Cultivable microbiota associated with *Aurelia aurita* and *Mnemiopsis leidyi*

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Abstract
The associated microbiota of marine invertebrates plays an important role to the host in relation to fitness, health, and homeostasis. Cooperative and competitive interactions between bacteria, due to release of, for example, antibacterial substances and quorum sensing (QS)/quorum quenching (QQ) molecules, ultimately affect the establishment and dynamics of the associated microbial community. Aiming to address interspecies competition of cultivable microbes associated with emerging model species of the basal animal phyla Cnidaria (*Aurelia aurita*) and Ctenophora (*Mnemiopsis leidyi*), we performed a classical isolation approach. Overall, 84 bacteria were isolated from *A. aurita* medusae and polyps, 64 bacteria from *M. leidyi*, and 83 bacteria from ambient seawater, followed by taxonomically classification by 16S rRNA gene analysis. The results show that *A. aurita* and *M. leidyi* harbor a cultivable core microbiome consisting of typical marine ubiquitous bacteria also found in the ambient seawater. However, several bacteria were restricted to one host suggesting host-specific microbial community patterns. Interbacterial interactions were assessed by (a) a growth inhibition assay and (b) QS interference screening assay. Out of 231 isolates, 4 bacterial isolates inhibited growth of 17 isolates on agar plates. Moreover, 121 of the 231 isolates showed QS-interfering activities. They interfered with the acyl-homoserine lactone (AHL)-based communication, of which 21 showed simultaneous interference with autoinducer 2. Overall, this study provides insights into the cultivable part of the microbiota associated with two environmentally important marine non-model organisms and into interbacterial interactions, which are most likely considerably involved in shaping a healthy and resilient microbiota.

**KEYWORDS**
*Aurelia aurita*, cultivation, gelatinous zooplankton, *Mnemiopsis leidyi*, quorum quenching

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1 | INTRODUCTION

The marine environment covers more than 70% of the world’s surface and harbors approximately $3.6 \times 10^{28}$ microorganisms (Ammann, Ludwig, & Schleifer, 1995; Flemming & Wuertz, 2019; Magnabosco et al., 2018; Whitman, Coleman, & Wiebe, 1998). Marine microbial communities are highly diverse and have evolved under a variety of ecological conditions and selection pressures (Haubold & Rheinheimer, 1992). Those microbes are also known to form beneficial symbiotic relationships with various marine multicellular hosts, for example, sponges, corals, squids, and jellyfishes, and are assumed to produce unique biologically active compounds important for the homoeostasis of the host, which are additionally often pharmaceutically valuable compounds (Bosch & McFall-Ngai, 2011; McFall-Ngai et al., 2013). Recently, the potential role of associated microbiota became an important research focus in the fields of zoology, botany, ecology, and medicine, since each multicellular organism can be regarded as an entity with its associated microbes as a so-called “metaorganism” or “holobiont.” The microbes most likely have crucial functions for fitness and health of the host (Bosch & McFall-Ngai, 2011; McFall-Ngai et al., 2013), in addition to their function for the ecological role of the metaorganism in the respective environment. The role of bacteria during the development of various organisms, such as humans, as well as their importance for the host’s resilience in the control of pathogens and prevention of inflammatory diseases, has been intensively studied in recent years (reviewed in (Sommer, Anderson, Bharti, Raes, & Rosenstiel, 2017)). These studies also showed that the interactions within a metaorganism are complex. In order to understand this complexity, research studies addressing the impact of the microbiota on a host have mostly utilized well-studied model organisms, such as the Drosophila and mouse model. To understand the long-term evolutionary origin of the metaorganism, however, additional (model) organisms are urgently needed (Dawson & Martin, 2001; Jaspers, Fraune, et al., 2019). Here, evolutionarily ancient organisms, which are located at the base of the metazoan tree of life, are expected to provide important insight into host-microbe interactions. Two basal metazoan species, which are widely distributed in marine environments, partly due to their large adaptability (Dawson & Jacobs, 2001; Jaspers, Huwer, Weiland-Bräuer, & Clemmesen, 2018), are the moon jellyfish Aurelia aurita and the comb jelly Mnemiopsis leidyi (Figure 1a). Their ecological impacts are widely recognized (Bayha & Graham, 2014; Jaspers, Huwer, Antajan, et al., 2018), but the characterization of their associated microbial communities and interactions lacks behind; however, the relatively simple morphology with only two tissue layers as surfaces for microbial colonization definitely allows for such studies.

A. aurita is one of the most widely distributed Scyphozoans (Cnidaria) featuring a complex life cycle. In its diphasic life cycle, A. aurita alternates between a free-living pelagic medusa and a sessile polyp (McFall-Ngai et al., 2013). In its different successive stages of

![Figure 1](image-url)
life cycle—planula larva, sessile polyp, pelagic ephyra, and medusa—A. aurita is adapted to different marine environmental factors, for example, salinity, temperature, and food spectrum (Fuqua, Winans, & Greenberg, 1996). In a recent study, we disclosed that those different life stages and different compartments of a medusa as well as different subpopulations harbor distinct, specific microbiota (Weiland-Brauer, Neulinge, et al., 2015). The comb jelly M. leidiyi (Ctenophora) is one of the most successful invasive marine species worldwide (Bayha & Graham, 2014). M. leidiyi features an unusual mode of reproduction so-called dissozygosis (Jaspers et al., 2012), where small larval stages before metamorphosis are already sexually reproducing, while they also reproduce again after metamorphosis in the adult stage as simultaneous hermaphrodites (Sasson & Ryan, 2016). Although those jellies possess only two tissue layers for bacterial colonization, interactions at those interfaces can be manifold and take place between the host and the colonizing bacteria and among the bacteria.

Current molecular high-throughput techniques, like deep sequencing, are preferred methods to analyze such complex microbial communities and interactions (Lagkouvardos, Overmann, & Clavel, 2017). They enable the identification of microbes, normally missed by cultivation-based approaches, and ultimately allow for a broader picture of the entire environmental network (Lagkouvardos et al., 2017). However, these metagenomics-based approaches lack the possibility for additional experimental manipulation studies. Although the cultivation of certain bacteria is still challenging, several recent studies showed that the cultivation of host-associated bacteria is urgently needed to better study and understand their function in a metag organización context (Esser et al., 2018).

Consequently, this study aimed to isolate bacterial colonizers of A. aurita and M. leidiyi to disclose potentially specific microbial community patterns of these gelatinous zooplankton species compared to the ambient seawater as well as to compare the culturable community pattern to the reported microbial diversity based on 16S rRNA amplicon sequencing. The generation of such a bacterial archive of isolates is crucial for future colonization experiments. Finally, it was also intended to elucidate interbacterial interactions, for example, potential bacterial competition and quorum quenching (QQ) activities. Such bioactive compounds might be important for the maintenance of a healthy microbiota by defending competitors or pathogens due to inhibition of their growth or interference with their cell–cell communication.

2 | MATERIALS AND METHODS

2.1 | Sampling of A. aurita and M. leidiyi

Individual A. aurita (Linnaeus) medusae (with mean size umbrella diameter of 22 cm) were sampled from one location in the Kiel Bight. Baltic Sea (54°32.8′N, 10°14.7′E), in June 2015 using a dip net. Accordingly, M. leidiyi (Agassiz) adults (mean size of 4 cm) were sampled from the same location in May 2017. The animals were immediately transported to the laboratory and washed thoroughly with autoclaved artificial seawater to remove nonassociated microbes. Additionally, individuals were kept in artificial seawater (Tropical Marine Salts, 18 practical salinity units (PSU)) for ten days before thoroughly washing with autoclaved artificial seawater to remove nonassociated microbes and considered as husbandry individuals. In addition, A. aurita polyps of subpopulations Baltic Sea, North Sea, and North Atlantic (Roscoff) were kept in artificial seawater (Tropical Marine Salts, 18 PSU (Baltic Sea) and 30 PSU (North Sea, North Atlantic)) in 2-L plastic tanks originating from natural polyps sampled in the respective locations almost 15 years ago. Prior to bacterial enrichment and isolation, polyps were not fed with freshly hatched (un-manipulated) Artemia salina for at least three days to ensure empty guts and consequently least possible contamination with microbes. Moreover, 1L ambient water (Baltic Sea 54°32.8′N, 10°14.7′E; artificial seawater 18 and 30 PSU) was filtrated (0.22 µm pores, Millipore, 45 mm diameter) to enrich bacterial cells for further isolation.

2.2 | Bacterial enrichment and isolation

Bacterial enrichment and isolation were performed with sterile cotton swabs from the surface of the umbrella of native and kept A. aurita as well as M. leidiyi individuals (in total 10 medusae of each phylum were sampled), homogenized single A. aurita polyps of different subpopulations, and filters derived from ambient seawater filtration. In order to ensure high diversity during the isolation procedure, swabs, 100 µL of homogenized animal tissues, and ¼ of a filter were streaked/plated onto three different solid media (Marine Bouillon (Sizemore & Stevenson, 1970), R2A (Reasoner & Geldreich, 1985), Plate Count Medium (Buchbinder et al., 1951)) and all plates were incubated at 4, 20, and 30°C, respectively, for at least 16 h up to one week (for 4°C incubations). Obtained single colonies were picked and purified by streaking at least three times on the respective agar plates and incubated at the initial incubation temperature. Morphologically similar colonies (i.e., colony size, colony color, and colony shape) from different samples as well as morphologically different colonies from all samples were grown in the respective liquid medium at the respective incubation temperature. Pure cultures were stored as glycerol stocks (10%) at −80°C and subsequently were taxonomically classified by 16S rRNA analysis.

2.3 | Nucleic acid isolation

High-molecular weight genomic DNA of bacteria was isolated from 5 ml overnight cultures using the Wizard Genomic DNA Isolation Kit (Promega) according to the manufacturer’s instructions.

2.4 | 16S rRNA gene analysis

16S rRNA genes were PCR-amplified from 50 ng isolated genomic DNA using the bacterium-specific primer 27F (5′-AGAGTTTGATCCTGCGAGC-3′) and the universal primer

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1492R (5′-GGTACCTGTTACGACTT-3′) (Lane, 1991) resulting in a 1.5-kb bacterial PCR fragment. The fragment sequences were determined by the sequencing facility at the Institute of Clinical Molecular Biology, University of Kiel, Kiel, Germany (IKMB), using primer 27F (Phred quality score of 20). Sequence data are deposited under GenBank accession numbers MK967003–MK967227.

2.5 | Growth inhibition assay (modified after Moran, Crank, Ghabban, & Horsburgh, 2016)

First, all 231 isolated bacterial strains were grown on MB agar plates at 30 ºC overnight (Moran, Crank, Ghabban, & Horsburgh, 2016). Out of those 231 strains, 203 formed compact bacterial lawns on the agar plates under the selected growth conditions and were subsequently used for the growth inhibition assay as follows. First, agar disks with a diameter of 5 mm were cut out of those incubated agar plates comprising the respective living bacterial strain at the surface. Second, agar disks were prepared in prepared accurately fitting cavities of freshly generated agar plates (screening plates) on which bacterial strains to be tested have been plated (100 µl of an overnight culture). All 203 strains were tested against each other. Screening plates were incubated overnight at 30°C. Growth inhibition zones were detected, and the assay was verified with at least two biological replicates each with two technical replicates of initially identified inhibiting bacterial strains. Finally, inhibition zones were measured from the center of the agar disk to the edge of the halo. Moreover, an isolate was defined to have a growth-promoting effect on the strain present on the agar disk when this bacterium was overgrowing the edge of the agar disk.

