Pyruvate Oxidase Influences the Sugar Utilization Pattern and Capsule Production in Streptococcus pneumoniae
Carvalho, Sandra M.; Farshchi Andisi, Vahid; Gradstedt, Henrik; Neef, Jolanda; Kuipers, Oscar; Neves, Ana R.; Bijlsma, Jetta J. E.

Published in: PLoS ONE

DOI: 10.1371/journal.pone.0068277

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date: 2013

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.
Table S1 Genes with significantly higher expression profiles in *L. lactis* strain MG1363 suspended in KPi at pH 5.1, previously adapted to acid (grown at pH 5.1) compared with non-adapted cells (grown at 6.5).

<table>
<thead>
<tr>
<th>Function</th>
<th>Gene</th>
<th>Fold change</th>
<th>Description of gene product</th>
</tr>
</thead>
<tbody>
<tr>
<td>Energy production and conversion</td>
<td>gltA</td>
<td>3.7</td>
<td>methylcitrate synthase</td>
</tr>
<tr>
<td></td>
<td>icd</td>
<td>4.0</td>
<td>isocitrate dehydrogenase</td>
</tr>
<tr>
<td></td>
<td>cydB</td>
<td>2.0</td>
<td>cytochrome d ubiquinol oxidase, subunit II</td>
</tr>
<tr>
<td></td>
<td>atpC</td>
<td>2.8</td>
<td>F0F1 ATP synthase subunit epsilon</td>
</tr>
<tr>
<td></td>
<td>atpD</td>
<td>3.0</td>
<td>F0F1 ATP synthase subunit beta</td>
</tr>
<tr>
<td></td>
<td>atpG</td>
<td>2.9</td>
<td>F0F1 ATP synthase subunit gamma</td>
</tr>
<tr>
<td></td>
<td>atpA</td>
<td>2.2</td>
<td>F0F1 ATP synthase subunit alpha</td>
</tr>
<tr>
<td></td>
<td>atpF</td>
<td>2.5</td>
<td>F0F1 ATP synthase subunit B</td>
</tr>
<tr>
<td></td>
<td>atpB</td>
<td>2.9</td>
<td>F0F1 ATP synthase subunit A</td>
</tr>
<tr>
<td></td>
<td>atpE</td>
<td>2.2</td>
<td>F0F1 ATP synthase subunit C</td>
</tr>
<tr>
<td></td>
<td>ldh</td>
<td>2.6</td>
<td>L-lactate dehydrogenase</td>
</tr>
<tr>
<td></td>
<td>qor *</td>
<td>2.4</td>
<td>quinone oxidoreductase</td>
</tr>
<tr>
<td>Amino acid transport and metabolism</td>
<td>oppA</td>
<td>2.6</td>
<td>oligopeptide-binding protein oppA precursor</td>
</tr>
<tr>
<td></td>
<td>ilvH</td>
<td>2.3</td>
<td>acetolactate synthase 3 regulatory subunit</td>
</tr>
<tr>
<td></td>
<td>hisG</td>
<td>5.1</td>
<td>ATP phosphoribosyltransferase catalytic subunit</td>
</tr>
<tr>
<td></td>
<td>hisZ</td>
<td>4.7</td>
<td>ATP phosphoribosyltransferase regulatory subunit</td>
</tr>
<tr>
<td></td>
<td>busAB</td>
<td>2.4</td>
<td>glycine betaine-binding periplasmic protein precursor</td>
</tr>
<tr>
<td></td>
<td>glnB</td>
<td>2.7</td>
<td>nitrogen regulatory protein P-II</td>
</tr>
<tr>
<td></td>
<td>hisI</td>
<td>3.2</td>
<td>bifunctional phosphoribosyl-AMP</td>
</tr>
<tr>
<td></td>
<td>hisF</td>
<td>3.0</td>
<td>imidazoleglycerol-phosphate synthase cyclase</td>
</tr>
<tr>
<td></td>
<td>hisA</td>
<td>5.9</td>
<td>1-(5-phosphoribosyl)-5-imidazole glycerol phosphate synthase subunit</td>
</tr>
<tr>
<td></td>
<td>hisH</td>
<td>3.8</td>
<td>HisH</td>
</tr>
<tr>
<td></td>
<td>pepC</td>
<td>3.1</td>
<td>PepC protein</td>
</tr>
<tr>
<td></td>
<td>glnA</td>
<td>2.3</td>
<td>GlnA protein</td>
</tr>
<tr>
<td></td>
<td>arcB</td>
<td>3.0</td>
<td>ornithine carbamoyltransferase</td>
</tr>
<tr>
<td></td>
<td>arcA</td>
<td>2.3</td>
<td>ArcA protein</td>
</tr>
<tr>
<td></td>
<td>cysK</td>
<td>3.2</td>
<td>O-acetylserine sulfhydrylase</td>
