

Supplementary Information

Inhibitory Effects of Cinnamaldehyde Derivatives on Biofilm Formation and Virulence Factors in *Vibrio* Species

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Table S1. Minimum Inhibitory Concentration (MICs) of Cinnamaldehyde and its Derivatives Against *V. parahaemolyticus* and *V. harveyi*.

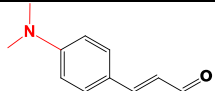
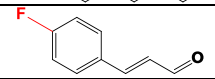
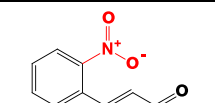
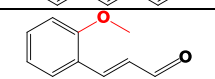
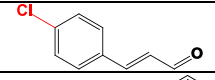
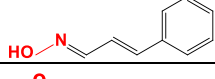
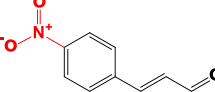
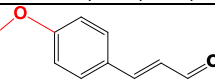
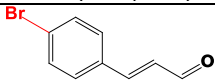
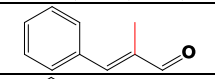
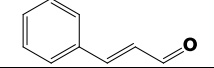
Chemical Name	Structure	<i>V. parahaemolyticus</i>	<i>V. harveyi</i>
4-DimethylaminoCNMA		>500	>500
4-FluoroCNMA		175	175
2-NitroCNMA		250	300
2-MethoxyCNMA		175	175
4-ChloroCNMA		50	50
CNMAoxime		>500	>500
4-NitroCNMA		50	50
4-MethoxyCNMA		300	275
4-BromoCNMA		50	50
α -MethylCNMA		>500	>500
CNMA		200	200

Table S2. Primer sequences for qRT-PCR.

Genes	Functions	Primer Sequences
<i>aphA</i>	Acid phosphatase AphA; Biofilm, motility	5'-ACACCCAACCGTTCGTGATG-3' 5'-GTTGAAGGCGTTGCGTAGTAAG-3'
<i>cpsA</i>	EPS production genes	5'-GCGCACAACGAAGAATATCG-3' 5'--3'CCATCTTATCGAGCGTGTCG
<i>luxI</i>	QS regulator	5'-GTG GAT GCT GGC GTT TAT TAC -3' 5'-TTT GGG AGC ACT CTG TTG AC -3'
<i>luxS</i>	Autoinducer binding domain- containing protein; QS	5'-GAT GGG ATG TCG CAC TGG TTT-3' 5'- ACT TGC TGT TCA GAA GGC GTA-3'
<i>mshA</i>	Type IV pilin MshA	5'-GGTTTCGTTTAGGTCACG -3' 5'-CGTCGAAATGTCGGCGG-3'
<i>opaR</i>	Transcriptional regulator OpaR; QS	5'-TGTCTACCAACCGCACTAACC-3' 5'-GCTCTTTCAACTCGGCTTCAC-3'
<i>oxyR</i>	DNA-binding transcriptional regulator OxyR; regulator of growth, biofilm formation and motility	5'-TCG TCA GCT AGA GGA AGG-3' 5'-TGG TCG CGT AAG CAA TGC-3'
<i>tnaA</i>	Tryptophanase	5'-TGA AGA AGT TGG TCC GAA TAA CGT G-3' 5'-CTT TGT ATT CTG CTT CAC GCT GCT T-3'
<i>qsvR</i>	an AraC-type transcriptional regulator QsvR; QS regulator to control virulence	5'-TAC ACC GCC ACC CAT AAC G-3' 5'-AGC CAT TCT CGC CAG GTA TG-3'
<i>fliA</i>	Motility/Chemotaxis	5'-TAAGCGTATTGCTCACCACCT-3' 5'-GCTCGCACCTTTAGAACCAT-3'
<i>tdh</i>	Thermostable direct hemolysin (TDH)	5'-GTAAAGGTCTCTGACTTTTGGAC-3' 5'-TGGAATAGAACCTTCATCTTCACC-3'
<i>vopS</i>	T3SS effector adenosine monophosphate-protein transferase VopS; virulence genes (secretion systems)	5'-AAGGTAGGGCAACGCAAAGA-3' 5'-AGCAGCACGACAGCAATACT-3'
<i>vmrA</i>	Sodium-coupled multidrug efflux MATE transporter VmrA	5'-GGTGTGTGTTTCGTGGTATTG-3' 5'-CTTGATGCTCGGTTCTACTG-3'
<i>vmeB</i>	Multidrug efflux RND transporter permease subunit VmeB	5'-CTGCGACCATTACACTGACTT-3' 5'-GTGTGTAAAGTCTGGATCGTC-3'
<i>ef-Tu</i>	Elongation factor Tu	5'-CACTAAACGGCGAAGAGCA-3' 5'-CCACGACCTTGGATTGAGAA-3'
<i>fadL</i>	Long-chain fatty acid outer membrane channel/bacteriophage T2 receptor	5'-ACGATAAAGGTCAGGAAATCAC-3' 5'-GTATTGGATGCTGTAATGTACGG-3'
<i>nusA</i>	Transcription termination factor NusA	5'-TGTTTATCACTCGTTCTAAGCCT-3' 5'-GTTTGTCAATTTGTTTTCCTGCG-3'
16S rRNA	Housekeeping gene	5'-TATCCTTGTGTTGCCAGCGAG-3' 5'-CTACGACGCACTTTTTGGGA-3'