2.6 | Identification of quorum sensing-interfering activities (QQ activities) of isolates

Quorum quenching assays with bacterial isolates were performed as described in Weiland-Brauer, Kisch, Pinnow, Liese, and Schmitz (2016); Weiland-Brauer, Pinnow, and Schmitz (2015). Briefly, QQ screening plates were prepared as follows: LB agar containing 0,8% agar at 50°C was supplemented with final concentrations of 100 µM N-[(β-ketocaproyl)]-L-homoserine lactone (Sigma-Aldrich, Munich, Germany), 100 g/mL ampicillin, 30 g/mL kanamycin, and 10% (vol/vol) exponentially growing culture of the reporter strain AI1-QQ1. LB agar plates were coated with the top agar mixture. AI-2 quorum quenching plates were prepared similarly, but the agar was supplemented with final concentrations of 50 mM 4-hydroxy-3-methyl-2-furanone (Sigma-Aldrich, Munich, Germany), 100 g/mL ampicillin, 30 g/mL kanamycin, and 5% (vol/vol) exponentially growing culture of the reporter strain AI2-QQ1. After 10 min of solidifying the top agar, 5 µl of the test substances were applied, followed by overnight incubation at 37°C. QQ activities were visualized by growth of the respective reporter strain. Preparation of cell-free cell extracts and culture supernatants from isolates was performed after growth of bacterial isolates in 5 mL of the respective isolation medium (MB, R2A, and PCA) overnight at the respective isolation temperature (4, 30, and 37°C) and 120 rpm. Cells were harvested by centrifugation at 7,000 xg, and the culture supernatant was subsequently filtered using 0,2-µm centrifugal filter units (Carl Roth, Karlsruhe, Germany). The cell extracts were prepared from the cell pellet using the Geno/Grinder 2000 (BT&C/OPS Diagnostics, Bridgewater, NJ). The cell pellet was resuspended in 500 µL 50 mM Tris-HCl (pH 8,0), and glass beads (0,1 mm and 2,5 mm) were added prior to mechanical cell disruption for 6 min at 1,300 strokes/min at RT. After centrifugation at 10,000 xg and 4°C for 25 min, the cell extracts were filtered through 0,2-µm filter units. Cell-free culture supernatants and cell extracts were stored at 4°C until used in the QQ assay. The reporter strains are only able to grow in the top agar when QS-interfering biomolecule is present in the culture supernatant or cell extract, since the lethal gene is under the control of a promoter, which is induced in the presence of the autoinducer (see details of the genetic/strategic design of the reporter strain in Weiland-Brauer, Pinnow, et al. (2015).

3 | RESULTS AND DISCUSSION

3.1 | Cultivated part of jelly-associated bacteria reflects host-specific microbiota

The overall goal of this study was to enrich and isolate bacterial colonizers of the moon jellyfish A. aurita and the comb jelly M. leidyi to unravel potential host-specific patterns of their microbial community structure based on a cultivation-dependent approach. In the long run, we aim to use these respective isolates in future controlled laboratory experiments to study their function in the metagenome in more detail (e.g., by recolonization of germ-free hosts with manipulated microbial communities). Moreover, we aimed to gain insights into interbacterial interactions and evaluate the isolates concerning their ability to interfere with growth of their neighbors and with QS, interactions that might affect the establishment of the host-associated microbiota.

A classical isolation approach was performed using three different solid media at three different incubation temperatures ranging from 4 to 20°C up to 30°C, thus comprising the range of current and expected ocean surface temperatures to ensure high diversity in enriched bacteria. Plate count agar was used for enrichment of the viable bacterial fraction of a sample without any selection, whereas R2A was used for enrichment of heterotrophic, aquatic bacteria, which tend to be slow-growing species and might be suppressed by faster-growing species on a richer culture medium. Marine Bouillon was used to select for marine bacteria preferring high-salt conditions. As expected, enrichment on Marine Bouillon resulted in highest diversity and colony-forming units (cfu) on plates, since the simulation of marine conditions in parallel to rich nutrient supply promoted bacterial growth even for low abundant ones. Only single and less diverse colonies were revealed on R2A agar. Highest cfu were further detected when incubated at 20°C in particular when...
compared to 4°C best matching ocean surface temperatures in summer. In total, we isolated 84 bacterial strains from *A. aurita* (Table 1 and Table A1; Accession No. MK967003–MK967227). In more detail, 17 bacteria were isolated from the umbrella surface of native Baltic Sea medusae and 8 bacteria from cultured medusa. From the benthic polyps cultured in the laboratory, 22 bacteria were isolated from the Baltic Sea subpopulation, 19 from the North Sea subpopulation, and 18 from the North Atlantic subpopulation (Table 1 and Table A1). The isolation procedure from *M. leidyi* resulted in the identification of 64 bacteria (Table 1 and Table A1), 49 bacteria were enriched from native Baltic Sea individuals and 15 from cultured ones. Moreover, 83 bacteria were isolated from the ambient seawater (Table 1 and Table A1). 16S rRNA gene analyses revealed the identification of eight different bacterial classes (Figure 1), representing 28 families.

| TABLE 1 | Presence of isolates in different sample types |
|----------|-----------------------------------------------|
|          | Native Medusa | Native Husbandry | Mediterranean Medusa | Native Adults | Native Husbandry | Mediterranean Adults | Ambient Baltic Sea | Ambient North Sea | Ambient North Atlantic |
| Acinetobacter | Baltic Sea | Baltic Sea | Baltic Sea | Baltic Sea | Baltic Sea | Baltic Sea | Baltic Sea | Baltic Sea | Baltic Sea |
| Aeromonas | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| Alteromonas | 1 | 0 | 0 | 1 | 0 | 3 | 2 | 0 | 4 |
| Arthrobacter | 0 | 3 | 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| Bacillus | 3 | 1 | 1 | 0 | 1 | 0 | 0 | 0 | 7 |
| Brevibacterium | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 4 |
| Celenrobacter | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Chryseobacterium | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| Cobelia | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 2 |
| Colerella | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Corynebacterium | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Enterococcus | 0 | 0 | 1 | 2 | 1 | 0 | 0 | 0 | 0 |
| Exiguobacterium | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Fictibacillus | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| Gordonia | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Halomonas | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Hydrogenophaga | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Hyphrobacter | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Lactobacillus | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Listeria | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Luteococcus | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 1 |
| Marinobacter | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 3 |
| Marinobacter | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Marinomonas | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Microbacterium | 1 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 |
| Micrococcus | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | 2 |
| Moraxella | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 | 0 |
| Octobacterium | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Oleysa | 0 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 0 |
| Pantoea | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Paracoccus | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| Paraglaciecola | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 1 |
| Phaeobacter | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Phaeocystidibacter | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Pseudoalteromonas | 1 | 2 | 3 | 10 | 2 | 10 | 0 | 1 | 3 |
| Pseudoclastivibrio | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 11 |
| Pseudomonas | 7 | 4 | 0 | 2 | 4 | 1 | 1 | 0 | 3 |
| Psychrobacter | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Rhodococcus | 0 | 0 | 0 | 2 | 2 | 1 | 0 | 0 | 1 |
| Ruegeria | 0 | 0 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| Sagittula | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| Salinibacterium | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Serratia plymuthica | 0 | 0 | 0 | 0 | 0 | 8 | 1 | 0 | 0 |
| Staphylococcus | 1 | 1 | 2 | 0 | 3 | 1 | 1 | 0 | 8 |
| Streptococcus | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Sulfitobacter | 1 | 2 | 2 | 1 | 2 | 0 | 0 | 0 | 1 |
| Thalassimonas | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| Vibrio | 2 | 3 | 0 | 0 | 2 | 2 | 0 | 0 | 0 |
| Uncultured bacterium | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 |
| TOTAL No. of isolates | 17 | 8 | 22 | 19 | 18 | 49 | 15 | 6 | 39 |

Presence and abundances (based on total number in percentage per sample, visualized as bars) of isolates in different sample types on genus level.
and 51 genera. In general, distinct differences in the microbial compositions were observed using the cultivation approach between ambient seawater and the two gelatinous zooplankton species (summarized in Figure 1, Table 1 and Table A1). Representatives of the classes Betaproteobacteria, Cytophagia, and unclassified bacteria were shown to be present on the surfaces of the gelatinous zooplankton organisms, but were not isolated from the surrounding seawater samples (Figure 1). Likewise, several bacteria were exclusively isolated from the ambient seawater and assigned to the genera *Celeribacter, Corynebacterium, Fictibacillus, Halomonas, Marinobacter, Salinibacterium*, and *Serratia* (Table 1 and Table A1). All mentioned bacteria are typically found in the marine environment, some of them also associated with marine eukaryotes (Egerton, Culloty, Whooley, Stanton, & Ross, 2018; Martin et al., 2015; van de Water, Allemand, & Ferrier-Pages, 2018; Weiland-Brauer, Neulinger, et al., 2015). These cultivation-dependent results are in line with several publications demonstrating that the microbiota associated with multicellular eukaryotic hosts is significantly different to the bacterial communities in the ambient seawater (Egerton et al., 2018; Martin et al., 2015; van de Water et al., 2018; Weiland-Brauer, Neulinger, et al., 2015). This argues for the presence of specific selection mechanisms, both on bacterial and on the host site to establish and maintain such a specific host-associated microbiota (Pietschke et al., 2017; Weiland-Bräuer, Fischer, Pinnow, & Schmitz, 2019). Notable are the frequencies with which the ubiquitous and high abundant occurring bacteria of the genera *Pseudoalteromonas* and *Pseudomonas* were isolated from all samples (Table 1). These occur in open waters, but are also able to colonize animal tissues (Galkiewicz, Pratte, Gray, & Kellogg, 2011; Tarnecki, Patterson, & Arias, 2016). Both genera are well-known marine inhabitants found in symbiotic associations with sponges, corals, and algae and additionally are known for their versatile biotechnological potential with respect to the production of antimicrobials and enzymes of industrial interest (Borchert et al., 2017; Holmström, James, Neilan, White, & Kjelleberg, 1998; Röthig et al., 2016). Phylogenetic classification revealed that *A. aurita* is colonized by cultivable representatives of genera *Alteromonas*, *Arthrobacter*, *Bacillus*, *Brevibacterium*, *Chryseobacterium*, *Cobetia*, *Enterococcus*, *Gordonia*, *Hymenobacter*, *Luteococcus*, *Maribacter*, *Microbacterium*, *Micrococcus*, *Moraxella*, *Ollela*, *Paracoccus*, *Pseudoalteromonas*, *Pseudomonas*, *Rhodococcus*, *Ruegeria*, *Shewanella*, *Streptococcus*, *Sulfotiobacter*, and *Vibrio* (Table 1 and Table A1). In more detail, *Bacillus* was exclusively isolated from Baltic Sea specimens, *Enterococcus* from benthic polyps, and *Luteococcus* from polyps kept under high-salt conditions (30 PSU) (Table 1). Regarding an important function of those bacteria for the host can only be speculated, but the tropodithioc acid-producing genus *Ruegeria* of the Roseobacter clade, which was exclusively isolated from *A. aurita* polyps, is a globally distributed marine bacterial species found primarily in the upper open ocean and has primarily been isolated from marine aquatic environment, where *Ruegeria* strains have probiotic potential (Beyersmann et al., 2017; Sonnenschein et al., 2017). Additionally, *Luteococcus* has been isolated from the marine environment and was often found in the intestinal tracts of animals (Fan, Zhang, Li, & Zhang, 2014). A highly specific colonization of *A. aurita* has been previously shown in a 16S rRNA amplicon sequencing approach demonstrating jellyfish-specific microbial patterns, which were even different in different compartments of a medusa, between different subpopulations, and among different life stages (Weiland-Brauer, Neulinger, et al., 2015). The diverse but highly specific colonization of both jellies, *A. aurita* and *M. leidy*, was recently also demonstrated in a comprehensive microbial community structure analysis (amplicon and metagenomics sequencing) of several metaorganisms (Rausch et al., 2019). In agreement with those reports, all bacteria isolated from *A. aurita* have been found in the respective deposited 16S amplicon data sets (Rausch et al., 2019; Weiland-Brauer, Neulinger, et al., 2015), suggesting that the isolated bacteria indeed reflect the cultivable part of the moon jellyfish microbiota. Besides, our present cultivation-based study likewise indicates host-specific community patterns. Moreover, we were able to cultivate a high proportion of representatives, for *A. aurita* 14 out of 24 genera and for *M. leidy* 16 out of 19 genera identified by 16S amplicon sequencing (Rausch et al., 2019; Weiland-Brauer, Neulinger, et al., 2015). However, the limitations of the cultivation-dependent approach became apparent for instance on the highly abundant taxon *Mycoplasma*, which was massively detected on the umbrella of *A. aurita* medusa using next-generation sequencing (Weiland-Brauer, Neulinger, et al., 2015), but was not isolated in the present study. The genus *Mycoplasma* is one of the best-known representatives of the bacterial class Mollicutes. *Mycoplasma* often lives in a mutualistic or parasitic lifestyle, but they are also known as commensals in vertebrates and invertebrates (Citti & Blanchard, 2013; Razin, Yoge, & Naot, 1998). Unique characteristics of *Mycoplasma* are the absence of a cell wall, their small cell sizes as well as a reduced genome and a simplified metabolism, which points to an endosymbiotic lifestyle and the requirement of host-specific metabolic compounds for successful growth. So far, *Mycoplasma* was detected in several life stages and subpopulations of *A. aurita* as well as in the sea anemone *Nematostella vectensis* using next-generation sequencing (Daley, Urban-Rich, & Moisander, 2016; Mortzfeld et al., 2016; Weiland-Brauer, Neulinger, et al., 2015). However, cultivation of the potentially common associate of marine gelatinous zooplankton organisms is extremely challenging due to the mentioned characteristics and novel isolation techniques have to be developed and applied to overcome the bottlenecks in cultivation.