</tr>
<tr>
<td></td>
<td>metC</td>
<td>4.3</td>
<td>cystathionine gamma-synthase/cystathionine betalyase</td>
</tr>
<tr>
<td></td>
<td>ilvC *</td>
<td>2.2</td>
<td>ketol-acid reductoisomerase</td>
</tr>
<tr>
<td></td>
<td>ilvB *</td>
<td>2.1</td>
<td>acetolactate synthase catalytic subunit</td>
</tr>
<tr>
<td></td>
<td>gltD *</td>
<td>2.1</td>
<td>glutamate synthase subunit beta</td>
</tr>
<tr>
<td></td>
<td>hisK *</td>
<td>3.9</td>
<td>histidinol-phosphatase</td>
</tr>
<tr>
<td>Nucleotide transport and metabolism</td>
<td>deoD</td>
<td>2.1</td>
<td>DeoD protein</td>
</tr>
<tr>
<td></td>
<td>ptcC</td>
<td>2.4</td>
<td>cellobiose-specific PTS system IIC component</td>
</tr>
<tr>
<td>Carbohydrate</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Function</td>
<td>Gene</td>
<td>Fold change</td>
<td>Description of gene product</td>
</tr>
<tr>
<td>----------------------------------------</td>
<td>----------</td>
<td>-------------</td>
<td>----------------------------------------------------------------</td>
</tr>
<tr>
<td>transport and metabolism</td>
<td>gapA</td>
<td>2.4</td>
<td>glyceraldehyde 3-phosphate dehydrogenase</td>
</tr>
<tr>
<td></td>
<td>eno</td>
<td>2.6</td>
<td>enolase</td>
</tr>
<tr>
<td></td>
<td>gpmA</td>
<td>2.0</td>
<td>phosphoglycerate mutase</td>
</tr>
<tr>
<td></td>
<td>pgi</td>
<td>2.4</td>
<td>glucose-6-phosphate isomerase</td>
</tr>
<tr>
<td></td>
<td>-</td>
<td>6.1</td>
<td>putative transport protein</td>
</tr>
<tr>
<td></td>
<td>nagA</td>
<td>2.5</td>
<td>NagA protein</td>
</tr>
<tr>
<td></td>
<td>pyk</td>
<td>2.4</td>
<td>pyruvate kinase</td>
</tr>
<tr>
<td></td>
<td>pgk</td>
<td>2.3</td>
<td>phosphoglycerate kinase</td>
</tr>
<tr>
<td>Coenzyme transport and metabolism</td>
<td>-</td>
<td>2.9</td>
<td>hypothetical protein Ilmg_2158</td>
</tr>
<tr>
<td></td>
<td>nadR</td>
<td>2.2</td>
<td>putative nicotinamide-nucleotide adenylyltransferase</td>
</tr>
<tr>
<td></td>
<td>nadE</td>
<td>2.0</td>
<td>NAD synthetase</td>
</tr>
<tr>
<td></td>
<td>ilvC *</td>
<td>2.2</td>
<td>ketol-acid reductoisomerase</td>
</tr>
<tr>
<td></td>
<td>ilvB *</td>
<td>2.1</td>
<td>acetalactate synthase catalytic subunit</td>
</tr>
<tr>
<td>Translation</td>
<td>gltX</td>
<td>2.0</td>
<td>glutamyl-tRNA synthetase</td>
</tr>
<tr>
<td></td>
<td>-</td>
<td>4.3</td>
<td>hypothetical protein Ilmg_1293</td>
</tr>
<tr>
<td></td>
<td>serS</td>
<td>2.1</td>
<td>seryl-tRNA synthetase</td>
</tr>
<tr>
<td></td>
<td>rpmB</td>
<td>2.2</td>
<td>50S ribosomal protein L28</td>
</tr>
<tr>
<td></td>
<td>yfIA</td>
<td>4.6</td>
<td>putative sigma 54 modulation protein</td>
</tr>
<tr>
<td>Transcription</td>
<td>hrcA</td>
<td>2.7</td>
<td>heat-inducible transcription repressor</td>
</tr>
<tr>
<td></td>
<td>vacB1</td>
<td>2.2</td>
<td>putative exoribonuclease R</td>
</tr>
<tr>
<td></td>
<td>- *</td>
<td>2.4</td>
<td>hypothetical protein Ilmg_2163</td>
</tr>
<tr>
<td>Replication, recombination and repair</td>
<td>recA</td>
<td>2.0</td>
<td>recombinase A</td>
</tr>
<tr>
<td></td>
<td>hllA</td>
<td>2.4</td>
<td>HU-like DNA-binding protein</td>
</tr>
<tr>
<td></td>
<td>tnp712</td>
<td>2.1</td>
<td>transposase for insertion sequence element IS712H</td>
</tr>
<tr>
<td></td>
<td>-</td>
