

Genome Sequence of Strain TW15, a Novel Member of the Genus *Ruegeria*, Belonging to the Marine *Roseobacter* Clade[∇]

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***Ruegeria* sp. TW15, which belongs to the family *Rhodobacteraceae*, was isolated from an ark clam in the South Sea of Korea. Here is presented the draft genome sequence of *Ruegeria* sp. TW15 (4,490,771 bp with a G+C content of 55.7%), a member of the marine *Roseobacter* clade, which comprises up to 20% of the bacterioplankton in the coastal and oceanic mixed layer.**

Bacterioplankton species play a significant role in the biochemical processes of the marine environment. Approximately 10 to 20% of the bacterioplankton in the surface water of both the open sea and coastal waters is composed of *Roseobacter* cells (2, 3, 5). The marine *Roseobacter* clade is a metabolically versatile bacterioplankton using labile substrates and influences the biochemical status of seawater (8, 9). In this study, the genome sequence of *Ruegeria* sp. TW15, a member of the marine *Roseobacter* group, was decoded. The genus *Ruegeria* was first introduced by Uchino et al. in 1998 (11) and currently comprises seven species. Based on the 16S rRNA gene sequences of published *Ruegeria* species, isolate TW15 exhibits the highest similarity to *R. lacuscaerulensis* (97.9%) (10), which was isolated from the Blue Lagoon geothermal lake in Iceland. Within the genus *Ruegeria*, the complete genome sequence has been reported only for *R. pomeroyi* DSS-3^T (4). *Ruegeria* sp. TW15 was isolated from a tissue homogenate obtained from an ark clam from the South Sea of Korea.

The genome sequence of *Ruegeria* sp. TW15 was constructed by means of a shotgun strategy using Roche 454 GS (FLX Titanium) pyrosequencing (performed by GnCIBIO Inc., Daejeon, Republic of Korea). A total of 465,577 reads spanning 196 Mb were generated, which represents 43.7-fold coverage of the genome. Genome sequences from pyrosequencing were processed using Roche's software according to the manufacturer's instructions. Based on the assembly of the obtained reads using Newbler Assembler 2.3 (454 Life Science), 28 large contigs with bases containing quality scores of 40 and above were represented. The annotation was determined by combining results from the rapid annotation using subsystem technology (RAST) pipeline (1), tRNAscan-SE 1.23 (7), and RNAmmer 1.2 (6).

The unclosed draft genome includes 4,490,771 bp with a 55.7% G+C content. One copy of the 16S-23S-5S rRNA gene operon was predicted, along with 43 tRNA genes. According to

the RAST results, the genome includes 4,485 predicted coding sequences (CDSs). Twelve genes are annotated to encode carbon monoxide dehydrogenases, which are responsible for sinking CO in surface seawater.

R. pomeroyi DSS-3^T, whose publicly available genome represents the closest relative of isolate TW15, is known to use a lithoheterotrophic strategy (9). Comparative analyses of TW15 and *R. pomeroyi* show that *R. pomeroyi* assimilates urea and ammonium as nitrogen sources, while it does not use nitrite and nitrate; however, *Ruegeria* sp. TW15 contains seven genes that are putatively involved in nitrate and nitrite ammonification for metabolism of nitrite and nitrate. In addition, *R. pomeroyi* comprises 32 genes involved in motility and chemotaxis, whereas *Ruegeria* sp. TW15 harbors only 4 genes.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AEYW00000000. The version described in this paper is the first version, with accession no. AEYW01000000. The 28 large contigs contained in the genome have been deposited under accession numbers AEYW01000001 through AEYW01000028.

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