
Supplementary information

Coral microbiomes as reservoirs of unknown genomic and biosynthetic diversity

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Coral microbiomes as reservoirs of unknown genomic and biosynthetic diversity

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Supplementary notes

Exploring host-association of BGC-rich microbial species

Coral host transcriptomics and generalised dissimilarity models

We leveraged previously sequenced transcriptomic samples from the coral host *Pocillopora*¹⁵² to explore host transcriptomic responses to microbiome community composition (16S amplicons)¹³⁴ along with algal symbiont community composition (ITS2 amplicons)¹⁵², environmental (pH, temperature, oxygen concentration, and nutrients)⁵⁴, host phylogenetic distance¹⁵³, and host biomarker data¹⁵⁴. Distances based on normalised transcript-per-million were used as the response variable in a Generalised Dissimilarity Model (GDM)¹⁵⁵.

Firstly, several predictor variables were pre-processed to reduce dimensionality. Community compositions were rarefied using rtk (v0.93.2) to 20,000 reads for 16S amplicons and 4,000 reads for ITS2 amplicons. 16S gene and ITS2 sequences were subsequently aligned against the SILVA SSU reference tree (NR99; release 138) using SINA (v1.6.0). The alignment was processed using MOTHUR (v1.41.0) (filter.seqs) and used to build a phylogenetic tree with FastTree (v2.1.11) (options *-gtr -nt -fastest -mlnni 4*). The rarefied abundances (after excluding ASVs with total abundances below 20 and 4 for microbiome and symbiome data, respectively) together with the phylogenies were then used to reduce the dimensionality of both datasets by grouping 16S and ITS2 ASVs into 116 bins with PhyCA¹⁵⁶. Environmental and biomarker dimensions were reduced by selecting the columns listed in Supplementary Table 8.

We subsequently computed the model using the R package gdm (v1.5)¹⁵⁵, with host transcriptomic distances as the response variable and the other variables (after range normalisation) as predictors, across the 28 samples for which all data types were available (Supplementary Table 8). In addition, a simpler GDM was built using host transcriptomic distances as the response variable and all Acidobacteriota ASVs with total rarefied abundance greater than five across the 57 samples where both data types were available (Supplementary Table 8). Predictor importance was computed with the gmd.varImp function using 100 permutations.

We found the most important predictor to be a microbiome cluster exclusively containing Acidobacteriota spp. (Extended Data Fig. 3b; Supplementary Table 8). Furthermore, when assessing individual abundances of Acidobacteriota spp. (the most BGC-rich bacteria identified in this study; Fig. 4a) for their predictability of host transcriptomic dissimilarities, several candidate superproducer genera and candidate superproducer-containing lineages stood out as the explanatory features (Extended Data Fig. 3c).

Screening for ELPs in host-associated microbial species

We found BGC-rich microbial species in general, and Acidobacteriota spp. in particular, to be more enriched in ELPs (Extended Data Fig. 2b) than other previously reported coral symbionts such as *Endozoicomonas* spp.^{157,158}.

Improving Sulfidibacter corallicola and Acanthopleuribacter pedis genomes

To improve the genome qualities of *S. corallicola*¹⁵⁹ and *A. pedis*¹⁶⁰, we produced fresh isolates of both strains. We cultivated the bacteria at 28 °C on 1/10 marine broth (MB) agar plates containing 3.74 g/L MB (BD Difco™ Marine Broth 2216), 30.6 g/L sea salts (Tropic Marin Pro-Reef), and 12 g/L agar (BD Difco™ Agar Noble). We inoculated 30 mL of liquid 1/10 MB medium containing 3.74 g/L MB (BD Difco™ Marine Broth 2216) and 30.6 g/L sea salts (Tropic Marin Pro-Reef) with a single colony and incubated the culture at 28 °C to an OD₆₀₀ of 0.4. Genomic DNA was extracted using the Quick-DNA™ Miniprep Plus Kit (Zymo Research) and sent to Plasmidsaurus Inc. (UK) for hybrid long-read (Oxford Nanopore Technology) and short-read (Illumina) sequencing. Resulting *S. corallicola* and *A. pedis* genome assemblies and annotations—generated with the Plasmidsaurus pipeline—were submitted to ENA (PRJEB81969).

