CORA Cork Open Research Archive
Cartlann Taighde Oscailte Chorcaí

Title	Microbial population changes in decaying Ascophyllum nodosum result in Macroalgal-Polysaccharide-Degrading bacteria with potential applicability in enzyme-assisted extraction technologies
Authors	Ihua, Maureen W.;Guihéneuf, Freddy;Mohammed, Halimah;Margassery, Lekha M.;Jackson, Stephen A.;Stengel, Dagmar B.;Clarke, David J.;Dobson, Alan D. W.
Publication date	2019-03-29
Original Citation	Ihua, M.W., Guihéneuf, F., Mohammed, H., Margassery, L.M., Jackson, S.A., Stengel, D.B., Clarke, D.J. and Dobson, A.D., 2019. Microbial Population Changes in Decaying Ascophyllum nodosum Result in Macroalgal-Polysaccharide-Degrading Bacteria with Potential Applicability in Enzyme-Assisted Extraction Technologies. Marine Drugs, 17(4), (200). DOI:10.3390/md17040200
Type of publication	Article (peer-reviewed)
Link to publisher's version	https://www.mdpi.com/1660-3397/17/4/200 - 10.3390/md17040200
Rights	© 2019 by the authors. Licensee MDPI, Basel, Switzerland - https://creativecommons.org/licenses/by/4.0/
Download date	2025-04-17 18:52:21
Item downloaded from	https://hdl.handle.net/10468/9058

UCC
University College Cork, Ireland
Coláiste na hOllscoile Corcaigh

marine drugs

MDPI

Article

Microbial population changes in decaying *Ascophyllum nodosum* result in macroalgal-polysaccharide-degrading bacteria with potential applicability in enzyme-assisted extraction technologies.

Maureen W. Ihua[1], Freddy Guihéneuf[2], Halimah Mohammed[1], Lekha M. Margassery[1], Stephen A. Jackson[1], Dagmar B. Stengel[3], David J. Clarke[1,4], Alan D.W. Dobson[1,5 *]

[1]School of Microbiology, University College Cork, Cork, Ireland; w.ihua@umail.ucc.ie (M.I.); halimahmoh8@gmail.com (H.M.); lekha513@gmail.com (L.M.); sjackson@ucc.ie (S.J.); a.dobson@ucc.ie (A.D.)

[2]Laboratoire d'Océanographie de Villefranche-sur-Mer (LOV) France; freddy.guiheneuf@obs-vlfr.fr (F.G.)

[3]Botany and Plant Science, School of Natural Sciences, Ryan Institute for Environmental, Marine and Energy Research, National University of Ireland Galway, Galway, Ireland; dagmar.stengel@nuigalway.ie (D.S.)

[4]APC Microbiome Institute, University College Cork, Cork, Ireland; david.clarke@ucc.ie (D.C.)

[5]Environmental Research Institute, University College Cork, Cork, Ireland; a.dobson@ucc.ie (A.D.)

[*]Correspondence: a.dobson@ucc.ie (A.D.)

Keywords: *Ascophyllum nodosum*, algal cell wall degrading enzymes, enzyme-assisted extraction, iChip device

marine drugs

Legends to Supplementary figures

Table S1

Ascophyllum nodosum associated bacterial isolates, their closest BLAST relative and observed enzymatic activities. Bacterial strains were examined for their hydroxyethyl cellulose (HE-cellulase), lichenase and pectinase activities. Enzymatic activity is indicated by a (+) sign while a (-) sign indicates that no enzymatic activity was observed under the conditions tested

Figure S1

Relative abundances at genus level of bacteria associated with the cultivable surface microbiota of (a) intact *Ascophyllum nodosum* and decaying *Ascophyllum nodosum* at 2, 4 and 6 weeks of decay at (a) 18 °C; 2_18, 4_18, 6_18 (b) 25 °C; 2_25, 4_25, 6_25 (c) 30 °C; 2_30, 4_30, 6_30 which were obtained by maceration culture isolation method and (e) obtained by ichip culture isolation method. 16S rRNA gene sequences were obtained from the bacterial isolates and taxonomic analyses were performed. The relative distribution of phyla in each group is represented as a percentage

