**Table S1.** Oligonucleotide probes targeting 16S rRNA from bacteria of the *Vibrio* genus (collected in the scientific literature of the last 20 years). They are shown for each of the probes: the sequence, the population with which they hybridize and the reference.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **PROBE** | **SEQUENCE (5’→3’)** | **HYBRIDIZATION** | **REFERENCE** | | |
| GV841 | AGGCCACAACCTCCAAGTAG | *Vibrio* genus (except *V. cholerae* and *V. mimicus*) | | 1-5 |
| MS6 | AGTTTTACATTTGCGACC | *V. shiloi* | | 6 |
| Vchomin 1276 | ACTTTGTGAGATTCGCTCCACCTCG | *V. cholerae, V. mimicus* | | 7-9 |
| VIB | ACAGTACTCTAGTCTGCCAG | *Vibrio* genus | | 10,11 |
| Vib 1 | GTGGTAGTGTTAATAGCACT | *V. vulnificus* | | 12 |
| Vib 2 | TCTAGCGGAGACGCTGGA | *V. vulnificus* | | 12 |
| Vib 3R | GCTCACTTTCGCAAGTTGGCC | *V. vulnificus* | | 12 |
| Vib-16S-1 | AGGAGCTTCGCTTGC | *Vibrio* genus | | 13 |
| VIB572a | ACCACCTGCATGCGCTTT | *Vibrio* genus (occasionally *Photobacterium* and *Listonella)* | | 5,14-16 |
| VIB572b | ACCGCCTGCATGCGCTTT | *Vibrio, Photobacterium* | | 14 |
| Vib749 | TCGCATCTGAGTGTCAGT | *Vibrio, Aliivibrio* | | 5 |
| Vvul3 | TCCTCACGACTGAAAG | *V. vulnificus* | | 7 |

1. Giuliano, L.; De Domenico, M.; De Domenico, E.; Höfle, M.; Yakimov, M. Identification of culturable oligotrophic bacteria within naturally occurring bacterioplankton communities of the Ligurian Sea by 16S rRNA sequencing and probing. *Microb. Ecol.* **1999**, *37*, 77-85. doi: 10.1007/s002489900132.

2. Arboleda. M.; Reichardt, W. Epizoic communities of prokaryotes on healthy and diseased scleractinian corals in Lingayen Gulf, Philippines. *Microb. Ecol.* **2009***, 5:*117-28. doi: 10.1007/s00248-008-9400-0.

3. Tada, Y.; Taniguchi, A.; Hamasaki, K. Phylotype-specific productivity of marine bacterial populations in eutrophic seawater, as revealed by bromodeoxyuridine immunocytochemistry combined with fluorescence in situ hybridization. *Microbes Environ.* **2009**, *24*, 315-321. doi: 10.1007/s00248-008-9400-0.

4. Oberbeckmann, S.; Fuchs, B.M.; Meiners, M.; Wichels, A.; Wiltshire, K.H.; Gerdts, G. Seasonal dynamics and modeling of a *Vibrio* community in coastal waters of the North Sea. *Microb. Ecol.* **2012**. *63*, 543-551. doi: 10.1007/s00248-011-9990-9.

5. Girard, L.; Peuchet, S.; Servais, P.; Henry, A.; Charni-Ben-Tabassi, N.; Baudart, J. Spatiotemporal dynamics of total viable *Vibrio* spp. in a NW Mediterranean coastal area. *Microbes Environ.* **2017**, *32*, 210-218. doi: 10.1264/jsme2.ME17028.

6. Sussman, M.; Loya, Y.; Fine, M.; Rosenberg, E. The marine fireworm *Hermodice carunculata* is a winter reservoir and spring-summer vector for the coral-bleaching pathogen *Vibrio shiloi*. *Environ. Microbiol.* **2003**, *5*, 250–255. doi: 10.1046/j.1462-2920.2003.00424.x

7. Heidelberg, J.F.; Heidelberg, K.B.; Colwell, R.R. Bacteria of the gamma-subclass Proteobacteria associated with zooplankton in Chesapeake Bay. *Appl. Environ. Microbiol.* **2002**, *68*, 5498–5507. doi: 10.1128/aem.68.11.5498-5507.2002.

