**Supplementary Materials**

**Table S1.** List of studies that isolated and identified sponge-associated bacteria using culture-dependent techniques.

**Table S2.** Culture characteristics of *Haliclona* sp. 1KI cultured bacteria.

**Table S3.** Culturable bacteria associated with *Haliclona* sp. 1KI and their nearest match from the GenBank (March 2020).

**Table S4.** Sampling site, date and taxonomic identification of sponge sample collected from Kuwait marine environment.

**Table S5.** The documented numbers of sponges-associated prokaryotes raw 16S rRNA amplicon next generation sequencing reads, prokaryotic operational taxonomic units (OTUs) and genera.

**Table S6.** Number of spots containing the filtered bacterial sequence (cultured bacterial isolates) found in *Haliclona* sp. NGS reads (SRX14840950).

**Table S7.** Antimicrobial activity of bacterial isolates obtained from in *Haliclona* sp. 1Kl.

**Figure S1.** Sponge samples collected from Kuwait marine environment and identified as (A) *Haliclona* sp., sample code 1KI, (B) *Haliclona* sp. sample code 5KI (C) *Chondrilla australiensis* sample code 4KI, (D) *Niphates sp.*1sample code 2NW, (E) *Niphates sp.*2sample code 5NW, (F) *Niphates sp.3* sample code 2KI, (G) *Amphimedon sp.* sample code 6KI. Sampling site and date: KI= Kubbar Island (August, 2017), NW= Nuwaiseeb intertidal (February, 2018).

**Figure S2.** Rarefaction curves of 16S rRNA gene diversity for 7 sponge sample collected from Kuwait.

**Table S1.** List of studies that isolated and identified sponge-associated bacteria using culture-dependent techniques.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Location** | **Sponge species** | **Types of culturing media** | **Selected and dominant bacterial phyla** | **Reference** |
| Mediterranean SeaLimski kanalBanjoleSt. Giovanni | *Chondrilla nucula, Tethya aurantium,**Suberites domuncula, Acanthella acuta*.*Chondrosia reniformis**Clathrina clathris, Agelas oroides,**Ircinia* sp. | Semisynthetic polycarbon agar (HSPC), GPYNS agar, Chitin agar, Actinomycetes isolation agar (AIA), FS agar with 4 different YE concentration | Proteobacteria(Alphaproteobacteria, Gammaproteobacteria), and Actinobacteria, | Muscholl-silberhorn et al. (2008) |
| South east India.Vizhinjam coast | *Dendrilla nigra* | 14 different culturing media  | Actinobacteria and Proteobacteria | Selvin et al. (2009) |
| Brazil Cagarras Archipelago and Praia Vermelha beach | *Clathrina aurea, Dragmacidon reticulatus, Geodia corticostylifera, Haliclona sp., Mycale microsigmatosa, Paraleucilla magna, petromica citrina, Polymastia janeirensis and Tedania ignis* | Brain heart infusion (BHI) media, Marine Agar (MA), Marine agar in seawater (MSW) | Proteobacteria(Alphaproteobacteria, Gammaproteobacteria), and Firmicutes | Santos et al. (2010) |