Figure S2

Neighbor-joining phylogenetic tree representing bacterial phyla cultured from *Ascophyllum nodosum* sample before induced decay (T_0). The evolutionary relationships of each phylum identified are shown with reference sequences from NCBI included. This phylogenetic analysis was performed using single representative 16S rDNA sequences from each group

identified by Fastgroup program. The number of similar sequences represented by each sequence is shown in brackets. This tree was drawn using MEGA program (version 7) and bootstrapping percentages (1000 replicates) above 50% are shown

Figure S3

Neighbor-joining phylogenetic tree representing bacterial phyla cultured from *Ascophyllum nodosum* sample at week 2 of induced decay from ● 18 ºC, ■ 25 ºC and ▲ 30 ºC. The evolutionary relationships of each phylum identified are shown with reference sequences from NCBI included. This phylogenetic analysis was made using single representative 16S rDNA sequences from each group identified by Avalanche NextGen Workbench version 2.30. The number of similar sequences represented by each sequence is shown in brackets. This tree was drawn using MEGA program (version 7) and bootstrapping percentages (1000 replicates) above 50% are shown

Figure S4

Neighbor-joining phylogenetic tree representing bacterial phyla cultured from *Ascophyllum nodosum* sample at at week 4 of induced decay from ● 18 ºC, ■ 25 ºC and ▲ 30 ºC. The evolutionary relationships of each phylum identified are shown with reference sequences from NCBI included. This phylogenetic analysis was made using single representative 16S rDNA sequences from each group identified by Avalanche NextGen Workbench version 2.30. The number of similar sequences represented by each sequence is shown in brackets. This tree was drawn using MEGA program (version 7) and bootstrapping percentages (1000 replicates) above 50% are shown.

Figure S5

Neighbor-joining phylogenetic tree representing bacterial phyla cultured from *Ascophyllum nodosum* sample at the end of the decay period (week 6) from ● 18 ºC, ■ 25 ºC and 30 ºC .The evolutionary relationships of each phyla identified are shown with reference sequences from NCBI included. This phylogenetic analysis was made using single representative 16S rDNA sequences from each group identified by Avalanche NextGen Workbench version 2.30. The number of similar sequences represented by each sequence is shown in brackets. This neighbor joining tree was drawn using MEGA program (version 7) and bootstrapping percentages (1000 replicates) above 50% are shown.

Figure S6

Neighbour-joining phylogenetic tree representing bacterial phyla cultured from ● 18 ºC, ■ 25 ºC and 30 ºC using the iChip device. The evolutionary relationships of each phylum identified are shown with reference sequences from NCBI included. This phylogenetic analysis was performed using single representative 16S rDNA sequences from each group identified by Fastgroup. The number of similar sequences represented by each sequence is shown in brackets. This neighbor joining tree was drawn using MEGA program (version 7) and bootstrapping percentages (1000 replicates) above 50% are shown

