**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 |

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**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.