8. Kirschner, A.K.T.; Schauer, S.; Steinberger, B.; Wilhartitz, I.; Grim, C.J.; Huq, A.; Colwell, R.R.; Herzig, A.; Sommer, R. Interaction of *Vibrio cholerae* non-O1/non-O139 with Copepods, Cladocerans and competing bacteria in the Large Alkaline Lake Neusiedler See, Austria. *Microb. Ecol.* **2010**, *61*, 496-506. doi: 10.1007/s00248-010-9764-9

9. Schauer, S.; Sommer, R. ; Farnleitner, A.H.; Kirschner, A.K. Rapid and sensitive quantification of *Vibrio cholerae* and *Vibrio mimicus* cells in water samples by use of Catalyzed Reporter Deposition Fluorescence In Situ Hybridization combined with Solid-Phase Cytometry. *Appl. Environ. Microbiol.* **2012**, *78*, 7369–7375. doi: 10.1128/AEM.02190-12.

10. Moreno, Y.; Arias, C.R.; Meier, H.; Garay, E.; Aznar, R. *In situ* analysis of the bacterial communities associated to farmed eel by whole-cell hybridization. *Lett. Appl. Microbiol.* **1999**, *29*, 160–165. doi: 10.1046/j.1365-2672.1999.00588.x.

11. Cañigral Cárcel, I. Desarrollo de métodos moleculares para la detección y caracterización de bacterias patógenas emergentes del género *Vibrio* en aguas y alimentos. PhD Thesis, Universitat Politècnica de València, Spain, **2011**.

12. Kim, M.S.; Jeong, H.D. Development of 16S rRNA targeted PCR methods for the detection and differentiation of *Vibrio vulnificus* in marine environments. *Aquaculture.* **2001**, *193*, 199-211. doi: 10.1016/S0044-8486(00)00495-6.

13. Zhang, X.; Li, K.; Wu, S.; Shuai, J.; Fang, W. Peptide nucleic acid fluorescence in-situ hybridization for identification of *Vibrio* spp. in aquatic products and environments. *Int. J. Food Microbiol.* **2015**, *206*, 39-44. doi: 10.1016/j.ijfoodmicro.2015.04.017.

14. Huggett, M.J.; Crocetti, G.R.; Kjelleberg, S.; Steinberg, P.D. Recruitment of the sea urchin *Heliocidaris erythrogramma* and the distribution and abundance of inducing bacteria in the field. *Aquat. Microb. Ecol.* **2008**, *53*, 161-171. doi: 10.3354/ame01239.

15. Pereira, C.; Salvador, S.; Arrojado, C.; Silva, Y.; Santos, A.L.; Cunha, A.; Gomes, N.C.M.; Almeida, A. Evaluating seasonal dynamics of bacterial communities in marine fish aquaculture: a preliminary study before applying phage therapy. *J. Environ. Monit*. **2011**, *13*, 1053-1058. doi: 10.1039/C0EM00434K.

16. Bellés-Garulera, J.; Vila, M.; Borrull, E.; Riobó, P.; Franco, J.M.; Sala, M.M. Variability of planktonic and epiphytic vibrios in a coastal environment affected by *Ostreopsis* blooms. *Sci. Mar*. **2016**, *80S1*, 97-106. doi: 10.3989/scimar.04405.01A..

**Table S2.** Coverage and specificity, expressed as percentages, for the probes GV841, Vib-16S-1 and VIB572a (SILVA database). Those taxa whose values exceed 75% for both characteristics are shown.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **TAXA** | **PROBES** | | | | | |
| **GV 841** | | **Vib-16S-1** | | **VIB572a** | |
| **Coverage**  **(%)** | **Specificity (%)** | **Coverage (%)** | **Specificity (%)** | **Coverage (%)** | **Specificity (%)** |
| Alteromonadales; Alteromonadaceae; *Gayadomonas* | 0 | 0 | 100 | 99.3 | 0 | 0 |
| Alteromonadales; Gallaecimonadaceae; *Gallaecimonas* | 0 | 0 | 100 | 99.3 | 0 | 0 |
| Enterobacteriales; Enterobacteriaceae; endosymbionts10 | 0 | 0 | 100 | 99.3 | 0 | 0 |
| Vibrionales; Vibrionaceae; *Candidatus Photodesmus* | 50 | 99.3 | 100 | 99.3 | 25 | 99.3 |
| Aeromonadales; Aeromonadaceae; *Oceanisphaera* | 0 | 0 | 94.4 | 99.3 | 0 | 0 |
| Pasteurellales; Pasteurellaceae; *Avibacterium* | 0 | 0 | 94.1 | 99.3 | 0 | 0 |
| Alteromonadales; Alteromonadaceae; *Catenovulum* | 0 | 0 | 92.3 | 99.3 | 0 | 0 |
| Vibrionales; Vibrionaceae; *Vibrio* | 89.9 | 99.9 | 92.1 | 99.9 | 94 | 100 |
| Vibrionales | 78 | 100 | 76.1 | 99.9 | 78.9 | 100 |
| Vibrionales; Vibrionaceae | 78 | 100 | 76.1 | 99.9 | 78.9 | 100 |
| Vibrionales; Vibrionaceae; *Aliivibrio* | 60.2 | 99.4 | 1.4 | 99.3 | 95.6 | 99.4 |
| Vibrionales; Vibrionaceae; *Catenococcus* | 93.8 | 99.3 | 56.3 | 99.3 | 93.8 | 99.3 |

