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GENOME ANNOUNCEMENT

Draft Genome of *Pseudomonas stutzeri* Strain ZoBell (CCUG 16156), a Marine Isolate and Model Organism for Denitrification Studies

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***Pseudomonas stutzeri* strain ZoBell, formerly a strain of *Pseudomonas perfectomarina* (CCUG 16156 = ATCC 14405), is a model organism for denitrification. It was isolated by ZoBell in 1944 from a marine sample, and here we report the first genome draft of a strain assigned to genomovar 2 of the species *P. stutzeri*.**

Pseudomonas stutzeri is a species of extremely broad phenotypic and genotypic diversity. Results of DNA-DNA hybridization justify the recognition of 18 genomic groupings (genomovars) within the species (3, 5), with 15 to 50% DNA-DNA similarity values between them. Genomovars are also reflected in phylogenetically coherent groupings (5). Within prokaryotes, many relevant advances in the biochemical characterization of denitrification have been achieved with *P. stutzeri*, a species considered a model system for this process. Most investigations have been focused on *P. stutzeri* strain ZoBell, formerly a strain of *Pseudomonas perfectomarina* (CCUG 16156 = ATCC 14405) (10), which was isolated by ZoBell in 1944 from a marine sample taken in the Pacific Ocean (California) and reclassified as a member of genomovar 2 of *P. stutzeri* in 1993 (7).

So far, whole-genome sequences of 3 *P. stutzeri* strains of genomovar 1 are publicly available: the type strain of the species (of clinical origin) (CGMCC 1.1803 = ATCC 17588) (2) and two dinitrogen fixers isolated from the rhizosphere (A1501 and CMT.9.A) (8, 9). Therefore, analysis of the marine strain ZoBell, the first sequenced strain representative of genomovar 2, will help us gain insight into the evolution of the species by analyzing members of a different genomovar and studying the adaptation of *P. stutzeri* strains to marine habitats.

The draft genome sequence of *P. stutzeri* strain ZoBell was obtained using the 454 GS FLX system and Titanium platforms (454 Life Sciences). A total of 275,630 reads (99.92% coverage) were *de novo* assembled with the 454 Newbler assembler. The obtained genome sequence included 130 large contigs (>500 bp in size), with a calculated genome size of 4.9 Mb and a G+C mole percentage of 61.4%.

Gene prediction and annotation were carried out using the RAST Server (1) and further manually curated. A total of 4,232 protein-coding sequences were identified. The frequency of individual reads is consistent with the chromosomal size and the presence of 4 copies of the genes for 5S, 16S, and 23S rRNA, as described for strains of the species (4). Putative genes for complete tricarboxylic acid, glycolysis, and pentose phosphate pathways are present. Genes coding for discriminating metabolic and physiological properties of the species were detected, including the complete sets of genes for the denitrification pathway, for starch metabolism, and for flagellum synthesis. No nitrogen fixation genes (*nif*) or extrachromosomal elements were found. Predicted phage-related sequences, transposons, and insertion elements were detected.

Comparative genome analysis confirmed that strain ZoBell exhibited overall similarity to the 3 strains of genomovar 1 that were previously sequenced (in terms of genome size and G+C content). Genomovars were discriminated by average nucleotide identities based on BLAST (ANIb values) (6), with identities higher than 96% between strains of gv1 and identities of 85.44 to 85.93% between gv1 strains and strain ZoBell. ANIb values with strains of other *Pseudomonas* species were lower than 77%.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AGSL00000000. The version described in this paper is the first version, AGSL01000000.

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REFERENCES

1. **Aziz RK, et al.** 2008. The RAST Server: rapid annotations using subsystems technology. BMC Genomics **9**:75.
2. **Chen M, et al.** 2011. Complete genome sequence of the type strain *Pseudomonas stutzeri* CGMCC 1.1803. J. Bacteriol. **193**:6095.
3. **Cladera A, Bennasar A, Barceló M, Lalucat J, García-Valdés E.** 2004. Comparative genetic diversity of *Pseudomonas stutzeri* genomovars, clonal structure and phylogeny of the species. J. Bacteriol. **186**:5239–5248.
4. **Lalucat J, Bennasar A, Bosch R, García-Valdés E, Palleroni NJ.** 2006. Biology of *Pseudomonas stutzeri*. Microbiol. Mol. Biol. Rev. **70**:510–547.
5. **Mulet M, et al.** 2008. Phylogenetic analysis and siderotyping as useful tools in the taxonomy of *Pseudomonas stutzeri*: description of a novel genomovar. Int. J. Syst. Evol. Microbiol. **58**:2309–2315.

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6. **Richter M, Rosselló-Móra R.** 2009. Shifting the genomic gold standard for the prokaryotic species definition. Proc. Natl. Acad. Sci. U. S. A. **106**: 19126–19131.
7. **Rosselló-Mora RA, García-Valdés E, Lalucat J.** 1993. Taxonomic relationship between *Pseudomonas perfectomarina* strain ZoBell and *Pseudomonas stutzeri.* Int. J. Syst. Bacteriol. **43**:852–854.
8. **Yan Y, et al.** 2008. Nitrogen fixation island and rhizosphere competence traits in the genome of root-associated Pseudomonas stutzeri A1501. Proc. Natl. Acad. Sci. U. S. A. **105**:7564–7569.
9. **Yu H, et al.** 2011. Complete genome sequence of the nitrogen-fixing and rhizosphere-associated bacterium *Pseudomonas stutzeri* strain DSM4166. J. Bacteriol. **193**:3422–3423.
10. **Zumft WG.** 1997. Cell biology and molecular basis of denitrification. Microbiol. Mol. Biol. Rev. **61**:533–616.