

Supplementary Information

Table S1. Antimicrobial Activity of the *Pseudovibrio* RAPD group representatives against the pathogen *S. aureus* NCDO 949, with *Pseudovibrio* isolates grown on MA vs. SYP-SW.

<i>Pseudovibrio</i> Isolate	MA	SYP-SW
JIC5	++	<+
JIC6	++	-
JIC17	+	<+
W10	+	<+
W19	-	-
W62	++	+
W63	++	<+
W64	+++	<+
W65	++	+
W69	++	-
W71	+	<+
W74	++	<+
W85	++	<+
W78	+	<+
W89	+++	<+
W94	++	+
W96	+	<+
W99	++	<+
WM31	++	+
WM33	+	<+
WM34	++	<+
WM40	++	+
WM50	-	-
WC13	++	<+
WC15	+	-
WC21	++	<+
WC22	++	-
WC30	+	<+
WC32	++	-
WC41	++	+
WC43	++	<+
HC6	++	+
HMMA3	+	<+

Diameter Inhibition: <+ = <1 mm; + = ≥1 mm; ++ = ≥2 mm; +++ = ≥4 mm.

Table S2. Indicator strains used for testing bioactivity of marine isolates.

Strain	Description	Source/Reference
<i>Yersinia ruckerri</i>	Type strain	DSMZ [#]
<i>Edwardsiella tarda</i>	Type strain	DSMZ
<i>Vibrio anguillarum</i> LMG 4410	Type strain	DSMZ
<i>Escherichia coli</i> MUH 103	Clinical Isolate	MUH *
<i>Escherichia coli</i> NCIMB 15943	Type strain	MDCC UCC
<i>Morganella morganii</i> MUH 988	Clinical isolate	MUH
<i>Salmonella</i> Typhimurium LT2	Type strain	MDCC UCC
<i>Salmonella</i> Typhimurium C5369	Type strain	MDCC UCC
<i>Pandoraea sputorum</i> LMG18819	CF clinical Isolate	E. Caraher [§]
<i>Salmonella arizona</i> e	Type strain	Shinfield, UK/MDCC UCC
<i>Staphylococcus aureus</i> NCDO 949	Type strain	Shinfield, UK/MDCC UCC

DSM Collection, Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Braunschweig, Germany;

* Mercy University Hospital, Cork; [§] Centre of Microbial Host Interactions, ITT Dublin, Tallaght, Dublin 24, Ireland;

[^] Microbiology Department Culture Collection, University College Cork.

Table S3. A selection of marine sponge isolates were compound extracted for TDA production. Both sensitive and tolerant isolates were tested for TDA production.

	Isolate	Nearest Neighbour	TDA Producer *
Tolerant to TDA	B98C31	<i>Vibrio</i>	×
	B98C32	<i>Micrococcus</i>	×
	B98C34a	<i>Salinibacterium amurskyense</i>	×
	B98C36	<i>Halomonas boliviensis</i>	×
	B98C38	<i>Maribacter</i>	×
	B98C49	<i>Alteromonas</i>	×
	B98C52	<i>Planococcus</i>	×
	B98C53	<i>Salinibacterium</i>	×
	B98C53b	<i>Psychrobacter</i>	×
	B98C56	<i>Alcanivorax</i>	×
Sensitive to TDA	B98C69a	<i>Flavobacterium</i>	×
	B98S22a	<i>Oceanobacillus</i>	×
	B98C7	<i>Staphylococcus saprophyticus</i>	×
	B98C30a	<i>Marinobacter maritimus</i>	√
	B98C44a	<i>Idiomarina</i>	×
	B98SM7	<i>Rhodococcus</i>	×

* TDA production: × = no TDA; √ = yes TDA production.

