

Draft Genome Sequence of the Hydrocarbon-Degrading and Emulsan-Producing Strain *Acinetobacter venetianus* RAG-1^T

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We report the draft genome sequence of *Acinetobacter venetianus* strain RAG-1^T, which is able to degrade hydrocarbons and to synthesize a powerful biosurfactant (emulsan) that can be employed for oil removal and as an adjuvant for vaccine delivery. The genome sequence of *A. venetianus* RAG-1^T might be useful for bioremediation and/or clinical purposes.

Acinetobacter venetianus strain RAG-1^T (ATCC 31012) was first isolated from seawater near a beach in Tel Baruch, Israel (11, 12). It was affiliated with the genus *Arthrobacter* (12), species *A. lwoffii* (1) or *A. calcoaceticus* (5). More recently, it has been demonstrated that RAG-1^T belongs to the species *Acinetobacter venetianus* (7, 19, 20).

The importance of this strain mainly resides in its bioremediation potential, since it is capable of degrading *n*-alkanes and, also, because it produces a potent amphipathic polysaccharide bioemulsifier (emulsan) (12–14) that is involved in the capture and transport of *n*-alkanes into the cell (10, 21) and whose structure might be responsible for macrophage stimulation (9).

The genome sequence of *A. venetianus* RAG-1^T might provide useful insights into its metabolism with regard to the search for biodegradable surfactants and crude oil viscosity modifiers, as well as vaccine adjuvants and drug delivery vehicles (3, 8, 9).

The *A. venetianus* RAG-1^T genome was sequenced using Illumina HiSeq2000, and the 3,019,963 reads (109-bp long) were assembled using Abyss software version 1.2.6 (15). The assembled genome has a length of 3,464,338 bp, consists of 87 contigs (>500 bp; average length, 39,819 bp) and has an overall GC content of 39.38%, similar to that of the other *Acinetobacter* genomes sequenced so far. Genome annotation was performed with the RAST annotation system (2), allowing the identification of 3,196 open reading frames (ORFs), 73 tRNAs, and 8 rRNA operons. Of the identified ORFs, 2,403 (75.18%) could be assigned to at least one Cluster of Orthologous Groups (COG) (16).

The presence in the *A. venetianus* RAG-1^T genome of genes encoding homologs to the Alk (AlkB, -F, -G, -H, -L, -J, -K, -S, -T, and -N) from *Pseudomonas putida* GPo1 (18), the soluble cytochrome P450 monooxygenases from *Acinetobacter* sp. EB104 (6), AlmA from *Acinetobacter* sp. DSM 17874 (17), and the LadA protein from *Geobacillus thermodenitrificans* (4) was checked.

Among the set of the genes that are commonly required for the metabolism of *n*-alkanes, *A. venetianus* RAG-1^T possesses *alkB*, *alkH*, *alkJ*, and *alkK*, which were found on different contigs, suggesting that they are scattered throughout the *A. venetianus* RAG-1^T chromosome, unlike in *P. putida*, where all the *alk* genes are clustered in the OCT plasmid (18). Additionally, the four genes encoding rubredoxin (*rubA*), rubredoxin reductase (*rubB*), AlmA, and LadA were found. No close homolog was found for AlkL, -S, -T, or -N. Lastly, despite the fact that *A. venetianus*

RAG-1^T is able to grow in the presence of long-chain alkanes, it is missing the soluble cytochrome P450 monooxygenase that is probably involved in long-chain alkane degradation (6).

Consistent with the presence of *A. venetianus* RAG-1^T in contaminated environments, its genome harbors several systems involved in resistance to or tolerance of toxic compounds, including cobalt, cobalt-zinc-cadmium, arsenic, and chromium, as well as 15 genes encoding multidrug resistance efflux pumps.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AKIQ0000000](https://doi.org/10.1093/nucleotide/AKIQ0000000). The version described in this paper is the first version, AKIQ01000000.

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