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GENOME ANNOUNCEMENT

Complete Genome Sequence of the Naphthalene-Degrading Bacterium *Pseudomonas stutzeri* AN10 (CCUG 29243)

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***Pseudomonas stutzeri* AN10 (CCUG 29243) can be considered a model strain for aerobic naphthalene degradation. We report the complete genome sequence of this bacterium. Its 4.71-Mb chromosome provides insights into other biodegradative capabilities of strain AN10 (i.e., benzoate catabolism) and suggests a high number of horizontal gene transfer events.**

Pseudomonas stutzeri AN10 (CCUG 29243) is a naphthalene-degrading strain that was isolated from polluted marine sediments of the West Mediterranean Sea (9, 14). The genes involved in naphthalene degradation (*nahAaAbAcAdBFCED*, *nahGTHINLOMKJ*, *nahW*, and *nahR*) have been characterized (1–3, 10). Those operons are flanked by entire copies and remnants of insertion sequences (IS). The transposition of two of them (IS*Pst9*, IS*Ppu12*) was highly induced by a novel stimulus widespread in *Pseudomonas*: conjugative interaction (5, 6).

The genome sequence of *P. stutzeri* AN10 was generated using Celera Assembler version 7.0 (11) from 322,269 8-kb mate pair reads (23-fold coverage) obtained with the 454 GS FLX Titanium system. Gaps were closed using the assembly information obtained with the Velvet program (18) from 4,285,714 500-bp paired-end reads (100-fold coverage) generated with Illumina HiSeq 2000 platform. A single scaffold of 4,709,064 bp in length was obtained. Contig order in the scaffold was confirmed by PCR with specific primers. Genome annotation and analysis was done using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP; http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html), the KEGG Automatic Annotation Server (KAAS) (12), the IS-Finder (15), and the PhiSiGns database (8).

P. stutzeri AN10 is the first strain of genomovar 3 of the species to be sequenced. Its genome has a G+C content of 62.7%, shows a coding density of 88.7%, and contains 4,300 coding sequences (CDSs), 4 entire rRNA operons, and 62 tRNA genes.

Putative genes that cover all major metabolic pathways were found, as expected for heterotrophic bacteria. As in other *P. stutzeri* strains (4, 13, 16, 17), the complete set of genes for denitrification, starch metabolism, flagellum synthesis, and bacterial chemotaxis was found. The genome also contains more than 150 genes related to ABC transporters and two-component systems. Other transport systems, such as types II, IV, and VI secretion systems, and the Sec pathway were also detected.

Genome analysis revealed the presence of at least 44 plausible transposase-encoding genes, belonging to 10 different IS families. Seventy percent of them were found in a 400-kb region of the chromosome (coordinates 1,310,557 to 1,744,602), thus suggesting a hot spot for transposition. All previously characterized *nah* genes (1–3) are also located in this region. Furthermore, all genetic determinants needed for the degradation of benzoate were also found beside this IS-enriched region. However, growth on benzoate was not observed in previous laboratory experiments (9, 14). Twenty-one integrase-like-encoding genes have also been annotated. Seven of them are located in the 400-kb region previously mentioned. Among those, the gene product AFM32726 is homologous (49% identity, 67% similarity) to the well-characterized integrase of the In*PstQ* integron of *P. stutzeri* strain Q (7). Finally, a putative prophage sequence (42.7 kb in length) was also detected within the 400-kb region (coordinates 1,476,863 to 1,524,049). All these data suggest that this region might be a specific area of the chromosome used to stabilize foreign genetic material. In relation to this, as observed in other *P. stutzeri* strains (4, 16), the complete repertoire of genes needed for the acquisition of foreign DNA by natural transformation (*pilA*, *pilBCD*, *pilTU*, *exbB*, and *comA*) has been detected.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited in the DDBJ/EMBL/GenBank databases under the accession number CP003677. The version described in this report corresponds to the first version.

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