


Nineteen Whole-Genome Assemblies of *Yersinia pestis* subsp. *microtus*, Including Representatives of Biovars *caucasica*, *talassica*, *hissarica*, *altaica*, *xilingolensis*, and *ulegeica*

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The etiologic agent of plague, *Yersinia pestis*, includes two subspecies, of which *Y. pestis* subsp. *microtus* contains the strains that cause only occasional diseases in humans that are not accompanied by human-to-human transmission. Here, we report the draft genome sequences of 19 *Y. pestis* strains (across 6 biovars of *Y. pestis* subsp. *microtus*).

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The etiologic agent of plague, bacterial species *Yersinia pestis*, includes several phylogenetic groups (1–4). Some of them that display “universal” hypervirulence for different mammal species (epidemic strains or *Y. pestis* subsp. *pestis*) were responsible for three devastating pandemics, while endemic strains circulating in populations of rodents belonging to the genus *Microtus* (*Y. pestis* subsp. *microtus*) were characterized by high virulence to their main hosts, voles, and laboratory mice but as a rule were of low virulence or avirulent for guinea pigs and caused only occasional diseases in humans that were not accompanied by outbreaks of human-to-human transmission of infection (5). The availability of these two closely related *Y. pestis* subspecies that differ in their selective virulence (host specificity) makes it possible to identify by comparing their whole-genome sequences the pathogenicity-determining genes, potential molecular targets for prophylaxis, and treatment of plague.

In this study, we sequenced 19 *Y. pestis* subsp. *microtus* strains (from six biovars: *ulegeica*, *caucasica*, *xilingolensis*, *hissarica*, *talassica*, *altaica*) isolated from different foci.

Whole-genome sequencing was performed using the Ion Torrent PGM (Life Technologies, USA), according to the manufacturer’s instructions. Ion PGM Reagents 400 Kit (Life Technologies, USA) and Ion 318 Chip Kit (Life Technologies, USA) were used for sequencing. For each genome, reads were *de novo* assembled using 2.9 Newbler assembler (Roche). Finally, we obtained from 180 to 341 contigs for each genome (Table 1). The genome size ranged from 4.51 to 4.64 Mb. Each genome contains 3,711 to 4,008 coding sequences. Only 7 strains have all three plasmids (pMT, pCD, pPCP).

The comparative genomic analysis among *Y. pestis* subsp. *microtus* strains under study and other available *Y. pestis* isolates will provide information on the speciation and evolution of *Y. pestis* and might explain the mechanisms of the selective virulence (host

specificity) of *Y. pestis* vole strains. A detailed report of a full comparative genomic analysis will be included in a future publication.

Nucleotide sequence accession numbers. The GenBank accession numbers for all 19 genomes are listed in Table 1.

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REFERENCES

- Cui Y, Yu C, Yan Y, Li D, Li Y, Jombart T, Weinert LA, Wang Z, Guo Z, Xu L, Zhang Y, Zheng H, Qin N, Xiao X, Wu M, Wang X, Zhou D, Qi Z, Du Z, Wu H, Yang X, Cao H, Wang H, Wang J, Yao S, Rakin A, Li Y, Falush D, Balloux F, Achtman M, Song Y, Wang J, Yang R. 2013. Historical variations in mutation rate in an epidemic pathogen, *Yersinia pestis*. *Proc Natl Acad Sci USA* 110:577–582. <http://dx.doi.org/10.1073/pnas.1205750110>.
- Platonov ME, Evseeva VV, Dentovskaya SV, Anisimov AP. 2013. Molecular typing of *Yersinia pestis*. *Mol Genet Microbiol Virol* 28:41–45. <http://dx.doi.org/10.3103/S0891416813020067>.
- Platonov ME, Evseeva VV, Efremenko DV, Afanas’ev MV, Verzhutski DB, Kuznetsova IV, Shestopalov MY, Dentovskaya SV, Kulichenko AN, Balakhonov SV, Anisimov AP. 2015. Intraspecies classification of rhamnase-positive *Yersinia pestis* strains from natural plague foci of Mongolia. *Mol Genet Microbiol Virol* 30:24–29. <http://dx.doi.org/10.3103/S0891416815010073>.
- Riehm JM, Vergnaud G, Kiefer D, Damdindorj T, Dashdavaa O, Khurelsukh T, Zöller L, Wölfel R, Le Flèche P, Scholz HC. 2012. *Yersinia pestis* lineages in Mongolia. *PLoS One* 7:e30624. <http://dx.doi.org/10.1371/journal.pone.0030624>.
- Anisimov AP, Lindler LE, Pier GB. 2004. Intraspecific diversity of *Yersinia pestis*. *Clin Microbiol Rev* 17:434–464. <http://dx.doi.org/10.1128/CMR.17.2.434-464.2004>.

