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PROKARYOTES

Draft Genome Sequences of Five Novel *Ochrobactrum* spp. Isolated from Different Avian Hosts in Nigeria

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ABSTRACT Here, we present the draft genome sequences of five multidrug-resistant novel *Ochrobactrum* species strains isolated from a pigeon, a duck, and chickens from Nigeria in 2009.

Ochrobactrum spp. are Gram-negative, nonfermentative, aerobic, non-spore-forming bacilli normally isolated from various environments, such as water, soil, plants, and animals (1–3). The genus *Ochrobactrum* is composed of 20 species regarded as opportunistic pathogens, such as *Ochrobactrum anthropi* and *Ochrobactrum intermedium* (4–6). *Ochrobactrum gallinifaecis* has been isolated from fecal matter collected from chicken farms (7), *Ochrobactrum anthropi* and *Ochrobactrum pecoris* have been isolated from the cecal contents of commercial turkeys (8), and 24 other *Ochrobactrum* spp. have been isolated from broiler chickens (9).

Here, we present the draft genome sequences of five multidrug-resistant *Ochrobactrum* species isolates from a Nigerian pigeon, a duck, and chickens that were also coinfected with Newcastle disease virus. As the evolutionary relationships among members of the genus *Ochrobactrum* cannot be resolved using the 16S rRNA gene, we examined the *rpoB* and *dnaK* sequences to distinguish these isolates from other members of the genus *Ochrobactrum* (10). The *rpoB* and *dnaK* sequences were 94.9% and 95.4% similar to *Ochrobactrum anthropi* ATCC 49687 (GenBank accession number CP008820) (11) and *O. anthropi* (GenBank accession no. LT671861), respectively, hence showing them to be different from other known *Ochrobactrum* species. The average nucleotide identity with other members of genus *Ochrobactrum* was <88% (12).

Media from oral swabs were streaked on Farrell's medium for colony isolation. Genomic DNA from *Ochrobactrum* isolates was 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, according to the manufacturer's instructions (Life Technologies, Inc., Waltham, MA). The Illumina libraries were prepared using the Nextera XT DNA library preparation kit and Nextera XT index primers (Illumina, San Diego, CA). The library fragment size distribution was checked using the Bioanalyzer 2100 using the Agilent high-sensitivity DNA kit (Agilent Technologies, Santa Clara, CA) and quantified using the Qubit DNA HS assay kit in a Qubit fluorometer (Thermo Fisher Scientific, USA). The generated libraries were sequenced using MiSeq reagent kit version 3 with 600 cycles and a paired-end read length of 2 × 300 bp on an Illumina MiSeq platform. Sequence data were assembled using MIRA version 3.4.1 (13) within a customized workflow on the Galaxy platform (14). The genome sequence was annotated via the

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TABLE 1 Statistics of the genome assembly and annotation

Organism	Isolation source	Genome size (bp)	N_{50} (bp)	No. of contigs	GC content (%)	No. of tRNAs	Total no. of genes	Accession no.	Antibiotic resistance genes
Ochrobactrum sp. 689/2009	*Columba livia*	4,935,855	855,839	13	57.8	52	4,766	PCQU00000000	*aac3-IIc, strA, strB,* bla_{OCH2}*, tetG, tetR, floR*
Ochrobactrum sp. 695/2009	*Anas platyrhynchos*	4,937,528	946,216	19	57.8	52	4,774	PCQT00000000	*aac3-IIc, strA, strB,* bla_{OCH2}*, tetG, floR*
Ochrobactrum sp. 715/2009	*Gallus gallus*	4,936,674	451,323	18	57.8	52	4,772	PCQS00000000	*aac3-IIc, strA, strB,* bla_{OCH2}*, tetG, floR*
Ochrobactrum sp. 720/2009	*G. gallus*	4,936,858	495,115	18	57.8	52	4,769	PCQR00000000	*aac3-IIc, strA, strB,* bla_{OCH2}*, tetG, floR*
Ochrobactrum sp. 721/2009	*G. gallus*	4,938,583	999,630	18	57.8	52	4,768	PCQQ00000000	*aac3-IIc, strA, strB,* bla_{OCH2}*, tetG, floR*

NCBI Prokaryotic Genome Annotation Pipeline (15). The assembly and annotation statistics are shown in Table 1.

Antibiotic resistance genes were identified using ARG-ANNOT (16). All of the isolates had at least one extended-spectrum β-lactamase (ESBL) resistance gene. The isolates harbored genes conferring resistance to aminoglycosides, β-lactamase, tetracycline, and chloramphenicol, consistent with their reported phenotypes.

The detection of novel multidrug-resistant *Ochrobactrum* species indicates that their presence in avian reservoirs is poorly documented and suggests the need for additional studies on the role of antibiotics on environmental bacterial ecology.

Accession number(s). This whole-genome project has been deposited at DDBJ/ENA/GenBank under BioProject number PRJNA407325, and the accession numbers are listed in Table 1.

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