Specific associated bacterial communities can also be proposed for *M. leidy*, where, likewise, a diverse set of associated colonizers was isolated, which were assigned to the genera *Acinetobacter*, *Aeromonas*, *Alteromonas*, *Bacillus*, *Chryseobacterium*, *Colwellia*, *Exiguobacterium*, *Hydrogenophaga*, *Lacinutrix*, *Leisingera*, *Marinomonas*, *Microbacterium*, *Micrococcus*, *Ochrobactrum*, *Ollela*, *Pantoea*, *Pheaoctydibacter*, *Pseudoalteromonas*, *Pseudoclavibacter*, *Pseudomonas*, *Psychrobacter*, *Rhodococcus*, *Sagittula*, *Shewanella*, *Staphylococcus*, *Thalassomonas*, and *Vibrio* (Table 1 and Table A1). In addition, bacteria belonging to the genera *Alteromonas*, *Bacillus*, *Chryseobacterium*, *Micrococcus*, *Ollela*, *Pseudoalteromonas*, *Pseudomonas*, *Rhodococcus*, *Shewanella*, *Staphylococcus*, and *Vibrio* were isolated from both species, *M. leidy*. 


and A. aurita, and most of them also from the ambient seawater (Table 1). These bacteria are most likely ubiquitous marine bacteria, whose abundances in the open waters might differ from their abundances on the animals. Several bacteria were exclusively isolated from M. leidyi, such as Acinetobacter, Aeromonas, Colwellia, Exiguobacterium, Hydrogenophaga, Lacinutrix, Marinomonas, Ochrobactrum, Pantoaea, Phaeocystidibacter, Pseudoclavibacter, Psychrobacter, Sagittula, and Thalassomonas, which also have been detected in a recent 16S rRNA gene amplification study of the M. leidyi-associated microbiota (Jaspers, Weiland-Bräuer, et al., 2019). Several of those bacteria were previously described in association with M. leidyi (Daniels & Brettar, 2012; Hao, Gerdts, Peples, & Wichels, 2015; Saeedi et al., 2013). For instance, Aeromonas was already isolated from M. leidyi of the North Sea population (Saeedi et al., 2013). Marinomonas was even described as the dominant phylotype of the comb jelly in a 16S amplicon-based study (Hao et al., 2015), and Colwellia was isolated from several marine animal and plant tissues (Martin et al., 2015). Besides, Colwellia has already been identified on various brown algae and the red alga Delisea pulchra using shotgun sequencing, where it was present on diseased thallus and absent from healthy thalli of this red alga (Fernandes, Steinberg, Rusch, Kjelleberg, & Thomas, 2012). However, the hypothesis that those bacteria indeed play crucial roles for the comb jelly, in particular during the invasion process, has still to be proven by functional approaches.

Taken together, our cultivation-dependent approach revealed that the moon jellyfish A. aurita and the comb jelly M. leidyi harbor a cultivable core microbiota consisting of typically marine and ubiquitous bacteria, which can partly be found in the ambient seawater, but in quite different abundances. These microbes were also found associated with other marine organisms such as brown algae or fish gut (Egerton et al., 2018; Martin et al., 2015; van de Water et al., 2018). In contrast, several bacteria not detected in the ambient water were exclusively isolated from one of the investigated gelatinous zooplankton organisms, suggesting that the animals have their individual host-specific microbial communities, even if they share the same environment. There might be at least three possibilities, why strains were exclusively isolated from the animals, but not from ambient water. The more supposable one is simply based on the abundance of bacteria in ambient water. Bacterial abundancies on the jellies might be much higher than the corresponding colonizer pools in the ambient water, since they might be specifically enriched in the jelly mucus, thus missing them during isolation. Second, there might be a bias during cultivation. Third, bacteria might be vertically transmitted and planula larvae already harbor those bacteria. The metaorganism, as entity of the host and its microbiota, has to control and modulate the microbial colonization of the host tissues to establish and maintain the specific microbiota, which most likely contributes to its overall fitness and health. Ultimately, the established collection of bacterial isolates can now be used for recolonization experiments with artificial (reduced) bacterial communities allowing functional analysis of how the microbes influence the host.

3.2 Interbacterial interactions control microbial community structure

In nature, bacteria grow in communities, where they are continuously interacting with each other in a cooperative or competitive manner (Geesink et al., 2018). Bacterial community composition and functioning as well as growth and fitness of a single bacterium highly depend on these interactions (Braga, Dourado, & Araújo, 2016; Hibbing, Fuqua, Parsek, & Peterson, 2010; Pande & Kost, 2017), which are often mediated by small molecules secreted by the bacteria. In this respect, the bacterial release of a plethora of primary and secondary metabolites into their environment might play an important role. Particularly, secondary metabolites, which in most cases act as repressing agents, like antibiotics or signaling compounds such as quorum sensing molecules, can have important ecological functions as they can positively or negatively affect the growth of neighboring bacteria (Cornforth & Foster, 2013; Hibbing et al., 2010; Pande & Kost, 2017). For instance, competition between bacteria due to nutritional competition or the production of antimicrobial compounds often leads to exclusion of particular species or strains within a community, consequently often causing community shifts (Sapp et al., 2007). Negative as well as positive bacterial interactions based on competition/cooperation can be monitored with growth inhibition assays as described by Moran et al. (Moran et al., 2016). The assay is used to detect growth inhibition and its degree or growth promotion of the neighboring bacteria. Combining such data on bacterial interactions with 16S rRNA community data ultimately

![Figure 2](image-url) Growth inhibition assay. (a) Original photograph shows growth inhibition of isolate 9 (Vibrio alginolyticus) in the presence of isolate 111 (Brevibacterium frigoritolerans). (b) Original photograph visualizes growth promotion of isolate 25 (Vibrio anguillarum) in the presence of isolate 81 (Pseudoalteromonas issachenkoni).
### TABLE 2 Growth inhibition of neighboring bacteria

| Isolate No. | Identified species by 16S rRNA | Isolates 111, 193, 209, and 113 inhibited the growth of the listed bacteria in a growth inhibition assay performed on MB agar plates overnight at 30°C. The assay was verified with two biological replicates. Mean sizes of corrected growth inhibition zones (corrected by 2.5 mm radius of 5-mm-agar disk) are listed with respective standard deviations as radius in mm. |
|-------------|--------------------------------|---------------------------------------------------------------------------------|
| 111         | Brevibacterium frigoritolerans  | 7 ± 2                                                                            |
| 193         | Fictibacillus phosphorivorans  | 5 ± 2                                                                            |
| 209         | Paraglaciecola                  | 2 ± 1                                                                            |
| 210         | Sulfitobacter ponticus          | 9 ± 2                                                                            |
| 113         | Sulfitobacter sp.               | 6 ± 3                                                                            |
| 111         | Brevibacterium frigoritolerans  | 7 ± 2                                                                            |
| 193         | Fictibacillus phosphorivorans  | 5 ± 1                                                                            |
| 209         | Paraglaciecola                  | 2 ± 1                                                                            |
| 210         | Sulfitobacter ponticus          | 9 ± 2                                                                            |
| 113         | Sulfitobacter sp.               | 6 ± 3                                                                            |

Note: Isolates 111, 193, 209, and 113 inhibited the growth of the listed bacteria in a growth inhibition assay performed on MB agar plates overnight at 30°C. The assay was verified with two biological replicates. Mean sizes of corrected growth inhibition zones (corrected by 2.5 mm radius of 5-mm-agar disk) are listed with respective standard deviations as radius in mm.

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Weiland-Brauer, Neulinger, et al., 2015), and their colonization and/or abundance might thus be controlled by microbial community members like Brevibacterium and Sulfitobacter. Moreover, we observed growth-promoting effects of several Pseudoalteromonas strains (in total 18) exclusively on Vibrio strains (isolates 81, 77, 68, 70, 7, 242, and 213) (Table 3). Pseudoalteromonas is a ubiquitous marine bacterium, which often serves as initial bacterial attractant for surrounding bacteria through secretion of chitinases, proteases, or hydrolytic enzymes enabling access to nutrients and thus colonization of biotic surfaces (Everuss, Delpin, & Goodman, 2008). Pseudoalteromonas has been identified to support the accumulation of Vibrio strains and consequently often found in aggregates and fouling communities with Vibrio (Dang & Lovell, 2002; Long & Azam, 2001; Rao, Webb, & Kjelleberg, 2006), which is in line with our observations on growth-promoting effects of Pseudoalteromonas on Vibrio strains. Although molecular mechanisms of the identified interactions are so far unknown, the results of this study indicate that neighboring bacteria have competitive and enables identifying correlations between microbial community patterns and competitive exclusion (Hibbing et al., 2010; Libberton, Coates, Brockhurst, & Horsburgh, 2014). In the present study, we screened for growth-inhibiting as well as growth-promoting effects of the 231 isolated bacteria (Table A1). Secondary metabolites are already known to play important ecological roles in the interactions with other organisms. For instance, several studies have demonstrated that secondary metabolites produced by bacteria can serve as weapons in microbial warfare or they protect or stimulate the eukaryotic host (Cornforth & Foster, 2013; van Dam, Weinhold, & Garbeva, 2016; Foster & Bell, 2012; Ryu et al., 2003). Therefore, agar disks comprising bacterial lawn of the competing bacteria (feasible for 203 isolates, 28 isolates not used for functional assays are highlighted in Table A1) were placed in prepared cavities of freshly plated agar plates (Figure 2). All isolates were grown on MB-rich medium at 30 °C to make the practical effort appropriate, but being aware of the bias during functional assays. All 203 isolates were tested against each other. Isolates 111, 193, 209 (different Brevibacterium frigoritolerans strains), and 113 (Sulfitobacter ponticus) inhibited the growth of 18 isolates belonging to the bacterial families Rhodobacteraceae, Alteromonadaceae, and Vibrionaceae (Table 2) (inhibition zones of 2 to 9 mm). Brevibacterium species are strictly aerobic chemo-organotrophic bacteria and B. frigoritolerans was already described as isolated from environmental samples, such as different soils (Onraedt, Soetaert, & Vandamme, 2005). Moreover, Brevibacterium is known to produce antimicrobial substances, which inhibit the growth of many food poisoning and pathogenic bacteria as well as several yeasts and molds (Bikash, Ghosh, Sienkiewicz, & Krenkel, 2000; Jones & Keddle, 1986; Onraedt et al., 2005; Rattray & Fox, 1999). Sulfitobacter widely exists in coastal and open ocean environments and is known for the synthesis of secondary metabolites with antibacterial, antitumor, and antiviral activities (Martins & Carvalho, 2007; Müller, Brümmer, Batel, Müller, & Schröder, 2003). Representatives of the bacterial families inhibited are highly abundant in the marine environment and in particular on gelatinous zooplankton organisms (Elfantz, Horn, Ayon, Cohen, & Minz, 2013; Rausch et al., 2019; Thompson, Iida, & Swings, 2004; Thompson, Randa, et al., 2004; Vergin, Done, Carlson, & Giovannoni, 2013; Weiland-Brauer, Neulinger, et al., 2015), and their colonization and/or abundance might thus be controlled by microbial community members like Brevibacterium and Sulfitobacter. Moreover, we observed growth-promoting effects of several Pseudoalteromonas strains (in total 18) exclusively on Vibrio strains (isolates 81, 77, 68, 70, 7, 242, and 213) (Table 3). Pseudoalteromonas is a ubiquitous marine bacterium, which often serves as initial bacterial attractant for surrounding bacteria through secretion of chitinases, proteases, or hydrolytic enzymes enabling access to nutrients and thus colonization of biotic surfaces (Everuss, Delpin, & Goodman, 2008). Pseudoalteromonas has been identified to support the accumulation of Vibrio strains and consequently often found in aggregates and fouling communities with Vibrio (Dang & Lovell, 2002; Long & Azam, 2001; Rao, Webb, & Kjelleberg, 2006), which is in line with our observations on growth-promoting effects of Pseudoalteromonas on Vibrio strains. Although molecular mechanisms of the identified interactions are so far unknown, the results of this study indicate that neighboring bacteria have competitive and
cooperative relationships, which most likely both affect the bacterial community composition and ultimately impact on a host.

