Draft Genome Sequences of Three *Ochrobactrum* spp. Isolated from Different Avian Hosts in Pakistan

Poonam Sharma,a Lindsay F. Killmaster,a Jeremy D. Volkening,b Stivalis Cardenas-Garcia,a Abdul Wajid,c Shaqfat Fatima Rehmani,d Asma Basharat,d Patti J. Miller,a Claudio L. Afonsoa

aExotic and Emerging Avian Viral Disease Research Unit, Southeast Poultry Research Laboratory, U.S. National Poultry Research Center, ARS, USDA, Athens, Georgia, USA
bBASE2BIO, Oshkosh, Wisconsin, USA
cDepartment of Biotechnology, Virtual University of Pakistan, Lahore, Pakistan
dQuality Operations Laboratory (QOL), University of Veterinary and Animal Sciences, Lahore, Pakistan

**ABSTRACT** Here, we present the draft genome sequences of three *Ochrobactrum* sp. strains with multidrug-resistant properties, isolated in 2015 from a pigeon and two chickens in Pakistan.

*Ochrobactrum* spp. are Gram-negative, rod-shaped bacilli that belong to the family *Brucellaceae* and inhabit diverse niches, including water, soil, plants, and animals (1–3). Some species are regarded as emerging human opportunistic pathogens, with *Ochrobactrum anthropi* and *Ochrobactrum intermedium* being the most frequently studied species causing infections in immunocompromised patients (4–6).

There are few reports on the isolation of *Ochrobactrum* spp. from avian hosts. *Ochrobactrum gallinacea* has been isolated from chicken feces in Germany (7), and *Ochrobactrum anthropi* and *Ochrobactrum pecoris* have been isolated from the cecal contents of commercial turkeys (8). More recently, *Ochrobactrum intermedium* and *Ochrobactrum tritici* were recovered from broiler chickens (9), and a novel species has been reported in Nigeria (10).

Here, we present the draft genome sequences of three multidrug-resistant *Ochrobactrum* isolates from a pigeon and chickens that were coinfected with Newcastle disease virus. The distance between these and other members of the genus *Ochrobactrum* cannot be resolved using the 16S rRNA phylogeny (11), and therefore we examined the *rpoB* and *dnaK* sequences to distinguish the new isolates. The maximum similarity levels with *rpoB* and *dnaK* were 94.7% and 95.3%, with *O. anthropi* ATCC 49687 (GenBank accession no. CP008820) (12) and *O. anthropi* (GenBank accession no. LT671861), respectively, which distinguish these strains from other *Ochrobactrum* species. The average nucleotide identity among these isolates was 99.99% and varied between 96.96% and 97.05% with the five novel *Ochrobactrum* spp. recently reported from Nigeria (10, 13). This 3 to 4% of genomic variation supports the finding that the Pakistani isolates belong to a novel avian *Ochrobactrum* sp. (10).

Oral swabs were plated onto Farrell’s agar medium for purification as previously reported (10). Genomic DNA isolates were extracted using the blood and tissue genomic DNA extraction kit (Qiagen, Germantown, MD). Extracted DNA was quantified using the Qubit double-stranded DNA (dsDNA) high-sensitivity (HS) assay kit (Life Technologies, Inc., Waltham, MA). The libraries were prepared using the Nextera XT DNA library preparation kit and Nextera XT index primers (Illumina, San Diego, CA). The concentrations of the libraries were checked using the Qubit DNA HS assay kit in a Qubit fluorometer (Thermo Fisher Scientific, USA), and the fragment size distribution was checked using the Bioanalyzer 2100 with an Agilent high-sensitivity DNA kit (Agilent Technologies, Santa Clara, CA). The generated libraries were sequenced using the Nextera XT cluster generation kit on an Illumina HiSeq 2500.
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