<td>4.9</td>
<td>putative transposase helper protein for IS712G</td>
</tr>
<tr>
<td></td>
<td>matR</td>
<td>2.5</td>
<td>maturase</td>
</tr>
<tr>
<td>Cell wall/membrane biogenesis</td>
<td>ps356</td>
<td>4.1</td>
<td>endolysin</td>
</tr>
<tr>
<td></td>
<td>-</td>
<td>2.4</td>
<td>hypothetical protein Ilmg_0162</td>
</tr>
<tr>
<td>Posttranslational modification, protein turnover, chaperones</td>
<td>htrA</td>
<td>2.9</td>
<td>housekeeping protease</td>
</tr>
<tr>
<td></td>
<td>dnaK</td>
<td>2.7</td>
<td>molecular chaperone DnaK</td>
</tr>
<tr>
<td></td>
<td>clpE</td>
<td>2.5</td>
<td>ATP-dependent Clp protease ATP-binding subunit clpE</td>
</tr>
<tr>
<td></td>
<td>groEL</td>
<td>2.5</td>
<td>chaperonin GroEL</td>
</tr>
<tr>
<td></td>
<td>gcp</td>
<td>2.0</td>
<td>O-sialoglycoprotein endopeptidase</td>
</tr>
<tr>
<td></td>
<td>ahpC</td>
<td>3.6</td>
<td>alkyl hydroperoxide reductase subunit C</td>
</tr>
<tr>
<td></td>
<td>ahpF</td>
<td>4.6</td>
<td>alkyl hydroperoxide reductase subunit F</td>
</tr>
<tr>
<td>Function</td>
<td>Gene</td>
<td>Fold change</td>
<td>Description of gene product</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>---------</td>
<td>-------------</td>
<td>----------------------------------------------</td>
</tr>
<tr>
<td>Inorganic ion transport and metabolism</td>
<td>osmC</td>
<td>2.9</td>
<td>osmotically inducible protein C</td>
</tr>
<tr>
<td></td>
<td>clpB</td>
<td>2.1</td>
<td>ATP-dependent Clp protease</td>
</tr>
<tr>
<td>Secondary metabolites biosynthesis, transport</td>
<td>sodA</td>
<td>2.2</td>
<td>SodA protein</td>
</tr>
<tr>
<td>and catabolism</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>General function prediction only</td>
<td></td>
<td>2.1</td>
<td>amidase</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>putative NADH-flavin reductase</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.9</td>
<td>hypothetical protein Ilmg_1135</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.1</td>
<td>hypothetical protein Ilmg_1253</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.3</td>
<td>hypothetical protein Ilmg_0584</td>
</tr>
<tr>
<td></td>
<td>hadL</td>
<td>2.5</td>
<td>cryptic haloacid dehalogenase 1</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.8</td>
<td>aldo/keto reductase family oxidoreductase</td>
</tr>
<tr>
<td></td>
<td>ps350</td>
<td>3.5</td>
<td>hypothetical protein Ilmg_0844</td>
</tr>
<tr>
<td></td>
<td>gltD *</td>
<td>2.1</td>
<td>glutamate synthase subunit beta</td>
</tr>
<tr>
<td></td>
<td>hisK *</td>
<td>3.9</td>
<td>histidinol-phosphatase</td>
</tr>
<tr>
<td></td>
<td>qor *</td>
<td>2.4</td>
<td>quinone oxidoreductase</td>
</tr>
<tr>
<td>Function unknown</td>
<td>mycA</td>
<td>2.2</td>
<td>Myosin-crossreactive streptococcal antigen homologue</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3.5</td>
<td>hypothetical protein Ilmg_1257</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.0</td>
<td>hypothetical protein Ilmg_0152</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.5</td>
<td>hypothetical protein Ilmg_0150</td>
</tr>
<tr>
<td>Signal transduction mechanisms</td>
<td></td>
<td>3.0</td>
<td>hypothetical protein Ilmg_0093</td>
</tr>
<tr>
<td></td>
<td>uspA2</td>