| United states of AmericaMonterey, California | *Haliclona* (*gellius*) sp. | agar plates (nineteen different culturing media),Liquid media and floating filters. | Proteobacteria(Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria and Deltaproteobacteria),Bacteroidetes, Actinobacteria, Firmicutes, Verrucomicrobia, and Planctomycetes | Sipkema et al. (2011) |
| Southern coast of Portugal | *Sarcotragus spinosulus****,****Ircinia variabilis* | MA | Proteobacteria,Bacteriodetes,Firmicutes, and Actinobacteria | Esteves et al. (2013) |
| Eastern Mediterranean coast of TurkeyBeşparmak Island, Dana Island and Akkuyu Bay | *Ircinia variabilis, Petrosia ficiformis, Axinella damicornis, Dysidea avara, Agelas oroides, Sarcotragus spinosulus, Ircinia* sp., *Chondrosia reniformis, Sarcotragus fasciculatus, Phorbas fictitious, Axinella polypoides, Spirastrella cunctatrix,Axinella damicornis, Chondrilla nucula*, and *Oscarella lobularis.* | M1, M6, R2A, Actinomycetes isolation agar, SE medium (sponge extract), AW medium (agar water), ISP4 (with 6% NaCl), and SMP | A total of 7578 Actinomycetes colonies. | Öner et al. (2014) |
| Abra Harbor, Guam | *Rhabdastrella globostellata* | Diffusion growth chambers  | Proteobacteria (Alpha and Gammaproteobacteria), Bacteroidetes, Actinobacteria and Firmicutes | Steinert et al., (2014) |
| BrazilComprida Island and Pargos Island | *Oscarella* spp | BHI and MA | Proteobacteria (Gammaproteobacteria) and Firmicutes (Bacilli) | Laport et al. (2017) |
| South AfricaAlgoa Bay, Port Elizabeth. | *Isodictya compressa* and *Higginsia bidentifera* | 23 different culturing media  | Actinobacteria, Firmicutes and Proteobacteria (Alphaproteobacteria andGammaproteobacteria). | Matobole et al. (2017) |
| Kenting National Park, southern Taiwan | *Theonella swinhoei* | Soil agar, Gause modified agar, actinomycete isolation agar, M1A agar, glucose-peptone-yeast extract agar, Gause mineral agar, and peptone-yeast extract agar. | Firmicutes, Actinobacteria, and Proteobacteria | Kuo et al. (2019) |
| South-west Iceland | *Halichondria panicea* | MA | Proteobacteria (Alpha and Gammaproteobacteria), Flavobacteriia, Planctomycetia, Verrucomicrobiae. | Knobloch et al. (2019) |
| Southeast coast of India | *Pirastrella inconstans*, *Cliona* sp., *Haliclona implexa*, *Callyspongia diffusa*, *Stylissa* sp., *Orina sagittaria*, *Tethya diploderma* and 2 unidentified sponges. | MA and seawater nutrient agar (SWNA). | Proteobacteria (Gammaproteobacteria), Firmicutes and Actinobacteria | Rajasabapathy et al. (2020) |

