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

Maud Flécharde¹, Émeline Bouffartigues¹, Rachel Duchesne¹, Julie Hardouin, Olivier Maillot¹, Nicole Orange¹, Marc G. J. Feuilloley¹, Pierre Cornelis¹ and Sylvie Chevalier¹.

¹Laboratory 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			
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	-2.06
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 sugar 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 H1A	-2.37
PA4687	<i>hcr1</i>	iron-iron-binding periplasmic protein H1A	-2.27
PA5217	<i>oprG</i>	probable binding protein component of ABC iron transporter	-2.38
PA0215	<i>malZ</i>	malonate transporter MalZ	15.91
PA0216	<i>malM</i>	malonate transporter MalM	6.93
PA0280	<i>cysE</i>	cellular transport protein CysA	2.75
PA0603	<i>oprE</i>	ATP-binding cassette (ABC) transporter complex, substrate-binding subunit-containing	8.66
PA0604	<i>oprE</i>	ATP-binding cassette (ABC) transporter complex, substrate-binding subunit-containing	14.81
PA0755	<i>oprH</i>	cis-acconitate porin OprH1	1.58
PA0866	<i>amiE</i>	transmembrane amino acid transport protein AmiE2	3.95
PA1074	<i>hcr1</i>	transmembrane amino acid transport protein H1A2	2.79
PA1339	<i>amiE</i>	amino acid ABC transporter ATP binding protein	2.61
PA1342	<i>amiE</i>	ABC-type amino acid transport/transduction systems, periplasmic component/domain	2.45
PA1946	<i>rbcB</i>	binding protein component precursor of ABC ribose transporter	2.78
PA1947	<i>rbcB</i>	thiosulfonate-specific ABC ribose transporter	4.75
PA1948	<i>rbcC</i>	membrane protein component of ABC ribose transporter	3.29
PA2329	<i>oprC</i>	probable ATP-binding component of ABC transporter	2.79
PA2338	<i>oprC</i>	probable binding protein component of ABC maltoheptaose/transport protein	4.35
PA2339	<i>oprC</i>	probable binding-protein-dependent maltoheptaose/transport protein	3.89
PA2340	<i>oprC</i>	probable binding-protein-dependent maltoheptaose/transport protein	4.42
PA2341	<i>oprC</i>	probable ATP-binding component of ABC maltoheptaose/transport protein	3.96
PA2711	<i>oprC</i>	probable periplasmic spermidine/potrescine-binding protein	2.14
PA3038	<i>oprC</i>	probable porin	14.88
PA3891	<i>oprC</i>	OprC ABC transporter, ATP-binding protein	2.10
PA4498	<i>oprC</i>	probable binding protein component of ABC transporter	5.29
PA4497	<i>oprC</i>	probable binding protein component of ABC transporter	5.69
PA4501	<i>oprD</i>	Dicaine-glutamate dipeptide porin OprD	3.28
PA4910	<i>oprD</i>	branched chain amino acid ABC transporter ATP binding protein	2.61
PA4913	<i>oprD</i>	probable binding protein component of ABC transporter	5.08
PA5094	<i>oprD</i>	probable ATP-binding component of ABC transporter	6.66
PA5096	<i>oprD</i>	probable binding protein component of ABC transporter	3.78
PA5153	<i>oprD</i>	amino acid (lysine/arginine/ornithine/histidine) ABC transporter periplasmic binding protein	2.44

Many porins encoding genes were downregulated while several amino acids transporters were upregulated in PAOSX grown in LB medium compared to *P. aeruginosa* H103.

The absence of SigX leads to increased expression of many genes that are involved in amino acids and carbon metabolisms.