Meanwhile, it is well known that bacterial cell–cell communication, so-called quorum sensing (QS) and its interference (quorum quenching, QQ), has a crucial role in cooperative and competitive microbial interactions, both within a species and between species (Abisado, Benomar, Klaus, Dandekar, & Chandler, 2018). QS is the fundamental system of bacteria regulating cell density-dependent behaviors by the synthesis and detection of small signal molecules (Camilli & Bassler, 2006). Gram-negative bacteria use...
N-acetyl-homoserine lactones (AHL) for communication, whereas Gram-positive bacteria use short oligopeptides for QS regulation (Eberl, 1999; Kleerebezem, Quadri, Kuipers, & de Vos, 1997; Miller & Bassler, 2001). Besides this intraspecific communication, AI-2—a furanone-based small molecule—acts as autoinducer in the universal communication among different species (Bassler & Miller, 2013; Bassler, Wright, Showalter, & Silverman, 1993; Chen et al., 2002; Schauder, Shokat, Surette, & Bassler, 2001). QS can be interfered by so-called quorum quenching (QQ) molecules, which, for instance, inactivate autoinducer synthetases, degrade or modify the autoinducers, or interfere with the autoinducer receptors through signal analogs. QQ molecules are synthesized by various bacteria, which ultimately interfere QS-regulated coordinated behaviors like microbial colonization. Thus, QQ activity might represent a crucial mechanism for outcompeting other microbes and might have significant consequences in shaping the structure of polymicrobial communities (Greig & Travisano, 2004; Popat et al., 2015; Rainey & Rainey, 2003; Velicer, Kroos, & Lenski, 2000). Moreover, many bacterial species use QS to control the production of toxins: for example, bacteriocins in Streptococcus species (Fontaine et al., 2007; van der Ploeg, 2005) and type VI secretion effectors in B. thailandensis (Majerczyk, Schneider, & Greenberg, 2016). Here, QQ activities prevent the increase of potential pathogens and the detrimental altering of community dynamics. QS and its respective interference have meanwhile been evaluated as important to maintain the healthy stability of the microbiota and the metaorganism, and prevent colonization by pathogens (Thompson, Oliveira, & Xavier, 2016; van de Water et al., 2018; Xavier, 2018). Consequently, we evaluated the frequency of QQ activities present in gelatinous zooplankton-associated bacteria. All isolated bacteria were screened for QS-interfering activities using the established reporter strains AI1-QQ.1 and AI2-QQ.1 (Weiland-Brauer, Pinnow, et al., 2015). Screening of cell-free cell extracts and culture supernatants demonstrated that 121 out of the 231 isolated bacteria showed AHL-interfering activities (52%), of which 21 (9%) showed simultaneous interference with AHL and AI-2 (Table A1, Figure 3). In more detail, QQ activities were identified for representatives of Actinobacteria, Bacilli, Flavobacteria, Alpha-, Beta-, and Gammaproteobacteria, whereas QQ activities were absent for representatives of Actinomycetes and Cytophaga. Notable is the high frequency of QQ activities identified for Gammaproteobacteria mostly represented by Pseudomonas, Pseudoalteromonas, and Vibrio. The high frequency of QS-interfering bacteria strongly argues that QS and the respective interference are important to establish and maintain a healthy and stable microbiota and consequently a healthy metaorganism, for example, by preventing the colonization of pathogens (J. A. Thompson et al., 2016; van de Water et al., 2018; Xavier, 2018). These findings are also in accordance with recent reports on the occurrence of marine bacteria with AHL-QQ activities in pelagic and marine surface-associated communities (Romero, Acuna, & Otero, 2012; Romero, Martin-Cuadrado, Roca-Rivada, Cabello, & Otero, 2011). Remarkably, different isolated strains of bacterial species showed either exclusive interference with AHL or interference with both AHL and AI-2 (Table A1), indicating that different interference mechanisms may have evolved. This is for instance reflected within the Pseudoalteromonas species. In summary, the identification of <50% QQ-active bacterial isolates demonstrated a high abundance of QS-interfering bacteria from the marine environment, in particular associated with surfaces of our tested gelatinous zooplankton organisms. We further detected differences in QQ activities on different jellies, which are most likely different not only because of different community patterns, but also because of different QQ expression patterns adapted to ever-changing environmental conditions. Detected QQ activities mainly interfered with Gram-negative AHL communication, which is primarily present in the marine environment (Liu et al., 2018; Rehman & Leiknes, 2018). Overall, this study provides insights into the cultivable part of the microbiota associated with two gelatinous zooplankton species. In line with deep sequencing approaches, our cultivation-dependent approach revealed that the moon jellyfish A. aurita and the comb jelly M. leidyi harbor a core microbiota, but both also feature an animal-specific microbiota. A healthy and stable microbiota, which contributes to the overall fitness and health of the metaorganism, has to be established and maintained through attraction and defense mechanisms of the host and its associated microbiota (Bang et al., 2018). We identified interbacterial interactions of those cultivated bacteria in terms of growth-promoting and growth-inhibiting as well as QQ activities. Brevisbacterium frigoritolerans and Sulfitobacter sp. inhibited several bacterial isolates, whereas Pseudoalteromonas spp. promoted growth of Vibrio strains. Moreover, with over 50% we identified a high frequency of QS-interfering bacteria from the marine environment, which mainly interfere AHL communication primarily present in the marine environment (Liu et al., 2018; Rehman & Leiknes, 2018). Cooperative and competitive interactions, in particular QS and QQ, appear to have an important ecological role in marine environments, particularly in dense microbial communities on biological surfaces. Interbacterial interactions are most likely crucial for maintaining a healthy microbiota of a metaorganism. Thus, identifying and analyzing such attraction or defense mechanisms between microbes as well as between microbes and the host allows gaining insights into the fundamental, but complex interactions within such multi-organismal partnerships and ultimately enables for a better understanding of the establishment and maintenance of a healthy microbiota.

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CONFLICT OF INTEREST
None declared.

AUTHORS CONTRIBUTION
Nancy Weiland-Bräuer: Conceptualization (equal); Formal analysis (equal); Investigation (lead); Resources (equal); Supervision (equal); Visualization (lead); Writing-original draft (lead); Writing-review & editing (supporting).
Daniela Prasse: Formal analysis (supporting); Investigation (supporting); Writing-original draft (supporting).
Annikka Brauer: Investigation (supporting).
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Thorsten B. H. Reusch: Resources (equal); Writing-review & editing (supporting).
Ruth A. Schmitz: Conceptualization (equal); Funding acquisition (lead); Supervision (equal); Writing-original draft (equal); Writing-review & editing (lead).

ETHICS STATEMENT
None required.

DATA AVAILABILITY STATEMENT
All data generated or analyzed during this study are included in this published article (and its Appendix 1). Sequence data is deposited under GenBank accession numbers MK967003–MK967227.

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### Table A1 Bacteria isolated from *Aurelia aurita*, *Mnemiopsis leidyi*, and ambient seawater

| Isolate | Origin          | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|-----------------|---------------------------------------------------------------------------|--------------------------|-------------------|-------------|
|         |                 |                                                                          | Phylum                   | Class             | Order       | Family      | AHL | AI−2 |          |
| 14      | *A. aurita* medusa Baltic Sea | *Microbacterium* sp. ZV-2-1 (KT597025.1, 99%)                          | Actinobacteria           | Actinobacteria    | Actinomycetales | Microbacteriaceae | Light yellow, round | ++ | -   |
| 13      | *A. aurita* medusa Baltic Sea | *Bacillus* cereus strain YB1806 (MH633934.1, 99%)                     | Firmicutes               | Bacilli           | Bacillales     | Bacillaceae  | White, oval | -   | -   |
| 16      | *A. aurita* medusa Baltic Sea | *Bacillus* sp. BAM561 (AB330413.1, 98%)                                 | Firmicutes               | Bacilli           | Bacillales     | Bacillaceae  | White, round | -   | -   |
| 17      | *A. aurita* medusa Baltic Sea | *Bacillus* cereus (KF624695.1, 98%)                                    | Firmicutes               | Bacilli           | Bacillales     | Bacillaceae  | White, round | -   | -   |
| 5       | *A. aurita* medusa Baltic Sea | Uncultured *Staphylococcus* sp. (FR690777.1, 93%)                     | Firmicutes               | Bacilli           | Bacillales     | Staphylococcaceae | White, smeary | +++ | -   |
| 15      | *A. aurita* medusa Baltic Sea | *Sulfotobacter* sp. strain B28-5 (MG388121.1, 99%)                     | Proteobacteria           | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | White with orange spots, smeary | +++ | -   |
| 12      | *A. aurita* medusa Baltic Sea | *Alteromonas genoviensis* strain PQQ33 (KT730058.1, 99%)              | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Alteromonadaceae | White, smeary | +++ | -   |
| 4       | *A. aurita* medusa Baltic Sea | *Pseudoalteromonas* sp. DL-6 (CP019770.1, 99%)                           | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Pseudoalteromonadaceae | White, smeary | -   | -   |
| 3       | *A. aurita* medusa Baltic Sea | *Pseudomonas marincola* strain 002-Na3 (MG456871.1, 94%)               | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | White, round, smeary | -   | -   |
| 1       | *A. aurita* medusa Baltic Sea | *Pseudomonas* sp. JXH−219 (KR012212.1, 100%)                            | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellowish-white, smeary | -   | -   |
| 2       | *A. aurita* medusa Baltic Sea | *Pseudomonas* sp. (KR012034.1, 99%)                                    | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Orange, round | ++ | -   |
| 8       | *A. aurita* medusa Baltic Sea | *Pseudomonas* sp. JXH–340 (KR012328.1, 99%)                            | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellow, round | ++ | -   |
| 9       | *A. aurita* medusa Baltic Sea | *Pseudomonas* sp. JXH–219 (KR012212.1, 99%)                            | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellow, roundish | + | -   |
| 10      | *A. aurita* medusa Baltic Sea | *Pseudomonas* sp. JXH–36 (KR012034.1, 99%)                             | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellow, roundish | ++ | -   |
| 11      | *A. aurita* medusa Baltic Sea | *Pseudomonas* sp. HN–2 (KJ452338.1, 97%)                                | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellow, roundish | ++ | -   |