Testing holobiont–S. corallicola interactions

To examine the effect of the coral host on the growth, transcription profile, and actual metabolite production of an acidobacterial strain, we used the only acidobacterial strain isolated from a reef-building coral (*Porites lutea*) to date, *S. corallicola*¹⁵⁹ (of which we could match the 16S rRNA gene at 100% identity to a representative in our data). We performed an experiment as follows: A pre-culture of *S. corallicola* was prepared by inoculating 30 mL of 1/10 MB medium from a cryostock. After incubation at 28 °C with shaking (180 rpm) in the dark to an OD₆₀₀ of 0.4, *S. corallicola* cells were washed three times by centrifugation (3,500 × g, room temperature, 5 min), resuspended in artificial seawater (34 g/L sea salts; Tropic Marin Pro-Reef), and then adjusted to an OD₆₀₀ of 0.5. Using filtered calcium-/magnesium-free seawater (400 mM NaCl, 10 mM KCl, 7 mM Na₂SO₄, 0.005 mM NaHCO₃) and an airbrush at 5 bar, we blasted the tissue off of domestic *Porites* (procured from Zoologischer Garten Basel) fragments. We homogenised the tissue slurry using a Polytron PT 1200 E with the aggregate PT-DA 07/2SYN-E082 at maximum speed for a minute without cooling. Next, we performed two freeze–thaw cycles (–80 °C for 30 min and 35 °C until thawed completely) to disrupt the host cells. The resulting tissue slurry was added to dissolved organic matter exuded by *Porites* into autoclaved artificial seawater during 48 h to increase the volume and filtered three times. We prepared the culture medium as 1/10 full MB in 9/10 dissolved organic matter derived from *Porites* tissue extracts (or 9/10 artificial seawater for the control without coral organic matter). We again filtered both media (with and without coral additives) three times, kept an aliquot without bacteria as control (for growth curves and metabolite analysis), and spiked the remainder (980 mL) with 1 mL of the *S. corallicola* culture and divided the culture into three 1 L Erlenmeyer flasks per treatment. The flasks were incubated at 28 °C and gently shaken at 150 rpm in the dark. For enumerating the microbial cells, we stained bacteria with SYBR-Green I (final concentration 1:20,000) and incubated them in the dark and at room temperature for 20 min. For each sample, we recorded forward scatter (FSC) and green fluorescence (488 nm, SYBR) to identify bacterial cells. Flow rates did not exceed 30 µL/min to limit the abortion rate of sample during a 30 s sample acquisition time. Data were analysed with CytExpert (v2.5).

To measure the transcription profile, we sampled 50 mL of culture six days after inoculation (stationary phase; Extended Data Fig. 4d). After centrifugation (3,500 × g, room temperature, 5 min), we removed the supernatant by vacuum suction and immediately resuspended the

pellets in 450 μ L of RLT lysis buffer (QIAGEN) with 1% β -mercaptoethanol (Sigma-Aldrich). Resuspended cells were transferred into 1.5 mL screw-capped tubes pre-filled with 600 mg of 100 μ m Zirconium beads (OPS Diagnostics), plunged into liquid nitrogen, and stored at -80 °C for two weeks. RNA was extracted using the RNeasy Mini Kit (QIAGEN) and a QIAvac 24 Plus manifold (QIAGEN) following the QIAGEN RNeasy Mini Handbook (06/2023) and the protocols “Purification of Total RNA from Plant Cells and Tissues and Filamentous Fungi” and “Optional On-Column DNase Digestion with the RNase-Free DNase Set”. After thawing, the cells were subjected to bead beating (30 Hz, 5 min) with a Mixer Mill M400 (Retsch). Lysates were spun down and passed through a QIAshredder column (QIAGEN) by centrifugation (11,000 $\times g$, 1 min) to remove beads. Cleared lysates (350 μ L) were mixed with 350 μ L ethanol (99.8%; Merck), passed through an RNeasy spin column followed by DNase-treatment (QIAGEN RNase-free DNase set) and washing. RNA extracts were eluted with two times 30 μ L UltraPure DNase/RNase-Free Distilled Water (Invitrogen) and their integrity confirmed by TapeStation.