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**Figure S1.** Sponge samples collected from Kuwait marine environment and identified as (A) *Haliclona* sp., sample code 1KI, (B) *Haliclona* sp. sample code 5KI (C) *Chondrilla australiensis* sample code 4KI, (D) *Niphates sp.*1sample code 2NW, (E) *Niphates sp.*2sample code 5NW, (F) *Niphates sp.3* sample code 2KI, (G) *Amphimedon sp.* sample code 6KI. Sampling site and date: KI= Kubbar Island (August, 2017), NW= Nuwaiseeb intertidal (February, 2018).

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**Figure S2.** Rarefaction curves of 16S rRNA gene diversity for 7 sponge sample collected from Kuwait.

**Table S2.** Culture characteristics of *Haliclona* sp. 1KI cultured bacteria.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Isolate** | **Colony size** | **Color** | **Form** | **Margin** | **Elevation** | **Gram stain** | **Cell morphology** | **Cell size (µm)** |
| **Length** | **Width** |
| KS55 | m | Beige | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS59 | m | Beige | Irregular | Undulate | Flat | G-ve | Rod | 2 | 1 |
| KS58 | pp | Beige | Circular | Entire | Convex | G-ve | Rod | 4 | 0.8 |
| KS42 | m | Beige | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS50 | s | Cream  | Circular | Entire | Convex | G+ve | Rod | 3 | 1 |
| KS48 | s | Cream  | Circular | Entire | Convex | G+ve | Rod | 3.5 | 1 |
| KS9 | m | Cream  | Circular | Entire | Convex | G-ve | Coccobacilli | 1.5 | 1 |
| KS7 | m | Cream  | Circular | Entire | Convex | G-ve | Coccobacilli | 1.4 | 1 |
| KS18 | pp | Cream  | Circular | Entire | Raised | G-ve | Rod | 2.5 | 1 |
| KS30 | m | Cream  | Circular | Entire | Convex | G-ve | Rod | 3 | 1 |
| KS26 | m | Cream  | Circular | Entire | Convex | G-ve | Rod | 2.5 | 1 |
| KS27 | s | Cream  | Circular | Entire | Raised | G-ve | Rod | 3 | 1 |
| KS28 | m | Cream  | Circular | Entire | Convex | G-ve | Coccobacilli | 1.5 | 1 |
| KS38 | m | cream | circular | entire | convex | G-ve | Rod | 2 | 1 |
| KS44 | s | Cream  | Circular | Entire | Convex | G-ve | Rod | 3 | 1 |
| KS54 | m | Translucent cream | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS45 | s | Translucent Cream  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS16 | s | Translucent Cream  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS8 | pp | Translucent Cream  | Circular | Entire | Convex | G-ve | Rod | 4 | 1 |
| KS36 | s | Translucent Cream  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS37 | m | Translucent Cream  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS34 | m | Translucent Cream  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS52 | pp | Translucent Cream  | Circular | Entire | Convex | G-ve | Rod | 3 | 1 |
| KS49 | s | Translucent Cream  | Irregular  | Undulate | Raised | G+ve | Rod | 2.8 | 0.8 |
| KS40 | m | Translucent cream | Circular | Entire | Convex | G-ve | Rod | 2.5 | 1 |
| KS61 | pp | Translucent Cream  | Circular  | Entire | Convex | G-ve | Rod | 2.5 | 1 |
| KS31 | s | Translucent Cream - pink | Circular  | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS13 | s | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Long Rod | 5 | 2 |
| KS3 | s | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Rod | 3 | 1.5 |
| KS4 | m | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Coccobacilli | 1.5 | 1 |
| KS10 | s | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Rod | 2.5 | 1 |
| KS22 | L | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Coccobacilli | 1.5 | 1 |
| KS19 | l | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Rod | 2 | 1.5 |
| KS2 | m | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Coccobacilli | 1.5 | 1 |
| KS17 | m | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS32 | pp | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS29 | s | Translucent Cream -yellow | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS1 | s | Translucent Cream -orange  | Circular | Entire | Convex | G-ve | Rod | 3 | 1.5 |
| KS6 | s | Translucent Cream -orange  | Circular | Entire | Convex | G-ve | Long Rods | 5 | 0.8 |
| KS20 | s | Translucent Cream -orange  | Circular | Entire | Convex | G-ve | Long threads | 12 | 0.5 |
| KS24 | s | Translucent Cream -orange  | Irregular | Undulate | Raised | G-ve | Rod | 5 | 1 |
| KS12 | s | Translucent Cream -orange  | Circular | Entire | Convex | G-ve | Rod | 4 | 1.5 |
| KS25 | m | Translucent Cream -orange  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS11 | m | Translucent Cream -orange  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS33 | s | Translucent Cream -orange  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS5 | s | Translucent  | Irregular | Undulate | Raised | G-ve | Long Rods | 6 | 0.5 |
| KS15 | s | Translucent  | Irregular | Undulate | Raised | G-ve | Long threads | 12 | 0.4 |
| KS41 | s | Translucent  | Circular | Entire | Convex | G-ve | Long Rod | 6 | 1.5 |
| KS51 | m | Yellow | Circular | Entire | Convex | G+ve | Rod | 3 | 1.5 |
| KS53 | s | White | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |
| KS47 | s | White | Irregular  | Undulate | Raised | G+ve | Rod | 4 | 2 |
| KS57 | m | White | Circular | Entire | Convex | G-ve | Rod | 3 | 1 |
| KS14 | m | White | Circular | Entire | Convex | G-ve | Rod | 2.5 | 1.2 |
| KS39 | m | White | Circular | Entire | Convex | G-ve | Rod | 2.5 | 1 |
| KS46 | s | White | Circular | Entire | Convex | G+ve | Rod | 3 | 1 |
| KS60 | s | White | Circular | Entire | Raised | G+ve | Rod | 4 | 0.8 |
| KS56 | s | Orange  | Circular | Entire | Raised | G+ve | Rod | 2 | 1 |
| KS35 | m | Orange  | Circular | Entire | Convex | G-ve | Rod | 2 | 1 |