Table S4. All-vs-all blastp similarity values between *tdaA* genes in the different species.

	tdaA_EF139200	tdaA_JE062 g1641	tdaA_PGA1 _262p00980	tdaA_PGA2 _239p0970	tdaA_PSE _2264	tdaA_Pden _1600	tdaA_W64 g2177	tdaA_W74 g3196	tdaA_WM33 g4179
tdaA_EF139200	100								
tdaA_JE062_g1641	48.7	100							
tdaA_PGA1_262p00980	42.29	65.88	100						
tdaA_PGA2_239p0970	43.28	66.22	98.65	100					
tdaA_PSE_2264	48.7	98.71	65.88	66.22	100				
tdaA_Pden_1600	41.12	53.12	54.73	55.4	53.12	100			
tdaA_W64_g2177	46.11	91.29	65.86	66.21	91.29	52.78	100		
tdaA_W74_g3196	46.11	91.29	65.86	66.21	91.29	52.78	100	100	
tdaA_WM33_g4179	46.11	90.97	65.86	66.21	90.97	51.32	99.03	99.03	100

Pseudovibrio sp. W64: tdaA_W64_g2177; *Pseudovibrio* sp. W74: tdaA_W74_g3196; *Pseudovibrio* sp. W33: tdaA_WM33_g4179; *Pseudovibrio* sp. FO-BEG1: tdaA_PSE_2264; *Pseudovibrio* sp. JE062: tdaA_JE062_g1641; *Phaeobacter gallaeciensis* DSM 17395: tdaA_PGA1_262p00980; *Phaeobacter gallaeciensis* 2.10: tdaA_PGA2_239p0970; *Ruegeria* sp. TM1040: tdaA_EF139200; *Paracoccus denitrificans* PD1222: tdaA_Pden_1600.

Table S5. All-vs-all blastp similarity values between *tdaB* genes in the different species.

	tdaB_EF139201	tdaB_JE062 g1639	tdaB_PGA1 _262p00970	tdaB_PGA2 _239p0960	tdaB_PSE _2263	tdaB_Pden _1599	tdaB_W64 g2176	tdaB_W74 g3195	tdaB_WM33 g4178
tdaB_EF139201	100								
tdaB_JE062_g1639	51.36	100							
tdaB_PGA1_262p00970	55.07	67.41	100						
tdaB_PGA2_239p0960	55.07	67.86	98.71	100					
tdaB_PSE_2263	50	94.83	66.52	66.96	100				
tdaB_Pden_1599	50.92	53.33	52.09	52.56	51.43	100			
tdaB_W64_g2176	51.85	83.17	61.81	61.81	82.21	50.79	100		
tdaB_W74_g3195	51.32	83.65	62.31	62.31	82.69	51.32	96.63	100	
tdaB_WM33_g4178	51.67	84.05	62.05	62.05	84.05	51.9	94.23	95.67	100

Pseudovibrio sp. W64: tdaB_W64_g2176; *Pseudovibrio* sp. W74: tdaB_W74_g3195; *Pseudovibrio* sp. W33: tdaB_WM33_g4178; *Pseudovibrio* sp. FO-BEG1: tdaB_PSE_2263; *Pseudovibrio* sp. JE062: tdaB_JE062_g1639; *Phaeobacter gallaeciensis* DSM 17395: tdaB_PGA1_262p00970; *Phaeobacter gallaeciensis* 2.10: tdaB_PGA2_239p0960; *Ruegeria* sp. TM1040: tdaB_EF139201; *Paracoccus denitrificans* PD1222: tdaB_Pden_1599.

