# Genome Sequences of 72 Bacterial Strains Isolated from Ectocarpus subulatus: A Resource for Algal Microbiology

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# Genome Sequences of 72 Bacterial Strains Isolated from *Ectocarpus subulatus*: A Resource for Algal Microbiology

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## Abstract

Brown algae are important primary producers and ecosystem engineers in the ocean, and *Ectocarpus* has been established as a laboratory model for this lineage. Like most multicellular organisms, *Ectocarpus* is associated with a community of microorganisms, a partnership frequently referred to as holobiont due to the tight interconnections between the components. Although genomic resources for the algal host are well established, its associated microbiome is poorly characterized from a genomic point of view, limiting the possibilities of using these types of data to study host–microbe interactions. To address this gap in knowledge, we present the annotated draft genome sequences of seventy-two cultivable *Ectocarpus*-associated bacteria. A screening of gene clusters related to the production of secondary metabolites revealed terpene, bacteriocin, NRPS, PKS-t3, siderophore, PKS-t1, and homoserine lactone clusters to be abundant among the sequenced genomes. These compounds may be used by the bacteria to communicate with the host and other microbes. Moreover, detoxification and provision of vitamin B pathways have been observed in most sequenced genomes, highlighting potential contributions of the bacterial metabolism toward host fitness and survival. The genomes sequenced in this study form a valuable resource for comparative genomic analyses and evolutionary surveys of alga-associated bacteria. They help establish *Ectocarpus* as a model for brown algal holobionts and will enable the research community to produce testable hypotheses about the molecular interactions within this complex system.

**Key words:** brown algae, holobiont, alga-associated bacteria, biosynthetic gene clusters, detoxification, metabolic networks.

## Introduction

Brown macroalgae are important primary producers and major ecosystem engineers on marine rocky shores, providing both shelter and nutrients for other forms of life (Brodie et al. 2017). They belong to the stramenopiles, an evolutionarily distinct lineage from the Achaeplastida, which comprise red and green algae as well as land plants (Charrier et al. 2008) and are of commercial importance in several regions of the world (Koru 2013; Raja et al. 2013; Venkatesan et al. 2015). *Ectocarpus* is a genus of brown algae that has been established as a laboratory model for this lineage (Peters et al. 2004) due to its small genome (Cock et al. 2010), the possibility of cultivation in the lab, and its short life cycle.

Like most if not all multicellular eukaryotes, brown algae, including *Ectocarpus*, are associated with bacteria (Paix et al. 2019). These interactions may be so intimate that the term holobiont has been suggested to describe the functional unit of a host and its associated microbiome (Zilber-Rosenberg and Rosenberg 2008; Douglas and Werren 2016). For instance, it has been estimated that approximately half of all algae (including 49 out of 83 surveyed stramenopiles) rely on their bacteria associated to provide them with vitamin B12 (Croft et al. 2005; Tang et al. 2010). In *Ectocarpus*, associated

bacteria are known to provide functions related to developmental transitions and growth of the algae (Pedersen 1968; Tapia et al. 2016). Furthermore, they may impact their capacity to tolerate environmental stressors (Dittami et al. 2016).

Collections of cultivable bacteria provide a valuable resource to study the mechanisms underlying these interactions, and in *Ectocarpus* three recent papers describe the generation of culture collections. In *Ectocarpus siliculosus* Tapia et al. (2016) have reported the isolation of 9 bacterial strains, and in *Ectocarpus subulatus* KleinJan et al. (2017) cultivated 46 strains corresponding to 33 different bacterial genera from algal surfaces. An additional 95 strains corresponding to 27 different genera have also recently been isolated from field material of *E. subulatus* (Dittami et al. 2019).

In present study, we describe genomic resources for 72 of these cultivable *Ectocarpus*-associated bacteria. Sixty-two genomes were sequenced specifically for this study, plus ten previously sequenced genomes from the same culture collection (Burgunter-Delamare et al. 2019) were also included. These genomes constitute a valuable resource both to study the genomic adaptations of bacteria to life on the surface of brown algae, but also to generate hypotheses on potential beneficial interactions between the bacteria and their host, for example, via metabolic complementarity-based approaches (Frioux et al. 2018). They furthermore constitute a first step toward filling a big gap in our current knowledge: The fact that currently (September 2019), based on our research through Marine Metagenomics Portal (Robertsen et al. 2017; Klemetsen et al. 2018), only ~100 draft and complete bacterial genomes isolated from algae/seaweed are publicly available in GenBank. Thus, the genomes from this study could add a great amount of information to algal microbiomes and will promote other studies aiming to decipher algal-microbial associations.