marine drugs

MDPI

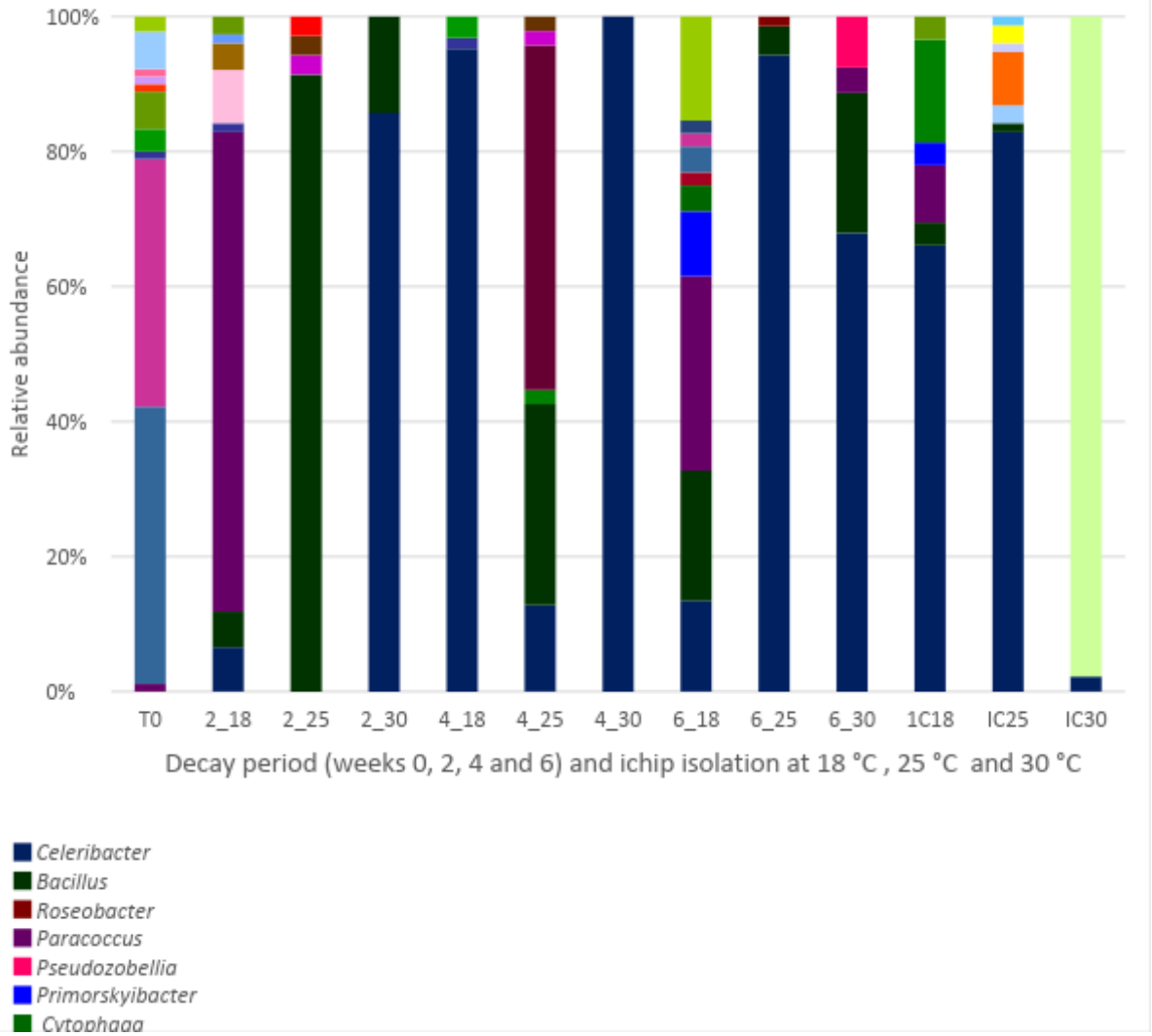
Table S1

SAMPLE ID	TOP BLAST HIT	IDENTITY (%)	ALGAL CELL WALL POLYSACCHARIDE DEGRADING ACTIVITIES		
			HE-cellulase	Lichenase	pectinase
AN218_A2	*Bacillus safensis* strain Rb1S1	100	-	+	-
AN218_H5	*Bacillus* sp. M101(2010) strain M101	100	+	+	-
AN225_A5	*Bacillus altitudinis* strain CT10	99	-	+	-
AN225_A11	*Bacillus licheniformis* strain HQB814	99	+	-	+
AN225_B8	*Bacillus licheniformis* strain AG-06	100	-	-	+
AN225_B9	*Bacillus licheniformis* strain ST7	99	-	-	+
AN225_C1	*Bacillus pumilus* strain ASpB9	99	-	+	-
AN225_C7	*Bacillus aerius strain* APBSMLB109	99	-	+	-
AN225_C11	*Bacillus* sp. 11RB3	99	-	+	+
AN225_D1	*Bacillus licheniformis* strain APBSWPTB167	100	+	-	+
AN225_D4	*Bacillus subtilis* strain HDXJ04	99	+	+	+
AN225_D6	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN225_E1	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN225_E6	*Bacillus licheniformis* strain JMB003	99	-	-	+
AN225_E7	*Bacillus licheniformis* strain V24	100	-	-	+
AN225_E8	*Bacillus licheniformis* strain V24	100	-	-	+
AN225_E9	*Bacillus* sp. strain SKS7	99	-	-	+
AN225_E10	*Bacillus licheniformis* strain KB102	99	-	-	+
AN225_E11	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN225_F6	*Bacillus* sp. strain 703	100	-	-	+
AN225_F9	*Bacillus* sp. strain C60	99	-	+	
AN225_F12	*Bacillus licheniformis* strain V24	100	+	-	+

