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PROKARYOTES

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

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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 gallinifaecis* 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* spp. (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

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TABLE 1 Statistics of the genome assembly and annotation

Strain	Source	Genome size (bp)	N_{50} (bp)	No. of contigs	GC content (%)	No. of tRNAs	Total no. of genes	GenBank accession no.	Antibiotic resistance genes
Ochrobactrum sp. 23A/997/2015	*Columba livia*	4,855,883	793,849	22	57.8	52	4,778	PCFM00000000	*aadB*, *aadA2*, *aac6-Ib*, *strA*, *strB*, bla_{och2}, *carb2*, *tetG*, *floR*, *sulI*, *dfrA10*
Ochrobactrum sp. 27A/999/2015	*Gallus gallus*	4,856,529	671,229	23	57.8	52	4,780	PCFL00000000	*aadB*, *aadA2*, *aac6-Ib*, *strA*, *strB*, bla_{och2}, *carb2*, *tetG*, *floR*, *sulI*, *dfrA10*
Ochrobactrum sp. 30A/1000/2015	*Gallus gallus*	4,860,377	431,306	24	57.8	52	4,782	PCFK00000000	*aadB*, *aadA2*, *aac6-Ib*, *strA*, *strB*, bla_{och2}, *carb2*, *tetG*, *floR*, *sulI*, *dfrA10*

MiSeq reagent kit version 3 (600 cycles), with a paired-end read length of 2 × 300 bp on an Illumina MiSeq platform. Sequence data were assembled using MIRA version 3.4.1 (14) on the Galaxy platform (15). The genome sequence was annotated with the NCBI Prokaryotic Genome Annotation Pipeline (16). The statistics of library assembly and annotation are shown in Table 1.

The antibiotic resistance genes were identified using ARG-ANNOT (17). The isolates harbored genes conferring resistance to aminoglycosides, β-lactamase, tetracycline, and chloramphenicol. We also found additional antibiotic resistance genes conferring resistance to sulfonamide and trimethoprim.

Accession number(s). This whole-genome project has been deposited at DDBJ/ENA/GenBank under BioProject number PRJNA407326, and the accession numbers are listed in Table 1.

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