The following appendix accompanies the article

Recruitment of the sea urchin *Heliocidaris erythrogramma* and the distribution and abundance of inducing bacteria in the field

Megan J. Huggett[1,2,4,*], Gregory R. Crocetti[2,3], Staffan Kjelleberg[2,3], Peter D. Steinberg[1,2]

[1]School of Biological, Earth and Environmental Sciences (BEES), [2]Centre for Marine Biofouling and Bio-Innovation, and [3]School of Biotechnology and Biomolecular Sciences (BABS), University of New South Wales, Sydney 2052, Australia

[4]*Present address:* Hawaii Institute of Marine Biology, University of Hawaii at Manoa, PO Box 1346, Kaneohe, Hawaii 96744, USA

*Email: huggett@hawaii.edu

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Appendix 1. Information on the probes targeting the 3 genera *Pseudoalteromonas*, *Vibrio* and *Shewanella*

Table A1. Alignment of the VIB572a probe target sequence with 16S rRNA sequences from organisms and clones. Strains used as positive and negative controls in determination of optimal formamide concentration with VIB572a are shown in bold. Dashes indicate matches to the target sequence

	16S rRNA target sequence (572–589)
VIB572a probe target	AAAGCGCAUGCAGGUGGU
***Vibrio harveyii* (DQ0055908)**	– – – – – – – – – – – – – – – – – – [a]
***Vibrio alginolyticus* (DQ005910)**	– – – – – – – – – – – – – – – – – – [a]
***Photobacterium phosphoreum* (DQ099331)**	– – – – – – – – – – – – – C – – – [a]
***Aeromonas salmonicida* ACM2475 (DQ099332)**	– – – – – – – – – C – – – – C – – –
Cellvibrio mixtus (AF448515**)**	– – – – – – – – – C – U – – – – – –

[a]Determined in the present study

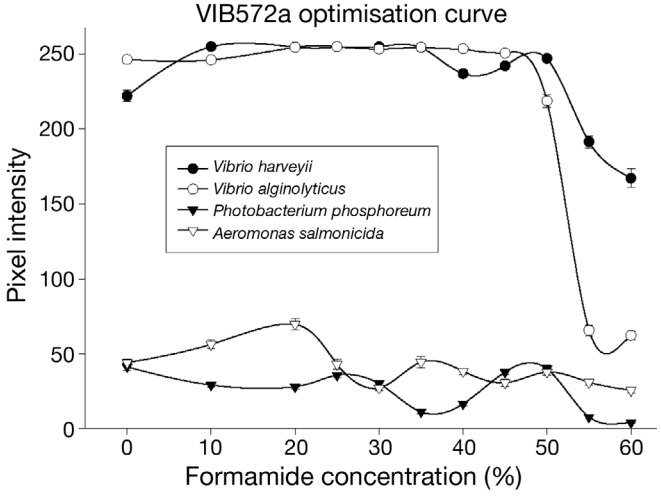

Fig. A1. Optimisation curves for development of *Vibrio* FISH probe VIB572a

Table A2. Alignment of the SHEW227 probe target sequence with 16S rRNA sequences from organisms and clones. Strains used as positive and negative controls in determination of optimal formamide concentration with SHEW227 are shown in bold. Dashes indicate matches to the target sequence

	16S rRNA target sequence (227–249)
SHEW227 probe target	GATGwACCTAGGTGGGATTAGCT [a]
***Shewanella* sp. A317 (DQ005868)** – isolated from *Amphiroa anceps*	– – –T– – – – – – – – – – – – – – – – – – – [b]
***Shewanella* sp. C111 (DQ005889)** – isolated	– – –A– – – – – – – – – – – – – – – – – – – [b]
Vibrio harveyii (DQ005908)[c]	– – –A– G – – – – – – – – – – – – – – – – – [b]
***Aeromonas salmonicida* ACM2475 (DQ099332)**	– – –A– – – C – – – – – – – – – – – – – – –
Pseudomonas stutzeri (U26418)	– – – –AG – – – – – – – –C– – – – – – – – –

[a]W = A/T
[b]Determined in the present study
[c]Reverse complement of cSHEW227 probe

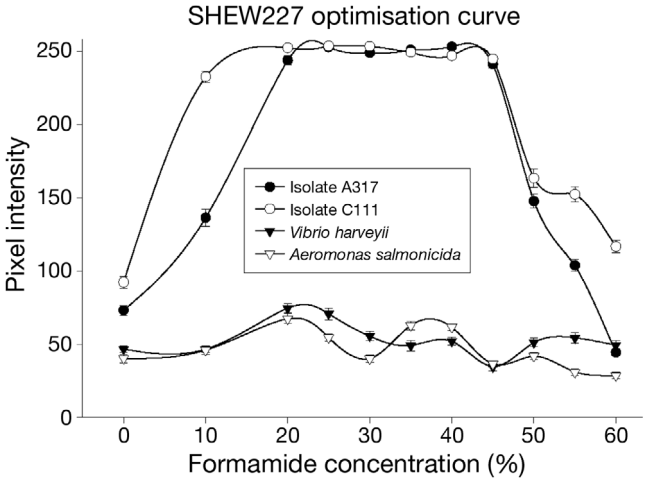

Fig. A2. Optimisation curve for development of *Shewanella* FISH probes SHEW227

Table A3. Alignment of the PSU730 probe target sequence with 16S rRNA sequences from organisms and clones. Strains used as positive and negative controls in determination of optimal formamide concentration with PSU730 are shown in bold. Dashes indicate matches to the target sequence

	16S rRNA target sequence (730–747)
PSU730 probe target	GGCAGCCACCTGGGTCAA
***Pseudoalteromonas* sp. A213 (DQ005864)**	– – – – – – – – – – – – – – – – – – [a]
***Pseudoalteromonas tunicata* D2 (DQ005902)**	– – – – – – – – – – – – – – – – – –
***Telluria mixta* ACM1762 (DQ005909)**	– – – – – – – – – – – – – – – – – – [a]
Azovibrio restrictus (AF011348)	– – – – – – – C – – – – – – – – G –
Rhodocyclus tenuis (D16208)	– – – – – – – C – – – – – – C – – –

[a]Isolated from *Amphiroa anceps* in the present study

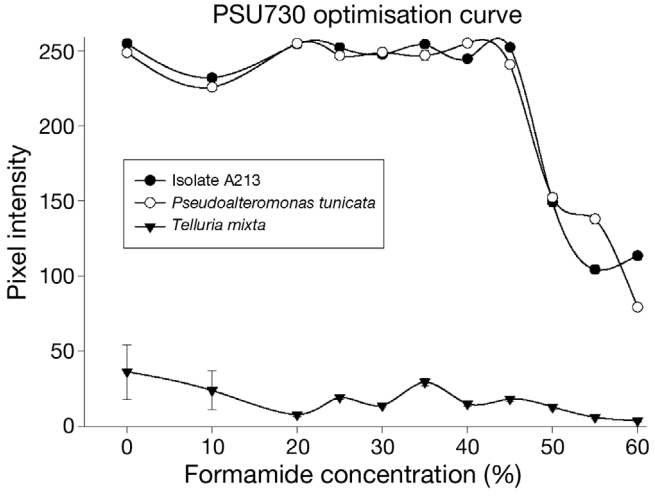

Fig. A3. Optimisation curve for development of *Pseudoalteromonas* FISH probe PSU730