AN225_G2	*Bacillus* sp. strain SKS7	100	+	-	+
AN225_G3	*Bacillus* sp. (in: Bacteria) strain VI/7	100	-	-	+
AN225_G6	*Bacillus subtilis* strain AKKVG-2-18	100	-	+	+
AN225_G8	*Bacillus* sp. (in: Bacteria) strain VI/7	100	-	-	+
AN230_A10	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN230_B4	*Bacillus* sp. strain SKS7	100	+	-	+
AN230_B11	*Bacillus mycoides* strain LBUM203	99	+	-	+
AN230_D9	*Bacillus licheniformis* strain V24	100	+	-	+
AN230_D11	*Bacillus licheniformis* strain V24	100	+	-	+
AN230_E3	*Bacillus* sp. (in: Bacteria) strain V52	100	-	-	+
AN230_E4	*Bacillus* sp. Ph_25A	100	-	+	-
AN425_D9	*Bacillus* sp. strain CZL003	100	+	+	+
AN425_D11	*Bacillus licheniformis* strain 8B-B92	99	+	-	+
AN425_D12	*Bacillus* sp. strain SKS7	100	+	-	+
AN425_E4	*Bacillus* sp. strain BS155	100	+	+	+
AN425_G7	*Bacillus* sp. strain BS155	100	+	-	+
AN618_A1	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN618_A2	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN618_B10	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN618_D11	*Bacillus pumilus* strain ASpB9	100	+	+	-
AN618_H4	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN625_A10	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN625_D7	*Bacillus pumilus* isolate TD22	100	-	+	-
AN625_G10	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN630_A12	*Bacillus hwajinpoensis* strain 16E11	99	-	+	-
AN630_D1	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN630_D2	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN630_G12	*Bacillus pumilus* strain ASpB9	100	-	+	-
AN630_H8	*Bacillus safensis* strain Rb1S1	100	-	+	-
IC18_D5	*Vibrio oceanisediminis* strain S37	98	-	-	+
IC18_D6	*Vibrio anguillarum* strain INTA11	100	-	-	+
IC18_D7	*Vibrio anguillarum* strain X0906	99	-	-	+

IC18_D8	*Vibrio oceanisediminis* strain S37	99	-	-	+
IC18_D9	*Vibrio anguillarum* strain X0906	99	-	-	+
IC18_E2	*Vibrio oceanisediminis* strain S37	98	-	-	+
IC18_E6	*Vibrio anguillarum* strain KAP1	100	-	-	+
IC18_E7	*Vibrio oceanisediminis* strain S37	99	-	-	+
IC18_E8	*Vibrio anguillarum* strain INTA11	100	-	-	+
IC25_C11	*Micrococcus yunnanensis*	100	-	-	+
IC25_F10	*Micrococcus yunnanensis*	100	-	-	+