## Materials and Methods

### Bacterial Strains and DNA Extraction

Bacterial strains were isolated from a laboratory culture of *E.subulatus* (strain CCAP 1310/19; KleinJan et al. 2017) as well as from field samples of the same species (Dittami et al. 2019). Field samples were collected in March 2017 from two locations along the Hopkins River, Victoria, Australia, a few km upstream of Hopkins River falls, the original collection site of strain CCAP 1310/19 (West and Kraft 1996): Framlingham Forest reserve (–38.297064, 142.668291) and Kent's Ford (–38.191574, 142.698058). All bacterial strains were identified by Sanger-sequencing of the 16S rDNA gene using the 8F and the 1492R primer pair (Weisburg et al. 1991). Bacteria were grown on 90 mm Petri dishes with R2A medium (Reasoner and Geldreich 1985) Sigma–Aldrich at 19 °C for 4–7 days. Subsequently, a single colony was selected and grown at 25 °C in liquid R2A medium overnight. The bacterial genomic DNA was extracted using Promega Wizard Genomic DNA purification kit following the manufacturer's instructions. The extracted DNA was quantified using a Qubit and its quality was determined using agarose gel electrophoresis.

### Genome Sequencing, Assembly, and Annotation

Paired-end DNA libraries with an average insert size of 500 bp were prepared using the Nextera XT DNA library kit (library average size ~1,100 bp). Libraries were then sequenced using the Illumina MiSeq technology (V3, paired-end, 2 × 300 bp reads) at GENOMER platform (Station Biologique de Roscoff), multiplexing ~20 bacterial genomes per run. Raw reads were first examined using FastQC (Andrews 2010). Low-quality sequences were trimmed or removed using Trimmomatic v.0.38 and a sliding window with a quality score of 15 as well as a minimal read length of 36 bp as filters. Trimmed read pairs were used for genome assembly with SPAdes v.3.12.0 (Bankevich et al. 2012) using default parameters. Genomic sequences encoding parts of the ribosome were identified using Barrnap v. 0.8 (https://github.com/tseemann/barrnap) and 16S rDNA sequences used to search for complete reference genomes in the GenBank. These reference genomes were used for scaffolding with Medusa version 1.6. Finally, gaps in the scaffolds were filled wherever possible using GapCloser 1.12 (Li et al. 2010) and the resulting draft genomes were annotated and prepared for submission to public databases using the MicroScope platform (Vallenet et al. 2017). The genomes were deposited at the European Nucleotide Archive.

### Phylogenomic Analyses

Phylogenomic relationships among all studied strains were confirmed by running genome clustering based on pairwise distances and Average Nucleotide Identity (ANI) between all selected genomes using the Neighbor-Joining algorithm in MicroScope. Furthermore, the closest genome has been provided for all genomes, based on their resulting Tetranucleotide signature correlation index via the JSpeciesWS tool (Richter et al. 2016).

### In Silico Analysis of Bacterial Metabolism

Models of primary metabolism for each sequenced bacterium were generated using the Pathway tools pipeline implemented in the MicroScope platform. The output of this pipeline is a pathway completion value, that is, the ratio between the number of reactions for a specific pathway in a bacterium and the total number of reactions for that pathway defined in the MetaCyc (Caspi et al. 2018) or KEGG (Kanehisa et al. 2008) databases. In addition, secondary metabolite-related gene clusters were predicted using antiSMASH (Blin et al. 2017).

## Results and Discussion

### Genome Characteristics

Here, we report the sequencing of 62 and the analysis of 72 genomes of *Ectocarpus*-associated bacterial strains corresponding to 43 different genera and 16 different orders. The individual strains as well as key attributes of their genome sequences are listed in table 1. The genome size of all strains ranged from 2.4 Mb to 6.8 Mb. The largest genome was that of *Imperialibacter* sp. strain SDR9 from the *Bacteroidetes* and the smallest was that of *Micrococcus* sp. strain 11B from the *Actinobacteria*. The analyzed genomes showed diverse GC contents with strains belonging to the *Bacteroidetes* and *Firmicutes* exhibiting GC contents <40% (e.g., 30% in *Flavobacterium* sp. 9AF) contrary to *Actinobacteria*, where most strains exhibit GC contents over 70%. Overall, the GC content was positively correlated with genome size (Pearson correlation $r = 0.73$, $P = 0.042$). CheckM analyses (Parks et al. 2015) suggest that the sequenced genomes are nearly complete (>98%, table 1) and free of or with very low levels of contamination (<2.5%; supplementary table S1, Supplementary Material online). The only exception was *Arthrobacter* sp. strain 9V with 4.8% contamination (22 marker genes). This indicates that, overall, the presented genomes are suitable for downstream analyses such as comparisons of metabolic capacities.