We sent the RNA extracts on dry ice to BMK (Biomarker Technologies GmbH, Germany) for library preparation and RNA sequencing. Briefly, ribosomal RNA was depleted with the RiboCop rRNA Depletion Kit (Lexogen) and the library constructed with the ALFA-SEQ Directional RNA Lib Prep Kit (Findrop) and sequenced on a NovaSeq 6000 platform (Illumina) to produce 3 Gbp of $\sim$ 150 bp paired-end reads per sample. Raw RNA sequencing reads were cleaned by removing adaptor sequences, low-quality-end trimming, and removal of low-quality reads using BBTools (v38.18, Bushnell, B., BBDMap, available from: <https://sourceforge.net/projects/bbmap/>). The exact commands used for quality control can be found on the Methods in Microbiomics webpage (Sintsova, A., Data Preprocessing — Methods in Microbiomics v0.0.1 documentation, available from: <https://methods-in-microbiomics.readthedocs.io/en/latest/preprocessing/preprocessing.html>). The quality-controlled reads were aligned against the *S. corallicola* genome assembly (ERZ25037212) using BWA aligner (v0.7.17)¹⁰⁹. Transcript abundances were quantified using HTseq count (v2.0.2)¹⁶¹. This resulted in an average of 5.7M gene feature counts per sample ($\pm$ 0.4M counts, $n = 6$). Differential gene expression analysis was performed using Bioconductor R package DESeq2 (v1.37.4)¹⁶², which identified 291 genes that were differentially expressed when comparing cultures with and without coral additives (adjusted p-value < 0.05, absolute log₂-fold change > 0.585). BGCs were annotated in the genome of *S. corallicola* (ERZ25037212) using antiSMASH (v7.1.0)¹⁶³, resulting in 44 predicted BGC regions.

Before chemically extracting the samples, we separated cells and supernatants by centrifugation (7,000 $\times g$, 4 °C, 30 min). The supernatants were extracted with 3 $\times$ 300 mL of ethyl acetate and the combined organic phases were evaporated to dryness (yielding 15 mg and 6 mg for *S. corallicola* with and without coral additives, respectively). We also extracted 50 mL of the controls (no *S. corallicola*) with and without coral additives with 3 $\times$ 20 mL ethyl acetate, evaporating the organic phases to dryness (yielding 1 mg and 1 mg for medium with and without coral additives, respectively). The pellets were dissolved in 15 mL methanol and incubated with a magnetic stirrer for 1 h at 4 °C and 900 rpm. The pellets were then transferred to an ultrasonic water bath for 30 min and afterwards filtered and dried (yielding 67 mg and 23 mg for *S. corallicola* with and without additives, respectively). The supernatant, control, and pellet extracts were dissolved in methanol to obtain final

concentrations of 1.5 mg/mL, 1.5 mg/mL, and 6 mg/mL, respectively. Samples were analysed using high-performance liquid chromatography (HPLC; Dionex Ultimate 3000) coupled to heated electrospray ionisation high-resolution tandem mass spectrometry (HESI-HRMS/MS; Thermo Scientific Q Exactive) with the following gradient method: 99:1 A/B from 0–3 min, ramped to 5:95 A/B from 3–19 min, maintained at 5:95 A/B from 19–23 min, diminished to 99:1 A/B from 23–23.1 min, and maintained at 99:1 A/B from 23.1–25 min (solvent A: water + 0.1% formic acid; solvent B: acetonitrile + 0.1% formic acid; column: Kinetex™ 2.6 µm XB-C18 100 Å (150 × 4.6 mm); flow rate: 1 mL/min). Columns were maintained at 27 °C. The mass spectrometer was operated in positive ionisation mode at a scan range of 200–2000 *m/z* and a resolution of 17,500 (spray voltage: 3.5 kV; capillary temperature: 300 °C). Data were analysed using Xcalibur 4.1 (Thermo Fisher) and GNPS¹⁶⁴ to construct a molecular network.

We found that upon exposure to dissolved organic matter derived from *Porites* tissue extracts, *S. corallicola* transcribed more BGCs (Extended Data Fig. 4a) and produced a set of specific metabolites (Extended Data Fig. 4bc) while its growth was unaffected (Extended Data Fig. 4d). Whether similar BGC transcription and expression changes occur upon exposure to organic matter from other sources is currently unknown.

The RNAseq raw data were uploaded as project PRJEB81969. All files used for analysing holobiont–*S. corallicola* interactions were deposited on Zenodo (<https://zenodo.org/doi/10.5281/zenodo.14050210>)¹⁴⁶.

Functional characterisation of the *aci* cluster

In silico analysis

The *aci* BGC (TARA_SAMEA6023455_MAG_00000007-scaffold_11-biosynth_1), annotated by antiSMASH¹⁶² and curated by sequence similarity searches¹⁶³, encodes two lanthipeptide precursors and a type III lanthionine synthetase homologue. AntiSMASH annotated this cluster as encoding a type IV lanthipeptide but closer examination revealed the lack of conserved zinc-binding motifs in *AciKC* (the lanthionine synthetase homologue), suggesting a type III lanthipeptide-encoding BGC. Additionally, genes encoding transcriptional regulators and ABC transporter related proteins are encoded in the BGC.

