regulator bindings sites (BS) have been identified for all three *P. aeruginosa* strains with the following consensus sequences: Lux-Box – ACCTACCAGATCTTGTAGTTGAGCCGGTACGAGCGTTCTGTGTTTTATGCAATCCACATCAGCGACC AGGGATGCTGGCTATTTGAAACACTTCACGGAATGACGCTGAAAGTCTTCGCGACCTCGTCTGTCCG CACCTTAACGAAAGCATTGCGAATCCATTACCGACAGGTTTCCAAAAGAAACCCGGGATGAAACTC CTATTGCCTTTCGAAAATTGGAAACGACAGGCCGAACATATGTAACGCGAAA; LasR-BS – ACCTACCAGATCTTGTAGTT; RsaL-BS – TATGCAATCCACATC; QscR-BS (=PhzR-BS) – ACCTGCCCCGGAAGGGCAGGTTGTCCC; VqsR-BS – TCGCCCCGGCGGGCGGCGA; AmrZ-BS – (i) CGAATTGCCATGA, (ii) CAATTCGGCATTGA.

Table S1. Primers used in this study.

Primer name	Sequence 5'→3'	Application
PA14Δphz knockout generation		
Op1_left_for	gaattcgagctcggtacGCCTGTCCAAGCTGTACC	Knockout PA14 <i>phzA1-G1,S,M</i>
Op1_left_rev	cgatccgctCGACCGAAGACTGAGAAGAG	
Op1_right_for	cttcggtcgAGCGGATCGTCGACCTG	
Op1_right_rev	gtcgactctagagatccCGGCTTCATCGGTTTCTTCG	
Op2_left_for	gaattcgagctcggtacATGCATATCCCGCCCGAG	Knockout PA14 <i>phzA2-G2</i>
Op2_left_rev	ttgaaagggTTGGAGCCCATCCAACCG	
Op2_right_for	ggctccaaCCCTTTCAACCGTTGGTACTCTC	
Op2_right_rev	gtcgactctagagatccCGGTGGGCAAGACCTACG	
pEMG_for	CGGGCCTCTTCGCTATTAC	Confirmation of cointegration and knockout
pEMG_rev	TTATGCTTCCGGCTCGTATG	
Op1_Gen_L_for	AAGGTCAACGCGGTACAG	
Op1_Gen_R_rev	CACCGCCGAACCTCTATCC	
Op1_KO_rev	GCGCGAATACGAAGAAGC	
Op2_Gen_L_for	CGCATCGACGATATGAAACG	
Op2_Gen_R_rev	CGTCCCGGAAAGCAATGTG	
Op2_KO_rev	AGATTCCCTACGGGCAGCAG	
Strain KRP1 Sequencing of phenazine gene regions		
OP1-1 (for)	TGCCCGGTGTTGCTAGCG	KRP1: phz operon 1 and 2 PCR amplification
OP1-2 (rev)	TCGGCAGGTCGACGATCC	
OP2-1 (for)	TCGTCTGGCGCGAATTCTG	
OP2-2 (rev)	GAGAGCCGTTCTACGGTTTCC	
OP1-1-S1	TTCCACCTGGTTGCGGTAG	KRP1: phz operon 1 sequencing
OP1-882-S2	GCAGGATCATCTGCAGTTC	
OP1-1861-S3	GGCCGTTGAGGATGATCTG	
OP1-2618-S4	GGTAGACCTCGATGGGAAAG	
OP1-3610-S5	GGCGATCATCGAGGTGAAG	
OP1-4451-S6	AGCAACTGGCGGAAGAAAC	
OP1-5453-S7	GGAAGTAGCGCTGCATGTC	
OP1-6326-S8	CGCATAGCCCTTGAGAATC	
OP1-7219-S9	GTCCTGGCCTTTGGTATTC	
OP1-8052-S10	TGGAAACCTGTCGGTAATGG	
OP1-8916-S11	TCGGCGAAGACTTCTACAG	
OP2-1-S1	TCGTCTGGCGCGAATTCTG	KRP1: phz Operon 2 sequencing
OP2-940-S2	GTGAGGGACTCGGAAATG	
OP2-1701-S3	TCTCCGACAGGTTTCATCTC	
OP2-2624-S4	ATCGGAGTGACGCACGATG	
OP2-3518-S5	GATCTGCCGGTAGGGAATC	
OP2-4449-S6	ATCGCAGAGGCTGGTGTAG	
OP2-5333-S7	CGTTCTCGGCATGGTGGTC	
OP2-6334-S8	CTCGAAGATCCGCACGTTG	
OP2-7244-S9	CTTGAGCATCTCGGTTTCC	

Table S2. DNA sequence identity (in %) of the phenazine genes in a pair-wise comparison of the three *P. aeruginosa* strains. The number in the bracket indicates the number of nucleotide miss-matches.

Gene	PA14-PAO1	PA14-KRP1	PAO1-KRP1
<i>phzA1</i>	98.98%, (5)	98.98%, (5)	100%
<i>phzB1</i>	98.36%, (8)	99.18%, (4)	98.77%, (6)
<i>phzC1</i>	99.26%, (9)	98.85%, (14)	98.61%, (17)
<i>phzD1</i>	99.36%, (4)	99.84%, (2)	98.87%, (7)
<i>phzE1</i>	99.15%, (16)	99.30%, (13)	99.42%, (11)
<i>phzF1</i>	99.52%, (4)	99.16%, (7)	99.40%, (5)
<i>phzG1</i>	99.38%, (4)	99.54%, (3)	99.84%, (1)
<i>phzM</i>	99.30%, (7)	99.40%, (6)	99.70%, (3)
<i>phzS</i>	98.10%, (23)	98.18%, (22)	99.59%, (5)
<i>phzA2</i>	98.98%, (5)	99.59%, (2)	98.98%, (5)
<i>phzB2</i>	99.18%, (4)	99.59%, (2)	99.59%, (2)
<i>phzC2</i>	99.43%, (7)	98.77%, (15) (88.92% with 120n gap) ^a	98.85%, (14), (89.00%, with 120n gap) ^a
<i>phzD2</i>	99.20%, (5)	99.68%, (2)	98.88%, (7)
<i>phzE2</i>	98.99%, (19)	99.15%, (16)	99.42%, (11)
<i>phzF2</i>	99.52%, (4)	99.16%, (7)	99.40%, (5)
<i>phzG2</i>	99.23%, (5)	99.38%, (4)	99.85%, (1)

^a The obtained sequences for *phzC2* from KRP1 contained a 120 nucleotide gap. It is not clear yet, if this is due to difficulties in sequencing for this area or if the gene contains a 120bp deletion.

References:

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