KS: Kuwait sponge. s: small. vpp: very pinpoint.

m: medium. pp: pinpoint. l: large.

**Table S3.** Culturable bacteria associated with *Haliclona* sp. 1KI and their nearest match from the GenBank (data retrieved from NCBI on March 2020).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Accession No.** | **E-value** | **Similarity %** | **Nearest GenBank match** | **Phylum** | **Base compared** | **Total base pair** | **Isolate name** |
| MG972446.1 | 0.0 | 100 | *Shewanella corallii* strain JKB2 | Proteobacteria | 487/487 | 487 | *Shewanella* sp. KS1 |
| MT269637.1 | 0.0 | 99 | *Vibrio brasiliensis* strain DS1907-1YS\_1\_2 | Proteobacteria | 486/490 | 490 | *Vibrio* sp. KS2 |
| CP031472.1 | 0.0 | 100 | *Vibrio coralliilyticus* strain RE22 | Proteobacteria | 465/465 | 465 | *Vibrio* sp. KS3 |
| CP031472.1 | 0.0 | 99 | *Vibrio coralliilyticus* strain RE22 | Proteobacteria | 482/484 | 484 | *Vibrio* sp. KS4 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 490/496 | 496 | *Ferrimonas* sp. KS5 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 483/487 | 487 | *Ferrimonas* sp. KS6 |
| JN871709.1 | 0.0 | 99 | *Vibrio brasiliensis* strain FD W9 | Proteobacteria | 490/497 | 497 | *Vibrio* sp. KS7 |
| MH283837.1 | 0.0 | 100 | *Pseudovibrio denitrificans* strain SCSIO\_43753 | Proteobacteria | 442/442 | 442 | *Pseudovibrio* sp. KS8 |
| KX418475.1 | 0.0 | 99 | *Vibrio harveyi* strain 50161 | Proteobacteria | 493/495 | 495 | *Vibrio* sp. KS9 |
| JN871710.1 | 0.0 | 99 | *Vibrio sinaloensis* strain FD O5-12 | Proteobacteria | 498/502 | 502 | *Vibrio* sp. KS10 |
| MK308628.1 | 0.0 | 99 | *Vibrio coralliilyticus* strain SC53 | Proteobacteria | 485/488 | 488 | *Vibrio* sp. KS11 |
| KY655377.1 | 0.0 | 99 | *Spongiobacter* sp. strain EA276 | Proteobacteria | 490/493 | 493 | *Spongiobacter* sp. KS12 |
| KY655377.1 | 0.0 | 99 | *Spongiobacter* sp. strain EA276 | Proteobacteria | 497/498 | 498 | *Spongiobacter* sp. KS13 |
| MF125195.1 | 0.0 | 99 | *Vibrio azureus* strain WUDI8 | Proteobacteria | 497/499 | 499 | *Vibrio* sp. KS14 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 470/475 | 475 | *Ferrimonas* sp. KS15 |
| MF417434.1 | 0.0 | 100 | *Shewanella corallii* strain fav-2-10-05 | Proteobacteria | 493/493 | 493 | *Shewanella* sp*.* KS16 |
| MF417426.1 | 0.0 | 100 | *Vibrio sinaloensis* strain F17C1 | Proteobacteria | 465/470 | 470 | *Vibrio* sp. KS17 |
| MG972446.1 | 0.0 | 100 | *Shewanella corallii* strain JKB2 | Proteobacteria | 495/495 | 495 | *Shewanella* sp*.* KS18 |