### Phylogenomic Tree

Several of the sequenced bacteria in this study correspond to bacteria with no or only few closely related sequences in the databases. Notably, *Enterobacterales* bacterium 8AC, and *Moraxellaceae* bacterium 17A could be confidently identified only to the family level through RDP classifier (supplementary table S1, Supplementary Material online), making these strains candidates for new species or genera. Besides, fifteen strains including *Imperialibacter* sp. EC-SDR9, *Marinoscillum* sp. 108, *Sphingomonas* sp., AX6, and *Novosphingobium* sp., and *Burkholderiales* bacterium 8X have low similarity (*z*-score below cutoff < 0.989) with their closest genome-sequenced relatives (based on the tetra-nucleotide signature correlation index, table 1 and supplementary fig. S1, Supplementary Material online). This phylogenomic analysis yielded a tree generally grouping together bacteria from the same taxon (supplementary fig. S1, Supplementary Material online). However, *Imperialibacter* sp. EC-SDR9 and *Sphingobacterium* sp. 8BC from *Bacteroidetes* clustered with *Firmicutes*.

### Secondary Metabolic Activities and Potentially Symbiosis-Related Metabolites

Algal-associated microbes are likely to interact with both the host and other microbes within the community. Secondary metabolites are metabolites not essential for normal growth of microorganisms, but they play a major role as chemical signals for interaction with other microorganisms (Netzker et al. 2015), restriction of pathogens (antimicrobial activities), and biofouling (Wiese et al. 2009; Nasrolahi et al. 2012; Susilowati et al. 2015). For instance, terpenes as the largest class of natural compounds have protective roles against competitors and are involved in interspecies signaling (Gershenzon and Dudareva 2007; Yamada et al. 2015). Similarly, bacteriocins, peptidic toxins produced by bacteria, have been suggested to play a role in pathogenesis by induction of cell lysis (Li and Tian 2012). The annotation of the 72 bacterial genomes with respect to genes involved in secondary metabolism obtained from AntiSMASH via the MicroScope platform showed that all analyzed strains except *Oceanicaulis* sp. strain 350, had at least one secondary biosynthetic gene cluster. Furthermore, 68% of genomes have at least one predicted terpene cluster gene, followed by bacteriocin (40.2%), nonribosomal Peptide Synthetases (NRPS, 36%), Type 3 polyketide synthases (PKS-t3, 33.33%), siderophores (23.6%), Type 1 polyketide synthases (PKS-t1, 20.8%), and homoserine lactone synthesis genes (16.6%; fig. 1 and supplementary table S1, Supplementary Material online). These genes are likely to be at least partially involved in the communication with the host and between microbes.

### Detoxification Role of Symbionts and Provision of Vitamins

In terms of detoxification mechanisms, one pathway that was complete in all studied genomes was the capacity to degrade superoxide radicals. Moreover, 46 strains of 72 possessed the complete pathway for glutaredoxin synthesis (fig. 1). This mechanism is important for the degradation reactive oxygen species (ROS), which are formed by the algae through metabolic processes and in response to different stressors (Cosse et al. 2007). ROS can cause significant damage to the cell; thus, microorganisms have developed defense systems to detoxify ROS in order to survive.

Furthermore, the cyanate degradation pathway was complete or semicomplete in all bacteria except in strains 8BE, 8AC, and 8AQ. Cyanate is a common compound in marine environments and may serve as both an energy source for marine microbes (Palatinszky et al. 2015) as well as a potential source of nitrogen (Kamennaya et al. 2008; Sáez et al. 2019). Whether this pathway also plays a role during the interactions of microbes with their algal host, for example, by enabling the microbes to provide nitrogen to their host, remains to be tested.

Finally, most genomes analyzed encoded nearly complete or complete pathways for production of B vitamins like biotin (B7), folate (B9), riboflavin (B2), thiamine (B1), and pyridoxine (B6) (fig. 1). They may thus be contributors of vitamin B for the algal host, as has previously been suggested for diatom-bacteria associations (Behringer et al. 2018). All in all, these studied metabolic features highlight the possible contributions of the alga-associated bacteria to maintain host fitness and survival.