Figure S1


100%
80%
60%
40%
20%
0%
Relative abundance
T0
2_18
2_25
2_30
4_18
4_25
4_30
6_18
6_25
6_30
1C18
IC25
IC30
Decay period (weeks 0, 2, 4 and 6) and ichip isolation at 18 °C , 25 °C and 30 °C
Celeribacter
Bacillus
Roseobacter
Paracoccus
Pseudozobellia
Primorskyibacter
Cytophaga

marine drugs

Figure S2

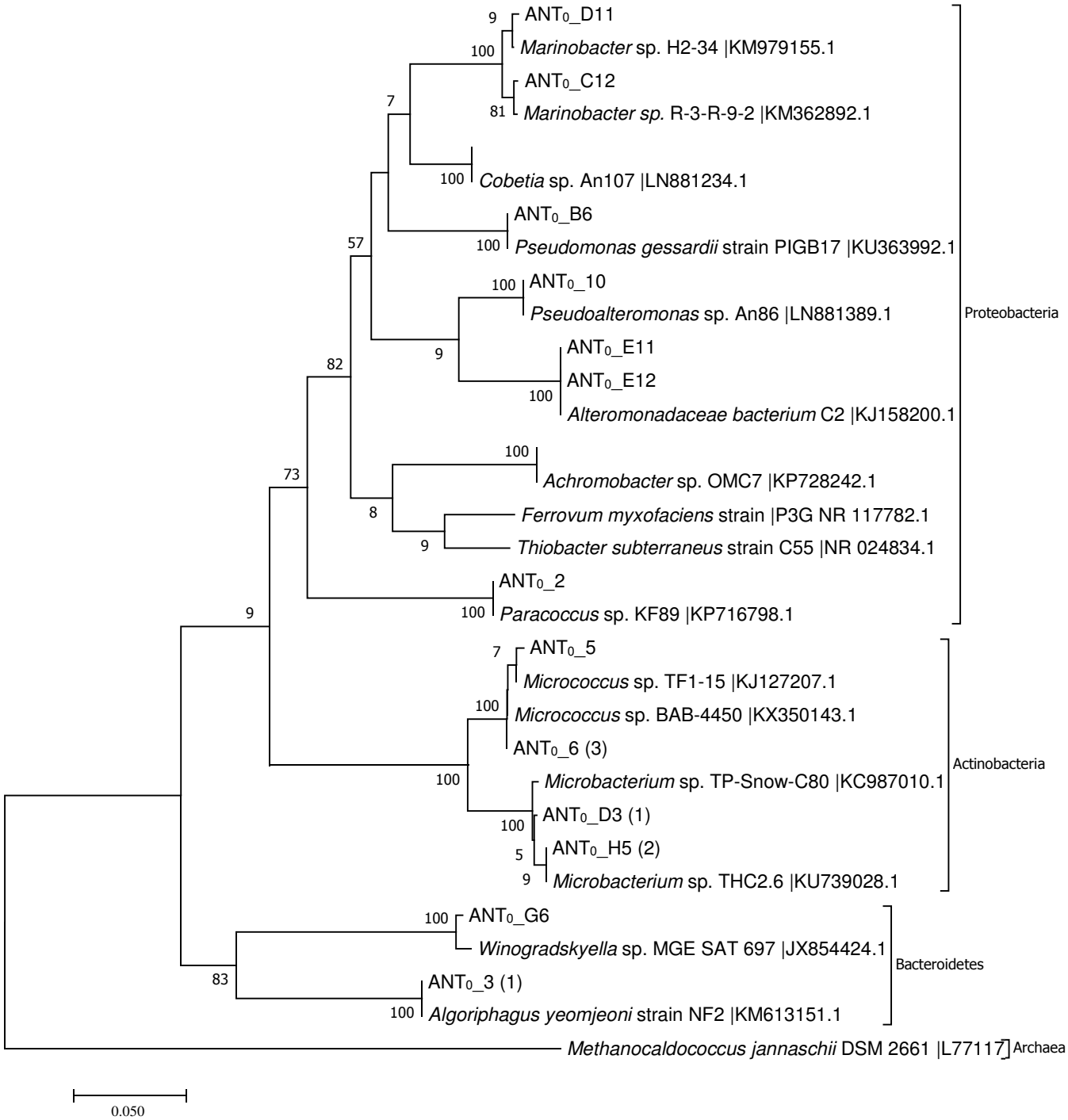


Figure S3

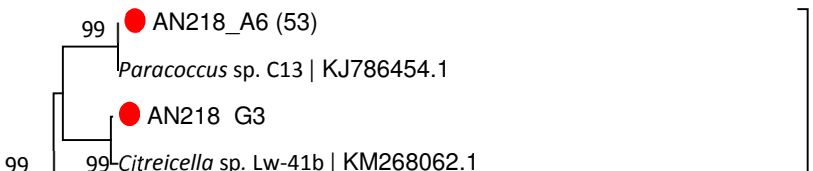


Figure S4

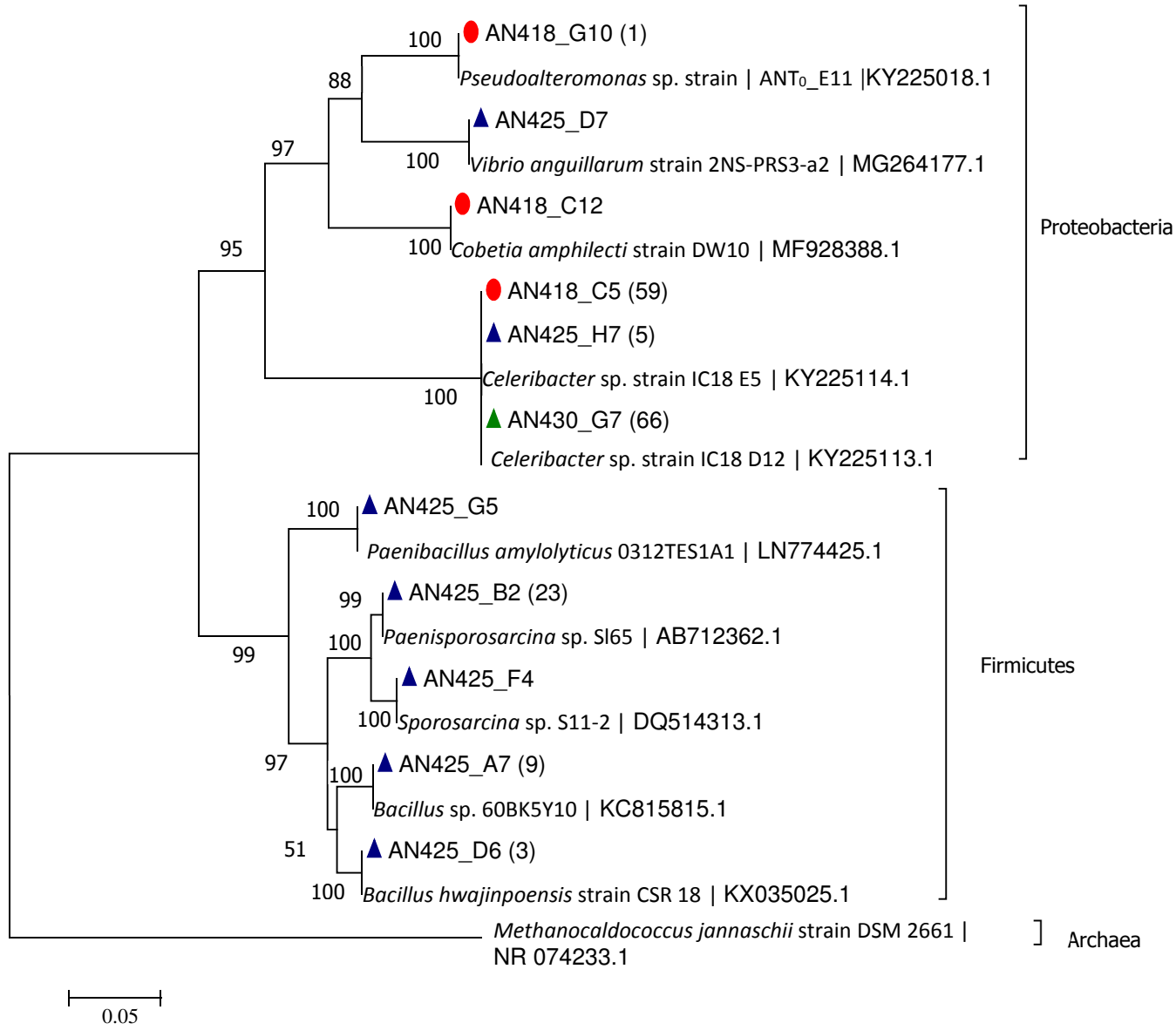

AN418_G10 (1)
Pseudoalteromonas sp. strain | ANT0_E11 |KY225018.1