| MF580374.1 | 0.0 | 99 | *Vibrio jasicida* strain OF-GM70 | Proteobacteria | 473/480 | 480 | *Vibrio* sp. KS19 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 490/494 | 494 | *Ferrimonas* sp. KS20 |
| MH283837.1 | 0.0 | 100 | *Pseudovibrio denitrificans* strain SCSIO\_43753 | Proteobacteria | 475/475 | 475 | *Pseudovibrio* sp. KS21 |
| JN871710.1 | 0.0 | 99 | *Vibrio sinaloensis* strain FD O5-12 | Proteobacteria | 487/491 | 491 | *Vibrio* sp. KS22 |
| CP031472.1 | 0.0 | 100 | *Vibrio coralliilyticus* strain RE22 | Proteobacteria | 485/485 | 485 | *Vibrio* sp. KS23 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 488/493 | 493 | *Ferrimonas* sp. KS24 |
| CP031472.1 | 0.0 | 100 | *Vibrio coralliilyticus* strain RE22 | Proteobacteria | 482/482 | 482 | *Vibrio* sp. KS25 |
| CP033138.1 | 0.0 | 99 | *Vibrio owensii* strain 1700302 | Proteobacteria | 494/496 | 496 | *Vibrio* sp. KS26 |
| CP033138.1 | 0.0 | 100 | *Vibrio owensii* strain 1700302 | Proteobacteria | 479/479 | 479 | *Vibrio* sp. KS27 |
| CP033138.1 | 0.0 | 100 | *Vibrio owensii* strain 1700302 | Proteobacteria | 479/479 | 479 | *Vibrio* sp. KS28 |
| CP031472.1 | 0.0 | 100 | *Vibrio coralliilyticus* strain RE22 | Proteobacteria | 482/482 | 482 | *Vibrio* sp. KS29 |
| MK318661.1 | 0.0 | 100 | *Vibrio harveyi* strain 2018MZ1 | Proteobacteria | 488/488 | 488 | *Vibrio* sp. KS30 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 486/490 | 490 | *Ferrimonas* sp. KS31 |
| MH283837.1 | 0.0 | 100 | *Pseudovibrio denitrificans* strain SCSIO\_43753 | Proteobacteria | 449/449 | 449 | *Pseudovibrio* sp. KS32 |
| MK308628.1 | 0.0 | 100 | *Vibrio coralliilyticus* strain SC53 | Proteobacteria | 500/500 | 500 | *Vibrio* sp. KSS33 |
| MK308628.1 | 0.0 | 99 | *Vibrio coralliilyticus* strain SC53 | Proteobacteria | 492/493 | 493 | *Vibrio* sp. KS34 |
| MH283839.1 | 0.0 | 100 | *Vibrio sinaloensis* strain SCSIO\_43755 | Proteobacteria | 493/493 | 493 | *Vibrio* sp. KS35 |
| MH283839.1 | 0.0 | 100 | *Vibrio sinaloensis strain* SCSIO\_43755 | Proteobacteria | 495/495 | 495 | *Vibrio* sp. KS36 |
| MH283839.1 | 0.0 | 99 | *Vibrio sinaloensis* strain SCSIO\_43755 | Proteobacteria | 488/489 | 489 | *Vibrio* sp. KS37 |
| MH283839.1 | 0.0 | 99 | *Vibrio sinaloensis* strain SCSIO\_43755 | Proteobacteria | 489/490 | 490 | *Vibrio* sp. KS38 |
| MH714891.1 | 0.0 | 100 | *Bacillus kochii* strain KB7 | Firmicutes | 482/482 | 482 | *Bacillus* sp. KS39 |
