Supplementary File

Table 1. List of Genes and Primer Sequences used for transcriptome analysis by qRT-PCR.

S. no	Gene name	Gene function	Forward primer sequence	Reverse primer sequence	Reference
1	*ftsZ*	Cell division protein	CTGAGATGCCTGCTGCTGAA	GATTGCTGTGGCTCAGATG ATG	[1]
2	*gyrA*	Encodes DNA gyrase subunit A	TTCGTACAAGTGTTGCCGA-TATCT	TCTAGGCGCATCACTTT-GACA	[1]
3	*gbpB*	Glucan binding protein - B	ATGGCGGTTATGGACACGTT	TTTGGCCACCTTGAACACCT	[2]
4	*relA*	Virulence phenotypes	ACAAAAAGGGTATCGTCCG-TACAT	AATCACGCTTGG-TATTGCTAATTG	[2]
5	*gtfC*	Extracellular polysaccha-ride synthesis	GGTTTAACGTCAAAATT-AGCTGTATTAGC	CTCAACCAACCGCCAC-TGTT	[2]
6	*atlA*	Autolysin like protein	GTTAGTTCTGGTTTTGACCG-CAAT	CCCTCAACAACAACATCAA AGGT	[2]
7	*spaP*	Adherence to saliva-coated tooth	GACTTTGG-TAATGGTTATGCATCAA	TTTGTATCAGCCG-GATCAAGTG	[2]
8	*immB*	Bacteriocin immunity proteins	GCTAGAGAGGCAAATGCACA	CAGCAGCAGCTGAGAA-GATG	[3]
10	*immA*	Bacteriocin immunity proteins	TCTCCCCTGCTTGTTCAGAT	GCTGGCAAATTCGCTTACTT	[3]
11	*bsmH*	Bacteriocin production	AGACATGTTAGCCGCTGTT-GAAG	AAGCGCCTGTTCCAATCG-TA	[3]
12	*bsmI*		GAAACAATGGATACAGA-GACG	GGAACAATAAGAGGAT-TTGG	[3]
13	*atpD*	Essential for acid toler-ance	CCAGGCGGTTCATTCATCTGA C	GGCGGGATTTCGG-TATTTACTG	[4]
14	*ldh*	Reversible enzyme in tricarboxylic acid cycle	ACTTCACTTGA-TACTGCTCGTT	AACACCAGCTACATTGG-CATGA	[5]
15	*dnaK*	Stress tolerance protein	GGTACAACAAACTCAGCAG-TTGCAGTTCTT	CCCCATCTTAGATTT-GATGGAAAGAATTGT	[6]
16	*recA*	Involved in DNA repair	GGATCCGAGAAAAA-GATTGGCCAAAAGAAT	TAAAGACTCGGGCTTGG-GACCTATTTTTAT	[7]
17	*brpA*	Cell division, stress tol-erance, biofilm formation	GGAGGAGCTGCATCAG-GATTC	AACTCCAGCACATCCAG-CAAG	[2]
18	*comDE*	Competence histidine kinase and response regulator	ACAATTCCTTGAG-TTCCATCCAAG	TGGTCTGCTGCCTGTTGC	[2]
19	*comB*	Competence develop-ment	CCAGTCCAAACCGTCAGACT	GCTGCTTTCCTTGTCTTTCG	[3]
20	*comA*		ACGAGCCTAACAAGGGGATT	CCCTGAGGCATTTGTTCAAT	[3]
21	*covR*	Regulation of EPS syn-thesizing enzymes	ACACGATTACAGCCTTT-GATGG	CTTCTTAGCCACTTCAA-GACC	[1]
22	*vicR*	Promotes biofilm archi-tecture	TGACACGATTACAGCCTTT-GATG	CGTCTAGTTCTGG-TAACATTAAGTCCAATA	[2]
23	*comX*	Competence develop-ment	CTGTTTGTCAAGTGGCGGTA	GCATACTTTGCCTTCCCAAA	[3]
24	*luxS*	Autoinducer-2 synthesis	ACTGTTCCCCTTTTGGCTGTC	AACTTGCTTT-GATGACTGTGGC	[8]

Table 2. The CI values for individual combinations of Baicalein and Fluoride. For all the tested combinations CI < 1 indicating synergy. (CI=1 indicates addictiveness while CI>1 indicates antagonism).

Baicalein Conc. (µM)	Fluoride Conc. (ppm)	Effect	CI	Interpretation
200.0	31.25	0.85	0.21	Synergistic
200.0	15.63	0.99	5.12E-6	Synergistic
200.0	7.81	0.93	0.09	Synergistic
200.0	3.9	0.89	0.16	Synergistic
200.0	1.95	0.96	0.05	Synergistic
100.0	31.25	0.63	0.57	Synergistic
100.0	15.63	0.81	0.16	Synergistic
100.0	7.81	0.87	0.095	Synergistic
100.0	3.9	0.69	0.32	Synergistic
100.0	1.95	0.77	0.20	Synergistic
50.0	31.25	0.62	0.40	Synergistic
50.0	15.63	0.8	0.08	Synergistic
50.0	7.81	0.79	0.09	Synergistic
50.0	3.9	0.62	0.24	Synergistic
50.0	1.95	0.47	0.72	Synergistic
25.0	31.25	0.63	0.25	Synergistic
25.0	15.63	0.69	0.1	Synergistic
25.0	7.81	0.69	0.09	Synergistic
25.0	3.9	0.53	0.32	Synergistic
25.0	1.95	0.49	0.38	Synergistic
12.5	15.63	0.6	0.20	Synergistic
12.5	7.81	0.68	0.05	Synergistic
12.5	3.9	0.53	0.24	Synergistic

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