**Table 1**

Genome Features of Algal-Associated Bacteria Analyzed in This Study

| Strain | Complete-ness (%)[a] | Genome Size (Mb) | Coverage (X) | N50 (Mb) | %GC | Scaffold Nb. | CDS Nb. | Mean CDS Length | tRNA Nb. | rRNA Nb. | Closest Relative | Accession Numbers |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Actinobacteria*** | | | | | | | | | | | | |
| *Aeromicrobium* sp. 9AM | 99.7 | 4.2 | 144 | 2.98 | 68 | 9 | 4,422 | 897 | 46 | 3 | *Aeromicrobium* sp. Root236 | LR733303–LR733311 |
| *Arthrobacter* sp. 8AJ | 99.7 | 4.3 | 88 | 4.22 | 66 | 4 | 4,228 | 944 | 51 | 5 | *Moraxella osloensis* NCTC10465 | LR733289–LR733292 |
| *Arthrobacter* sp. 9AX | 99.7 | 4.4 | 230 | 4.41 | 66 | 7 | 4,453 | 918 | 50 | 6 | *Pseudarthrobacter siccitolerans* 4J27 | LR733289–LR733292 |
| *Arthrobacter* sp. 9V | 99.7 | 5.1 | 221 | 4.82 | 62 | 158 | 5,091 | 925 | 62 | 9 | *Arthrobacter* sp. EpRS71 | LR732912–LR733069 |
| *Citricoccus* sp. K5 | 99.2 | 3.9 | 324 | 3.74 | 69 | 9 | 3,708 | 974 | 47 | 5 | *Citricoccus muralis* DSM 14442 | LR732817–LR732825 |
| *Curtobacterium* sp. 8I–2 | 99 | 3.6 | 109 | 2.80 | 71 | 5 | 3,767 | 911 | 47 | 6 | *Curtobacterium flaccumfaciens* UCD-AKU | LR732826–LR732830 |
| *Frigoribacterium* sp. 9N | 98.5 | 3.3 | 151 | 2.53 | 71 | 16 | 3,339 | 926 | 45 | 5 | *Frigoribacterium* sp. Leaf8 | LR733390–LR733405 |
| *Microbacterium* sp. 8M | 99.5 | 3.7 | 185 | 3.68 | 71 | 2 | 3,659 | 961 | 44 | 4 | *Microbacterium azadirachtae* DSM 23848 | LR733284–LR733285 |
| *Micrococcus* sp. 116 | 98.6 | 2.6 | 215 | 2.49 | 73 | 19 | 2,526 | 943 | 48 | 5 | *Micrococcus luteus* 2385 | LR732370–LR732388 |
| *Micrococcus* sp. 11B | 98.1 | 2.4 | 450 | 1.89 | 73 | 52 | 2,398 | 952 | 48 | 5 | *Micrococcus luteus* 2385 | LR733070–LR733121 |
| *Micrococcus* sp. 80W | 98.1 | 2.5 | 224 | 1.78 | 73 | 80 | 2,521 | 942 | 48 | 4 | *Micrococcus luteus* 2385 | LR732389–LR732468 |
| *Nocardioides* sp. AX2bis | 98.7 | 4.2 | 221 | 3.96 | 73 | 37 | 4,397 | 915 | 45 | 4 | *Marmoricola aurantiacus* DSM 12652* | LR733215–LR733251 |
| *Plantibacter* sp. T3 | 99.5 | 4 | 287 | 3.98 | 69 | 3 | 4,131 | 924 | 48 | 4 | *Plantibacter flavus* VKM Ac-2504 | LR733286–LR733288 |
| *Pseudoclavibacter* sp. 8L | 98.2 | 4.1 | 98 | 1.43 | 68 | 30 | 4,137 | 921 | 45 | 4 | *Microbacterium* sp. TS-1* | LR733185–LR733214 |
| ***Bacteroidetes*** | | | | | | | | | | | | |
| *Imperialibacter* sp. SDR9 | 100 | 6.8 | 111 | 0.96 | 47 | 65 | 5,767 | 1069 | 38 | 4 | *Arcticibacter pallidi-corallinus* CGMCC 1.9313* | LR701573–LR701637 |
| *Marinoscillum* sp. 108 | 99.1 | 5.2 | 83 | 3.73 | 46 | 12 | 4,489 | 1086 | 37 | 4 | *Marinoscillum furvescens* DSM 4134* | LR734808–LR734819 |
| *Chryseobacterium* sp. 8AT | 100 | 4.7 | 114 | 4.43 | 34 | 31 | 4,483 | 931 | 70 | 7 | *Chryseobacterium scophthalmum* DSM 16779 | LR733314–LR733344 |
| *Flavobacterium* sp. 9AF | 98.9 | 4.2 | 101 | 2.95 | 30 | 74 | 3,871 | 992 | 51 | 5 | *Flavobacterium* sp. 316* | LR733556–LR733629 |
| *Flavobacterium* sp. 9R | 99.6 | 3.6 | 184 | 3.42 | 35 | 16 | 3,175 | 1006 | 42 | 6 | *Flavobacterium succinicans* DD5b* | LR733413–LR733428 |
