

Increased leukotoxin production: Characterization of 100 base pairs within the 530 base pair leukotoxin promoter region of *Aggregatibacter actinomycetemcomitans*

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Supplementary Table. S1. Oligonucleotides used in this study

Oligonucleotides	Sequence (5'→3')
<i>ltxA</i> promoter deletion	
530USSUpF	ATACT <u>CCCGGGA</u> AGTGCGGTGATTCTTTCTTCTTGCGGTGATGAAG
530UpR	CTAAATAAAATAACCAAACCACAATATCCAGTATGCCATCATTA ³ AAAG
530DnF	CTTTTAATGATGGCATACTGGATATTGTGGTTTGGTTATTTTATTTAG
530DnR	TACTAC <u>GAGCTCG</u> CAGGAGCAAATAAAGTTAAGCC
400UpR	CTAAATAAAATAACCAAACCACAATAGTTGGTAAAATTAGATTTAAAATG
400DnF	CATTTTAAATCTAATTTTACCAACTATTGTGGTTTGGTTATTTTATTTAG
300UpR	CTAAATAAAATAACCAAACCACAATAGTCTGCGTAATAAGCAAGAGAAG
300DnF	CTTCTCTTGCTTATTACGCAGACTATTGTGGTTTGGTTATTTTATTTAG
200UpR	CTAAATAAAATAACCAAACCACAATAATTTTTAAAATTACAATGGAAAC
200DnF	GTTTCCATTGTAATTTTAAAAATTATTGTGGTTTGGTTATTTTATTTAG
100UpR	CTAAATAAAATAACCAAACCACAATATATTTAAGCTTTATTATTTTGC
100DnF	GCAAATAATAAAGCTTAAATATATTGTGGTTTGGTTATTTTATTTAG
80UpR	ATAAAATAACCAAACCACAATATTGTTAAACAACAAATAGAAATATAAC
80DnF	GTTATATTTCTATTTGTGTTTAAACAATATTGTGGTTTGGTTATTTTAT
530UpFI	GGGCCCAATTAATGGCGATTCTTTCTTCTTGCGGTGATGAAG
530DnRI	TACTAGTTCGAATAACGCAGGAGCAAATAAAGTTAAGCC
-nagUpR	CTTATTTAACCTTATATTATAGGAATAATTTTTAAAATTACAATGGAAAC
-nagDnF	GTTTCCATTGTAATTTTAAAAATTATTCCTATAATATAAGGTTAAATAAG
<i>nagC</i> disruption	

NAGC3R	TACTAGTTCGAATAACAGGCGGATATTGTGATCAGTTCC
nagCDNFNew	CGCACTTTAAGGCTGTAAACGCTTTTTTCTCCCGAAAAGATAAG
3619R	GGGCCCAATTAATGGCGAATGGTGCGGGACGAGGGACTTG
nagCURNew	CTTATCTTTTCGGGAGAAAAAAGCGTTTACAGCCTTAAAGTGCG
<i>nagC</i> mutant screening	
NAGC4R	GAGGTGTTGGTGGAAAAGCTGG
3843R	CCAATAAATTGTATAGTGGAAGC
<i>mlc</i> disruption	
mlcUF	GGGCCCAATTAATGGCCGTTCTTCACGTTGCGAACCGCC
mlcUR	ATTGAGCTAAAACAAAGTTTAAATAATTCGGTATTTTTTA
mlcDNF	TAAAAAATACGGAATTATTTAAACTTTGTTTTAGCTCAAT
mlcDNR	TACTAGTTCGAATAACCTATGCTTTATACCAAGCTCAC
<i>mlc</i> mutant screening	
mlc5'	CCGTGCCGTAACGACGCAAATCAC
mlc3'	GTCGGAGTCGGCATTATTCGAC
qRT-PCR & RT-PCR	
orfXqF	CACTTTGTGAATACTGGCAACTT
orfXqR	GTGCCAATGATTTGTGCGAATA
orfXJnF	CGAGTATGTCCAGTACAGAATATGC
ltxAqF	GCGGCTCTACTTACTTGCA
ltxAqR	GCAATACCTAGGAAAGAC
ltxCqF	GGGCAAATTTAAGCCTTGAG

ltxCqR

GCGCAATCCAATCAATAAAC

Sequences underlined are the restriction enzyme recognition sites

Supplementary Figure. S1. The nucleotide sequence showing 530 bp ltxA promoter deletion and regulatory elements binding sites

The *glyA* stop is shown as the stop codon for *glyA* gene. The Mlc binding site is highlighted in bold face. A -35 and -10 region preceding to *orfX* is highlighted. The start codon of *orfX* is ATG and is shown in bold face and the orfXJnF primer (in blue) binding site is highlighted. The 530 bp deletion starts from 1 to 530 and is shown in small letters. The *orfX* stop (tag) codon is shown in bold face. The encircled (red) bases are the proposed predicted stem loop structure. The probable NagC binding sites were also highlighted. The *ltxC* SD sequence and the start codon are highlighted in bold face.