The proteins annotated as precursor proteins contain cysteine- and serine-rich putative core regions followed by unusual glycine-rich C-terminal regions, which, to our knowledge, are not yet described in type III lanthipeptides. The two precursors showed no homologues with significant similarity in the NCBI non-redundant protein sequence database.

Functional characterisation of AciKC

Functional characterisation was carried out by heterologous expression of genes encoding an N-terminal fusion of His₆-bdSUMO with either *AciA1* or *AciA2* by expression from a pACYC plasmid in *E. coli* BL21(DE3). In addition to the precursor genes, plasmid pET-24(+)-*acikc* was introduced and simultaneously expressed. Protein production and subsequent purification by nickel-nitrilotriacetic acid (Ni-NTA) and proteolysis by endoprotease GluC followed by liquid-chromatography-mass spectrometry (LC-MS)

revealed up to seven dehydrations (-126 Da) installed by AcIKC on both precursors (Extended Data Fig. 6). Fragmentation ions of the proteolytically digested peptides suggested dehydration in the serine-rich putative core region (Extended Data Fig. 7), and no dehydrations in the C-terminal glycine-rich region (containing one to two serines theoretically available for dehydration in this region). The lack of b- and y-ions in the MS/MS fragmentation pattern in the putative core region suggested (multiple) macrocyclisation events through (methyl-)lanthionine and/or labionin formation.

Functional characterisation of the *tha* cluster

In silico analysis

The *tha* BGC (TARA_SAMEA6034818_MAG_00000048-scaffold_6), annotated by antiSMASH¹⁶⁵ and curated by sequence similarity searches¹⁶⁶, encodes a lanthipeptide precursor (*thaA*) that shares sequence similarity with mersacidin/lichenicidin family type 2 lantibiotics. Two small open reading frames on the boundaries of the cluster are annotated as putative lanthipeptides but share no sequence similarity to known proteins and were disregarded. Additionally, a gene encoding a class-II lanthionine synthetase homologue (*thaM*) is present as well as genes encoding transcriptional regulators and ABC-transporter related proteins and a C39 peptidase. Finally, a gene encoding a homologue of a GMC-family oxidoreductase (*thaO*) is located downstream of the lanthionine synthetase gene, suggesting that the enzyme could be part of the BGC. Multimeric AlphaFold2 predictions of the putative precursor with the enzymes suggested possible interactions with the core sequence predicted to bind near the active site (Extended Data Fig. 7). Genome neighbourhood diagrams^{167,168} showed no clear evolutionary conserved cluster architectures when queried with the protein sequences for ThaA and ThaO.

Functional characterisation of ThaM

We heterologously expressed genes encoding an N-terminal fusion of His₆-bdSUMO with ThaA by expression from a pACYC plasmid in *E. coli* BL21(DE3). In addition to the precursor gene, plasmids pET-24(+)-tham, pET-24(+)-thao, or pET-24(+)-tham-thao were supplied and simultaneously expressed. Protein production and subsequent purification by Ni-NTA and proteolysis by trypsin followed by LC-MS revealed two dehydrations (-36 Da) installed by ThaM and a further mass loss of 20 Da when ThaM and ThaO were both produced (Extended Data Fig. 7). Expression of ThaO alone with ThaA did not lead to any apparent mass loss. Iodoacetamide derivatisation suggested formation of two lanthionine bridges in the twice dehydrated compound as only three (out of five) were modified by the reagent (Extended Data Fig. 6). The lack of fragmentation ions of Ser2 in the C-terminal region supported this observation (Extended Data Fig. 7). To investigate the ring topology, we produced mutants with each serine, threonine, and cysteine residue in the core region independently mutated to alanines. Out of the three amino acids suitable for dehydration, two were dehydrated. Tha-T6A was only dehydrated once, suggesting Thr6 to be dehydrated (Extended Data Fig. 7). While both Tha-S2A and Tha-T12A were dehydrated twice, Tha-S2A was only dehydrated once in co-production with ThaO and then further modified by ThaO, suggesting that while Ser2 is usually dehydrated, Thr12 can be dehydrated by ThaM in the absence of Ser2. This is supported by the lack of fragmentation

ions from Ser2 to the C-terminus in the native ThaA precursor (Extended Data Fig. 7). Mutants Tha-S2A and Tha-C16A produced similar fragmentation ions, as did mutants Tha-T6A and Tha-C13A, suggesting that Ser2 formed a lanthionine with Cys16, and Thr6 formed a lanthionine with Cys13 (Extended Data Fig. 7). At the same time, these results suggested only partial lanthionine formation of both macrocycles in these mutants. The absolute configuration was determined by Marfey's analysis and revealed D,L-lanthionine and D,L-methyllanthione formation (Extended Data Fig. 6).