TABLE 1 Strain-identifying information and basic statistics on assemblies and annotations

| Strain name | Alternate strain name | Focus ^a | Raw data accession no. | Assembly accession no. | Size (bp) | No. of contigs | No. of CDS ^b | No. of genes | Plasmid ^c | | | |
|---|-----------------------|--------------------|------------------------|------------------------|-----------|----------------|-------------------------|--------------|----------------------|-------------|---------------|--|
| | | | | | | | | | pMT/ pFra | pCD/ pYV | pPCP/ pPst | |
| <i>Y. pestis</i> subsp. <i>microtus</i> | | | | | | | | | | | | |
| bv. <i>caucasica</i> | | | | | | | | | | | | |
| SCPM-O-B-6904 | C-537 | 39 | SRR2094286, SRR2094287 | LIYP00000000 | 4,510,568 | 190 | 3,916 | 4,203 | + | + | - | |
| SCPM-O-B-7761 | C-590 | 4 | SRR2094294 | LIYQ00000000 | 4,560,303 | 207 | 4,008 | 4,249 | + | + | - | |
| SCPM-O-B-6990 | C-290 | 4 | SRR2094306 | LIYU00000000 | 4,561,770 | 180 | 3,952 | 4,245 | + | + | - | |
| SCPM-O-B-6974 | C-197 | 6 | SRR2124156, SRR2124157 | LIYX00000000 | 4,522,840 | 270 | 3,916 | 4,255 | + | + | - | |
| SCPM-O-B-6757 | C-235 | 7 | SRR2124162, SRR2124163 | LIYY00000000 | 4,554,747 | 228 | 3,956 | 4,253 | + | + | - | |
| SCPM-O-B-6984 | C-267 | 6 | SRR2124165, SRR2124167 | LIZY00000000 | 4,555,511 | 231 | 3,864 | 4,251 | + | + | - | |
| SCPM-O-B-7832 | C-359 | 5 | SRR2124169, SRR2124170 | LIZB00000000 | 4,557,841 | 205 | 3,854 | 4,265 | + | + | - | |
| SCPM-O-B-6300 | C-291 | 7 | SRR2124185 | LIZC00000000 | 4,559,661 | 202 | 3,893 | 4,250 | + | + | - | |
| SCPM-O-B-6536 | C-346 | 4 | SRR2124186 | LIZE00000000 | 4,560,069 | 204 | 3,931 | 4,243 | + | + | - | |
| SCPM-O-B-6540 | C-666 | 5 | SRR2124207 | LIZF00000000 | 4,559,559 | 183 | 3,863 | 4,247 | + | + | - | |
| <i>Y. pestis</i> subsp. <i>microtus</i> | | | | | | | | | | | | |
| bv. <i>talassica</i> | | | | | | | | | | | | |
| SCPM-O-B-7019 | A-1804 | 40 | SRR2124154, SRR2124155 | LIYW00000000 | 4,626,244 | 275 | 3,984 | 4,308 | + | + | + | |
| SCPM-O-B-7074 | A-1807 | 40 | SRR2094300 | LIYT00000000 | 4,565,589 | 207 | 3,966 | 4,237 | + | + | + | |
| <i>Y. pestis</i> subsp. <i>microtus</i> | | | | | | | | | | | | |
| bv. <i>altaica</i> | | | | | | | | | | | | |
| SCPM-O-B-7812 | I-3455 | 36 | SRR2094311 | LIYV00000000 | 4,575,487 | 223 | 3,939 | 4,261 | + | + | + | |
| SCPM-O-B-7075 | A-513 | 36 | SRR2124168 | LIZA00000000 | 4,595,298 | 229 | 3,923 | 4,263 | + | + | + | |
| <i>Y. pestis</i> subsp. <i>microtus</i> | | | | | | | | | | | | |
| bv. <i>ulegeica</i> | | | | | | | | | | | | |
| SCPM-O-B-6706 | I-3189 | M13 | SRR2093957 | LIYO00000000 | 4,636,832 | 189 | 3,969 | 4,281 | + | + | + | |
| SCPM-O-B-6906 | I-2422 | M02 | SRR2124208, SRR2124209 | LIZG00000000 | 4,520,537 | 341 | 3,711 | 4,212 | - | + | + | |
| SCPM-O-B-6213 | I-2239 | M01 | SRR2511857 | LIZD00000000 | 4,636,905 | 189 | 3,979 | 4,288 | + | + | + | |
| <i>Y. pestis</i> subsp. <i>microtus</i> | | | | | | | | | | | | |
| bv. <i>xilingolensis</i> | | | | | | | | | | | | |
| SCPM-O-B-6216 | I-3134 | M20 | SRR2094295 | LIYR00000000 | 4,587,862 | 230 | 3,920 | 4,255 | + | + | + | |
| <i>Y. pestis</i> subsp. <i>microtus</i> | | | | | | | | | | | | |
| bv. <i>hissarica</i> | | | | | | | | | | | | |
| SCPM-O-B-6304 | 5307-Gis | 34 | SRR2094296 | LIYS00000000 | 4,531,080 | 209 | 3,847 | 4,169 | + | - | + | |

^a Focus numbers are indicated according to references 1 and 4.

^b CDS, coding sequences.

^c -, not present; +, present.