AN425_D7
Vibrio anguillarum strain 2NS-PRS3-a2 | MG264177.1
AN418_C12
Cobetia amphilecti strain DW10 | MF928388.1
AN418_C5 (59)
AN425_H7 (5)
Celeribacter sp. strain IC18 E5 | KY225114.1
AN430_G7 (66)
Celeribacter sp. strain IC18 D12 | KY225113.1
Proteobacteria
AN425_G5
Paenibacillus amylolyticus 0312TES1A1 | LN774425.1
AN425_B2 (23)
Paenisporosarcina sp. SI65 | AB712362.1
AN425_F4
Sporosarcina sp. S11-2 | DQ514313.1
AN425_A7 (9)
Bacillus sp. 60BK5Y10 | KC815815.1
AN425_D6 (3)
Bacillus hwajinpoensis strain CSR 18 | KX035025.1
Firmicutes
Methanocaldococcus jannaschii strain DSM 2661 | NR 074233.1
Archaea
0.05

Figure S5

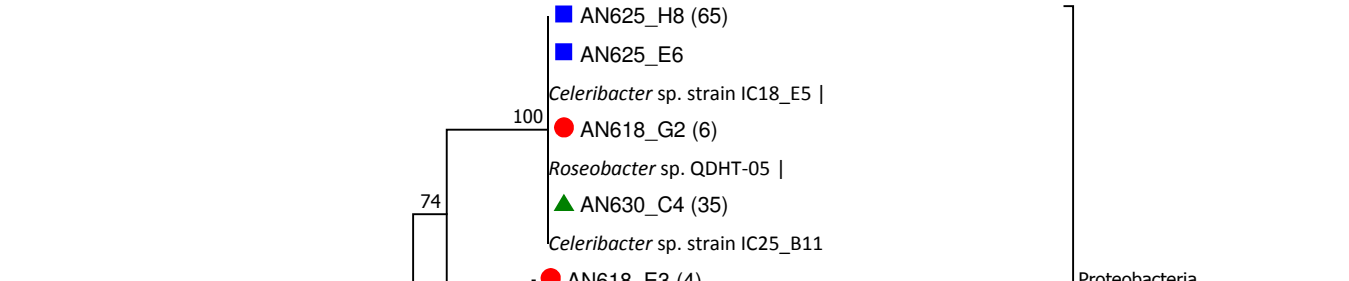
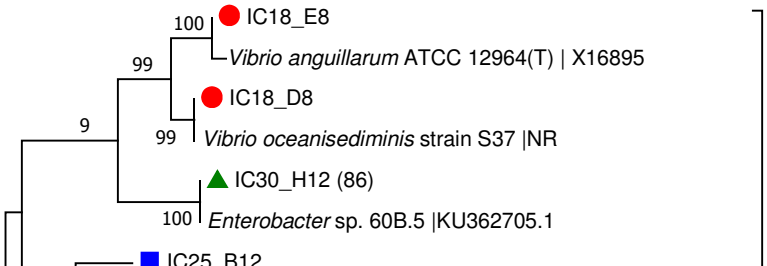

AN625_H8 (65)
AN625_E6
Celeribacter sp. strain IC18_E5 |
AN618_G2 (6)
Roseobacter sp. QDHT-05 |
AN630_C4 (35)
Celeribacter sp. strain IC25_B11
Proteobacteria

Figure S6


100
IC18_E8
Vibrio anguillarum ATCC 12964(T) | X16895
99
IC18_D8
9
99
Vibrio oceanisediminis strain S37 |NR
IC30_H12 (86)
100
Enterobacter sp. 60B.5 |KU362705.1
IC25_B12

marine drugs

MDPI