Functional characterisation of ThaO

The exact mass loss catalysed by ThaO corresponded to 20.0272 Da in TB. We conducted co-expression of genes for the precursor and the enzymes in ^{13}C - and ^{15}N -labelled medium and observed the same mass loss, 20.0312 Da in ISOGRO- ^{15}N and 20.0270 Da in ISOGRO- ^{13}C (Extended Data Fig. 7). This excluded carbon and nitrogen loss and led us to believe a loss of four protons and one oxygen atom as the likely source of the 20 Da mass loss. Tandem MS fragmentation suggested that the mass loss can be localised to the glycine–cysteine residues adjacent to the dehydrated serine residue, with the presence of unmodified y_{15} and modified y_{17} – y_{21} ions in the AspN digest, and y_{15} and y_{18} , y_{19} , and y_{21} ions in the trypsin digest, respectively (Extended Data Fig. 7). Cysteine derivatisation by iodoacetamide and Raney nickel independently supported that only two cysteines are available compared to three cysteines in the dehydrated compound (Extended Data Fig. 6). Point mutation of Cys1 to Ala abolished production of the further modified compound and was only dehydrated twice, further supporting that Cys1 (together with the adjacent Gly-1) is modified by ThaO (Extended Data Fig. 7). To characterise the modification, we performed NMR experiments that revealed a peak in the ^1H -NMR at 8.20 ppm, coupled to a ^{13}C in the HSQC at 124.27 ppm, and two ^{13}C at 148.63 and 170.33 ppm in the HMBC spectra (Extended Data Fig. 8). These peaks are characteristic for thiazole formation and are in agreement with previously reported thiazole-containing peptides^{169,170}. Taken together, these findings support that ThaO catalyses unusual thiazole formation in ThaA in the presence of ThaM. FAD-dependent oxidation of cysteine to a thioaldehyde, followed by thioenolisation, nucleophilic ring closure onto the amide carbonyl, and subsequent elimination of H_2O is in agreement with FAD-dependent cysteine oxidation observed in the initial steps of aminovinyl-cysteine-containing peptide biosynthesis^{171,172,173}. Widespread thiazole and (methyl-)oxazole biosynthesis in RiPPs is typically catalysed by a pair of enzymes, a YcaO-domain containing enzyme catalysing ring formation and a dehydrogenase catalysing ring oxidation^{49,174}.

Functional characterisation of the homologous *the* cluster

In silico analysis

To further explore the family of RiPP-modifying GMC-oxidoreductases, we searched for homologues of ThaO through blastp against the NCBI nr database. We manually curated hit sequences and selected BGCs encoding for precursor sequences with additional amino acids between GGC motifs and the first serine or threonine in the putative core peptide for closer analysis. We reasoned that this strategy might yield GMC-oxidoreductase homologues that are more independent of lanthionine synthetase encoded in the same

BGC. The selected *the* BGC (MAG, GenBank accession: GCA_035278895.1), annotated by antiSMASH¹⁶⁵ and curated by sequence similarity searches¹⁶⁶, encodes a lanthipeptide precursor (*theA*) that shares sequence similarity with mersacidin/lichenicidin family type 2 lantibiotic precursors. The cluster further encodes a GMC-family oxidoreductase (*theO*) and a class-II lanthionine synthetase homologue (*theM*) as well as a gluconate 2-dehydrogenase subunit 3-like protein (*theB*) and a GCN5-related *N*-acetyltransferase homologue (*theN*).

Functional characterisation of TheO

Upon co-production of an N-terminal fusion of His₆-bdSUMO and TheA with TheO, we observed a 20.0247 Da mass loss, suggesting similar thiazole formation as observed for ThaA co-produced with ThaO in the *tha* cluster (Extended Data Fig. 9). Tandem MS fragmentation and mutations of glycine residues near the putatively modified cysteine further supported thiazole formation as the source of the 20 Da loss. In a series of C-terminal truncations of the TheA core, we observed wildtype-like efficiency for TheA₂₀, TheA₁₄, and TheA₈, which consist of 20, 14, or 8 amino acid long core sequences, respectively (Extended Data Fig. 9). Further truncations were not modified by TheO. For production of a cargo-fused precursor, we fused the Protegrin-1 sequence to the C-terminus of the TheA₈ truncation to minimise the distance between the thiazole-forming site and the protein cargo. Upon co-production of this fusion protein, we observed the same mass loss of 20.0228 Da in the tryptic fragment, suggesting thiazole formation N-terminal of the Protegrin-1 sequence (Extended Data Fig. 9).

