Genetic loci associated with fluoride resistance in streptococcus mutans

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**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>
</tr>
</thead>
<tbody>
<tr>
<td>eno</td>
<td>Forward</td>
<td>CGGATATGATGTTCGTGAT</td>
<td>Real-time PCR</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>ACCAAGAATAGCATTAGCA</td>
<td></td>
</tr>
<tr>
<td>glpF</td>
<td>Forward</td>
<td>GTTACCAGATACATTACCA</td>
<td>Real-time PCR</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>TACTGCTCTACTCGTTAT</td>
<td></td>
</tr>
<tr>
<td>mut</td>
<td>Forward</td>
<td>ATGGTGAGCGATATGTA</td>
<td>Real-time PCR</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>TGTATTAGAAAGACGAATGACT</td>
<td></td>
</tr>
<tr>
<td>perA</td>
<td>Forward</td>
<td>TTAATCTGCTCTGCTTGTTGA</td>
<td>Real-time PCR</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>TGCTGATAAGGTAAATCTGTAG</td>
<td></td>
</tr>
<tr>
<td>perB</td>
<td>Forward</td>
<td>AGATGCTAATCTTGGTA</td>
<td>Real-time PCR</td>
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<tr>
<td></td>
<td>Reverse</td>
<td>TATGGTCTTCCCTTCAA</td>
<td></td>
</tr>
<tr>
<td>pepX</td>
<td>Forward</td>
<td>TATGGCTGACTGGACTAA</td>
<td>Real-time PCR</td>
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<tr>
<td></td>
<td>Reverse</td>
<td>TTCCGCAATAATGACCTTA</td>
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<tr>
<td>pyk</td>
<td>Forward</td>
<td>GGTГГАAGATGGCTATTTGG</td>
<td>Real-time PCR</td>
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<tr>
<td></td>
<td>Reverse</td>
<td>CATTTGCTCCCTCTGTAAAT</td>
<td></td>
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<tr>
<td>mutp_gfp</td>
<td>Forward</td>
<td>CATATGAGCCTCTCTTTACTTTAA</td>
<td>Construction of reporter strains</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>GCAITGCATGATATCTTGGCTATTTA</td>
<td></td>
</tr>
</tbody>
</table>
### Supplementary Table 2. Single nucleotide polymorphisms identified from the genomes of *S. mutans* UA159 and UA159-FR

<table>
<thead>
<tr>
<th>SNP base</th>
<th>Amino acid</th>
<th>mutation type</th>
<th>Gene annotation</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>UA159</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
| G | V | T | T | F | non
| T | F | C | S | non
| C | S | G | * | non
| AA | N | CG | R | non
| C | R | T | C | non
| C | T | T | I | non
| A | E | G | G | non
| T | T | T | I | non
| **UA159-FR** | | | |
| G | V | T | T | F | non
| T | F | C | S | non
| C | S | G | * | non
| AA | N | CG | R | non
| C | R | T | C | non
| C | T | T | I | non
| A | E | G | G | non
| T | T | T | I | non

**A** | A | E | G | G | non
**A** | S | G | P | non
**G** | P | A | L | non
**A** | T | intergenic region | Downstream: SMU_t14
**C** | T | intergenic region | Downstream: SMU_t14
**A** | G | intergenic region | Downstream: hippocrute hydrolase (SMU_318)
**G** | A | intergenic region | Downstream: hippocrute hydrolase (SMU_318)
**A** | G | intergenic region | Downstream: hippocrute hydrolase (SMU_318)
**A** | G | intergenic region | Downstream: hippocrute hydrolase (SMU_318)
**G** | A | intergenic region | Downstream: glycerol uptake facilitator protein (glpF); x-prolyl-dipeptidyl aminopeptidase (pepX)
**C** | A | intergenic region | Downstream: Mg²⁺/citrate transporter (SMU_1013c); hypothetic protein (SMU_1014)
**C** | A | intergenic region | Upstream: hypothetic proteins (SMU_1546 and SMU_1547c)
**C** | T | intergenic region | Downstream: transcriptional regulator (SMU_1647c)
**C** | T | intergenic region | Downstream: SMU_t42

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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. *** $p < 0.0005$. 