Table S6. All-vs-all blastp similarity values between *tdaC* genes in the different species.

	tdaC_EF139202	tdaC_JE062_g1638	tdaC_PGA1_262p00960	tdaC_PGA2_239p0950	tdaC_PSE_2261	tdaC_Pden_1615	tdaC_W64_g2175	tdaC_W74_g3194	tdaC_WM33_g4176
tdaC_EF139202	100								
tdaC_JE062_g1638	57.72	100							
tdaC_PGA1_262p00960	60.12	71.76	100						
tdaC_PGA2_239p0950	60.12	71.76	99.5	100					
tdaC_PSE_2261	58.92	98.1	69.23	67.19	100				
tdaC_Pden_1615	55.09	60.31	64.33	64.33	60.23	100			
tdaC_W64_g2175	60	89.87	68.21	64.55	88.43	58.48	100		
tdaC_W74_g3194	60	89.87	68.21	64.55	88.43	58.48	100	100	
tdaC_WM33_g4176	59.06	89.87	67.94	67.94	89.24	57.25	98.1	98.1	100

Pseudovibrio sp. W64: tdaC_W64_g2175; *Pseudovibrio* sp. W74: tdaC_W74_g3194; *Pseudovibrio* sp. W33: tdaC_WM33_g4176; *Pseudovibrio* sp. FO-BEG1: tdaC_PSE_2261; *Pseudovibrio* sp. JE062: tdaC_JE062_g1638; *Phaeobacter gallaeciensis* DSM 17395: tdaC_PGA1_262p00960; *Phaeobacter gallaeciensis* 2.10: tdaC_PGA2_239p0950; *Ruegeria* sp. TM1040: tdaC_EF139202; *Paracoccus denitrificans* PD1222: tdaC_Pden_1615.

Table S7. All-vs-all blastp similarity values between *tdaD* genes in the different species.

	tdaD_EF139203	tdaD_JE062_g1637	tdaD_PGA1_262p00950	tdaD_PGA2_239p0940	tdaD_PSE_2260	tdaD_Pden_1614	tdaD_W64_g2174	tdaD_W74_g3193	tdaD_WM33_g4175
tdaD_EF139203	100								
tdaD_JE062_g1637	78.52	100							
tdaD_PGA1_262p00950	71.85	80.88	100						
tdaD_PGA2_239p0940	71.85	80.88	99.28	100					
tdaD_PSE_2260	78.52	99.31	80.88	80.88	100				
tdaD_Pden_1614	65.19	74.07	68.84	68.12	74.07	100			
tdaD_W64_g2174	77.04	93.06	80.43	80.43	92.36	72.59	100		
tdaD_W74_g3193	77.04	93.06	80.43	80.43	92.36	72.59	100	100	
tdaD_WM33_g4175	77.04	93.06	80.88	80.88	92.36	72.59	97.92	97.92	100

Pseudovibrio sp. W64: tdaD_W64_g2174; *Pseudovibrio* sp. W74: tdaD_W74_g3193; *Pseudovibrio* sp. W33: tdaD_WM33_g4175; *Pseudovibrio* sp. FO-BEG1: tdaD_PSE_2260; *Pseudovibrio* sp. JE062: tdaD_JE062_g1637; *Phaeobacter gallaeciensis* DSM 17395: tdaD_PGA1_262p00950; *Phaeobacter gallaeciensis* 2.10: tdaD_PGA2_239p0940; *Ruegeria* sp. TM1040: tdaD_EF139203; *Paracoccus denitrificans* PD1222: tdaD_Pden_1614.

Table S8. All-vs-all blastp similarity values between *tdaE* genes in the different species.

	tdaE_EF139204	tdaE_JE062 _g1636	tdaE_PGA1 _262p00940	tdaE_PGA2 _239p0930	tdaE_PSE _2259	tdaE_Pden _1613	tdaE_W64 _g2173	tdaE_W74 _g3192	tdaE_WM33 _g4174
tdaE_EF139204	100								
tdaE_JE062_g1636	69.05	100							
tdaE_PGA1_262p00940	66.86	68.34	100						
tdaE_PGA2_239p0930	67.14	68.84	97.73	100					
tdaE_PSE_2259	68.77	98.99	68.59	68.59	100				
tdaE_Pden_1613	63.71	64.29	64.94	65.19	64.29	100			
tdaE_W64_g2173	68.77	93.97	69.04	69.29	93.72	63.5	100		
tdaE_W74_g3192	68.48	93.47	69.04	69.29	93.47	63.5	99.25	100	
tdaE_WM33_g4174	68.48	93.72	69.04	69.29	93.72	63.5	99.5	99.75	100

