Draft Genome Sequences of Four *Alteromonas macleodii* Strains Isolated from Copper Coupons and Grown Long-Term at Elevated Copper Levels

Kathleen D. Cusick, Jason R. Dale, Brenda J. Little, Justin C. Biffinger

National Research Council, Washington, District of Columbia, USA; U.S. Naval Research Laboratory, Washington, District of Columbia, USA; U.S. Naval Research Laboratory, Stennis Space Center, Mississippi, USA

*Alteromonas macleodii* is a marine bacterium involved in the early stages of biofouling on ship hulls treated with copper as an antifouling agent. We report here the draft genome sequences of an *A. macleodii* strain isolated from copper coupons and three laboratory mutants grown long-term at elevated copper levels.

A marine bacterium was isolated from copper coupons at the Naval Research Laboratory (Key West [KW], FL) seawater corrosion test facility which demonstrated the ability to generate copper nanoparticles. The isolate was initially maintained in artificial seawater medium supplemented with elevated concentrations of copper (1 to 2.75 mM). Preliminary phylogenetic analysis based on sequencing of the 16S rRNA and gyrase subunit B genes identified it as a strain of *Alteromonas macleodii*, a ubiquitous marine gammaproteobacterium. The species clusters by molecular and phenotypic analyses into two ecotypes: one from surface marine gammaproteobacterium. The species clusters by molecular and phenotypic analyses into two ecotypes: one from surface

| Strain   | Mean coverage (×) | No. of contigs | Genome size (bp) | \(N_{\text{iso}}\) (bp) | G+C content (%) | No. of transcripts + RNA | Accession no.   |
|----------|-------------------|----------------|------------------|-------------------------|-----------------|-------------------------|-----------------|
| CUKW     | 102               | 78             | 5,250,689        | 498,754                 | 44.6            | 4,991                   | MIPW00000000    |
| KCC01    | 180               | 74             | 5,244,637        | 498,754                 | 44.6            | 4,982                   | MIPX00000000    |
| KCP01    | 134               | 86             | 5,249,355        | 499,040                 | 44.6            | 4,999                   | MIPY00000000    |
| KCPu01   | 172               | 70             | 5,249,355        | 498,754                 | 44.6            | 4,987                   | MIPZ00000000    |

* TABLE 1 Summary characteristics of whole-genome assembly and annotation

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Address correspondence to Kathleen D. Cusick, kdcusick@gmail.com.
sis between the original isolate and KCC01 will be described in a future publication.

**Accession number(s).** The whole-genome shotgun projects have been deposited in the DDBJ/ENA/GenBank under the accession numbers listed in Table 1. The versions described in this paper are their first versions.

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