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Genetic loci associated with fluoride resistance in streptococcus mutans

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DOI

[10.3389/fmicb.2018.03093](https://doi.org/10.3389/fmicb.2018.03093)

Publication date

2018

Document Version

Other version

Published in

Frontiers in Microbiology

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[Link to publication](#)

Citation for published version (APA):

Liao, Y., Yang, J., Brandt, B. W., Li, J., Crielaard, W., van Loveren, C., & Deng, D. M. (2018). Genetic loci associated with fluoride resistance in streptococcus mutans. *Frontiers in Microbiology*, 9, [3093]. <https://doi.org/10.3389/fmicb.2018.03093>

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Supplementary Table 1. Primers used in this study.

| Gene name | Primer | Sequence(5'-3') | Purpose |
|-----------------|---------|-----------------------------|----------------------------------|
| <i>eno</i> | Forward | CGGATATGATGTTTCGTGAT | Real-time PCR |
| | Reverse | ACCAAGAATAGCATTAGCA | |
| <i>glpF</i> | Forward | GTTACCAGATACATTACCA | Real-time PCR |
| | Reverse | TACTGCTCTACTCGTTAT | |
| <i>mut</i> | Forward | ATGGTGGAGCGATATGTA | Real-time PCR |
| | Reverse | TGTTTAGAAAGACGAATGACT | |
| <i>perA</i> | Forward | TTACTGCTGCTGGTATGG | Real-time PCR |
| | Reverse | TGCTGATAAGGTTAATACTGTTAG | |
| <i>perB</i> | Forward | AGATGCTAATCCTTGGTA | Real-time PCR |
| | Reverse | TATGGTCTTCCTCTTCAA | |
| <i>pepX</i> | Forward | TATGGCTGACTGGACTAA | Real-time PCR |
| | Reverse | TTCCGCAATAATGACCTTA | |
| <i>pyk</i> | Forward | GGTGAAGATGGCTATTGG | Real-time PCR |
| | Reverse | CATTGGCTCCTTCTGTAAT | |
| <i>mutp_gfp</i> | Forward | CATATGAGCCTCTCCTTTTACTTAAA | Construction of reporter strains |
| | Reverse | GCATGCACTGATATTACTGGCTATTTA | |

Supplementary Table 2. Single nucleotide polymorphisms identified from the genomes of *S. mutans* UA159 and UA159-FR

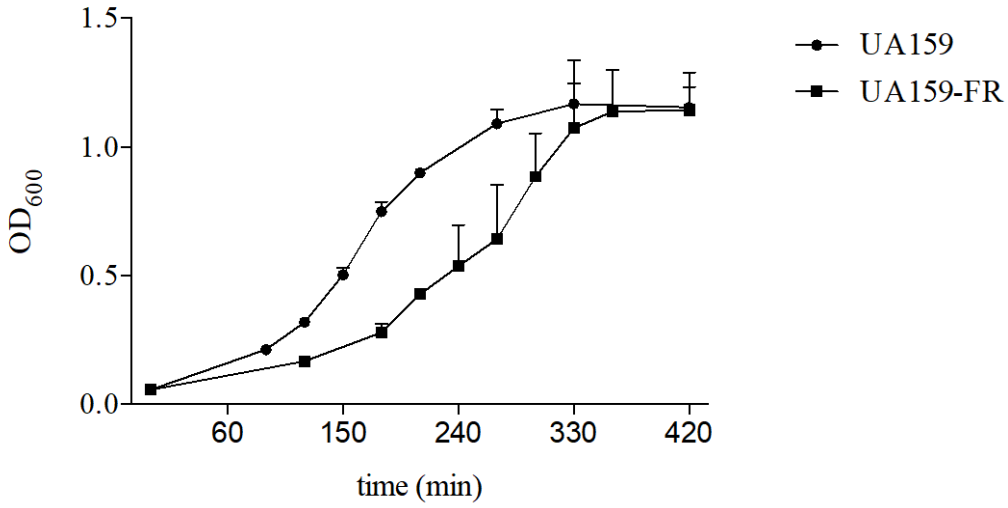
| UA159 | | UA159-FR | | mutation type | Gene annotation |
|----------|------------|----------|----------------|----------------------|---|
| SNP base | Amino acid | SNP base | Amino acid | | |
| G | V | T | F | non_syn ^a | transcriptional regulator (SMU_112c) |
| T | F | C | S | non_syn | hypothetical protein (SMU_448) |
| C | S | G | * ^b | non_syn | DNA-directed RNA polymerase subunit omega (<i>rpoZ</i>) |
| AA | N | CG | R | non_syn | glucosyltransferase-I (<i>gtfB</i>) |
| C | R | T | C | non_syn | GMP synthase (<i>guaA</i>) |
| C | T | T | I | non_syn | histidine kinase sensor CiaH (<i>ciaH</i>) |
| A | E | G | G | non_syn | pyruvate kinase (<i>pyk</i>) |
| C | T | T | I | non_syn | enolase (<i>eno</i>) |
| A | * | T | L | non_syn | hypothetical protein (SMU_1292c) |
| T | S | C | G | non_syn | transposase, ISSmu1 (SMU_565c) |
| A | S | G | P | non_syn | transposase, IS150-like (SMU_1370c) |
| G | P | A | L | non_syn | transposase, IS150-like (SMU_1370c) |
| A | | G | | intergenic region | Downstream ^c : SMU_t14 |
| C | | T | | intergenic region | Downstream: SMU_t14 |
| A | | G | | intergenic region | Downstream: hippurate hydrolase (SMU_318) |
| G | | A | | intergenic region | Downstream: hippurate hydrolase (SMU_318) |
| A | | G | | intergenic region | Downstream: hippurate hydrolase (SMU_318) |
| A | | G | | intergenic region | Downstream: hippurate hydrolase (SMU_318) |
| G | | A | | intergenic region | Downstream: glycerol uptake facilitator protein (<i>glpF</i>); x-prolyl-dipeptidyl aminopeptidase (<i>pepX</i>) |
| C | | A | | intergenic region | Downstream: Mg ²⁺ /citrate transporter (SMU_1013c); hypothetic protein (SMU_1014) |
| C | | A | | intergenic region | Upstream ^d : hypothetic proteins (SMU_1546 and SMU_1547c) |
| C | | T | | intergenic region | Downstream: transcriptional regulator (SMU_1647c) |
| C | | T | | intergenic region | Downstream: SMU_t42 |