Binomial naming of new acidobacterial lineages

For the three acidobacterial species represented by long-read MAGs, we propose the following names based on the International Code of Nomenclature of Prokaryotes (ICNP) and SeqCode¹⁷⁵ recommendations:

MAG48; TARA_SAMEA6034818_MAG_10000048; GCA_977880245 (one contig)

‘*Candidatus* Moanaiibacterium’ (Mo.a.na.i.i.bac.te’ri.um. N.L. neut. n. Moanaiibacterium, a composite of (Hine)Moana—Latinised as Moanaia, gen. Moanaiae, the Polynesian goddess of the sea, and bacterium; referring to the oceanic origin of the bacterial taxon);

‘*Candidatus* Moanaiibacterium opulentum’ (o.pu.len’tum. N.L. neut. adj. opulentum, rich, abundant, referring to the numerous biosynthetic gene clusters identified as well as the large genome size) is proposed as the type species of the genus *Ca.* Moanaiibacterium, which is represented by a long-read, chromosome-level metagenome-assembled genome as type material.

MAG13; TARA_SAMEA6035815_MAG_10000013; GCA_977880235 (two contigs)

‘*Candidatus* Tangaroaiibacterium’ (Tan.ga.ro.i.bac.te’ri.um. N.L. neut. n. Tangaroaiibacterium, a composite of Tangaroa—Latinised as Tangaroaius, gen. Tangaroaii, the Polynesian god of the sea, and bacterium; referring to the oceanic origin of the bacterial taxon);

'*Candidatus* Tangaroaiibacterium tarapacificum' (ta.ra.pa.ci'fi.cum. N.L. neut. adj. tarapacificum, referring to the *Tara* Pacific expedition from which the genome was recovered) is proposed as the type species of the genus *Ca. Tangaroaiibacterium*, which is represented by a long-read, chromosome-level metagenome-assembled genome as type material.

MAG20; TARA_SAMEA6034818_MAG_10000020; GCA_977880255 (seven contigs)

'*Candidatus* Taniwhaiibacterium' (Ta.niw.ha.i.i.bac.te'ri.um. N.L. neut. n. Taniwhaiibacterium, a composite of Taniwha—Latinised as Taniwhaius, gen. Taniwhaii, guardians of the sea, reefs, and other water bodies in Polynesian mythology, and bacterium; referring to the oceanic origin of the bacterial taxon);

'*Candidatus* Taniwhaiibacterium abditum' (ab.di'tum. N.L. neut. adj. abditum, hidden, referring to the more sporadic distribution of the taxon) is proposed as the type species of the genus *Ca. Taniwhaiibacterium*, which is represented by a long-read, chromosome-level metagenome-assembled genome as type material.

Proposed higher level taxonomy

On the basis of these clades, we further propose '*Candidatus* Moanaiibacteriaceae' (fam. nov.), '*Candidatus* Moanaiibacteriaceae' (fam. nov.), '*Candidatus* Tangaroaiibacteriales' (ord. nov.), and '*Candidatus* Tangaroaiibacteriia' (class nov.).

Research (UNCLOS) permits

Sampling permit for PANAMA under the reference 'SE/AP-18-16' delivered by the Direccion de Areas Protegidas y Vida Silvestre - LIC. Samuel Valdez Diaz Director - Ministerio de Ambiente – Republica de Panama on the 13/06/2016; Sampling permit for PANAMA under the reference '2016-0701-2019-2' delivered by the Smithsonian Tropical Research Institute Instituto Smithsonian de Investigaciones Tropicales - STRI Animal Care and Use Committee (ACUC) on the 28/06/2016; Sampling permit for PANAMA under the reference '2016-0701-2019-2-A1' delivered by the Smithsonian Tropical Research Institute Instituto Smithsonian de Investigaciones Tropicales - STRI Animal Care and Use Committee (ACUC) on the 21/06/2018; Sampling permit for COLOMBIA under the reference 'N°009' delivered by the MINISTERIO DE AMBIENTE Y DESARROLLO SOSTENIBLE PARQUES NACIONALES NATURALES DE COLOMBIA on the 04/03/2016; Sampling permit for CHILE under the reference '13270/24/457/Vrs' delivered by the Servicio Hidrografico y Oceanografico de la Armada de Chile (SHOA) – Patricio Carrasco Hellwig Contraalmirante Director on the 29/08/2016; Sampling permit for UNITED-KINGDOM (PITCAIRN ISLANDS) under the reference 'N/A' delivered by the Government of Pitcairn islands /Environmental, Conservation & Natural Resources Division Manager // Christian Michele on the 25/02/2016; Sampling permit for COOK under the reference '11-16' delivered by the Foundation for National Research – Cook Island Research Committee – Office of the Prime Minister – Elizabeth Wright-Koteka (Chairperson) on the 12/09/2016; Sampling permit for NIUE under the reference '34/16' delivered by the Government of Niue – Office for External Affairs on the 17/11/2016; Sampling permit for SAMOA under the reference 'Memorandum of Agreement' delivered by the THE GOVERNMENT OF THE INDEPENDENT STATE OF SAMOA acting

