Genetic loci associated with fluoride resistance in streptococcus mutans

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Published in:
Frontiers in Microbiology

DOI:
10.3389/fmicb.2018.03093

Citation for published version (APA):

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**Supplementary Table 1.** Primers used in this study.

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Primer</th>
<th>Sequence(5'-3')</th>
<th>Purpose</th>
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</thead>
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<tr>
<td>eno</td>
<td>Forward</td>
<td>CGGATATGATGTTCTGAT</td>
<td>Real-time PCR</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>ACCAAGAATAGCATTAGCA</td>
<td></td>
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<tr>
<td>glpF</td>
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<tr>
<td></td>
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<td>mut</td>
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<tr>
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<td>Reverse</td>
<td>TGTTTAGAAAGACGAATGACT</td>
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<td>perA</td>
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<tr>
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<td>Reverse</td>
<td>TGCTGATAAGGTAAAACTGTTAG</td>
<td></td>
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<tr>
<td>perB</td>
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<td></td>
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<td>mutp_gfp</td>
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<td>Construction of reporter strains</td>
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<tr>
<td></td>
<td>Reverse</td>
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**Supplementary Table 2.** Single nucleotide polymorphisms identified from the genomes of *S. mutans* UA159 and UA159-FR

<table>
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<tr>
<th>SNP base</th>
<th>Amino acid</th>
<th>SNP base</th>
<th>Amino acid</th>
<th>mutation type</th>
<th>Gene annotation</th>
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<td>T</td>
<td>F</td>
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<td>transcriptional regulator (SMU_112c)</td>
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<td>T</td>
<td>F</td>
<td>C</td>
<td>S</td>
<td>non_syn</td>
<td>hypothetical protein (SMU_448)</td>
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<tr>
<td>C</td>
<td>S</td>
<td>G</td>
<td>*(^b)</td>
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<td>DNA-directed RNA polymerase subunit omega (<em>rpoZ</em>)</td>
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<td>N</td>
<td>CG</td>
<td>R</td>
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<td>C</td>
<td>non_syn</td>
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<td>T</td>
<td>I</td>
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<td>histidine kinase sensor CiaH (<em>ciaH</em>)</td>
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<td>G</td>
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<td>pyruvate kinase (<em>pyk</em>)</td>
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<tr>
<td>C</td>
<td>T</td>
<td>T</td>
<td>I</td>
<td>non_syn</td>
<td>enolase (<em>eno</em>)</td>
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<td>L</td>
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<td>L</td>
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<td>transposase, IS150-like (SMU_1370c)</td>
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<td>Downstream: SMU_t14</td>
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<td>intergenic region</td>
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<td>A</td>
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<td>G</td>
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<td>intergenic region</td>
<td>Downstream: Mg(^{2+})/citrate transporter (SMU_1013c); hypothetical protein (SMU_1014)</td>
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<td>Upstream(^c): hypothetical proteins (SMU_1546 and SMU_1547c)</td>
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<td>Downstream: transcriptional regulator (SMU_1647c)</td>
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<td>Downstream: SMU_t42</td>
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</tbody>
</table>

\(^a\) nonsyn: non-synonymous coding SNP.  
\(^b\) *: stop codon.  
\(^c\) downstream: the gene / genes downstream the intergenic region with the SNP.  
\(^d\) upstream: the gene / genes upstream the intergenic region with the SNP.
Supplementary Figure 1. Growth curve of *S. mutans* UA159 and UA159-FR in the absence of NaF in BHI broth. Mean optical density at 600 nm ± standard deviation is shown. This experiment was performed with triplicates.
Supplementary Figure 2. Growth of *S. mutans* (A) UA159 and (B) UA159-FR in BHI broth supplemented with 0, 5, 10, 20, 40, 60 mM NaF. Data are expressed as means ± standard deviation of triplicates.
Supplementary Figure 3. Fluorescence intensities of *mutp* reporter strains, *S. mutans* UA159 containing the wild-type *mutp*, *mutp* from C180-2FR, or *mutp* from UA159-FR. ***p < 0.0005.