Many avian species have been found to carry antibiotic-resistant bacteria and resistance genes (1). Because of their ability to migrate to long distances in short periods, migratory birds are a possible source of antibiotic-resistant bacteria that colonize and/or infect human beings (2). Hirundo rustica (barn swallow) is the most widespread species of swallows in the world. Their global population is estimated to be approximately >190,000,000 individuals (3). In Japan, H. rustica populations migrate from Southeast Asia to the whole region during the spring and breed in and migrate back to Southeast Asia during autumn (4). This migratory population is estimated to be some hundreds of thousands of individuals. However, the incidence and type of antibiotic-resistant bacteria that are associated with migratory birds in East Asia remain unclear.

Multidrug-resistant Cellulosimicrobium sp. strain KWT-B was isolated on medium containing meropenem, ciprofloxacin, and amikacin from the feces of H. rustica, and its draft genome sequence is presented here. 16S rRNA sequence analysis revealed that strain KWT-B had 99% similarity to Cellulosimicrobium sp. strain PONa. Members of the genus Cellulosimicrobium are characterized as Gram-positive, rod-shaped, nonmotile chemoorganotrophs (5). They have been found in the soil, marine sponges, hot springs, Antarctic snow, compost, and agricultural soil, and Cellulosimicrobium bacteria can cause infections in humans (6–12).

The draft genome was sequenced by 300-bp paired-end sequencing on an Illumina MiSeq sequencing system (Fasmac Co. Ltd., Atsugi, Kanagawa, Japan). High-quality sequence reads (3,394,741 pairs) were assembled de novo using SPAdes version 3.6.0 (13). The final assembly of the genome produced 4,412,091 bp in 16 contigs, with an N50 of 821,157 bp and a G+C content of 74.6%. The assembled contigs were functionally annotated using the RAST server (14). The genomes contained 3,784 putative coding sequences (CDSs). One copy each of 23S rRNA and 16S rRNA and four copies of 5S rRNA in the draft genome were revealed. The strain KWT-B lacked detectable plasmids, but it had multidrug resistance. MIC values were >256 mg liter⁻¹ for amikacin, 12 mg liter⁻¹ for ciprofloxacin, 12 mg liter⁻¹ for imipenem, 24 mg liter⁻¹ for colistin, and 0.19 mg liter⁻¹ for vancomycin.

The genome of strain KWT-B encodes some multidrug-resistant proteins, resistance-nodulation-division (RND) family efflux transporters, Na⁺-driven multidrug efflux pump
proteins, the drug resistance transporter EmrB/QacA subfamily, two drug resistance transporter Bcr/Cra subfamilies, the multidrug efflux pump subunit AcrB, the arabino-

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ase, efflux permease major facilitator superfamily (MFS), vancomycin-resistant protein W, and four metallo-hydrolase-like–metallo-β-lactamase (MBL)-fold superfamilies. They are

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Accession number(s). The draft genome sequence of Cellulosimicrobium sp. KWT-B has been deposited in the DDBJ/EMBL/GenBank with the accession number NED000000000.

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