(Continues)
| Isolate | Origin | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|--------|-----------------------------------------------------------------------------|-------------------------|------------------|-------------|
|         |        |                                                                             | Phylum                  | Class            | Order       | Family        | AHL | AI-2 |
| 6       | A. aurita medusa Baltic Sea | *Vibrio* sp. Bac180 (KP980718.1, 99%) | Proteobacteria Gammaproteobacteria Vibionales Vibionaceae | Light orange in center, round | +++ + |
| 7       | A. aurita medusa Baltic Sea | *Vibrio* sp. H1309/4.5 (LN871549.1, 97%) | Proteobacteria Gammaproteobacteria Vibionales Vibionaceae | White with orange spots, smeary | - - |
| 24      | A. aurita medusa Baltic Sea husbandry | *Maribacter* sp. SDRB-Phe2 (MG456900.1, 99%) | Bacteroidetes Flavobacteria Flavobacteriales Flavobacteriaceae | White-orange, smeary | + - |
| 22      | A. aurita medusa Baltic Sea husbandry | *Pseudoalteromonas* sp. MACL07 (EF198247.1, 99%) | Bacteroidetes Flavobacteria Flavobacteriales Flavobacteriaceae | White, smeary | |
| 19      | A. aurita medusa Baltic Sea husbandry | *Bacillus* sp. strain CL25 (MH605366.1, 99%) | Firmicutes Bacilli Bacillales Bacillaceae | Light orange, round | + - |
| 18      | A. aurita medusa Baltic Sea husbandry | *Staphylococcus aureus* subsp. aureus JCM 2874 (LC420068.1, 99%) | Firmicutes Bacilli Bacillales Staphylococcaceae | Orange, round | ++ - |
| 20      | A. aurita medusa Baltic Sea husbandry | *Sulfotobacter pontiacus* strain ACBC109 (MK156387.1, 87%) | Proteobacteria Alphaproteobacteria Rhodobacteriales Rhodobacteriaceae | White, smeary | + - |
| 23      | A. aurita medusa Baltic Sea husbandry | *Sulfotobacter* sp. S7-80 (KU999998.1, 99%) | Proteobacteria Alphaproteobacteria Rhodobacteriales Rhodobacteriaceae | White, round | ++ - |
| 21      | A. aurita medusa Baltic Sea husbandry | *Cobetia amphilecti* (NR_113404.1, 99%) | Proteobacteria Gammaproteobacteria Halomonadaeae Cobetia | White, round | ++ - |
| 25      | A. aurita medusa Baltic Sea husbandry | *Pseudoalteromonas issachenkonii* strain KMM3549 (CP011030.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadaeae Pseudoalteromonadaeae | Yellow, roundish-smeary | ++ + |
| 75      | A. aurita polyp Baltic Sea husbandry | *Arthrobacter* sp. MB182 (JF706644.1, 99%) | Actinobacteria Actinobacteria Actinomycetaeae Micrococcaceae | White, round | |
| 82      | A. aurita polyp Baltic Sea husbandry | *Arthrobacter* sp. MB182 (JF706644.1, 99%) | Actinobacteria Actinobacteria Actinomycetaeae Micrococcaceae | White, round | + - |
| Isolate | Origin                      | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|-----------------------------|---------------------------------------------------------------------------|--------------------------|-------------------|-------------|
| 84      | A. aurita polyp Baltic Sea  | Arthrobacter sp. MB182 (JF706644.1, 100%)                                  | Actinobacteria           | White, round (tiny) | ++          |
|         | husbandry                   |                                                                           | Actinobacteria Actinobacteria Actinomycetales Micrococcaceae |                   |             |
| 74      | A. aurita polyp Baltic Sea  | *Micrococcus luteus* strain BMC2N6_2 (MG996855.1, 99%)                     | Actinobacteria           | Light yellow, round |             |
|         | husbandry                   |                                                                           | Actinobacteria Actinobacteria Actinomycetales Micrococcaceae |                   |             |
| 83      | A. aurita polyp Baltic Sea  | *Gordonia terrae* strain DSOSB42 (KP860547.1, 99%)                         | Actinobacteria           | Light orange, round |             |
|         | husbandry                   |                                                                           | Actinobacteria Actinobacteria Actinomycetales Nocardiaceae |                   |             |
| 79      | A. aurita polyp Baltic Sea  | Olleya sp. MOLA 14 (AM990790.1, 99%)                                       | Bacteroidetes            | Orange, round     | +++ +       |
|         | husbandry                   |                                                                           | Flavobacteriia          |                   |             |
|         |                             |                                                                           | Flavobacteriales Flavobacteriaceae |                   |             |
| 76      | A. aurita polyp Baltic Sea  | *Bacillus weihenstephanensis* strain 261ZG8 (KF831379.1, 98%)             | Firmicutes               | White, irregular  | - -         |
|         | husbandry                   |                                                                           | Bacilli Bacillales Bacillaceae |                   |             |
| 85      | A. aurita polyp Baltic Sea  | *Staphylococcus warneri* strain D2-1X-27 (MK287635.1, 99%)                 | Firmicutes               | White-yellow, round | + -         |
|         | husbandry                   |                                                                           | Bacilli Bacillales Staphylococcaceae |                   |             |
| 87      | A. aurita polyp Baltic Sea  | *Staphylococcus* sp. C34 (JX482523.1, 99%)                                | Firmicutes               | Brownish, round   | + +         |
|         | husbandry                   |                                                                           | Bacilli Bacillales Staphylococcaceae |                   |             |
| 73      | A. aurita polyp Baltic Sea  | *Enterococcus casseliflavus* strain EC2 (MH376403.1, 99%)                  | Firmicutes               | White, roundish-smeary | + -         |
|         | husbandry                   |                                                                           | Bacilli Lactobacillales Enterococcaceae |                   |             |
| 88      | A. aurita polyp Baltic Sea  | *Paracoccus* sp. S1-12 (KP114216.1, 99%)                                   | Proteobacteria           | White, smearry    | - -         |
|         | husbandry                   |                                                                           | Alphaproteobacteria Rhodobacterales Rhodobacteraceae |                   |             |
| 86      | A. aurita polyp Baltic Sea  | *Ruegeria* sp. strain EA372 (KY655473.1, 96%)                              | Proteobacteria           | White, smearry    | - -         |
|         | husbandry                   |                                                                           | Alphaproteobacteria Rhodobacterales Rhodobacteraceae |                   |             |
| 89      | A. aurita polyp Baltic Sea  | *Ruegeria* sp. strain S5-4-3 (MK743969.1, 99%)                              | Proteobacteria           | White, round      | - -         |
|         | husbandry                   |                                                                           | Alphaproteobacteria Rhodobacterales Rhodobacteraceae |                   |             |
| 78      | A. aurita polyp Baltic Sea  | *Sulfitobacter* sp. SAG13 (KX268604.1, 99%)                                | Proteobacteria           | White, smerey     | ++ -        |
|         | husbandry                   |                                                                           | Alphaproteobacteria Rhodobacterales Rhodobacteraceae |                   |             |
| Isolate | Origin | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|--------|-------------------------------------------------|---------------------------|-------------------|------------|
| 91      | *A. aurita* polyp Baltic Sea husbandry | *Proseudoalteromonas prydzensis* strain S2A2 (MH362721.1, 98%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | White-brownish, smeary | +++ + |
| 90      | *A. aurita* polyp Baltic Sea husbandry | *Pseudomonas putida* strain KB3 (KU299960.1, 95%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | White-yellow, round | ++ ++ |
| 92      | *A. aurita* polyp Baltic Sea husbandry | *Pseudomonas putida* (GU191292.1, 99%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | White, round | ++ - |
| 93      | *A. aurita* polyp Baltic Sea husbandry | *Pseudomonas* sp. strain AS3-9 (MK193867.1, 99%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | White, round with dent | ++ - |
| 94      | *A. aurita* polyp Baltic Sea husbandry | *Pseudomonas* sp. RTW2 (LC43924.1, 99%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Orange, roundish | ++ - |
| 77      | *A. aurita* polyp Baltic Sea husbandry | *Vibrio anguillarum* strain 12222 (MH036330.1, 99%) | Proteobacteria Gammaproteobacteria Vibrionales Vibrionaceae | White-brownish, smeary | ++ - |
| 81      | *A. aurita* polyp Baltic Sea husbandry | *Vibrio anguillarum* strain 12222 (MH036330.1, 99%) | Proteobacteria Gammaproteobacteria Vibrionales Vibrionaceae | Yellow, round | +++ ++ |
| 80      | *A. aurita* polyp Baltic Sea husbandry | *Vibrio* sp. strain GBx3 (MK560194.1, 99%) | Proteobacteria Gammaproteobacteria Vibrionales Vibrionaceae | White-brown, smeary | +++ - |
| 111     | *A. aurita* polyp North Sea husbandry | *Brevibacterium frigoritolerans* (JF411310.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Brevibacteriaceae | White, round | +++ - |
| 107     | *A. aurita* polyp North Sea husbandry | *Luteococcus japonicas* (NR_119351.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Propioni-bacteriaceae | Orange, round, smeary | + - |
| 112     | *A. aurita* polyp North Sea husbandry | *Rhodococcus degradans* strain OTU62_1 (MK547263.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Nocardiaceae | White, smeary | ++ + |
| 109     | *A. aurita* polyp North Sea husbandry | *Rhodococcus erythropolis* 263AY3 (KF836533.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Nocardiaceae | White, roundish-smeary | - - |
| Isolate | Origin                  | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|-------------------------|-----------------------------------------------------------------------------|---------------------------|-------------------|-------------|
|         |                         |                                                                             | Phylum | Class           | Order   | Family             |               |
| 106     | *A. aurita* polyp        | *Hymenobacter psychrophilus* (NR_117214.1, 98%)                              | Bacteroidetes | Cytophagia     | Cytophagales | Hymenobacteraceae | Orange-pink, round |
| 108     | *A. aurita* polyp        | *Chryseobacterium hominis* (JX100820.1, 98-99%)                             | Bacteroidetes | Flavobacteria  | Flavobacteriales | Flavobacteriaceae | White, round + - |
| 98      | *A. aurita* polyp        | *Olleya marilimosa* strain KMM6714 (KC247324.1, 99%)                         | Bacteroidetes | Flavobacteria  | Flavobacteriales | Flavobacteriaceae | Yellow/orange, smery - - |
| 110     | *A. aurita* polyp        | *Enterococcus caninfluens* strain 0.14 (MK611096.1, 93%)                    | Firmicutes   | Bacilli         | Lactobacillales | Enterococcaceae   | Translucent, smery |
| 96      | *A. aurita* polyp        | *Enterococcus casseliflavus* strain EC2 (MH376403.1, 99%)                   | Firmicutes   | Bacilli         | Lactobacillales | Enterococcaceae   | White, round + - |
| 95      | *A. aurita* polyp        | Uncultured *Streptococcus* sp. (LT697039.1, 99%)                            | Firmicutes   | Bacilli         | Lactobacillales | Streptococcaceae  | White, round |
| 104     | *A. aurita* polyp        | *Ruegeria* sp. strain InS-294 (MF359523.1, 99%)                             | Proteobacteria | Alphaproteobacteria | Rhodobacteriales | Rhodobacteriaceae | Light, orange, smery ++ - |
| 113     | *A. aurita* polyp        | *Sulfobacter pontiacus* strain ACBC109 (MK156387.1, 99%)                   | Proteobacteria | Alphaproteobacteria | Rhodobacteriales | Rhodobacteriaceae | White, smery - - |
| 100     | *A. aurita* polyp        | *Sulfobacter* sp. SAG13 (KX268604.1, 99%)                                   | Proteobacteria | Alphaproteobacteria | Rhodobacteriales | Rhodobacteriaceae | White-yellow, smery +++ - |
| 105     | *A. aurita* polyp        | *Shewanella basaltis* (KC534403.1, 99%)                                    | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteriaceae | White-yellow, smery - - |
| 97      | *A. aurita* polyp        | *Shewanella putrefaciens* strain PF 15 (KY614355.1, 99%)                    | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteriaceae | Yellowish, smery + + |
| 102     | *A. aurita* polyp        | Uncultured *Alteromonas* sp. clone PD22_850 (HM340647.1, 99%)              | Proteobacteria | Gammaproteobacteria | Alteromonadales | Alteromonadaeae | White, brownish in center, round, smery + - |
| Isolate | Origin                | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|-----------------------|-----------------------------------------------------------------------------|--------------------------|-------------------|-------------|
| 99      | A. aurita polyp North Sea husbandry | *Pseudoalteromonas issachenkoni* strain K-W12 (JQ799065.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | Light orange, round | ++ +         |
| 101     | A. aurita polyp North Sea husbandry | *Pseudoalteromonas issachenkoni* strain KMM 3549 (CP010303.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | Very light orange, smearable | - -         |
| 103     | A. aurita polyp North Sea husbandry | *Pseudoalteromonas* sp. strain KYW1326 (MH782067.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | Brownish, smearable | +++ -        |
| 118     | A. aurita polyp North Atlantic husbandry | *Micrococcus* sp. strain Actino-43 (MH671539.1, 96%) | Actinobacteria Actinobacteria Actinomycetales Micrococccaceae | White, round |         |
| 128     | A. aurita polyp North Atlantic husbandry | *Rhodococcus erythropolis* strain 263AY3 (KF836533.1, 98%) | Actinobacteria Actinobacteria Actinomycetales Nocardiaceae | White, orange, round-smearable | +++ -        |
| 131     | A. aurita polyp North Atlantic husbandry | *Rhodococcus erythropolis* strain 263AY3 (KF836533.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Nocardiaceae | Translucent, round | +++ -        |
| 123     | A. aurita polyp North Atlantic husbandry | *Luteococcus japonicus* (NR_119351.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Propioni-bacteriaceae | White, round | + -         |
| 121     | A. aurita polyp North Atlantic husbandry | *Olleya* sp. MOLA 14 (AM990790.1, 99%) | Bacteroidetes Flavobacteria Flavobacteriales Flavobacteriaceae | Light orange, round | ++ -         |
| 129     | A. aurita polyp North Atlantic husbandry | *Staphylococcus aureus* strain WMK026R (MK643265.1, 99%) | Firmicutes Bacilli Bacillales Staphylococcaceae | White-yellow, roundish | - -         |
| 124     | A. aurita polyp North Atlantic husbandry | *Staphylococcus* sp. strain Ursilor/9a (MG948184.1, 97%) | Firmicutes Bacilli Bacillales Staphylococcaceae | White, smearable | - -         |
| 127     | A. aurita polyp North Atlantic husbandry | *Staphylococcus succinus* subsp. casei (NR_037053.1, 99%) | Firmicutes Bacilli Bacillales Staphylococcaceae | Orange, roundish | +++ -        |
| 116     | A. aurita polyp North Atlantic husbandry | *Enterococcus casseliflavus* strain Ta12 (MK517636.1, 99%) | Firmicutes Bacilli Lactobacillales Enterococcaceae | White, round |         |
| Isolate | Origin | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|--------|--------------------------------------------------------------------------|-------------------------|------------------|-------------|
|         |        | Phylum | Class            | Order | Family                      | AHL | AI-2 |
| 117     | A. aurita polyp | *Ruegeria* sp. strain 1334 - 60 (KY770284.1, 99%) | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Pink, smeary | +++ | - |
| 125     | A. aurita polyp | *Sulfitobacter* sp. SAG13 (KX288604.1, 99%) | Proteobacteria | Alphaproteobacteria | Rhodobacterales | White, round | - | - |
| 126     | A. aurita polyp | *Sulfitobacter* sp. strain B28-5 (MG388121.1, 99%) | Proteobacteria | Alphaproteobacteria | Rhodobacterales | White-orange, round | +++ | - |
| 122     | A. aurita polyp | *Paraglaciecola* sp. strain M202 (MF443579.1, 99%) | Proteobacteria | Gammaproteobacteria | Alteromonadales | White, smeary | - | - |
| 119     | A. aurita polyp | *Pseudoalteromonas prydzensis* strain S2A2 (MH362721.1, 99%) | Proteobacteria | Gammaproteobacteria | Alteromonadales | Light orange, round | ++ | - |
| 120     | A. aurita polyp | *Pseudoalteromonas* sp. MACL07 (EF198247.1, 99%) | Proteobacteria | Gammaproteobacteria | Alteromonadales | White-brownish, round | ++ | - |
| 115     | A. aurita polyp | *Moraxella osloensis* isolate TID−8 (LN871835.1, 99%) | Proteobacteria | Gammaproteobacteria | Pseudomonadales | White, round | - | - |
| 114     | A. aurita polyp | *Pseudomonas* sp. strain THAF187a (MG996698.1, 99%) | Proteobacteria | Gammaproteobacteria | Pseudomonadales | White-yellow, round | ++ | - |
| 130     | A. aurita polyp | *Pseudomonas* sp. TKCM64 (LC194999.1, 99%) | Proteobacteria | Gammaproteobacteria | Pseudomonadales | White, roundish | + | - |
| 59      | M. leidyi Baltic Sea | *Microbacterium oxydans* strain DSM 20578(T) (MH321609.1, 99%) | Actinobacteria | Actinobacteria | Actinomycetales | Microbacteriaceae | White, round | - | - |
| 63      | M. leidyi Baltic Sea | *Microbacterium* sp. strain ZMAI-4 (MK178502.1, 99%) | Actinobacteria | Actinobacteria | Actinomycetales | Microbacteriaceae | White, round | - | - |
| 255     | M. leidyi Baltic Sea | *Pseudoclavibacter* sp. (MK1938651, 99%) | Actinobacteria | Actinobacteria | Actinomycetales | Microbacteriaceae | Light yellow, round | - | - |
| 52      | M. leidyi Baltic Sea | *Micrococcus* sp. EF1B-B144 (KC545358.1, 98%) | Actinobacteria | Actinobacteria | Actinomycetales | Micrococcaceae | Light yellow, round | - | - |
## TABLE A1 (Continued)

