

Draft Genome Sequences of Two *Vibrionaceae* Species, *Vibrio ponticus* C121 and *Photobacterium aphoticum* C119, Isolated as Coral Reef Microbiota

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Here, the draft genome sequences of two *Vibrionaceae*, *Vibrio ponticus* C121 and *Photobacterium aphoticum* C119, which were isolated from the coral reef vicinity in Okinawa, Japan, are reported. The genome provides further insight into the genomic plasticity, biocomplexity, and ecophysiology, including pathogenicity and evolution, of these genera.

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The family *Vibrionaceae* encompasses diverse metabolically versatile marine bacteria that are associated with many significant events in the marine ecosystem, including fish/shellfish pathogenicity (1), mutual symbiosis with marine organisms (2, 3), and mediation of the nutrient cycle in the marine food web (4, 5). They are ubiquitous in marine environments and are characterized by high genomic plasticity (6). These dynamics have made the differentiation of sister species difficult (7). Interestingly, such characteristics have also nominated *Vibrionaceae* species as a great test model for genomic taxonomy (7).

To date, the family *Vibrionaceae* accounts for 142 validly described species and the number is growing continuously (<http://www.bacterio.net/-candidatus.html>). However, the rapid expansion of the family has also demanded more reliable, reproducible, and informative schemes to define a new species that can be attained using microbial genomic taxonomy. While the type strains of *V. ponticus* (8) and *P. aphoticum* (9) were described in 2004 and 2011, respectively, no genome sequence has been reported since then. Our study reports the first draft genome sequences of *V. ponticus* C121 and *P. aphoticum* C119, which were isolated from water samples taken near the coral reef vicinity of Iriomote-Ishigaki National Park, Okinawa, Japan. *V. ponticus* strain was isolated not only from seawater and mussels but also diseased sea bream (8) and Japanese sea bass (10). *P. aphoticum* was isolated from seawater (9). The species might be found closed as a clade of *P. rosenbergii* on the basis of multilocus sequence analysis (11). The data presented here is aimed to extend the current database of *Vibrionaceae* and subsequently assist further elucidation in the genomics, pathogenicity, and evolution of this group of bacteria.

The genome sequences of *V. ponticus* C121 and *P. aphoticum* C119 were sequenced with the Ion PGM System (Life Technologies, Carlsbad, CA) and assembled using Newbler version 2.8. The

annotation and genome analysis were performed by RAST (Rapid Annotation Subsystem Technology) (12). The size of the draft genome of *V. ponticus* C121 is 4,658,121 bp, comprising 98 contigs with a G+C content of 45.2%. On the other hand, the size of the draft genome of *P. aphoticum* C119 is 5,412,298 bp, comprising 56 contigs with a G+C content of 49.7%. The redundancies of both were 71 and 26, and N_{50} contig lengths were 128,889 bp and 217,077 bp, respectively. The numbers of putative coding sequences (CDS) were 5,654 for *V. ponticus* C121 and 6,976 for *P. aphoticum* C119; of rRNA sequences were 3 and 6; and of tRNA sequences were 78 and 61, respectively.

These strains have been deposited in the Japan Collection of Microorganisms as JCM 19238 (C121) and JCM 19237 (C119), respectively.

Nucleotide sequence accession numbers. The genome data have been deposited at DDBJ/EMBL/GenBank under the accession numbers [BBMI01000001](https://www.ncbi.nlm.nih.gov/nuccore/BBMI01000001) to [BBMI01000098](https://www.ncbi.nlm.nih.gov/nuccore/BBMI01000098) for *Vibrio ponticus* C121 and [BBMN01000001](https://www.ncbi.nlm.nih.gov/nuccore/BBMN01000001) to [BBMN01000056](https://www.ncbi.nlm.nih.gov/nuccore/BBMN01000056) for *Photobacterium aphoticum* C119.

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