Pseudovibrio sp. W64: tdaE_W64_g2173; *Pseudovibrio* sp. W74: tdaE_W74_g3192; *Pseudovibrio* sp. W33: tdaE_WM33_g4174; *Pseudovibrio* sp. FO-BEG1: tdaE_PSE_2259; *Pseudovibrio* sp. JE062: tdaE_JE062_g1636; *Phaeobacter gallaeciensis* DSM 17395: tdaE_PGA1_262p00940; *Phaeobacter gallaeciensis* 2.10: tdaE_PGA2_239p0930; *Ruegeria* sp. TM1040: tdaE_EF139204; *Paracoccus denitrificans* PD1222: tdaE_Pden_1613.

Table S9. All-vs-all blastp similarity values between *tdaF* genes in the different species.

	tdaF_EF139205	tdaF_JE062 _g1624	tdaF_PGA1 _262p00810	tdaF_PGA2 _239p0800	tdaF_PSE _2247	tdaF_Pden _1605	tdaF_W64 _g2160	tdaF_W74 _g3180	tdaF_WM33 _g4161
tdaF_EF139205	100								
tdaF_JE062_g1624	70.56	100							
tdaF_PGA1_262p00810	71.51	70.65	100						
tdaF_PGA2_239p0800	71.51	70.65	100	100					
tdaF_PSE_2247	70.56	99.5	70.65	70.65	100				
tdaF_Pden_1605	53.63	55.31	51.61	51.61	54.75	100			
tdaF_W64_g2160	70	96.98	70.11	70.11	96.48	54.75	100		
tdaF_W74_g3180	70	97.49	70.65	70.65	96.98	54.75	98.49	100	
tdaF_WM33_g4161	70.56	97.49	70.65	70.65	96.98	54.75	99.5	98.99	100

Pseudovibrio sp. W64: tdaF_W64_g2160; *Pseudovibrio* sp. W74: tdaF_W74_g3180; *Pseudovibrio* sp. W33: tdaF_WM33_g4161; *Pseudovibrio* sp. FO-BEG1: tdaF_PSE_2247; *Pseudovibrio* sp. JE062: tdaF_JE062_g1624; *Phaeobacter gallaeciensis* DSM 17395: tdaF_PGA1_262p00810; *Phaeobacter gallaeciensis* 2.10: tdaF_PGA2_239p0800; *Ruegeria* sp. TM1040: tdaF_EF139205; *Paracoccus denitrificans* PD1222: tdaF_Pden_1605.

Table S10. Genes amplified, primer sequences and probes used in RT-PCR experiments.

Gene	Primer Sequence (5'-3')	Universal Probe Library Number
<i>gyrB</i>	aacgtcgaccctgaaaat tggaaatctgcaccgtattca	15
<i>tdaA</i>	gtcttgccggtagcctgac caagcagattgctcacaacg	67
<i>tdaB</i>	ttatgtactgttcggcaccttg cactcgaggagaatttgg	44
<i>tdaC</i>	gcaagtccgtttgctgaga ccgatgtgctcgtaataatttgg	144
<i>tdaD</i>	tttgagatgcagcatgaaatg tgagtggaaagctgcattttgg	9
<i>tdaE</i>	gttcggctgtgacgctcctga gaaggctctgagctcctga	161
<i>tdaF</i>	acacccaatgccatcaactt ttatcggtggaccaggcttttc	56

Figure S1. (A) 400× microscopy of W74 cells after 6 h of growth, before brown pigment production. Cells exist here in a planktonic form; (B) shows cell aggregation at 24 h, subsequent to colour change.