by and through the Ministry of Natural Resources and Environment on the 29/11/2016; Sampling permit for WALLIS AND FUTUNA under the reference 'Arrêté n°2016-527' delivered by the Le Préfet, Administrateur supérieur des îles Wallis et Futuna on the 24/11/2016; Sampling permit for TUVALU under the reference 'MFAT : 449/16' delivered by the Government of Tuvalu – Ministry of Foreign Affairs on the 19/12/2016; Sampling permit for KIRIBATI under the reference '015/16' delivered by the Environment and Conservation Division – Republic of Kiribati on the 24/11/2016; Sampling permit for MICRONESIA under the reference 'Letter' delivered by the Deputy Assistant Secretary – Marine Resources Unit – Department of Resources and Development – Federated States of Micronesia on the 05/04/2017; Sampling permit for GUAM under the reference 'U2021-023' delivered by the Marine Scientific Research Coordinator Office of Ocean and Polar Affairs – United States Department of State Bureau of Oceans and International Environmental and Scientific Affairs on the 27/10/2021; Sampling permit for AMERICAN SAMOA under the reference 'U2021-022' delivered by the Marine Scientific Research Coordinator Office of Ocean and Polar Affairs – United States Department of State Bureau of Oceans and International Environmental and Scientific Affairs on the 27/10/2021; Sampling permit for JAPAN (Tokyo Prefecture; Ogasawara Island) under the reference '28-50' delivered by the Prefecture of Tokyo on the 01/23/2017; Sampling permit for JAPAN (Okinawa Prefecture; Sesoko Island) under the reference '28-74' delivered by the Prefecture of Okinawa on the 04/14/2017; Sampling permit for JAPAN (Japanese EEZ) under the reference 'N/A' delivered by the Ministry of Agriculture, Forestry and Fisheries on the 01/10/2017; Sampling permit for FIJI under the reference '456/2017' delivered by the Ministry of Foreign Affairs – Republic of Fiji on the 11/06/2017; Sampling permit for AUSTRALIA under the reference 'G17/39873.1' delivered by the Great Barrier Reef Marine Park Authority and Department of Foreign Affairs and Trade on the 30/08/2017; Sampling permit for NEW-CALEDONIA (SOUTH PROVINCIA) under the reference 'Arrêté n°2720-2017/ARR/DENV modifiant l'arrêté 1515-2017/ARR/DENV du 04 août 2017' delivered by the Président de l'Assemblée de la Province Sud de la Nouvelle-Calédonie on the 06/09/2017; Sampling permit for NEW-CALEDONIA (CHESTERFIELD) under the reference 'Arrêté n°2017-2069/GNC' delivered by the Haut-Commissariat de la République en Nouvelle-Calédonie – Gouvernement de Nouvelle-Calédonie – République Française on the 29/08/2017; Sampling permit for SOLOMON ISLANDS under the reference 'Form 01' delivered by the Solomon Islands Maritime Safety Administration on the 20/09/2017; Sampling permit for PAPUA NEW-GUINEA under the reference '907/2017 (diplomatic clearance n°0232)' delivered by the Department of Foreign Affairs and Trade of the Independent State of Papua New Guinea on the 27/10/2017; Sampling permit for PALAU under the reference 'RE-18-04' delivered by the Ministry of Natural Resources, Environment and Tourism – Republic of Palau on the 21/12/2017; Sampling permit for CHINA (HONG-KONG) under the reference 'CMO-N00811' delivered by the Marine Department, Hong-Kong, China on the 15/03/2018; Sampling permit for TAIWAN (Pingtung county) under the reference '10707821600' delivered by the Pingtung Agri-Fish; National Taiwan Ocean University on the 06/04/2018; Sampling permit for TAIWAN (Taitung county) under the reference '1070033041' delivered by the Taitung Agri-Fish; National Taiwan Ocean University on the 12/02/2018; Sampling permit for USA (HAWAII) under the reference 'U2018-010' delivered by the United States Department of State Bureau of Oceans and International Environmental and Scientific Affairs on the 06/06/2018; Sampling permit for MEXICO under the reference 'PPF/DGOPA-291/17' delivered by the Secretaria de Agricultura, Ganaderia, Desarrollo rural, pesca y alimentacion