| Isolate | Origin | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|--------|---------------------------------------------------------------------------|--------------------------|-------------------|-------------|
|         |        |                                                                           | Phylum | Class | Order | Family         | AHL | AI-2         |
| 58      | M. leidyi Baltic Sea | *Rhodococcus* sp. strain GK29 (MK424373.1, 96%) | Actinobacteria | Actinobacteria | Actinomycetales | Nocardiaceae | Orange, roundish-smeary | - | - |
| 61      | M. leidyi Baltic Sea | *Phaeocystidibacter luteus* strain PG2501 (NR_132329.1, 99%) | Bacteroidetes | Flavobacteriia | Flavobacteriales | Cryomorphaceae | Dark orange, oval | ++ | - |
| 54      | M. leidyi Baltic Sea | *Lacinutrix* sp. strain KMM 6784 (MK587648.1, 99%) | Bacteroidetes | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | White-orange, round | ++ | - |
| 57      | M. leidyi Baltic Sea | *Olelea marilimosa* strain KMM 6714 (KC247324.1, 99%) | Bacteroidetes | Flavobacteriia | Flavobacteriales | Flavobacteriaceae | Translucent, round | +++ | + |
| 270     | M. leidyi Baltic Sea | *Bacillus aryabhattai* strain MF−90 (MH177254.1, 99%) | Firmicutes | Bacillli | Bacillales | Bacillaceae | Black, round | - | - |
| 264     | M. leidyi Baltic Sea | *Exiguobacterium acetylicum* (MK478815.1, 99%) | Firmicutes | Bacillli | Bacillales | Bacillaceae | Orange, round | - | - |
| 51      | M. leidyi Baltic Sea | *Staphylococcus epidermidis* strain C2 (MH304282.1, 92%) | Firmicutes | Bacillli | Bacillales | Staphylococcaceae | Yellow, roundish-smeary | - | - |
| 269     | M. leidyi Baltic Sea | *Leisingera daeponensis* DSM 23529 strain TF−218 (NR_044026.1, 99%) | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | Translucent, yellow, oval | - | - |
| 62      | M. leidyi Baltic Sea | *Sagnostula* sp. BG−9-E2 (KF560336.1, 89%) | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | Yellowish, oval | - | - |
| 229     | M. leidyi Baltic Sea | *Shewanella algicola* (NR_149298.1, 99%) | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteraceae | Red, round | +++ | + |
| 228     | M. leidyi Baltic Sea | *Shewanella putrefaciens* (MH304323.1, 90%) | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteraceae | Yellow, round | ++ | ++ |
| 248     | M. leidyi Baltic Sea | *Shewanella putrefaciens* strain NCTC10737 (KF798527.1, 99%) | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteraceae | White-yellow, round | - | - |
| 237     | M. leidyi Baltic Sea | *Shewanella* sp. KMM 6721 (KC247331.1, 99%) | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteraceae | Red, round | ++ | - |
| 247     | M. leidyi Baltic Sea | *Shewanella* sp. Man17.1 (LR134321.1, 98%) | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteraceae | Translucent yellow, round | +++ | - |
| 260     | M. leidyi Baltic Sea | *Shewanella* sp. (KJ922533.1, 89%) | Proteobacteria | Betaproteobacteria | Alteromonadales | Oxalobacteraceae | White-red, round | +++ | + |
| 221     | M. leidyi Baltic Sea | *Aeromonas salmonicida* (HG941669.1, 98%) | Proteobacteria | Gammaproteobacteria | Aeromonadales | Aeromonadaceae | Translucent, round | ++ | - |
| Isolate | Origin       | Best homologue based on 16S full-length rRNA gene (Accession No., identity)                                                                 | Taxonomic classification                                                                 | Colony morphology                                                                 | QQ activity |
|---------|--------------|----------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------|-------------|
|         |              |                                                                                                                                        | Phylum                                                                                   | Class                                      | Order          | Family                | morphology  | AHL   | Al-2 |
| 53      | M. leidyi Baltic Sea | Alteromonas naphthalenivorans strain ACBC117 (MK156421.1, 96%)                                                                         | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Alteromonadaceae | White, roundish-smeary | ++   | -    |
| 60      | M. leidyi Baltic Sea | Alteromonas sp. 2c3 (AJ294361.1, 99%)                                                                                                    | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Alteromonadaceae | White, round, smeary    | ++   | -    |
| 223     | M. leidyi Baltic Sea | Uncultured Alteromonas sp. clone G9UC_PoM_0m_07 (KP076503.1, 98%)                                                                         | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Alteromonadaceae | White with black center, round | ++   | -    |
| 56      | M. leidyi Baltic Sea | Colwellia sp. BSs20120 (EU330346.1, 99%)                                                                                                  | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Colwelliaceae      | Light orange, round      | -    | -    |
| 254     | M. leidyi Baltic Sea | Pantoea agglomerans strain SXAU-S1 (MK875137.1, 96%)                                                                                      | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Enterobacteriales | Enterobacteriaceae | Red, round                | +++  | -    |
| 225     | M. leidyi Baltic Sea | Acinetobacter sp. (MH796223.1, 99%)                                                                                                      | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Halobacteriales | Moraxellaceae       | White, spreading          | -    | -    |
| 261     | M. leidyi Baltic Sea | Psychrobacter cryohalolentis (MH712970.1, 96%)                                                                                             | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Halobacteriales | Moraxellaceae       | White, spreading          | -    | -    |
| 222     | M. leidyi Baltic Sea | Marinomonas pontica (MG780341.1, 100%)                                                                                                    | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Oceanospirillae | Oceanospirillaceae | Translucent, round      | +++  | -    |
| 55      | M. leidyi Baltic Sea | Marinomonas sp. QHL13 (JQ809718.1, 98%)                                                                                                   | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Oceanospirillae | Oceanospirillaceae | Translucent, round      | +++  | -    |
| 262     | M. leidyi Baltic Sea | Oceanospirillae bacterium S-1-3 (AB550533.1, 99%)                                                                                         | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Oceanospirillae | Oceanospirillaceae | Translucent, round      | +++  | -    |
| 224     | M. leidyi Baltic Sea | Pseudoalteromonas lipolytica (MH725436.1, 97%)                                                                                                | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Pseudoalteromonadaceae | White, round              | +++  | +    |
| 232     | M. leidyi Baltic Sea | Pseudoalteromonas sp. (JQ406678.1, 99%)                                                                                                    | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Pseudoalteromonadaceae | Orange, round             | +    | -    |
| 234     | M. leidyi Baltic Sea | Pseudoalteromonas sp. 1.2015MBL_MicDiv (CP012738.1, 99%)                                                                                   | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Pseudoalteromonadaceae | Black, round              | +++  | -    |
| 240     | M. leidyi Baltic Sea | Pseudoalteromonas sp. (EU330378.1, 99%)                                                                                                   | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Pseudoalteromonadaceae | Yellow, round             | +++  | -    |
| 241     | M. leidyi Baltic Sea | Pseudoalteromonas sp. (MK421604.1, 99%)                                                                                                   | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Pseudoalteromonadaceae | White, round             | -    | -    |
| 250     | M. leidyi Baltic Sea | Pseudoalteromonas sp. (FR821214.1, 99%)                                                                                                   | Proteobacteria                                                                         | Gammaproteobacteria                                                                 | Alteromonadales | Pseudoalteromonadaceae | Violet, round             | +++  | -    |
| Isolate | Origin          | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|----------------|----------------------------------------------------------------------------|--------------------------|------------------|-------------|
|         |                |                                                                             | Phylum                   | Class            | Order       | Family                  |                          |
|         |                |                                                                             |                          |                  |             |                         |                          |
| 243     | M. leidyi Baltic Sea | *Pseudoalteromonas tunicata* (KY319053.1, 99%)                              | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Pseudoalteromonadaceae | Black, round | + | - |
| 251     | M. leidyi Baltic Sea | *Pseudoalteromonas tunicata* (KY319053.1, 99%)                              | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Pseudoalteromonadaceae | White, round | - | - |
| 256     | M. leidyi Baltic Sea | *Pseudoalteromonas tunicata* (KY319053.1, 99%)                              | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Pseudoalteromonadaceae | Yellow, round | + | - |