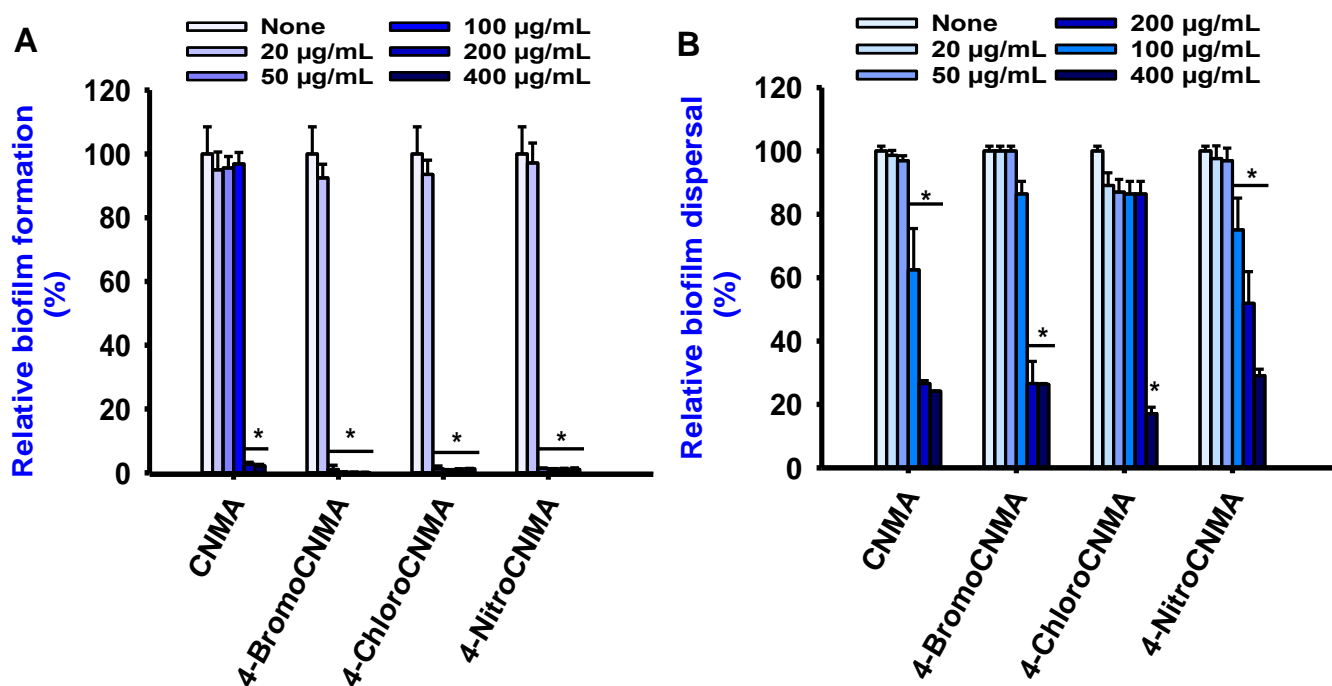


Figure S1. Antibiofilm activity of CNMA and its derivatives (A) and biofilm dispersing effects of CNMA and its derivatives against *V. parahaemolyticus* (B), * denotes a significant difference at $p < 0.05$.