| MK308628.1 | 0.0 | 99 | *Vibrio coralliilyticus* strain SC53 | Proteobacteria | 481/482 | 482 | *Vibrio* sp. KS40 |
| KY655377.1 | 0.0 | 100 | *Spongiobacter* sp. strain EA276 | Proteobacteria | 487/487 | 487 | *Spongiobacter* sp. KS41 |
| MH283839.1 | 0.0 | 100 | *Vibrio sinaloensis* strain SCSIO\_43755 | Proteobacteria | 480/480 | 480 | *Vibrio* sp. KS42 |
| MK308628.1 | 0.0 | 100 | *Vibrio coralliilyticus* strain SC53 | Proteobacteria | 480/480 | 480 | *Vibrio* sp. KS43 |
| MH283839.1 | 0.0 | 100 | *Vibrio sinaloensis strain* SCSIO\_43755 | Proteobacteria | 495/495 | 495 | *Vibrio* sp. KS44 |
| MH283839.1 | 0.0 | 100 | *Vibrio* *sinaloensis* strain SCSIO\_43755 | Proteobacteria | 495/495 | 495 | *Vibrio* sp. KS45 |
| MK346069.1 | 0.0 | 100 | *Bacillus* *pumilus* strain ASpB9 | Firmicutes | 460/460 | 460 | *Bacillus* sp. KS46 |
| MK611646.1 | 0.0 | 100 | *Bacillus toyonensis* strain B1 | Firmicutes | 488/488 | 488 | *Bacillus* sp. KS47 |
| MK156169.1 | 0.0 | 100 | *Bacillus mojavensis* strain DOK6 | Firmicutes | 473/473 | 473 | *Bacillus* sp. KS48 |
| MG719547.1 | 0.0 | 100 | *Bacillus aquimaris* strain L20 | Firmicutes | 482/482 | 482 | *Bacillus* sp. KS49 |
| MK156169.1 | 0.0 | 100 | *Bacillus mojavensis* strain DOK6 | Firmicutes | 482/482 | 482 | *Bacillus* sp. KS50 |
| MK106336.1 | 0.0 | 100 | *Bacillus megaterium* strain K13NAY002 | Firmicutes | 482/482 | 482 | *Bacillus* sp. KS51 |
| MK308628.1 | 0.0 | 99 | *Vibrio coralliilyticus* strain SC53 | Proteobacteria | 490/492 | 492 | *Vibrio* sp. KS52 |
| MH283839.1 | 0.0 | 100 | *Vibrio sinaloensis* strain SCSIO\_43755 | Proteobacteria | 495/495 | 495 | *Vibrio* sp. KS53 |
| MH283839.1 | 0.0 | 100 | *Vibrio sinaloensis* strain SCSIO\_43755 | Proteobacteria | 498/498 | 498 | *Vibrio* sp. KS54 |
| MK346068.1 | 0.0 | 100 | *Bacillus firmis* strain ASpB1 | Firmicutes | 487/487 | 487 | *Bacillus* sp. KS55 |
| MK346069.1 | 0.0 | 100 | *Bacillus pumilus* strain ASpB9 | Firmicutes | 482/482 | 482 | *Bacillus* sp. KS56 |
| MK346069.1 | 0.0 | 100 | *Bacillus pumilus* strain ASpB9 | Firmicutes | 462/462 | 462 | *Bacillus* sp. KS57 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 485/489 | 489 | *Ferrimonas* sp. KS58 |
| MK318662.1 | 0.0 | 99 | *Vibrio harveyi* strain 2018B22 | Proteobacteria | 497/498 | 498 | *Vibrio* sp. KS59 |
| MK346069.1 | 0.0 | 99 | *Bacillus pumilus* strain ASpB9 | Firmicutes | 474/475 | 475 | *Bacillus* sp. KS60 |
| AB682172.1 | 0.0 | 99 | *Ferrimonas* sp. NBRC 104252 | Proteobacteria | 488/492 | 492 | *Ferrimonas* sp. KS61 |

