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Draft Genome Sequence of the Putative Marine Pathogen *Aquimarina* sp. Strain I32.4

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ABSTRACT *Aquimarina* sp. strain I32.4 (formerly *Aquimarina* sp. 'homaria') is a putative pathogen involved in epizootic shell disease in the American lobster (*Homarus americanus*). We report here the draft genome sequence for *Aquimarina* sp. strain I32.4 and describe virulence factors that may provide insight into its mechanism of pathogenicity.

Epizootic shell disease (ESD) is a prevalent and uncontrolled disease affecting the carapace of the American lobster (*Homarus americanus*). ESD is characterized by the formation of lesions on the carapace that exhibit bacterial counts 2 to 4 orders of magnitude higher than those in the surrounding area (1). The cause of ESD is still debated within the scientific literature, but recent studies have suggested that the presence of *Aquimarina* sp. 'homaria' results in the exacerbation of lesions (2–4). *Aquimarina* sp. strain I32.4 is a Gram-negative chitin-degrading bacterium (5). To aid our understanding of its mechanism of pathogenicity, we announce here the draft genome sequence of *Aquimarina* sp. I32.4 and describe some of its potential virulence factors.

Aquimarina sp. I32.4 was grown in artificial seawater (Instant Ocean) supplemented with yeast extract (1 g/liter) and peptone (5 g/liter) at 25°C on an elliptical shaker (New Brunswick) for 48 h. Genomic DNA was isolated using the Promega Wizard DNA purification kit, and DNA was resuspended in 2 mM Tris-HCl buffer (Bio Basic, Inc.). DNA was quantified using a NanoDrop 1000 spectrophotometer (ND-1000) and checked for quality on a 1% agarose gel stained with ethidium bromide. DNA was sequenced on an Illumina MiSeq sequencer at the Genomics and Sequencing Center at the University of Rhode Island. Reads were trimmed using the CLC Genomic Workbench (version 8.5.1) for quality, ambiguous base pairs, adaptors, duplicates, and size, resulting in 1,329,308 paired-end reads. The draft genome was assembled using the *de novo* assembly algorithm of SPAdes assembler (version 3.1.1). Contigs with a coverage of >22 reads were processed using the CLC Microbial Genome Finishing module with *Aquimarina macrocephali* JAMB N27 (NCBI assembly accession number GCA_000520995) used as a reference genome. The completed draft genome is composed of 244 contigs, averaging 20,446 bp in size (total genome, 4,988,869 bp), with an average G+C content of 32.4%. The draft genome was annotated using the Rapid Annotations using Subsystem Technology (RAST) server and resulted in 4,469 open reading frames (6). The closest neighbor identified by SEED viewer 2.0 (7) was *Gramella forsetii* KT0803 (score, 541).

The genome of *Aquimarina* sp. I32.4 encodes type III and IV secretion systems. It has been reported that *Aquimarina* spp. can degrade the carapace of *H. americanus* (1).

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Accordingly, 16 putative chitinase genes were found, along with 3 hemolysins and 3 metalloproteases. Three iron acquisition systems were annotated, namely, TonB, including the full complement of proteins responsible for the formation of the TonB-ExbB-ExbD complex, and hemin and ferric siderophores, which were identified and could contribute to virulence associated with this strain. The RAST-annotated draft genome was entered into Antibiotics and Secondary Metabolite Analysis Shell (antiSMASH) for secondary metabolite biosynthesis gene cluster analysis (8). Identification of 10 clusters for secondary metabolism, including T1PKS-NRPS biosynthesis, NRPS, and Trans-ATPKS, were categorized by antiSMASH. Trans-ATPKS biosynthesis produces structurally diverse molecules in other bacteria, including the cytotoxic and antitumor compounds pederin and onnamide (9). Other species in this genus have been shown to have algicidal activity against toxic cyanobacterium strains (10).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [PGUB00000000](https://doi.org/10.1093/nar/gkv437). The version described in this paper is version PGUB01000000.

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