| 219     | M. leidyi Baltic Sea | *Pseudoalteromonas tunicata* (KY319053.1, 100%)                             | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Pseudoalteromonadaceae | Violet, round | +++ | - |
| 235     | M. leidyi Baltic Sea | *Shewanella baltica* strain 20LCp98 (MK642562.1, 99%)                       | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Shewanellaceae         | Yellow, round | ++ | - |
| 233     | M. leidyi Baltic Sea | *Shewanella baltica* BA175 (CP002767.1, 97%)                                 | Proteobacteria           | Gammaproteobacteria | Alteromonadales | Shewanellaceae         | White, round | - | - |
| 265     | M. leidyi Baltic Sea | *Pseudomonas sp.* (HG738847.1, 94%)                                         | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae       | Yellow, round | + | - |
| 249     | M. leidyi Baltic Sea | *Pseudomonas sp.* P4708 (MK104126.1, 99%)                                     | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae       | Black, round | ++ | - |
| 246     | M. leidyi Baltic Sea | *Pseudomonas veronii* strain Pvy (CP039631.1, 99%)                          | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae       | White-yellow, spreading | +++ | - |
| 213     | M. leidyi Baltic Sea | *Vibrio sp.* strain 201709CJkop−94 (MG867544.1, 98%)                        | Proteobacteria           | Gammaproteobacteria | Vibrionales      | Vibrionaceae           | Yellowish, round | +++ | + |
| 242     | M. leidyi Baltic Sea | *Vibrio sp.* S5SW(FK418795.1, 99%)                                          | Proteobacteria           | Gammaproteobacteria | Vibrionales      | Vibrionaceae           | Translucent, round | - | - |
| 72      | M. leidyi Baltic Sea husbandry | *Microbacterium sp.* MN2-1 (JQ396523.1, 99%)                                | Actinobacteria           | Actinobacteria     | Actinomycetales  | Microbacteriaceae      | Yellowish-white, round |                   |
| 257     | M. leidyi Baltic Sea husbandry | *Chryseobacterium sp.* (HQ9113691, 99%)                                      | Bacteroidetes            | Flavobacteria     | Flavobacterialae | Flavobacteriaceae      | Yellow-red, round | ++ | - |
| 227     | M. leidyi Baltic Sea husbandry | *Staphylococcus warneri* strain BPB10 (MK203007.1, 99%)                     | Firmicutes               | Bacilli            | Bacillae        | Staphylococcaceae      | Yellow-red, round | - | - |
| 71      | M. leidyi Baltic Sea husbandry | *Ochrobactrum anthropi* (MK284516.1, 99%)                                   | Proteobacteria           | Alphaproteobacteria | Rhizobiales     | Brucellaceae           | White, round |                   |
| 69      | M. leidyi Baltic Sea husbandry | *Falsirhodobacter deserti* strain W402 (KF268394.1, 99%)                   | Proteobacteria           | Alphaproteobacteria | Rhodobacterales | Rhodobacteriaceae      | Orange, round |                   |
| 67      | M. leidyi Baltic Sea husbandry | *Shewanella sp.* KMM 6721 (KC247331.1, 99%)                                  | Proteobacteria           | Betaproteobacteria | Alteromonadales | Oxalobacteriaceae      | Translucent, round | +++ | ++ |
| 217     | M. leidyi Baltic Sea husbandry | *Hydrogenophaga taeniospiralis* (AB795550.1, 99%)                           | Proteobacteria           | Betaproteobacteria | Burkholderiales | Comamonadaceae         | Translucent-red, round | - | - |
| Isolate | Origin | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|--------|--------------------------------------------------------------------------|------------------------|-------------------|-------------|
| 66      | M. leidyi Baltic Sea husbandry | *Alteromonas genovensis* strain DB29 (KM699284.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | White, round | ++ - |
| 267     | M. leidyi Baltic Sea husbandry | *Alteromonas macleodii* strain BF-12 (KT428054.1, 98%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | White, spreading | + - |
| 244     | M. leidyi Baltic Sea husbandry | Thalassomonas sp. (KC247368.1, 97%) | Proteobacteria Gammaproteobacteria Alteromonadales Colwelliaceae | Translucent-yellow, round | - - |
| 65      | M. leidyi Baltic Sea husbandry | Pseudoalteromonas sp. Strain B403 (MG388129.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | White, smearable | + + |
| 239     | M. leidyi Baltic Sea husbandry | Pseudoalteromonas sp. (LN871566.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | White-yellow, round | + - |
| 226     | M. leidyi Baltic Sea husbandry | *Pseudomonas aeruginosa* | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Light yellow, round | ++ - |
| 68      | M. leidyi Baltic Sea husbandry | *Vibrio gigantis* strain LPB0246 (MH989593.1, 98%) | Proteobacteria Gammaproteobacteria Vibrionales Vibrionaceae | Light orange, round | +++ + |
| 70      | M. leidyi Baltic Sea husbandry | *Vibrio gigantis* strain LPB0246 (MH989593.1, 99%) | Proteobacteria Gammaproteobacteria Vibrionales Vibrionaceae | White, orange in center, round | ++ - |
| 253     | Ambient water Baltic Sea | *Fictibacillus* sp. (MK101065.1, 98%) | Firmicutes Bacillales Bacillaceae | Translucent yellow, round | - - |
| 259     | Ambient water Baltic Sea | Pseudoalteromonas sp. (KF188488.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | Red, round | ++ - |
| 230     | Ambient water Baltic Sea | Pseudoalteromonas sp. P55 (EU935099.1, 98%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | White, round | +++ - |
| 266     | Ambient water Baltic Sea | Pseudoalteromonas tunicata strain D2 (CP031961.1, 97%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | Translucent yellow, round | + - |
| 214     | Ambient water Baltic Sea | Serratia plymuthica (KR611045.1, 99%) | Proteobacteria Gammaproteobacteria Enterobacteriales Yersiniaceae | Red, round | +++ - |
| 231     | Ambient water Baltic Sea | *Pseudomonas* sp. (JF766700.1, 99%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | White, spreading | - - |
| 156     | Artificial Seawater 18 PSU | *Micrococcus* sp. strain Actino-43 (MH671539.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Micrococcaceae | Yellow, round | |
| 168     | Artificial Seawater 18 PSU | *Salinibacterium* sp. BS-14B (KX000029.1, 99%) | Actinobacteria Actinobacteria Actinomycetales Microbacteriaceae | Yellow, round | |
| Isolate | Origin                | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|-----------------------|---------------------------------------------------------------------------|--------------------------|-------------------|-------------|
|         |                       |                                                                            | Phylum | Class                   | Order | Family              |                  |
| 143     | Artificial Seawater   | *Rhodococcus yunnanensis* strain IHBB 9200 (KR085831.1, 99%)             | Actinobacteria           | Actinobacteria       | Actinomycetales  | Nocardiaceae     | White, round    |
| 169     | Artificial Seawater   | *Luteococcus japonicus* strain DSM 10546 (NR_119351.1, 99%)               | Actinobacteria           | Actinobacteria       | Propionibacterales | Propioni-bacteriaceae | Orange, roundish|
| 157     | Artificial Seawater   | *Corynebacterium* sp. NML96-0244 (GU238410.1, 99%)                       | Actinobacteria           | Actinomycetales      | Corynebacteriaceae | Corynebacterium   | White, round    |
| 160     | Artificial Seawater   | *Staphylococcus aureus* JCM2874 (LC420068.1, 99%)                          | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | Yellow, round   |
| 162     | Artificial Seawater   | *Staphylococcus aureus* (CP039759.1, 99%)                                 | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | Orange, smeryy  |
| 149     | Artificial Seawater   | *Staphylococcus saprophyticus* strain AB697718.1 (MH491313.1, 98%)       | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | White, smeryy   |
| 145     | Artificial Seawater   | *Staphylococcus* sp. strain JLT103 (KX989231.1, 99%)                      | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | White, round ++ |
| 150     | Artificial Seawater   | *Staphylococcus* sp. strain JLT103 (KX989231.1, 99%)                      | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | White, round    |
| 151     | Artificial Seawater   | *Staphylococcus* sp. strain GD01 (MG214350.1, 99%)                        | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | White line, round|
| 152     | Artificial Seawater   | *Staphylococcus* sp. DVRSG-2 (KF779128.1, 99%)                            | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | White line, smeryy|
| 146     | Artificial Seawater   | Uncultured *Staphylococcus* sp. clone HEM419 (MF1481811, 99%)             | Firmicutes               | Bacilli              | Bacillales         | Staphylococcaceae | White, round    |
| 138     | Artificial Seawater   | *Celeribacter* sp. R−52665 (KT185135.1, 99%)                              | Proteobacteria           | Alphaproteobacteria  | Rhodobacterales   | Rhodobacteraceae  | White, smeryy   |
| 164     | Artificial Seawater   | *Celeribacter* sp. CY411 (KP201135.1, 99%)                                | Proteobacteria           | Alphaproteobacteria  | Rhodobacterales   | Rhodobacteraceae  | White, round    |
| 165     | Artificial Seawater   | *Celeribacter* sp. R−52665 (KT185135.1, 99%)                              | Proteobacteria           | Alphaproteobacteria  | Rhodobacterales   | Rhodobacteraceae  | White, light yellow center, smeryy |
| 166     | Artificial Seawater   | *Celeribacter* sp. R−52665 (KT185135.1, 99%)                              | Proteobacteria           | Alphaproteobacteria  | Rhodobacterales   | Rhodobacteraceae  | White, smeryy   |
| 147     | Artificial Seawater   | *Phaeobacter gallaeciensis* strain P63 (CP010784.1, 97%)                  | Proteobacteria           | Alphaproteobacteria  | Rhodobacterales   | Rhodobacteraceae  | White, round    |
| 137     | Artificial Seawater   | *Sulfitobacter* sp. SAG13 (KX268604.1, 99%)                               | Proteobacteria           | Alphaproteobacteria  | Rhodobacterales   | Rhodobacteraceae  | White, smeryy   |