KS: Kuwait sponge.

**Table S4.** Sampling site, date and taxonomic identification of sponge sample collected from Kuwait marine environment.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Location | date | Number of samples | Sample ID | Taxonomy |
| **Class**  | **Order** | **Family** | **species** |
| Nuwaiseeb | 17th Feb 2018 | 2 | 2NW,5NW | Demospongiae | Haplosclerida | Niphatidae | *Niphates* sp.1 |
| Kubbar Island | 1st Aug 2017 | 1 | 2KI | Demospongiae | Haplosclerida | Niphatidae | *Niphates* sp.3 |
| 1 | 6KI | Demospongiae | Haplosclerida | Niphatidae | *Amphimedon* sp. |
| 2 | 1KI,5KI | Demospongiae | Haplosclerida | Chalinidae | *Haliclona* sp. |
| 1 | 4KI | Demospongiae | Chondrillida | Chondrillidae | *Chondrilla australiensis* |

**Table S5.** The documented numbers of sponges-associated prokaryotes raw 16S rRNA amplicon next generation sequencing reads, prokaryotic operational taxonomic units (OTUs) and genera.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sponge species** | **Code** | **Mean read length bp** | **Number of reads bp** | **Total number of OTUs \*** | **Total number of genera** |
| ***Haliclona* sp.** | 1KI\*\* | 465 | 316,199 | 1,379 | 138 |
| 5KI | 466 | 235,203 | 1,266 | 123 |
| ***Niphates* sp.1** | 2NW\*\*\* | 470 | 192,875 | 1,917 | 215 |
| 5NW | 471 | 173,382 | 1,707 | 165 |
| ***Niphates* sp.3** | 2KI | 466 | 402,525 | 1,147 | 119 |
| ***Chondrilla australiensis*** | 4KI | 469 | 185,410 | 2,654 | 190 |
| ***Amphimedon* sp.1** | 6KI | 436 | 74,801 | 3,708 | 440 |

**\***excluding singletons and doubletons.

\*\* KI= Kubbar Island (August, 2017).

\*\*\*NW= Nuwaiseeb intertidal (February, 2018).

**Table S6.** Number of spots containing the filtered bacterial sequence (cultured bacterial isolates) found in *Haliclona* sp. NGS reads (SRX14840950).

