Genome of *Ochrobactrum anthropi* ATCC 49188T, a Versatile Opportunistic Pathogen and Symbiont of Several Eukaryotic Hosts

Patrick S. G. Chain,1,2 Dorothy M. Lang,3 Diego J. Comerci,4 Stephanie A. Malfatti,2,3 Lisa M. Vergez,2,3 Maria Shin,2,3 Rodolfo A. Ugalde,4 Emilio Garcia,3* and Marcelo E. Tolmasky5*

*Genome Science Group, Los Alamos National Laboratory, Los Alamos, New Mexico 87544; Microbial Program, Joint Genome Institute, Walnut Creek, California 94598; Physical and Life Sciences, Lawrence Livermore National Laboratory, Livermore, California 94550; Instituto de Investigaciones Biotecnologicas, Universidad Nacional de General San Martin (IIB-INTECH-CONICET), Av. Gral. Paz 5445, P.O. Box 30, 1650 San Martin, Buenos Aires, Argentina; and Center for Applied Biotechnology Studies, Department of Biological Science, California State University Fullerton, Fullerton, California 92831*

Received 18 May 2011/Accepted 6 June 2011

*Ochrobactrum anthropi* is a common soil alphaproteobacterium (7) that can interact with or colonize many eukaryotic organisms, leading to different outcomes, such as disease or even growth of some plants (references 4 and 13 and references therein). *O. anthropi*, a close relative of brucellae, has not garnered much attention (5, 8) but is becoming increasingly recognized as a potentially problematic opportunistic and nosocomial pathogen (13). A rising number of reported cases includes some potentially life-threatening infections, such as endocarditis (6, 9, 14). These reports, together with the organism’s intrinsic multiresistance to antibiotics (13), could lead to a situation resembling that of an *Acinetobacter* sp., whose importance as a highly problematic nosocomial pathogen skyrocketed in the past few years (12). The increasing relevance of *O. anthropi* to human health, together with its phylogenetic proximity to the highly pathogenic brucellae, make *O. anthropi* an attractive model of bacterial pathogenicity. Here we report the genome sequence of the type strain *O. anthropi* ATCC 49188, which revealed the presence of two chromosomes and four plasmids.

in other secondary chromosomes and plasmids of the *Rhizobiaceae* (18). Both chromosomes have an average G+C content of 56% and together comprise 4,424 protein-coding genes (~87% coding), along with 31 pseudogenes and 73 structural RNAs (tRNA, tRNA, and small RNA). Both chromosomes are highly similar to and colinear with the two chromosomes of *Brucella* spp.; however, the 1.5-Mb difference in size can be attributed to the acquisition of novel islands in *O. anthropi* and the degradation of a genome for the brucellae, as has been previously described (17).

In addition, the *O. anthropi* genome contains four plasmids, of which pOAN01, pOAN02, and pOAN03 have the characteristics expected of alphaproteobacterial plasmids, while pOAN04 is more puzzling, lacking known replication, partition, and conjugative systems. Plasmids pOAN01 (170,351 bp), pOAN02 (101,491 bp), and pOAN03 (93,589 bp) harbor one or more RepABC and/or RepC replication or replication-partition systems (2, 16). Genes known to be related to stabilization factors have also been found among these three plasmids, including genes encoding ParB-like, PilT-type, and toxin-antitoxin plasmid addiction systems. All three RepABC plasmids include a large number of genes encoding transposases and integrases from different families, but pOAN04 lacks such genes. Plasmid pOAN01 includes a complete set of type IV secretion system genes that suggest it is self-transmissible, and pOAN02 is the only other plasmid with homologs that suggest it is mobilizable (coding for antirestriction and mobilization proteins). All four plasmids may contribute to the fitness of *O. anthropi*, as they harbor several transporters, though metabolic genes are found only in pOAN01, pOAN03, and pOAN04.

A comparison of the genomics of *O. anthropi* to that of other pathogenic alphaproteobacteria will permit us to understand its mechanisms of virulence and take appropriate measures to prevent it from developing into a dangerous pathogen.
Nucleotide sequence accession numbers. The sequence data were deposited in NCBI GenBank under project accession numbers CP000758 to CP000763.

This work was partially supported by a grant from the California State University Program for Education and Research in Biotechnology (CSUPERB) and a minigrant from the CSU State Fund. The genome sequencing work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under contract number DE-AC02-05 CH11231.

REFERENCES

1. Reference deleted.
10. Reference deleted.
11. Reference deleted.
15. Reference deleted.