<td>3.7</td>
<td>universal stress protein A2</td>
</tr>
<tr>
<td></td>
<td>uspA</td>
<td>2.4</td>
<td>universal stress protein A</td>
</tr>
<tr>
<td></td>
<td>rcfB</td>
<td>3.2</td>
<td>universal stress protein A</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.2</td>
<td>transcriptional regulator</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.4</td>
<td>hypothetical protein Ilmg_2163</td>
</tr>
<tr>
<td>Intracellular trafficking and secretion</td>
<td></td>
<td>2.5</td>
<td>hypothetical protein Ilmg_1391</td>
</tr>
<tr>
<td>No prediction</td>
<td></td>
<td>2.7</td>
<td>putative secreted protein</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3.8</td>
<td>hypothetical protein Ilmg_1211</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.2</td>
<td>hypothetical protein Ilmg_0317</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.1</td>
<td>hypothetical protein Ilmg_0129</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2.1</td>
<td>hypothetical protein Ilmg_0589</td>
</tr>
<tr>
<td>Function</td>
<td>Gene</td>
<td>Fold change</td>
<td>Description of gene product</td>
</tr>
<tr>
<td>----------</td>
<td>-------</td>
<td>-------------</td>
<td>--------------------------------------</td>
</tr>
<tr>
<td>-</td>
<td>8.2</td>
<td>hypothetical protein llmg_0755</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>7.9</td>
<td>putative secreted protein</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>2.0</td>
<td>hypothetical protein llmg_0757</td>
<td></td>
</tr>
<tr>
<td>ps311</td>
<td>5.2</td>
<td>hypothetical protein llmg_0801</td>
<td></td>
</tr>
<tr>
<td>ps315</td>
<td>2.5</td>
<td>hypothetical protein llmg_0805</td>
<td></td>
</tr>
<tr>
<td>ps340</td>
<td>3.5</td>
<td>hypothetical protein llmg_0834</td>
<td></td>
</tr>
<tr>
<td>ps341</td>
<td>2.1</td>
<td>hypothetical protein llmg_0835</td>
<td></td>
</tr>
<tr>
<td>ps346</td>
<td>4.9</td>
<td>hypothetical protein llmg_0840</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>2.6</td>
<td>hypothetical protein llmg_1258</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>2.0</td>
<td>hypothetical protein llmg_1385</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>2.4</td>
<td>hypothetical protein llmg_1396</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>2.1</td>
<td>hypothetical protein llmg_1399</td>
<td></td>
</tr>
<tr>
<td>comX</td>
<td>2.5</td>
<td>competence regulator ComX</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>2.4</td>
<td>hypothetical protein llmg_1600</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>2.9</td>
<td>hypothetical protein llmg_1663</td>
<td></td>
</tr>
<tr>
<td>ps431</td>
<td>6.7</td>
<td>hypothetical protein llmg_2111</td>
<td></td>
</tr>
<tr>
<td>ps411</td>
<td>2.8</td>
<td>hypothetical protein llmg_2132</td>
<td></td>
</tr>
<tr>
<td>ps407</td>
<td>2.6</td>
<td>hypothetical protein llmg_2136</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>5.1</td>
<td>hypothetical protein llmg_2144</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>3.6</td>
<td>hypothetical protein llmg_2146</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td>3.9</td>
<td>hypothetical protein llmg_2211</td>
<td></td>
</tr>
</tbody>
</table>