|  |  |  |
| --- | --- | --- |
| **Bacterial genera** | **NCBI accession number** | **Number of spots containing the filtered sequence** |
| *Shewanella* sp*.* KS1 | MK558635 | 17 |
| *Shewanella* sp*.* KS16 | MK558650 | 17 |
| *Shewanella* sp*.* KS18 | MK558652 | 17 |
| *Vibrio* sp. KS2 | MK558636 | 1371 |
| *Vibrio* sp. KS3 | MK558637 | 1359 |
| *Vibrio* sp. KS4 | MK558638 | 1 |
| *Vibrio* sp. KS7 | MK558641 | 1371 |
| *Vibrio* sp. KS9 | MK558643 | 930 |
| *Vibrio* sp. KS10 | MK558644 | 1371 |
| *Vibrio* sp. KS11 | MK558645 | 1361 |
| *Vibrio* sp. KS14 | MK558648 | 64 |
| *Vibrio* sp. KS17 | MK558651 | 1 |
| *Vibrio* sp. KS19 | MK558653 | 7 |
| *Vibrio* sp. KS22 | MK558656 | 1371 |
| *Vibrio* sp. KS23 | MK558657 | 1346 |
| *Vibrio* sp. KS25 | MK558659 | 1365 |
| *Vibrio* sp. KS26 | MK558660 | 50 |
| *Vibrio* sp. KS27 | MK558661 | 931 |
| *Vibrio* sp. KS28 | MK558662 | 931 |
| *Vibrio* sp. KS29 | MK558663 | 1366 |
| *Vibrio* sp. KS30 | MK558664 | 930 |
| *Vibrio* sp. KS33 | MK558667 | 1365 |
| *Vibrio* sp. KS34 | MK558668 | 1371 |
| *Vibrio* sp. KS35 | MK558669 | 1371 |
| *Vibrio* sp. KS36 | MK558670 | 1371 |
| *Vibrio* sp. KS37 | MK558671 | 1 |
| *Vibrio* sp. KS38 | MK558672 | 1371 |
| *Vibrio* sp. KS40 | MK558674 | 1365 |
| *Vibrio* sp. KS42 | MK558676 | 1361 |
| *Vibrio* sp. KS43 | MK558677 | 1361 |
| *Vibrio* sp. KS44 | MK558678 | 1361 |
| *Vibrio* sp. KS45 | MK558679 | 1361 |
| *Vibrio* sp. KS52 | MK558686 | 22 |
| *Vibrio* sp. KS53 | MK558687 | 1360 |
| *Vibrio* sp. KS54 | MK558688 | 1365 |
| *Vibrio* sp. KS59 | MK558693 | 11 |
| *Pseudovibrio* sp. KS8 | MK558642 | 1 |
| *Pseudovibrio* sp. KS21 | MK558655 | 1 |
| *Pseudovibrio* sp. KS32 | MK558666 | 1 |
| *Ferrimonas* sp. KS5 | MK558639 | 1651 |
| *Ferrimonas* sp. KS6 | MK558640 | 1728 |
| *Ferrimonas* sp. KS15 | MK558649 | 2 |
| *Ferrimonas* sp. KS20 | MK558654 | 1721 |
| *Spongiobacter* sp. KS12 | MK558646 | 89 |
| *Spongiobacter* sp. KS13 | MK558647 | 1 |
| *Spongiobacter* sp. KS41 | MK558675 | 1  |
| *Bacillus* sp. KS39 | MK558673 | 13 |
| *Bacillus* sp. KS46 | MK558680 | 23 |
| *Bacillus* sp. KS47 | MK558681 | 12 |
| *Bacillus* sp. KS48 | MK558682 | 1 |
| *Bacillus* sp. KS49 | MK558683 | 13 |
| *Bacillus* sp. KS50 | MK558684 | 23 |
| *Bacillus* sp. KS51 | MK558685 | 12 |
| *Bacillus* sp. KS55 | MK558689 | 26 |
| *Bacillus* sp. KS56 | MK558690 | 23 |
| *Bacillus* sp. KS57 | MK558691 | 23 |
| *Bacillus* sp. KS60 | MK558694 | 23 |

**Table S7.** Antimicrobial activity of bacterial isolates obtained from *Haliclona* sp. 1Kl.

|  |  |
| --- | --- |
| **Isolate name /code** | **Zone of inhibition against tested microorganisms (mm)** |
|  | ***Staphylococcus aureus*** | ***Bacillus subtilis*** | ***Candida albicans*** |
|  | **Mean(minimum-maximum) standard deviation** |
| *Bacillus* sp. KS5d2 | 10(10-12)1 | 9(9-10)0.6 | - |
| *Bacillus* sp. KS5b1 | 10(10-11)0.05 | 1(1-1.1)0.5 | 11(10-13)1.1 |
| *Bacillus* sp. KS50 | 9(9-10)0.6 | 8(8-9)0.6 | - |
| *Bacillus* sp. KS47 | - | - | 10(10-11)0.5 |
| *Bacillus* sp. KS57 | 9(8-10)1 | 8(8-9)0.6 | - |
| *Bacillus* sp. KS46 | 11(11-12)0.6 | - | - |
| *Bacillus* sp. KS56 | - | 11(11-12)0.6 | - |
| Ampicillin | 20 | 15 |  |
| Kanamycin | 26 | 30 |  |
| Penicillin-G | 21 | 18 |  |
| Cycloheximide |  |  | 55 |

* **No microbial activity, ≥10 mm moderate activity, ≤10 mm weak activity.**

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