a) nonsyn: non-synonymous coding SNP.

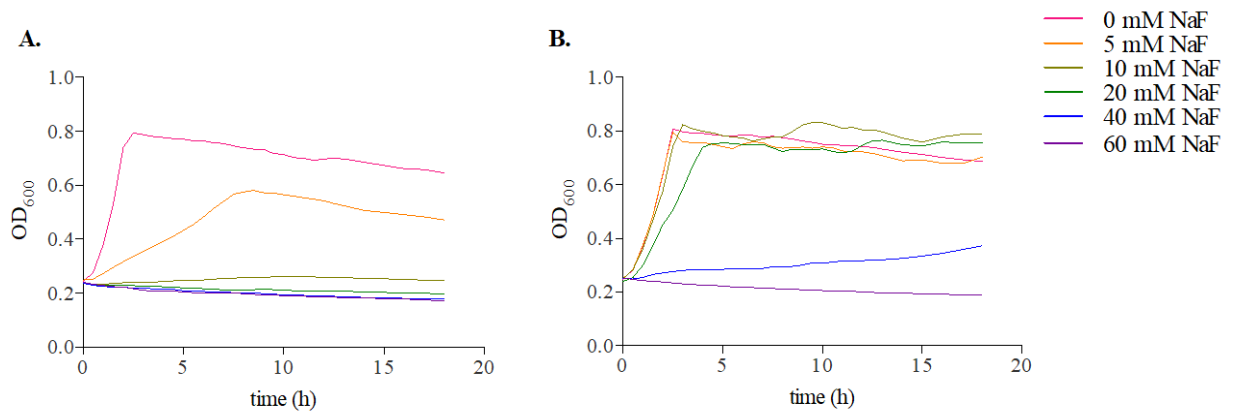
b) *: stop codon.

c) downstream: the gene / genes downstream the intergenic region with the SNP.

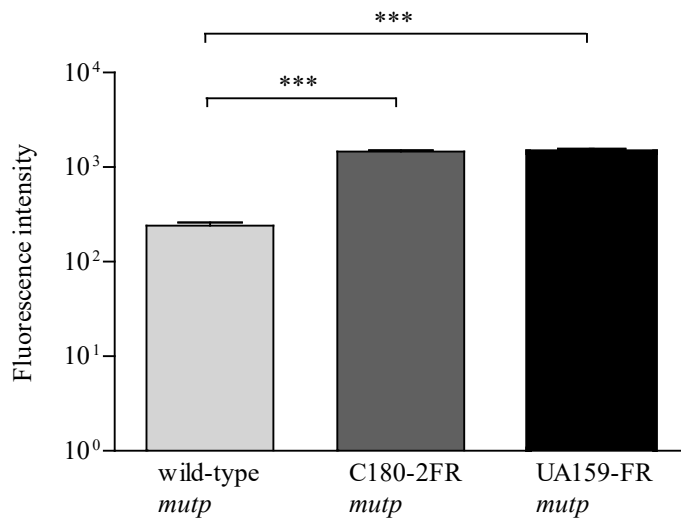
d) upstream: the gene / genes upstream the intergenic region with the SNP.



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 \pm 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 \pm 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. *** $p < 0.0005$.