| *Maribacter* sp. 151 | 99.7 | 4.4 | 59 | 4.35 | 36 | 4 | 3,857 | 1044 | 36 | 6 | *Maribacter litoralis* SDRB-Phe2 | LR733271–LR733274 |
| *Sphingobacterium* sp. 8BC | 100 | 5.8 | 129 | 5.73 | 40 | 14 | 5,379 | 960 | 70 | 9 | *Sphingobacterium multivorum* NCTC11343 | LR733857–LR733870 |
| ***Firmicutes*** | | | | | | | | | | | | |
| *Bacillus* sp. 348 | 99.6 | 3.8 | 246 | 3.58 | 41 | 5 | 4,070 | 846 | 79 | 9 | *Bacillus stratosphericus* LK33 | LR732831–LR732835 |
| *Bacillus* sp. 349Y | 99.3 | 4.5 | 114 | 0.12 | 48 | 85 | 4,616 | 839 | 97 | 9 | *Bacillus* sp. Leaf406 | LR733732–LR733816 |
| *Bacillus* sp. 71 | 99.3 | 5.7 | 116 | 5.69 | 35 | 14 | 6,092 | 796 | 98 | 18 | *Bacillus* cereus HuA2-4 | LR733376–LR733389 |
| *Bacillus* sp. 9J | 99.6 | 3.8 | 179 | 3.74 | 42 | 76 | 4,109 | 834 | 86 | 9 | *Bacillus* sp. Leaf49 | LR732836–LR732911 |
| *Exiguobacterium* sp. 8A | 99.3 | 3.1 | 184 | 2.87 | 48 | 77 | 3,234 | 868 | 63 | 13 | *Exiguobacterium* sp. AT1b | LR733630–LR733706 |
| *Exiguobacterium* sp. 8H | 99.3 | 3 | 296 | 0.87 | 48 | 40 | 3,154 | 868 | 63 | 14 | *Exiguobacterium* sp. AT1b | LR733429–LR733468 |
| *Exiguobacterium* sp. 9Y | 99.3 | 3 | 88 | 1.61 | 47 | 20 | 3,070 | 876 | 65 | 11 | *Exiguobacterium oxidotolerans* JCM 12280 | LR732308–LR732327 |
| *Staphylococcus* sp. 8AQ | 99.2 | 2.5 | 269 | 2.49 | 31 | 4 | 2,501 | 886 | 62 | 9 | *Staphylococcus pasteuri* BAB3 | LR733871–LR733874 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ***Proteobacteria*** | | | | | | | | | | | | |
| *Aeromonas* sp. 8C | 100 | 4.6 | 345 | 4.57 | 59 | 3 | 4,769 | 899 | 114 | 11 | *Aeromonas veronii* TTU2014-115ASC | LR732797–LR732799 |
| *Aeromonas* sp. 9A | 100 | 4.8 | 105 | 4.70 | 59 | 11 | 4,590 | 925 | 114 | 16 | *Aeromonas salmonicida* Y577 | LR732779–LR732789 |
| *Alteromonas* sp. 38 | 100 | 4.7 | 209 | 4.70 | 44 | 3 | 4,324 | 975 | 62 | 6 | *Alteromonas stellipolaris* LMG 21856 | LR733300–LR733302 |
| *Marinobacter* sp. HK377 | 100 | 4.4 | 172 | 4.34 | 57 | 7 | 4,176 | 976 | 45 | 6 | *Marinobacter salarius* R9SW1 | LR701480–LR701486 |
| *Marinobacter* sp. N1 | 100 | 4.4 | 152 | 4.35 | 57 | 2 | 4,125 | 978 | 45 | 6 | *Marinobacter salarius* R9SW1 | LR733269–LR733270 |
| *Burkholderia* sp. 8Y | 100 | 6.3 | 61 | 2.36 | 63 | 37 | 6,403 | 874 | 52 | 8 | *Burkholderia* sp. MR1 | LR733519–LR733555 |
| *Limnobacter* sp. 130 | 99 | 3.3 | 74 | 1.82 | 52 | 6 | 3,034 | 1007 | 37 | 3 | *Limnobacter* sp. MED105* | LR732328–LR732333 |
| *Massilia* sp. 9I | 100 | 5.5 | 195 | 5.51 | 66 | 9 | 5,242 | 984 | 70 | 7 | *Massilia alkalitolerans* DSM 17462 | LR733275–LR733283 |
| *Burkholderiales* bacterium 8X | 99.8 | 4.8 | 141 | 4.78 | 67 | 3 | 4,776 | 973 | 44 | 5 | *Variovorax* sp. WDL1* | LR732703–LR732705 |
| *Brevundimonas* sp. G8 | 99.7 | 3.3 | 375 | 3.32 | 66 | 1 | 3,308 | 927 | 47 | 3 | *Brevundimonas* sp. Leaf280 | LR732816–LR732816 |
| *Oceanicaulis* sp. 350 | 99.8 | 3.1 | 185 | 2.98 | 62 | 4 | 3,035 | 939 | 47 | 6 | *Oceanicaulis alexandrii* DSM 11625 | CABWMW010000001–CABWMW010000008 |
| *Pantoea* sp. 111 | 100 | 4.9 | 62 | 4.09 | 56 | 35 | 4,807 | 890 | 73 | 9 | *Pantoea brenneri* LMG 5343 | LR733469–LR733503 |
| *Enterobacterales bacterium* 8AC | 100 | 5.3 | 134 | 4.81 | 53 | 63 | 4,858 | 936 | 74 | 10 | *Serratia oryzae* J11-6 | LR733916–LR733978 |
