Draft Genome Sequence of Extended-Spectrum Beta-Lactamase-Producing Serratia fonticola BWK15 Isolated from Feces of Anas penelope

Takehiko Kenzaka, Katsuji Tani
Environmental Science and Microbiology, Faculty of Pharmacy, Osaka Ohtani University, Nishikiori-kita, Tondabayashi, Japan

ABSTRACT Migratory birds have been postulated as potential vehicles of antibiotic resistance. Here we isolated the extended-spectrum beta-lactamase (ESBL)-producing Serratia fonticola strain BWK15 from the feces of Anas penelope. The strain's draft genome sequence indicated that it harbors class A ESBL, class C beta-lactamase, and many multidrug efflux pumps.

Many avian species have been reported to carry drug-resistant bacteria harboring resistance genes (1). Owing to their ability to migrate long distances in short time periods, migratory birds are a potential source of antibiotic-resistant bacteria that colonize and/or infect humans (2). The Eurasian wigeon (Anas penelope) breeds in lowland freshwater marshes, slow-flowing rivers, and lakes in Eurasia and Northern America (3). A. penelope migrates from eastern Siberia to the mainland of Japan at the end of autumn and migrates back to eastern Siberia during spring (4). This migratory population is estimated to comprise hundreds of thousands of birds annually in Japan. However, the incidence and type of antibiotic-resistant bacteria that are associated with migratory birds in East Asia remain unclear.

Extended-spectrum beta-lactamase (ESBL)-producing Serratia fonticola BWK15 was isolated on CHROMagar ESBL medium (Kanto Chemical Co., Inc., Tokyo, Japan) from the feces of A. penelope, and the draft genome sequence of S. fonticola BWK15 was analyzed. S. fonticola is found in a wide range of environments, including drinking water, soil, and sewage (5, 6). S. fonticola has been isolated from clinical samples obtained from wounds and respiratory tracts and is regarded as a significant human pathogen causing a variety of infections (7).

Draft genomes were sequenced by 100-bp paired-end sequencing on an Illumina HiSeq 2000 sequencing system (Hokkaido System Science Co., Ltd., Sapporo, Hokkaido, Japan). High-quality sequence reads (45,069,214) were assembled de novo using CLC Genomics Workbench v6.5 (CLC bio, Cambridge, MA, USA). Approximately 99.6% of the sequenced reads were mapped again to the contigs. The final assembly of the genome produced 5,474,742 bp in 84 contigs with an N50 value of 184,845 bp and 53.9% GC content. The assembled contigs were functionally annotated using the RAST annotation server (8). The genomes contained 4,886 putative coding sequences (CDSs) and 72 RNA genes.

The genome of BWK15 encoded SFO family class A ESBL (CTX-M) and class C beta-lactamase. In addition, the genome encoded the following multidrug resistance proteins: streptothricin acetyltransferase, fosfomycin resistance protein, and mdtABCD multidrug resistance cluster. It also encoded the following multidrug resistance (MDR) efflux pumps: resistance-nodulation-division (RND) efflux system membrane fusion protein/inner membrane transporter/outer membrane lipoprotein (CmeA, CmeB, and CmeC).
CmeC), multidrug and toxic compound extrusion (MATE) family of MDR efflux pumps, multidrug efflux transporter major facilitator superfamily, macrolide-specific efflux protein MacA, macrolide export ATP-binding/permease protein MacB, and membrane fusion protein of RND family multidrug efflux pump.

These results suggest that *A. penelope* can spread multidrug-resistant *S. fonticola* through migration between Japan and eastern Siberia and that the bacteria can be transmitted from birds to humans and vice versa. The genome of *S. fonticola* BWK15 will facilitate the understanding of the ecology and global distribution of *S. fonticola* via migratory birds (9, 10). Studies on *S. fonticola* associated with *A. penelope* may help improve the understanding of antibiotic resistance dissemination in the environment.

**Accession number(s).** The draft genome sequence of the *S. fonticola* strain BWK15 has been deposited in the DDBJ/EMBL/GenBank with the accession number NQMP00000000.

**ACKNOWLEDGMENT**

This work was supported by the JSPS Grant-in-Aid for Scientific Research (C) (15K00571).

**REFERENCES**

1. Bonnedahl J, Järhult JD. 2014. Antibiotic resistance in wild birds. Ups J Med Sci 119:113–116. https://doi.org/10.3109/03009734.2014.905663.
2. Guenther S, Ewers C, Wieler LH. 2011. Extended-spectrum beta-lactamases producing *E. coli* in wildlife, yet another form of environmental pollution? Front Microbiol 2:246. https://doi.org/10.3389/fmicb.2011.00246.
3. Birdlife International. 2017. *Mareca penelope*. (Amended version published in 2016.) The IUCN red list of threatened species. http://www.iucnredlist.org/details/22680157/0.
4. Brazil M. 2009. Birds of East Asia: eastern China, Taiwan, Korea, Japan, eastern Russia. Christopher Helm Publishers, London.
5. Gavini F, Ferragut C, Izard D, Trinel PA, Leclerc H, Lefebvre B, Mossel DAA. 1979. *Serratia fonticola*, a new species from water. Int J Syst Evol Microbiol 29:92–101. https://doi.org/10.1099/00207713-29-2-92.
6. Tasic S, Obradovic D, Tasic I. 2013. Characterization of *Serratia fonticola*, an opportunistic pathogen isolated from drinking water. Arch Biol Sci 65:899–904. https://doi.org/10.2298/ABS1303899T.
7. Bollet C, Gainnier M, Sainty JM, Orhesser P, De Micco P. 1991. *Serratia fonticola* isolated from a leg abscess. J Clin Microbiol 29:834–835.
8. Aziz RK, Bartels D, Best AA, Dejongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics 9:75. https://doi.org/10.1186/1471-2164-9-75.
9. Carneiro AR, Jucá Ramos RT, Baraúna RA, de Sá PH, Marinho Almeida D, Barbosa S, Pereira A, Alves A, Egas C, Correia A, Henriques I, Silva A. 2013. Draft genome sequence of *Serratia fonticola* LMG 7882<sup>T</sup> isolated from freshwater. Genome Announc 1(6):e00971-13. https://doi.org/10.1128/genomeA.00971-13.
10. Aljorayid A, Viau R, Castellino L, Jump RLP. 2016. *Serratia fonticola*, pathogen or bystander? A case series and review of the literature. IDCases 5:6–8. https://doi.org/10.1016/j.idcr.2016.05.003.