Genome Sequence of *Comamonas testosteroni* ATCC 11996, a Representative Strain Involved in Steroid Degradation

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*Comamonas testosteroni* strains belong to the family of *Comamonadaceae* and are known for their ability to utilize steroid compounds as carbon source. Here, we present the draft genome sequence of strain ATCC 11996, with a G+C content of 61.48%.

Steroid compounds excreted by human beings and livestock can cause endocrine disruption of living organisms, and the removal of these pollutants from the environment by microorganisms such as bacteria has attracted considerable attention. Previously, *Comamonas testosteroni* ATCC 11996 (*C. testosteroni* ATCC 11996, Deutsche Sammlung von Mikroorganismen und Zellkulturen) was identified to be a strictly aerobic and Gram-negative bacterium which rarely attacks sugar but grows well on steroids and aromatic compounds. Therefore, it may be an attractive means for the bioremediation of steroid-contaminated environments (1, 16, 18). It has been suggested that two elements needed for an efficient utilization of steroid compounds by bacteria are the enzymes required for their degradation and the regulatory elements that control the expression of the catabolic enzymes (4–6, 11–14, 19, 20). Studies on *C. testosteroni* ATCC 11996 identified several catabolic enzymes, such as 3α-hydroxysteroid dehydrogenase/carbonyl reductase (3α-HSD/CR) and 3β,17β-hydroxysteroid dehydrogenase (3β,17β-HSD), as being responsible for the degradation of steroid compounds (2, 5, 11–14), but little is known about the catabolic pathway of steroids in this bacterium. Here, we present the draft genome sequence of this representative strain to provide more insight into the bacterial steroid metabolism.

The genome of *C. testosteroni* ATCC 11996 was sequenced using a Roche FLX Titanium genome sequencer. We obtained a total of 273,935 reads, amounting to over 113 million nucleotides (20.9-fold coverage of the genome). The short-read sequences were assembled using Newbler 2.3 software, which generated 63 contigs with a minimum contig length of 200 nucleotides (nt). The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) was employed for gene annotation (15). The open reading frames (ORFs) were predicted using Glimmer 3.0 software (3). The ORFs were analyzed using BLAST to search the nonredundant protein database (NR), and functional determinations were performed using the Clusters of Orthologous Genes (COGs) (17) and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases (8). tRNAscan-SE (10) and RNAmer software (9) were used for predicting genes encoding tRNA and rRNA, respectively.

The draft genome sequence of *C. testosteroni* ATCC 11996 comprises 5,415,699 bp, with an average G+C content of 61.48%. Of the 4,985 protein-coding sequences (CDSs) in the genome, 1,206 (24.2%) CDSs matched hypothetical coding sequences with unknown function in public databases. Sixty-nine tRNAs representing all 20 amino acids and single 5S, 16S, and 23S rRNA genes were predicted. Analysis of the whole-genome shotgun sequence showed that two gene clusters involved in steroid degradation (7) are present in *C. testosteroni* ATCC 11996, and these are responsible for the breakdown of the steroid A ring and B ring (7). Dioxygenases, hydroxylases, and oxidoreductases, which may be active in the metabolism of steroids and aromatic compounds such as benzoate, gentisate, 4-hydroxybenzoate, and vanillate, were found in the draft genome sequence of *C. testosteroni* ATCC 11996. In addition, the absence of genes encoding glucose-6-phosphate 1-dehydrogenase and 6-phosphogluconolactonase of the pentose phosphate pathway and genes encoding hexokinase and glucokinase for glucose catabolism is responsible for the poor ability of the strain to assimilate carbohydrates. Further genomic analysis should provide additional useful information to help elucidate the steroid-catabolic pathway in *C. testosteroni* ATCC 11996 and its physiological characteristics.

Nucleotide sequence accession numbers. The data for this whole-genome shotgun project have been deposited at DDBJ/EMBL/GenBank under the accession AHIL01000000. The version described in this paper is the first version, AHIL01000000.

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REFERENCES


Testosterone-inducible regulator is a kinase that drives steroid sensing and metabolism in *Comamonas testosteroni*. J. Biol. Chem. 283:17380–17390.