| *Halomonas* sp. 153 | 100 | 5.5 | 35 | 5.44 | 55 | 11 | 5,045 | 972 | 59 | 5 | *Halomonas titanicae* BH1 | LR733721–LR733731 |
| *Halomonas* sp. 98 | 100 | 5.5 | 109 | 5.43 | 55 | 14 | 5,029 | 975 | 59 | 6 | *Halomonas titanicae* BH1 | LR733707–LR733720 |
| *Acinetobacter* sp. 8BE | 100 | 4.4 | 144 | 3.94 | 41 | 35 | 4,368 | 891 | 61 | 7 | *Acinetobacter* sp. NIPH 809 | LR732744–LR732778 |
| *Acinetobacter* sp. 8I-beige | 100 | 3.5 | 138 | 2.08 | 41 | 7 | 3,452 | 895 | 73 | 7 | *Acinetobacter johnsonii* DSM 6963 | LR732790–LR732796 |
| *Moraxellaceae* bacterium 17A | 100 | 3 | 194 | 2.75 | 43 | 37 | 2,973 | 897 | 41 | 6 | *Moraxella osloensis* CCUG 57516 | LR732269–LR732305 |
| *Enhydrobacter* sp. 8BJ | 100 | 2.8 | 301 | 2.62 | 43 | 31 | 2,628 | 919 | 45 | 7 | *Moraxella osloensis* NCTC10465 | LR733345–LR733375 |
| *Enhydrobacter* sp. AX1 | 99.7 | 2.7 | 350 | 2.65 | 44 | 16 | 2,517 | 943 | 49 | 6 | *Enhydrobacter aerosaccus* SK60 | LR732800–LR732815 |
| *Pseudomonas* sp. 8AS | 98.1 | 4.3 | 199 | 4.26 | 66 | 7 | 4,113 | 945 | 57 | 4 | *Pseudomonas alcaligenes* NBRC 14159 | LR733406–LR733412 |
| *Pseudomonas* sp. 8BK | 100 | 4.5 | 145 | 4.38 | 60 | 11 | 4,205 | 960 | 63 | 9 | *Pseudomonas peli* DSM 17833 | LR733252–LR733262 |
| *Pseudomonas* sp. 8O | 99.8 | 5.2 | 78 | 1.61 | 62 | 6 | 4,949 | 949 | 60 | 5 | *Pseudomonas pseudoalcaligenes* AD6 | LR733263–LR733268 |
| *Pseudomonas* sp. 8Z | 99.4 | 4.8 | 144 | 1.12 | 61 | 12 | 4,625 | 935 | 61 | 8 | *Pseudomonas composti* CCUG 59231* | LR733824–LR733835 |
| *Pseudomonas* sp. 9Ag | 100 | 4.7 | 136 | 4.62 | 60 | 4 | 4,465 | 946 | 52 | 4 | *Pseudomonas* sp. 10B238 | LR733836–LR733839 |
| *Pseudomonas* sp. 9AZ | 99.7 | 4.5 | 235 | 4.46 | 60 | 4 | 4,260 | 961 | 60 | 8 | *Pseudomonas peli* DSM 17833 | LR733840–LR733843 |
| *Bosea* sp. 125 | 99.1 | 6.3 | 46 | 6.12 | 67 | 63 | 6,435 | 899 | 46 | 3 | *Bosea* sp. Root483D1 | LR733122–LR733184 |
| *Bosea* sp. 127 | 99.1 | 6.3 | 78 | 6.28 | 67 | 8 | 6,705 | 876 | 46 | 3 | *Bosea* sp. Root483D1 | LR733511–LR733518 |
| *Bosea* sp. 29B | 99.1 | 6.3 | 137 | 6.32 | 67 | 7 | 6,422 | 904 | 46 | 3 | *Bosea* sp. Root483D1 | LR733817–LR733823 |
| *Bosea* sp. 62 | 99.1 | 6.3 | 154 | 6.28 | 67 | 7 | 6,411 | 905 | 46 | 3 | *Bosea* sp. Root483D1 | LR733504–LR733510 |
| *Bosea* sp. HK365B | 99.1 | 6.3 | 133 | 1.03 | 67 | 18 | 6,738 | 876 | 46 | 3 | *Bosea* sp. Root483D1 | LR701663–LR701680 |
| *Hoeflea* sp. HK425 | 99.9 | 5.2 | 326 | 4.68 | 61 | 28 | 5,266 | 898 | 43 | 3 | *Hoeflea halophila* KCTC 23107 | LR701545–LR701572 |
| *Rhizobium* sp. SD404 | 100 | 4.2 | 148 | 4.22 | 62 | 18 | 4,192 | 920 | 42 | 3 | *Pararhizobium haloflavum* XC0140* | LR701442–LR701459 |
| *Roseovarius* sp. SD190 | 99.3 | 4.7 | 80 | 3.89 | 61 | 17 | 4,794 | 902 | 44 | 3 | *Roseovarius* sp. TM1035 | LR701460–LR701476 |
| *Erythrobacter* sp. HK427 | 99.1 | 3.1 | 157 | 3.12 | 63 | 3 | 3,097 | 947 | 45 | 3 | *Porphyrobacter* sp. AAP60* | LR701477–LR701479 |
| *Novosphingobium* sp. 9U | 99.6 | 4.6 | 221 | 2.82 | 65 | 75 | 4,843 | 867 | 49 | 5 | *Novosphingobium resinovorum* SA1* | LR732469–LR732543 |