– Comision Nacional de Acuacultura y Pesca – Direccion General de Ordenamiento Pesquero y Acuicola – Estados Unidos Mexicanos on the 28/08/2018; Sampling permit for CLIPPERTON under the reference 'HC/1195/CAB' delivered by the Haut-Commissariat de la République Polynésie Française on the 13/06/2018; Sampling permit for COSTA RICA under the reference M-C-SINAC-PNI-SE-002-2022 delivered by the Sistema Nacional de Áreas de Conservación (SINAC) on the 29/09/2022; Sampling permit for USA (MAINLAND) under the reference 'U2018-010' delivered by the United States Department of State Bureau of Oceans and International Environmental and Scientific Affairs on the 06/06/2018; Sampling permit for CANADA under the reference 'Letter of regularization' delivered by the Sécurité et relations de défense (IGR)/Affaires mondiales Canada on the 05/01/2022; Sampling permit for NEW-ZEALAND under the reference 'Letter of regularization' delivered by the Ministry of Foreign Affairs and Trade on the 05/10/2021; Sampling permit for IRELAND under the reference '572/22' delivered by the Department of Foreign Affairs on the 09/06/2022.

CITES permits

CITES export permit for PANAMA (I01) under the reference 'SEX/A-72-16' delivered by the Autoridad Nacional del Ambiente (ANAM) de la República de Panamá – Autoridad Administrativa CITES on the 28/07/2016; CITES final import permit under the reference 'FR1609100066-I' delivered the 04/08/2016 by the DRIEE ILE-DE-FRANCE; CITES export permit for PANAMA (I02) under the reference 'SEX/A-72-16' delivered by the Autoridad Nacional del Ambiente (ANAM) de la República de Panamá – Autoridad Administrativa CITES on the 28/07/2016; CITES final import permit under the reference 'FR1609100066-I' delivered the 04/08/2016 by the DRIEE ILE-DE-FRANCE; CITES export permit for PANAMA (I31) under the reference 'SEX/APO-1-2018' delivered by the Ministerio de Ambiente on the 30/08/2018; CITES final import permit under the reference 'FR1807523129-I' delivered the 19/10/2018 by the DRIEE ILE-DE-FRANCE; CITES export permit for PANAMA (I32) under the reference 'SEX/APO-1-2018' delivered by the Ministerio de Ambiente on the 30/08/2018; CITES final import permit under the reference 'FR1807523129-I' delivered the 19/10/2018 by the DRIEE ILE-DE-FRANCE; CITES export permit for COLOMBIA (I03) under the reference '41499' delivered by the Ministerio de Ambiente y Desarrollo Sostenible de la República de Colombia on the 13/02/2017; CITES final import permit under the reference 'FR1707506158-I' delivered the 17/03/2017 by the DRIEE ILE-DE-FRANCE; CITES export permit for CHILE (I04) under the reference '16CL000007WS' delivered by the Servicio Nacional de Pesca y Acuicultura on the 02/09/2016; CITES final import permit under the reference 'FR1607525599-I' delivered the 03/11/2016 by the DRIEE ILE-DE-FRANCE; CITES export permit for UNITED-KINGDOM (PITCAIRN ISLANDS; I05) under the reference 'FR1698700198-E' delivered by the Haut-Commissariat de la République en Polynésie Française on the 03/11/2016; CITES final import permit under the reference 'FR1607525646-I' delivered the 04/11/2016 by the DRIEE ILE-DE-FRANCE; CITES export permit for FRENCH POLYNESIA (GAMBIER – TUAMOTU; I06) under the reference 'FR1698700198-E' delivered by the Haut-Commissariat de la République en Polynésie Française on the 03/11/2016; CITES final import permit under the reference 'FR1607525646-I' delivered the 04/11/2016 by the DRIEE ILE-DE-FRANCE; CITES export permit for MOOREA (I07) under the reference 'FR1698700218-E' delivered by the Haut-Commissariat de la République en Polynésie Française on the 21/11/2016; CITES final

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