Draft Genome Sequences of Six *Yersinia pestis* Strains Isolated from a Natural Plague Focus in Mongolia

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**ABSTRACT** In this announcement, we report the draft genome sequences of six *Yersinia pestis* strains (biovar Medievalis) that were isolated from the Zamyn-Ude region in Mongolia. These genomes reveal the genetic characteristics of the *Y. pestis* population circulating in a local plague focus.

*Yersinia pestis*, a Gram-negative bacillus, is established in hundreds of natural plague foci around the world, where it causes sporadic epizootics, primarily in rodents (1), and has caused three major pandemics in history (2). Humans are at the greatest risk of exposure to *Y. pestis* during plague epizootics, because mass rodent die-offs increase the potential for human exposure to sick or dead animals and infected fleas (3). In recent years, plague has frequently occurred in many provinces and counties in Mongolia (4).

The Zamyn-Ude natural plague focus is located in Dornogovi Province, at the border between Mongolia and China. The six *Y. pestis* strains were isolated from the Zamyn-Ude region during the 2018 coinvestigation of the vectors, reservoirs, and pathogens in the natural foci of zoonotic infectious diseases in the selected border areas of Mongolia and China. All strains belong to the biovar Medievalis (5). *Y. pestis* strains were isolated from dead rats in the Zamyn-Ude natural plague focus (43.73N, 111.89E) in 2018, cultured on Hotinger’s agar (pH 6.9 to 7.1; prepared in the National Center for Zoonotic Diseases, Mongolia) at 28°C for 2 days by bacteriological methods, and identified with microscopic examinations (6), PCR methods, and a biochemical identification test (7). The Qiagen DNeasy blood and tissue kit was used to extract DNA samples.

The sequencing libraries were prepared using the MGIEasy universal DNA library preparation set (BGI, Shenzhen, China), and sequencing was performed on the Illumina NovaSeq 6000 sequencing platform, with a 150-bp paired-end library constructed according to the manufacturer’s instructions. We obtained 27,740,766 to 44,115,814 reads for each genome. The library insert size was 350 bp, and more than 0.9 Gb of clean data were generated for each strain. Adapter sequences and low-quality sequencing reads (Q, <20) were trimmed with Trimmomatic v0.38 (8) using the following options: ILLUMINACLIP:TruSeq3 PE 2:fa:2:30:10; LEADING:5; TRAILING:5; SLIDINGWINDOW:5:20; and MINLEN:50. After the raw data were filtered, we obtained more than 178 Mb of clean reads for each strain, and the average sequencing depth was 86×. SPAdes v3.12.0 ([http://cab.spbu.ru/software/spades](http://cab.spbu.ru/software/spades)) (9) was used to perform the assembly with default parameters. Finally, we obtained assembled genomes with an average genome size of 4.6 Mb. The GC content of the genomes is 47.55%. Each genome contains 202 to 224 contigs (Table 1). The coding
sequences of the six isolates were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (10).

Ethical approval was not required because these strains were isolated from dead rats.

Data availability. The draft genome assemblies reported here are available in GenBank under the accession numbers JAAEFC000000000, JAAEFB000000000, JAAEFA000000000, JAAEEZ000000000, JAAEEY000000000, and JAAEEX000000000. All raw sequencing reads have been deposited in the NCBI under the BioProject number PRJNA602786 (Table 1) and are available in the Sequence Read Archive (SRA).

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REFERENCES