(continued)

**Table 1** Continued

| Strain | Complete-ness (%)[a] | Genome Size (Mb) | Coverage (X) | N50 (Mb) | %GC | Scaffold Nb. | CDS Nb. | Mean CDS Length | tRNA Nb. | rRNA Nb. | Closest Relative | Accession Numbers |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Sphingomonas* sp. 8AM | 99.7 | 3.8 | 119 | 3.66 | 67 | 13 | 3,739 | 929 | 48 | 4 | *Sphingomonas phyllosphaerae* FA2 | LR733844–LR733856 |
| *Sphingomonas* sp. AX6 | 99.4 | 3 | 228 | 3.01 | 64 | 1 | 3,161 | 892 | 44 | 3 | *Sphingomonas echinoides* ATCC 14820* | LR733857–LR733870 |
| *Sphingomonas* sp. HK361 | 99.7 | 3.3 | 150 | 1.78 | 66 | 8 | 3,274 | 935 | 45 | 3 | *Hephaestia caeni* DSM 25527* | LR701487–LR701494 |
| *Sphingomonas* sp. SD391 | 99.5 | 4.6 | 114 | 4.15 | 66 | 34 | 4,682 | 903 | 49 | 5 | *Sphingomonas* sp. Leaf28 | LR701495–LR701528 |
| *Sphingomonas* sp. T1 | 99.3 | 4.5 | 243 | 3.83 | 66 | 41 | 4,647 | 900 | 50 | 3 | *Sphingomonas* sp. Leaf30 | LR733875–LR733915 |
| *Sphingorhabdus* sp. 109 | 99.2 | 3.6 | 97 | 3.56 | 58 | 5 | 3,585 | 928 | 45 | 6 | *Sphingorhabdus* sp. M41* | LR732707–LR732711 |
| *Luteimonas* sp. 9C | 100 | 3.3 | 77 | 2.83 | 69 | 2 | 3,207 | 957 | 48 | 3 | *Xanthomonas* sp. Mitacek01 | LR733312–LR733313 |

Note.—The closest relative with the similarity below Cut-off [z-score (<0.98)] is marked with asterisk. Nb, number; CDS, coding sequence.
[a]Determined using the CheckM tool.