(Continues)
| Isolate | Origin   | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|----------|---------------------------------------------------------------------------|--------------------------|-------------------|-------------|
|         |          |                                                                            | Phylum                    | Class             | Order        | Family         | AHL | AI-2 |
| 163     | Artificial Seawater 18 PSU | Aestuariibacter halophilus (LC221844.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | Orange, round     | +++ -         |
| 139     | Artificial Seawater 18 PSU | Alteromonas sp. JAM-GA15 (AB526338.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | Orange, round     | ++ -          |
| 140     | Artificial Seawater 18 PSU | Uncultured Alteromonas sp. clone PD22_850 (HM140647.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | White, smearable | ++ -          |
| 148     | Artificial Seawater 18 PSU | Uncultured Alteromonas sp. clone PD3_1355 (HM140650.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | White, smearable | + -           |
| 154     | Artificial Seawater 18 PSU | Uncultured Alteromonas sp. clone C146500156 (JX531176.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | White, smearable | ++ -          |
| 155     | Artificial Seawater 18 PSU | Marinobacter sp. Strain AN17_20.3 (MK780031.1, 98%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | White-yellowish, round | +++ -         |
| 153     | Artificial Seawater 18 PSU | Paraglaciecola sp. strain M202 (MF443579.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | White, round     | - -           |
| 167     | Artificial Seawater 18 PSU | Pseudoalteromonas sp. BSI20316 (DQ492738.1, 93%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | White-yellowish, round | ++ -          |
| 135     | Artificial Seawater 18 PSU | Moraxella sp. strain TS14 (MK591880.1, 99%) | Proteobacteria Gammaproteobacteria Halobacteriales Moraxellaceae | White, round     | ++ -          |
| 134     | Artificial Seawater 18 PSU | Pseudomonas anguilliseptica (JX177685.1, 99%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Light yellow, round | +++ -         |
| 136     | Artificial Seawater 18 PSU | Pseudomonas anguilliseptica (JX177685.1, 99%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | White-yellowish, round | - -           |
| 141     | Artificial Seawater 18 PSU | Pseudomonas cutrocinegasensis (JN644592.1, 98%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Yellow, round    | - -           |
| 132     | Artificial Seawater 18 PSU | Pseudomonas fluorescens strain G21 (MK874851.1, 98%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Light orange, smearable | - -           |
| 133     | Artificial Seawater 18 PSU | Pseudomonas sp. MBEF06 (AB733556.1, 97%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Light orange, round | - -           |
| 142     | Artificial Seawater 18 PSU | Pseudomonas sp. Iranica GH10 (KF742672.1, 97%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Orange, smearable | + -           |
| Isolate | Origin          | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity | AHL   | AI−2 |
|---------|-----------------|---------------------------------------------------------------------------|--------------------------|-------------------|-------------|-------|------|
|         |                 |                                                                           | Phylum                   |                   |             |       |      |
|         |                 |                                                                           | Class                    |                   |             |       |      |
|         |                 |                                                                           | Order                    |                   |             |       |      |
|         |                 |                                                                           | Family                   |                   |             |       |      |
| 158     | Artificial Seawater 18 PSU | *Pseudomonas* sp. Iranica GH10 (KF742672.1, 96%)                           | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Light yellow, smeary | +   | -   |
| 159     | Artificial Seawater 18 PSU | *Pseudomonas* sp. Iranica GH10 (KF742672.1, 96%)                           | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Light yellow, smeary | +   | -   |
| 171     | Artificial Seawater 18 PSU | *Pseudomonas* sp. Iranica GH10 (KF742672.1, 97%)                           | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellowish, round     | ++  | -   |
| 170     | Artificial Seawater 18 PSU | *Pseudomonas* sp. I-A-R-28 (KT922041.1, 99%)                               | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellow, round        | +++ | -   |
| 161     | Artificial Seawater 18 PSU | *Pseudomonas zhaodongensis* strain MT325 (MH725487.1, 97%)                 | Proteobacteria           | Gammaproteobacteria | Pseudomonadales | Pseudomonadaceae | Yellow-orange, smeary | -   | -   |
| 172     | Artificial Seawater 30 PSU | *Brevibacterium frigoritolerans* strain MER_TA_42 (KT719448.1, 99%)       | Actinobacteria           | Actinobacteria      | Actinomycetales  | Brevibacteriaceae | White, round         | -   | -   |
| 179     | Artificial Seawater 30 PSU | *Brevibacterium frigoritolerans* strain MER_TA_133 (KT719536.1, 99%)      | Actinobacteria           | Actinobacteria      | Actinomycetales  | Brevibacteriaceae | White, round         | -   | -   |
| 209     | Artificial Seawater 30 PSU | *Brevibacterium frigoritolerans* IHBB 6528 (KF758571.1, 99%)              | Actinobacteria           | Actinobacteria      | Actinomycetales  | Brevibacteriaceae | White, roundish      | -   | -   |
| 210     | Artificial Seawater 30 PSU | *Brevibacterium frigoritolerans* strain DSM 8801 (T) (MK424281.1, 99%)    | Actinobacteria           | Actinobacteria      | Actinomycetales  | Brevibacteriaceae | White, smeary        | ++  | -   |
| 192     | Artificial Seawater 30 PSU | *Microbacterium* sp. JL1103 (DQ985063.1, 99%)                              | Actinobacteria           | Actinobacteria      | Actinomycetales  | Microbacteriaceae | Light orange, smeary | -   | -   |
| 182     | Artificial Seawater 30 PSU | *Micrococcus* sp. EF1B-B144 (KCS545358.1, 99%)                            | Actinobacteria           | Actinobacteria      | Actinomycetales  | Microbacteriaceae | Pink, round          | -   | -   |
| 173     | Artificial Seawater 30 PSU | *Salinibacterium amurskyense* strain BBCC2678 (MK224796.1, 95%)             | Actinobacteria           | Actinobacteria      | Actinomycetales  | Microbacteriaceae | Light orange-white, round | -   | -   |
| 178     | Artificial Seawater 30 PSU | *Salinibacterium amurskyense* strain BBCC2678 (MK224796.1, 99%)             | Actinobacteria           | Actinobacteria      | Actinomycetales  | Microbacteriaceae | Yellowish, round     | -   | -   |
| 175     | Artificial Seawater 30 PSU | *Micrococcus* sp. strain Actino−43 (MH671539.1, 99%)                         | Actinobacteria           | Actinobacteria      | Actinomycetales  | Micrococcaceae   | Orange, roundish-smeary | -   | -   |
| 181     | Artificial Seawater 30 PSU | *Chryseobacterium* sp. WW-RP5 (KJ958497.1, 96%)                             | Bacteroidetes            | Flavobacteria       | Flavobacteriales | Flavobacteriaceae | Light orange, smeary | -   | -   |
| 177     | Artificial Seawater 30 PSU | *Marinobacter* sp. SDRB-Phe2 (MG456900.1, 98%)                             | Bacteroidetes            | Flavobacteria       | Flavobacteriales | Flavobacteriaceae | Yellow, smeary       | +   | -   |
| Isolate | Origin  | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|---------|---------------------------------------------------------------------------|--------------------------|-------------------|-------------|
|         |         |                                                                           | Phylum | Class | Order | Family |                   | AHL | AI-2 |
| 199     | Artificial Seawater 30 PSU | *Maribacter* sp. SDRB-Phe2 (MG456900.1, 93%) | Bacteroidetes | Flavobacteria | Flavobacteriales | Flavobacteriaceae | White, round, smeary in high density | -   | -   |
| 202     | Artificial Seawater 30 PSU | *Maribacter* sp. SDRB-Phe2 (MG456900.1, 99%) | Bacteroidetes | Flavobacteria | Flavobacteriales | Flavobacteriaceae | White, round, small | -   | -   |
| 189     | Artificial Seawater 30 PSU | *Bacillus* sp. strain KST183 (KX989449.1, 97%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | Pink, round | -   | -   |
| 193     | Artificial Seawater 30 PSU | *Bacillus* sp. SG109 (AB425366.1, 99%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | White, roundish | ++  | -   |
| 195     | Artificial Seawater 30 PSU | *Bacillus* sp. T1T (AM983464.1, 99%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | Translucent, round | -   | -   |
| 206     | Artificial Seawater 30 PSU | *Bacillus* sp. strain Sf1 (JN975958.1, 99%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | White-orange, brownish, smeary | -   | -   |
| 207     | Artificial Seawater 30 PSU | *Bacillus* sp. KP067r (KT200468.1, 100%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | White-orange, brownish, smeary | -   | -   |
| 184     | Artificial Seawater 30 PSU | *Bacillus thuringiensis* strain 263AG8 (KF836531.1, 99%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | White, brownish center, round | -   | -   |
| 187     | Artificial Seawater 30 PSU | *Bacillus vietnamensis* strain M52016 (KX683881.1, 99%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | Pink, smeary | -   | -   |
| 212     | Artificial Seawater 30 PSU | *Fictibacillus phosphorivorans* HT5 (MG547923.1, 98%) | Firmicutes | Bacilli | Bacillales | Bacillaceae | Translucent, smeary | -   | -   |
| 174     | Artificial Seawater 30 PSU | *Staphylococcus aureus* strain AR_475 (CP030323.1, 93%) | Firmicutes | Bacilli | Bacillales | Staphylococcaceae | White, round | -   | -   |
| 180     | Artificial Seawater 30 PSU | *Staphylococcus aureus* JCM 2874 (LC420068.1, 99%) | Firmicutes | Bacilli | Bacillales | Staphylococcaceae | White, brownish center, round | +++ | -   |
| 191     | Artificial Seawater 30 PSU | *Celeribacter* sp. CY411 (KP201135.1, 99%) | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | White, round | -   | -   |
| 188     | Artificial Seawater 30 PSU | *Sulfitobacter pseudonitrosochae* strain H3 (KF006321.2, 95%) | Proteobacteria | Alphaproteobacteria | Rhodobacterales | Rhodobacteraceae | White, smeary | +++ | -   |
| Isolate | Origin | Best homologue based on 16S full-length rRNA gene (Accession No., identity) | Taxonomic classification | Colony morphology | QQ activity |
|---------|--------|-------------------------------------------------|-------------------------|-------------------|-------------|
|         |        | Phylum Class Order Family AHL AI-2              |                         |                   |             |
| 204     | Artificial Seawater 30 PSU | *Sulfobacter* sp. strain B28-5 (MG388121.1, 99%) | Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae | White, round, smear in high density | -  |
| 185     | Artificial Seawater 30 PSU | *Alteromonas* sp. strain DT074 (MG099550.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | Orange, round | ++ |
| 186     | Artificial Seawater 30 PSU | *Alteromonas* sp. strain DT074 (MG099550.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | Brownish, round | ++ |
| 190     | Artificial Seawater 30 PSU | *Alteromonas* sp. 76-1 (LR136958.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Alteromonadaceae | Light orange, round | -  |
| 208     | Artificial Seawater 30 PSU | *Pseudoalteromonas prydzensis* strain S2A2 (MH362721.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | White-yellowish, smear | + |
| 200     | Artificial Seawater 30 PSU | *Pseudoalteromonas* sp. ZB23-4 (MG388173.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | Grey-white, round | ++ |
| 203     | Artificial Seawater 30 PSU | *Pseudoalteromonas* sp. strain SJS4-1 (MG383479.1, 99%) | Proteobacteria Gammaproteobacteria Alteromonadales Pseudoalteromonadaceae | White, round, smear in high density | ++ |
| 201     | Artificial Seawater 30 PSU | *Cobetia marina* strain QD34 (KF933690.1, 99%) | Proteobacteria Gammaproteobacteria Halomonadaceae Cobetia | White, round | + |
| 194     | Artificial Seawater 30 PSU | *Cobetia* sp. S2094 (FJ457279.1, 89%) | Proteobacteria Gammaproteobacteria Halomonadaceae Cobetia | Pink, round | + |
| 176     | Artificial Seawater 30 PSU | *Halomonas* sp. strain IceBac 363 (KF306352.1, 99%) | Proteobacteria Gammaproteobacteria Oceanospirillales Halomonadaceae | Light orange, round | - |
| 197     | Artificial Seawater 30 PSU | *Pseudomonas* sp. TKCM64 (LC194999.1, 99%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | White, round | - |
| 205     | Artificial Seawater 30 PSU | *Pseudomonas* sp. MR3 (JN082728.1, 83%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | White, round | - |
| 196     | Artificial Seawater 30 PSU | *Pseudomonas syringae pv. atrofaciens* strain GN-In (MK141010.1, 94%) | Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadaceae | Yellow, round | ++ |

Bacteria were isolated by classical enrichment on agar plates and taxonomically classified based on partial 16S rRNA gene sequences. QQ activities of isolates are stated in (−) no activity, (+) low, (++ mid, and (+++) high activity against acyl-homoserine lactone (AHL) and autoinducer-2 (AI-2); light grey highlighted isolates were not used for functional assays.