**Table S3.** Coverage (QC, query cover, %), identity (Ident, %), matches (Match) and E value (being the probability of finding the sequence - among all organisms - within this database), for the probes GV841, Vib-16S-1 and VIB572a (BLAST database). Those taxa whose values exceed 75% in coverage and identity for any of the three probes analyzed are shown.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **PROBES** | | | | | | | | | | | | |
|  | **GV 841** | | | | **Vib-16S-1** | | | | **VIB572a** | | | | |
| **TAXA** | **QC** | **Ident** | **Match** | **E** | **QC** | **Ident** | **Match** | **E** | | **QC** | **Ident** | **Match** | **E** | |
| Alteromonadales; Alteromonadaceae; *Gayadomonas* | 75 | 100 | 8/20 | 0.53 | 43 | 100 | 7/16 | 2.7 | | 94 | 88.24 | 15/18 | 0.11 | |
| Alteromonadales; Gallaecimonadaceae; *Gallaecimonas* | 70 | 92.86 | 13/20 | 25 | 43 | 100 | 7/16 | 774\* | | 77 | 92.86 | 13/18 | 19\* | |
| Enterobacteriales; Enterobacteriaceae; endosymbionts10 | 100-90 | 100 | 20/20-18/20 | 0.025-0.40 | 87 | 100 | 14/16 | 100\* | | 77 | 100 | 14/18 | 99\* | |
| Vibrionales; Vibrionaceae; *Candidatus Photodesmus* | 100 | 100 | 20/20 | 4 10-7\* | 62 | 100 | 7/16 | 13 | | 100 | 100 | 18/18 | 5 10-6\* | |
| Aeromonadales; Aeromonadaceae; *Oceanisphaera* | 45 | 100 | 9/20 | 138 | 100 | 100 | 12/16 | 0.029\* | | 77 | 92.86 | 13/18 | 30\* | |
| Pasteurellales; Pasteurellaceae; *Avibacterium* | 40 | 100 | 8/20 | 449\* | 100 | 100 | 12/16 | 1\* | | 44 | 100 | 10/18 | 385\* | |
| Alteromonadales; Alteromonadaceae; *Catenovulum* | 40 | 100 | 8/20 | 497\* | 100 | 100 | 8/16 | 0.3\* | | 94 | 88.24 | 15/18 | 108\* | |
| Vibrionales; Vibrionaceae; *Vibrio* | 100 | 100 | 20/20 | 0,004 | 100 | 100 | 16/16 | 0.49\* | | 100 | 100 | 18/18 | 0.031 | |
| Vibrionales | 100 | 100 | 20/20 | 0.004 | 100 | 100 | 16/16 | 0.51\* | | 100 | 100 | 18/18 | 0.033 | |
| Vibrionales; Vibrionaceae | 100 | 100 | 20/20 | 0,004 | 100 | 100 | 16/16 | 0,51\* | | 100 | 100 | 18/18 | 0.033 | |
| Vibrionales; Vibrionaceae; *Aliivibrio* | 100 | 100 | 20/20 | 1 10-4 | 100 | 100 | 13/16 | 0,92\* | | 100 | 100 | 18/18 | 0.002 | |
| Vibrionales; Vibrionaceae; *Catenococcus* | 100 | 100 | 20/20 | 2 10-7 | 50 | 100 | 7/16 | 6.7 | | 100 | 100 | 18/18 | 2 10-6 | |

\* The probe is complementary to non-16S rRNA genome regions.