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► To cite this version:

Maud Flechard, Emeline Bouffartigues, Rachel Duchesne, Julie Hardouin, Olivier Maillot, et al.. The absence of SigX may result in a nutritional stress response in *Pseudomonas aeruginosa*. Pseudomonas conference, Sep 2015, Washington (DC), United States. hal-02366396

HAL Id: hal-02366396

<https://normandie-univ.hal.science/hal-02366396>

Submitted on 21 Nov 2019

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The absence of SigX may result in a nutritional stress response in *Pseudomonas aeruginosa*.

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SigX is one of the 19 ECF sigma factor of *P. aeruginosa*. It is a master regulator of bacterial adaptation to osmotic stress that impacts more than 250 genes, among which genes involved in adaptation/protection, heat shock response, chemotaxis, motility/attachment, virulence and virulence-associated genes linked to the protein secretion/export apparatus or secreted factors. SigX was shown to be involved in modulation of fatty acid and phospholipid metabolisms and consequently in membrane lipidic composition. We have previously shown that a *sigX* mutant is severely altered during growth in LB rich broth but not in M9-glucose minimal medium. Since membrane homeostasis is required to fulfil important physiological functions including nutrients uptake, we wonder if the SigX mutant growth alterations observed in LB medium would be correlated to such metabolic pathways.

Microarrays (mRNA) and LTQ-orbitrap (Protein) assays were achieved on *P. aeruginosa* H103 and its isogenic *sigX* deletion mutant PAOSX grown in LB medium. A selection of the main dysregulated genes belonging to the "small molecules transport", "amino acids metabolism" and "carbon metabolism" Pseudocap functional classes, are presented, and the fold change between PAOSX and H103 is given in terms of mRNA and protein relative amounts (FC>2, Pvalue < 0.05).

Numerous genes transporters are dysregulated in the *sigX* mutant strain.

Locus	Gene	Product name	FC
Transport of small molecules			
PA0291	<i>oprB</i>	Amperibically-induced outer membrane porin OprB precursor	-2.63
PA0292	<i>oprD</i>	probable porphyrin-polymyxin binding protein	-3.33
PA0958	<i>oprD</i>	basic amino acid, basic peptide and imipenem outer membrane porin OprD	-5.55
PA1178	<i>oprH</i>	"PspQ" and low Mg ²⁺ -inducible outer membrane protein H1 precursor	-2.00
PA1183	<i>dctA</i>	c4-decarboxylase transport protein	-3.22
PA1863	<i>modA</i>	maltoheptaose-binding periplasmic protein precursor ModA	-3.45
PA2113	<i>oprB</i>	tryptophan-specific porin OprB	-5.00
PA3186	<i>oprB</i>	thiosulfonate-specific outer membrane porin OprB precursor	-2.70
PA3187	<i>oprB</i>	probable ATP-binding component of ABC transporter	-6.09
PA3188	<i>oprB</i>	probable periplasmic component of ABC transporter	-7.14
PA3189	<i>oprB</i>	probable periplasmic component of ABC transporter	-2.90
PA3190	<i>oprB</i>	probable binding protein component of ABC transporter	-2.00
PA3641	<i>oprC</i>	probable amino acid permease	-2.60
PA3790	<i>oprC</i>	putative copper transporter outer membrane porin OprC precursor	-4.35
PA3865	<i>oprC</i>	probable amino acid binding protein	-2.43
PA4067	<i>oprG</i>	Outer membrane protein OprG precursor	-1.51
PA4616	<i>oprG</i>	probable c4-decarboxylase-binding protein	-2.41
PA4617	<i>oprG</i>	similar to E. coli maltoheptaose outer membrane receptor H7A	-2.37
PA4687	<i>hcr1</i>	iron-iron-binding periplasmic protein HcrA	-2.27
PA5217	<i>oprC</i>	probable binding protein component of ABC transporter	-2.38
Carbon metabolism			
PA0133	<i>acrA</i>	acetoin:acetyl-CoA ligase, hcrA variant	4.03
PA0134	<i>acrA</i>	acetoin:acetyl-CoA ligase, hcrA variant	3.33
PA0135	<i>acrA</i>	acetoin:acetyl-CoA ligase, hcrA variant	14.3
PA0136	<i>acrA</i>	acetoin:acetyl-CoA ligase, hcrA variant	3.21
PA0137	<i>acrA</i>	acetoin:acetyl-CoA ligase, hcrA variant	16.1
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PA0142	<i>acrA</i>	acetoin:acetyl-CoA ligase, hcrA variant	16.1
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