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Finished Genome Assembly of Warm Spring Isolate *Francisella novicida* DPG 3A-IS

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We sequenced the complete genome of *Francisella novicida* DPG 3A-IS to closed and finished status. This is a warm spring isolate recovered from Hobo Warm Spring (Utah, USA). The final assembly is available in NCBI under accession number CP012037.

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Francisella tularensis subsp. *novicida* DPG 3A-IS was isolated in late December 2006 from Hobo Warm Spring, just north of Salt Lake City, Utah, USA (1). This isolate was recovered from the same area that strains U122 and UT01-4992 were isolated, in an attempt to further investigate *F. novicida* persistence and diversity (2, 3). By whole-genome mapping, the recent isolates of *F. novicida* from the hot springs are significantly different from the other *F. novicida* previously published, suggesting a greater species diversity than previously recognized. The sequences of the recent hot spring isolates will aid in the understanding of the status of *F. novicida* as a separate species from *F. tularensis* and the differences in virulence between *F. tularensis* and *F. novicida* in current animal models of tularemia disease.

High-quality genomic DNA of *F. novicida* DPG 3A-IS was extracted from a purified isolate using QIAgen Genome Tip-500. Specifically, 100-mL bacterial cultures were grown to stationary phase and nucleic acid was extracted per the manufacturer's recommendations with one minor variation. Genomic draft data, including both short- (300 ± 70 bp) and long-insert (10,434 ± 1,922 bp) paired-end Illumina data, were trimmed for quality and reduced to a total genome coverage of 342× for the assemblies. All raw data have been deposited to NCBI and are available in the SRA (SRP060258) (4). Draft data were assembled using Newbler version 2.6, Velvet version 1/2/08, AllPaths version 44837, and parallel Phrap version SPS 4.24 to generate a single closed contig of finished quality (5–8).

The final assembly consists of one closed 1,898,140-bp circular contig with 32.3% G+C. Preliminary review of the annotations found 2,037 coding regions, 10 rRNA sequences, and 38 tRNA sequences.

Nucleotide sequence accession number. The full genome sequence for *Francisella novicida* DPG 3A-IS has been deposited in NCBI under accession number CP012037.

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REFERENCES

1. **Whitehouse CA, Kesterson KE, Duncan DD, Eshoo MW, Wolcott M.** 2012. Identification and characterization of *Francisella* species from natural warm springs in Utah, USA. Lett Appl Microbiol **54:**313–324. http://dx.doi.org/10.1111/j.1472-765X.2012.03214.x.
2. **Brett ME, Respicio-Kingry LB, Yendell S, Ratard R, Hand J, Balsamo G, Scott-Waldron C, O'Neal C, Kidwell D, Yockey B, Singh P, Carpenter J, Hill V, Petersen JM, Mead P.** 2014. Outbreak of *Francisella novicida* bacteremia among Inmates at a Louisiana Correctional Facility. Clin Infect Dis **59:**826–833. http://dx.doi.org/10.1093/cid/ciu430.
3. **Molins-Schneekloth CR, Belisle JT, Petersen JM.** 2008. Genomic markers for differentiation of *Francisella tularensis* subsp. *tularensis* A.I and A.II strains. Appl Environ Microbiol **74:**336–341. http://dx.doi.org/10.1128/AEM.01522-07.
4. **Bennett S.** 2004. Solexa Ltd. Pharmacogenomics **5:**433–438. http://dx.doi.org/10.1517/14622416.5.4.433.
5. **Butler J, MacCallum I, Kleber M, Shlyakhter IA, Belmonte MK, Lander ES, Nusbaum C, Jaffe DB.** 2008. ALLPATHS: *de novo* assembly of whole-genome shotgun microreads. Genome Res **18:**810–820. http://dx.doi.org/10.1101/gr.7337908.
6. **Ewing B, Green P.** 1998. Base-calling of automated sequencer traces using Phred, II: error probabilities. Genome Res **8:**186–194. http://dx.doi.org/10.1101/gr.8.3.186.
7. **Ewing B, Hillier L, Wendl MC, Green P.** 1998. Base-calling of automated sequencer traces Using Phred, I: accuracy assessment. Genome Res **8:**175–185. http://dx.doi.org/10.1101/gr.8.3.175.
8. **Zerbino DR, Birney E.** 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res **18:**821–829. http://dx.doi.org/10.1101/gr.074492.107.