Locus	Gene name	Product name	PAOSX/mRNA	Protein	Chr/UB	Hfq
Amino acid metabolism						
PA0469	<i>argD</i>	acetylornithine 5-acetylornithine adenylyltransferase	2.31	X	X	
PA0699	<i>argA</i>	acetylornithine decarboxylase	2.42	X	X	
PA0981	<i>argA</i>	acetylornithine decarboxylase	2.25	X	X	
PA1338	<i>arg</i>	acetylornithine/ornithine/lysine transport	2.09	X	X	
PA1984	<i>argA</i>	NAD-dependent aldehyde dehydrogenase C-act	2.44	X	X	
PA2247	<i>argA</i>	oxaloacetate decarboxylase (alpha subunit)	4.39	2.7	X	X
PA2248	<i>argA</i>	oxaloacetate decarboxylase (beta subunit)	5.81	X	X	X
PA2249	<i>argA</i>	branched chain amino acid decarboxylase	6.04	2.2	X	X
PA2250	<i>argA</i>	transaminase dehydrogenase-VI	6.40	2.9	X	X
PA2251	<i>argA</i>	dehydrogenase transaminase	6.72	X	X	X
PA2308	<i>amiE</i>	branched chain amino acid permease	20.66	X	X	
PA2370	<i>amiE</i>	branched chain amino acid permease	13.12	X	X	
PA2371	<i>amiE</i>	branched chain amino acid permease	2.49	X	X	
PA2391	<i>amiE</i>	branched chain amino acid permease	3.02	X	X	
PA2692	<i>amiE</i>	maltoheptaose-5-phosphate lyase/transferase that hydrolyzes C10 binding protein	2.39	X	X	
PA2693	<i>amiE</i>	maltoheptaose-5-phosphate lyase/transferase that hydrolyzes C10 binding protein	15.8	X	X	
PA2694	<i>amiE</i>	maltoheptaose-5-phosphate lyase/transferase that hydrolyzes C10 binding protein	12.74	15	X	
PA2695	<i>amiE</i>	maltoheptaose-5-phosphate lyase/transferase that hydrolyzes C10 binding protein	10.45	6.9	X	
Carbon metabolism						
PA0153	<i>argD</i>	oxaloacetate 1,4-dihydropyridine lyase subunit	4.03	X	X	
PA0154	<i>argD</i>	oxaloacetate 1,4-dihydropyridine lyase subunit	3.33	11.6	X	
PA0211	<i>argD</i>	malate-CoA lyase/oxaloacetate lyase subunit	14.3	14.4	X	
PA0212	<i>argD</i>	malate-CoA lyase/oxaloacetate lyase subunit	3.21	14.4	X	
PA0213	<i>argD</i>	malate-CoA lyase/oxaloacetate lyase subunit	2.88	X	X	
PA0217	<i>argD</i>	malate-CoA lyase/oxaloacetate lyase subunit	20.9	17.5	X	
PA0228	<i>argD</i>	malate-CoA lyase/oxaloacetate lyase subunit	13.88	16.1	X	
PA0807	<i>argD</i>	acetylornithine 5-acetylornithine adenylyltransferase	2.88	X	X	
PA1092	<i>argD</i>	hypothetical protein	4.19	X	X	
PA1093	<i>argD</i>	hypothetical protein	4.04	X	X	
PA1094	<i>argD</i>	hypothetical protein	6.48	X	X	
PA1095	<i>argD</i>	hypothetical protein	7.32	X	X	
PA1096	<i>argD</i>	hypothetical protein	3.18	X	X	
PA1097	<i>argD</i>	hypothetical protein	4.47	X	X	
PA1098	<i>argD</i>	hypothetical protein	4.34	X	X	
PA1099	<i>argD</i>	hypothetical protein	4.52	X	X	
PA1099	<i>argD</i>	hypothetical protein	2.40	X	X	
PA1100	<i>argD</i>	hypothetical protein	4.34	X	X	
PA1101	<i>argD</i>	hypothetical protein	4.52	X	X	
PA1102	<i>argD</i>	hypothetical protein	2.40	X	X	
PA1103	<i>argD</i>	hypothetical protein	2.40	X	X	
PA1104	<i>argD</i>	NAD-dependent aldehyde dehydrogenase C-act	2.44	X	X	
PA1105	<i>argD</i>	oxaloacetate decarboxylase	2.97	5.4	X	
PA1207	<i>argD</i>	branched chain amino acid permease	10.95	25.5	X	
PA2208	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.02	8.5	X	
PA2209	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	7.39	8.5	X	
PA2210	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2211	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2212	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2213	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2214	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2215	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2216	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2217	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2218	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2219	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2220	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2221	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2222	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2223	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2224	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2225	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2226	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2227	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2228	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2229	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2230	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2231	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2232	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2233	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2234	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2235	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2236	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2237	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2238	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2239	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2240	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2241	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2242	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2243	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2244	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2245	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2246	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2247	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2248	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2249	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2250	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2251	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2252	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2253	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2254	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2255	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2256	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2257	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2258	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2259	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2260	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2261	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2262	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2263	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
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PA2266	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2267	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2268	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2269	<i>argD</i>	maltoheptaose-5-phosphate lyase/transferase	10.16	10.4	X	
PA2270	<i>argD</i>	maltoheptaose-5-phosphate lyase/transfer				