

The rhodamine isothiocyanate analogue as a quorum sensing inhibitor has the potential to control microbe-induced biofouling

Appendix: Supplementary information

Table S1. Alpha diversity of biofilm microbial in various groups. The parameter values are presented as the mean \pm standard deviation from five measurements.

Samples	Richness	Chao 1	Shannon	Simpson
A-36h	2847.4 \pm 719.6	2849.9 \pm 719.42	3.854 \pm 0.996	0.3424 \pm 0.1536
B-36h	2150.6 \pm 279.4	2153.8 \pm 278.96	3.332 \pm 0.278	0.2848 \pm 0.0492
C-36h	2968 \pm 577	2970.2 \pm 576.38	4.408 \pm 0.722	0.189 \pm 0.059
D-36h	2739.6 \pm 258.4	2742.3 \pm 259	3.522 \pm 0.668	0.3494 \pm 0.2156
E-36h	2674.4 \pm 343.6	2676.6 \pm 342.92	3.51 \pm 0.45	0.3704 \pm 0.1416
A-80h	3378.8 \pm 929.2	3381.0 \pm 929.94	6.302 \pm 0.238	0.04628 \pm 0.01082
B-80h	3122.2 \pm 632.8	3124.7 \pm 633.98	5.9 \pm 0.34	0.0649 \pm 0.0278
C-80h	3620.2 \pm 734.8	3622.5 \pm 735.1	6.596 \pm 0.734	0.0379 \pm 0.0126
D-80h	3618.6 \pm 976.4	3620.9 \pm 977.36	6.028 \pm 0.592	0.05584 \pm 0.01626
E-80h	3523.2 \pm 839.8	3525.4 \pm 840.42	6.356 \pm 0.414	0.04546 \pm 0.02084
A-180h	3960.2 \pm 300.8	3962.9 \pm 300.3	7.056 \pm 0.654	0.03476 \pm 0.02204
B-180h	3702.6 \pm 247.4	3705.4 \pm 247.16	6.794 \pm 0.406	0.0468 \pm 0.0313
C-180h	3955 \pm 815	3957.8 \pm 814.32	6.984 \pm 0.266	0.03292 \pm 0.01368
D-180h	4063.6 \pm 275.4	4066.2 \pm 274.96	7.336 \pm 0.164	0.02354 \pm 0.00616
E-180h	3935.8 \pm 363.2	3938.6 \pm 363.16	7.17 \pm 0.23	0.0265 \pm 0.0125

Figure S1. The phenotypic response of biofilm formation subjected to QSI substances. The representative images of biofilm following a 80-h incubation were shown. The signs for biofilm status are divided into three levels, namely ‘+’, mild biofouling; ‘++’, moderate biofouling; and ‘+++’, severe biofouling.

