



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

Maud Flechard, Emeline Bouffartigues, Rachel Duchesne, Julie Hardouin, Olivier Maillot, Nicole Orange, Marc Feuilloley, Pierre Cornelis, Sylvie Chevalier

### ► 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

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Maud Flécharde<sup>1</sup>, Émeline Bouffartigues<sup>1</sup>, Rachel Duchesne<sup>1</sup>, Julie Hardouin, Olivier Maillot<sup>1</sup>, Nicole Orange<sup>1</sup>, Marc G. J. Feuilloley<sup>1</sup>, Pierre Cornelis<sup>1</sup> and Sylvie Chevalier<sup>1</sup>.

<sup>1</sup>Laboratory of Microbiology Signals and Microenvironment, LMSM EA4312, University of Rouen, France

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			
PA0201	<i>oprB</i>	Anaerobically-induced outer membrane porin OprB precursor	-2.63
PA0205	<i>oprB</i>	Probable periplasmic polysaccharide binding protein	-3.33
PA0558	<i>oprD</i>	Basic amino acid, basic peptide and imipenem outer membrane porin OprD	-5.55
PA1178	<i>oprH</i>	PspQ and low Mg <sup>2+</sup> inducible outer membrane protein H1 precursor	-2.06
PA1183	<i>actA</i>	C4-decarboxylate transport protein	-3.22
PA1183	<i>modA</i>	Involinate-binding, periplasmic, protein precursor ModA	-3.45
PA2113	<i>oprO</i>	Pyroglutamate porin OprO	-5.00
PA3186	<i>oprB</i>	Glucose/carbohydrate 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 permease of ABC sugar transporter	-7.14
PA3189	<i>oprB</i>	Probable permease of ABC sugar transporter	-2.90
PA3190	<i>oprB</i>	Probable binding protein component of ABC sugar transporter	-2.00
PA3641	<i>oprB</i>	Probable amino acid permease	-2.40
PA3790	<i>oprC</i>	Putative copper transport 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-decarboxylate-binding protein	-2.41
PA4617	<i>actA</i>	Similar to E. coli anaerobic outer membrane receptor actA	-2.37
PA4687	<i>hcrA</i>	Ironer non-binding periplasmic protein HcrA	-2.27
PA5217	<i>oprB</i>	Probable binding protein component of ABC iron transporter	-2.38
Carbon metabolism			
PA0153	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0154	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0155	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0156	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0157	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0158	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0159	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0160	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0161	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0162	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0163	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0164	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0165	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0166	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0167	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0168	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0169	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0170	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0171	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0172	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	15.91
PA0173	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	15.91
PA0174	<i>hcrA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	1.98
PA0175	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	1.54
PA0176	<i>hcrA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	1.54
PA0177	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	2.39
PA0178	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	2.39
PA0179	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, beta subunit	2.39
PA0180	<i>actA</i>	Ironer-citric acid 1,4-dicarbonyl, alpha subunit	2.61
PA1542	<i>oprB</i>	ABC-type amino acid transport signal transduction system, periplasmic component/domain	2.45
PA1946	<i>rhaB</i>	Ironer binding protein component of ABC rhaB transporter	2.76
PA1947	<i>rhaB</i>	Ironer binding protein component of ABC rhaB transporter	2.76
PA1948	<i>rhaB</i>	Ironer binding protein component of ABC rhaB transporter	2.76
PA1949	<i>rhaB</i>	Ironer binding protein component of ABC rhaB transporter	2.76
PA2328	<i>oprB</i>	Probable binding protein component of ABC malose/mannitol transporter	4.29
PA2329	<i>oprB</i>	Probable binding protein component of ABC malose/mannitol transporter	3.89
PA2330	<i>oprB</i>	Probable binding protein component of ABC malose/mannitol transporter	3.89
PA2341	<i>oprB</i>	Probable ATP-binding component of ABC malose/mannitol transporter	1.96
PA2342	<i>oprB</i>	Probable ATP-binding component of ABC malose/mannitol transporter	1.96
PA2711	<i>oprB</i>	Probable periplasmic, spermidine/putrescine-binding protein	2.14
Iron metabolism			
PA0308	<i>oprB</i>	Ironer binding protein	14.89
PA0391	<i>oprB</i>	Ironer binding protein, ATP-binding protein	2.10
PA4490	<i>oprB</i>	Probable binding protein component of ABC transporter	5.28
PA4491	<i>oprB</i>	Probable binding protein component of ABC transporter	5.28
PA4501	<i>oprD</i>	Glycine-glutamate dipeptide porin OprD	3.69
PA4910	<i>oprB</i>	Branch chain amino acid ABC transporter ATP binding protein	2.61
PA4913	<i>oprB</i>	Probable binding protein component of ABC transporter	5.08
PA4914	<i>oprB</i>	Probable binding protein component of ABC transporter	5.08
PA5096	<i>oprB</i>	Probable binding protein component of ABC transporter	3.78
PA5154	<i>oprB</i>	Amino acid (tyrosine/arginine/ornithine/histidine/tyrosine) ABC transporter	2.44