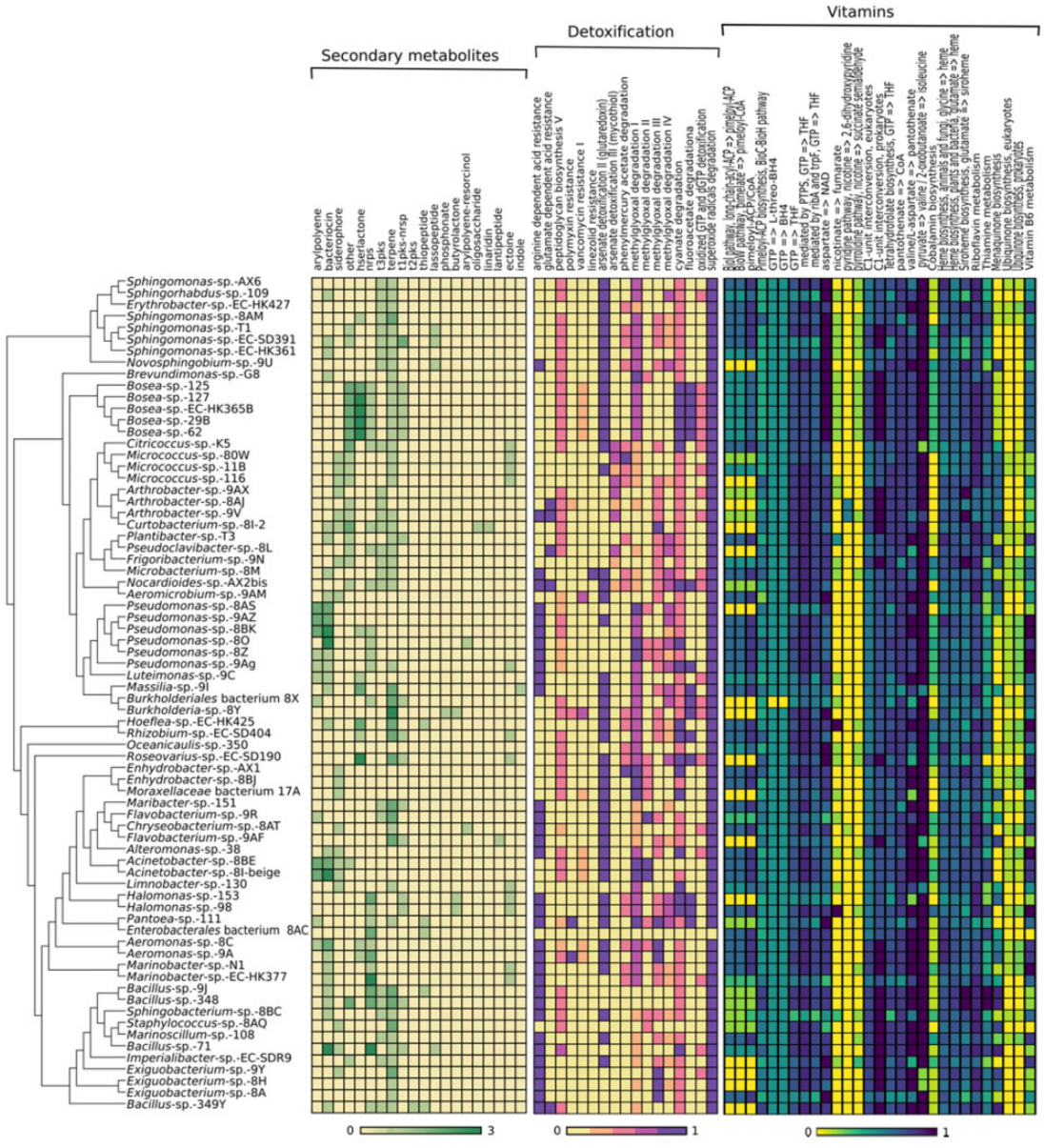


**Fig. 1.**—Heatmap of representative secondary metabolite clusters, detoxification-, and vitamin biosynthetic genes in the studied bacterial genomes. The dendrogram represents a whole-genome phylogeny, secondary metabolite gene clusters were predicted via AntiSMASH, detoxification genes were identified based on the MicroCyc database, and vitamin biosynthesis capacities were assess based on KEGG entries. The color code represents the number of genes per cluster (secondary metabolites) or the proportion of genes found in a particular organism and pathway.

The genomic resources provided here constitute a valuable resource for comparative genomic analyses and evolutionary surveys of alga-associated bacteria and will allow us to produce testable hypotheses about the molecular interactions between the microbes and their host. They may, among other uses, facilitate metabolic complementarity centered approach as proposed by Dittami et al. (2014), to identify potential beneficial interactions between the partners. They will also form the bases for more targeted molecular approaches, for example, gene knockouts or gene expression analyses once specific interactions are being targeted in coculture experiments.

## Supplementary Material

Supplementary data are available at *Genome Biology and Evolution* online.

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## Author Contributions

E.K. participated in the conception and design of the study, sample processing, genome sequencing and assembly, data analysis, writing the manuscript. E.G. participated in the genome assembling, submission of genomes to MicroScope, and helped with the preparation of the figures. H.K. participated in the isolation of bacteria and genome sequencing. G.T. and E.L. both contributed to the sequencing of the genomes. E.C. participated in the assembling protocol and revision. S.M.D. participated in the conception and design of the study, isolation of bacteria, genome assembly and writing the manuscript. All authors approved the final draft.

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