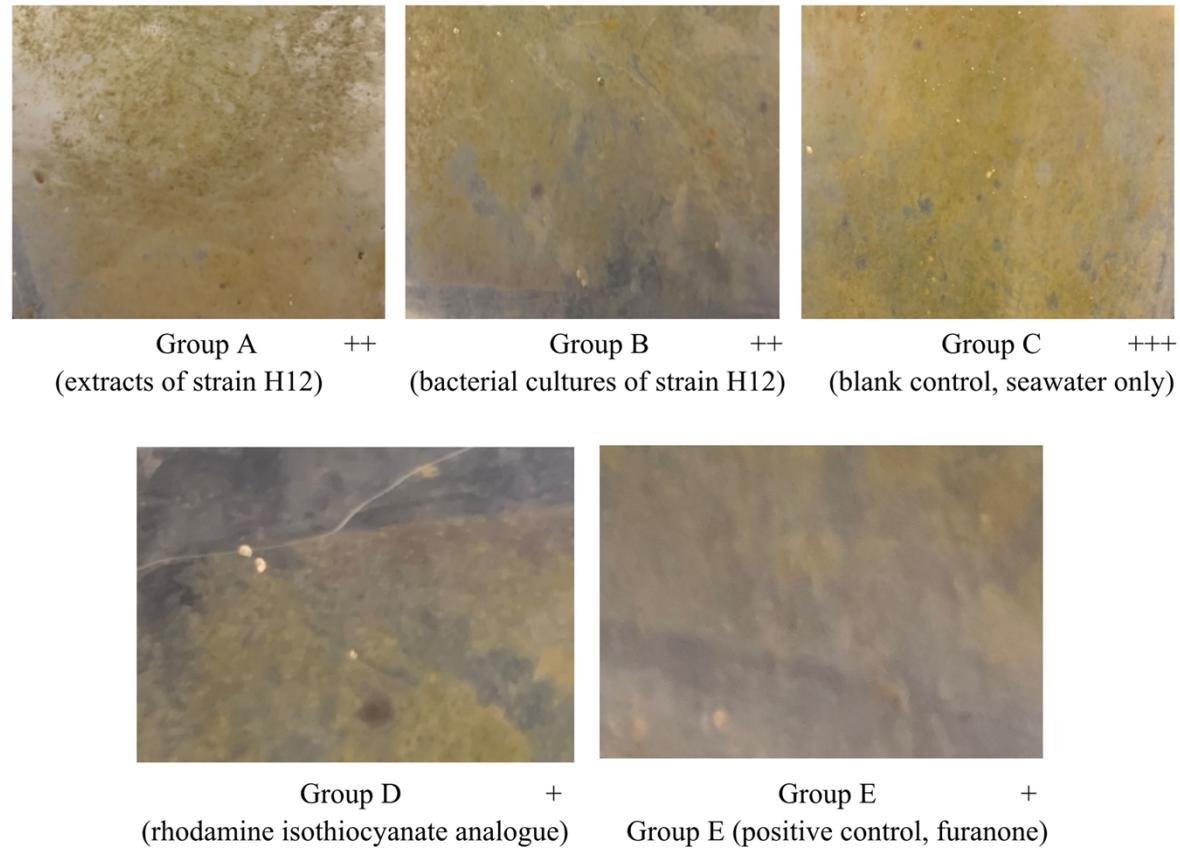
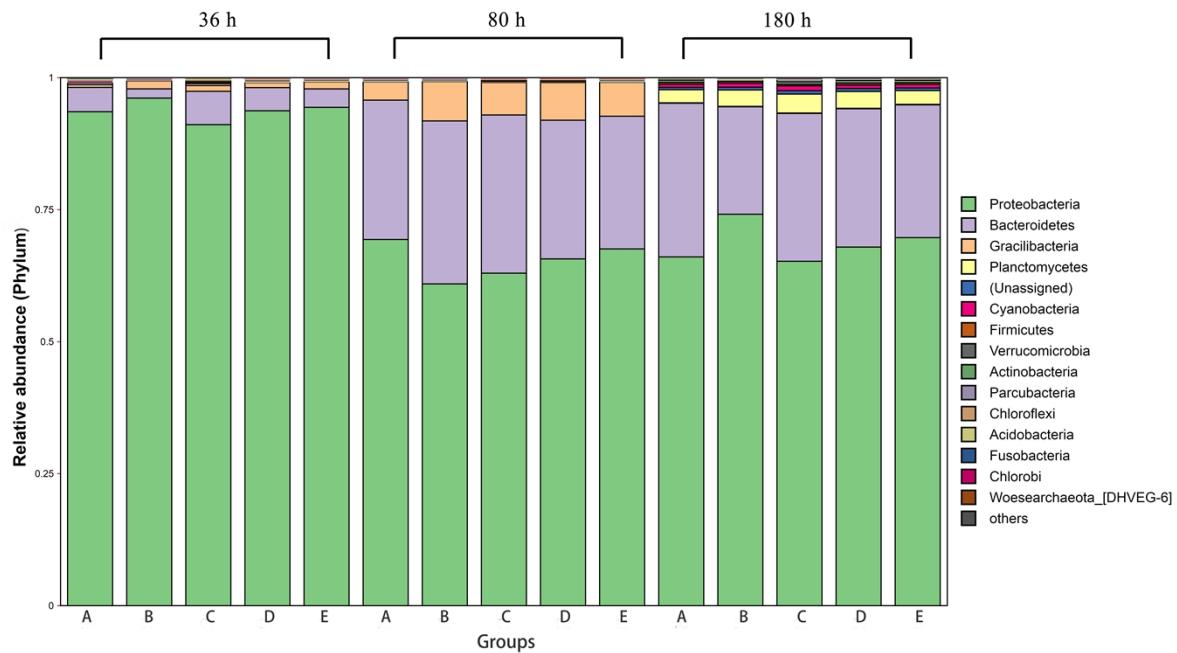


Figure S2. The microbiome structure of bacterial in five treatment groups across three time points at phylum (A) and family (B) levels .

A



B

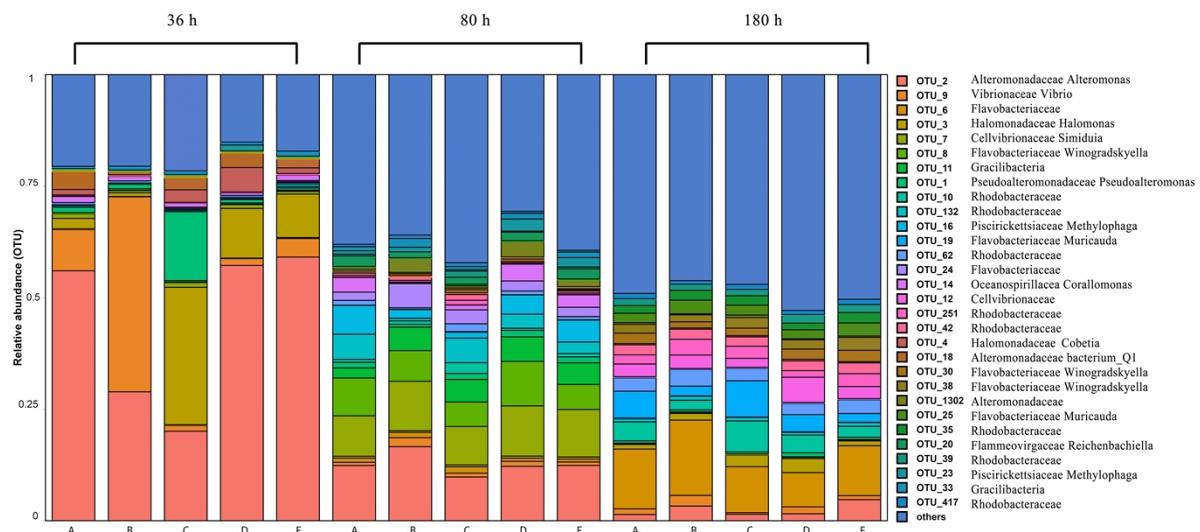


Figure S3. The effect of environmental parameters on microbial community.

