

# Draft Genome Sequence of *Legionella pneumophila* D-5864, a Serogroup 6 Strain

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***Legionella pneumophila* is the leading etiology of legionellosis infections in North America and Europe. Here we report the draft genome sequence of *L. pneumophila* D-5864, a serogroup 6 strain, which was isolated from a bronchial alveolar lavage specimen of a male patient from Arizona in 2009. Genes within the lipopolysaccharide (LPS)-biosynthesis region could potentially be determinants of serogroup specificity.**

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*Legionella pneumophila* is a Gram-negative bacterium found in natural freshwater environments worldwide. However, it can also colonize manmade water systems such as cooling towers, whirlpool spas and potable water systems (1). In man-made water systems, *L. pneumophila* can be transmitted into a susceptible human host by inhalation of aerosolized water containing this organism (1). Several studies have shown that *L. pneumophila* serogroup (sg) 6 is the second most common serogroup associated with clinical cases, following only the well-studied and documented sg 1 (2–6). Here we report a draft genome sequence of *L. pneumophila* strain D-5864 (sg6). This strain was isolated from the lower respiratory tract (bronchial alveolar lavage) of a male patient in Arizona in 2009. This draft genome will be helpful to the *Legionella* research community to aid in research efforts to elucidate functional and pathogenic differences within this serogroup and allow a more comprehensive understanding of the genetics of different legionellae, including other serogroups of *L. pneumophila*. Further analyses of these data may also lead to improvements in the characterization and detection methods for all *L. pneumophila* serogroups.

The genome was sequenced using the Roche 454-pyrosequencing (Branford, CT, USA) and Illumina (San Diego, CA, USA) sequencing platforms. After removal of low-quality sequence reads and read trimming, a total of 12,086,080 single-end reads were used for the downstream analysis. A *de novo* assembly was performed using CLC Genomics which resulted in a draft genome of 35 contigs, with a total length of 3,390,488 bp and a G+C content of 38.2%. The genome sequence was annotated by the Rapid Annotations using Subsystem Technology (RAST) server (7). RAST identified 3,292 genomic features consisting of 3,249 coding sequences (predicted), 40 tRNAs, and 3 rRNAs. Also, we mapped sequence reads to the genome of *L. pneumophila* Thunder Bay sg 6 (8) to show relatedness. The mapping resulted in a high sequence similarity of approximately 98.8%.

The LPS-biosynthesis region has been shown to be useful in the

classification of *L. pneumophila* into serogroups and subgroups by monoclonal antibodies (9–11). A correlation between the presence and absence of genes within the LPS biosynthesis region may be linked to *L. pneumophila* serogroup classification (12). In a gene comparison of this region between *L. pneumophila* strains Philadelphia (sg1), Paris (sg1), Thunder Bay (sg6), and D-5864 (sg6), we identified a similar pattern of gene presence/absence as seen by Cazalet et al. (12). While both sg 1 strains contained all 28 genes of the LPS region (*lpp0814*–*lpp0843* as per *L. pneumophila* Paris nomenclature), 13 out of 28 genes were present in both sg 6 strains (*lpp0814*–*lpp0826*). An in-depth comparative genomics study will be performed in the future.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at GenBank under the accession number [JRMJ000000000](https://www.ncbi.nlm.nih.gov/nuccore/JRMJ000000000). The version described in this paper is version [JRMJ010000000](https://www.ncbi.nlm.nih.gov/nuccore/JRMJ010000000).

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## REFERENCES

- Fields BS, Benson RF, Besser RE. 2002. *Legionella* and Legionnaires' disease: 25 years of investigation. *Clin Microbiol Rev* 15:506–526. <http://dx.doi.org/10.1128/CMR.15.3.506-526.2002>.
- Reingold AL, Thomason BM, Brake BJ, Thacker L, Wilkinson HW, Kuritsky JN. 1984. Legionella pneumonia in the United States: the distribution of serogroups and species causing human illness. *J Infect Dis* 149: 819. <http://dx.doi.org/10.1093/infdis/149.5.819>.
- McKinney RM, Kuffner TA, Bibb WF, Nokkaew C, Wells DE, Arnow PM, Woods TC, Plikaytis BD. 1989. Antigenic and genetic variation in *Legionella pneumophila* serogroup 6. *J Clin Microbiol* 27:738–742.
- Marston BJ, Lipman HB, Breiman RF. 1994. Surveillance for Legionnaires' disease: risk factors for morbidity and mortality. *Arch Intern Med* 154: 2417–2422. <http://dx.doi.org/10.1001/archinte.1994.00420210049006>.

5. Visca P, Goldoni P, Lück PC, Helbig JH, Cattani L, Giltri G, Bramati S, Castellani Pastoris M. 1999. Multiple types of *Legionella pneumophila* serogroup 6 in a hospital heated-water system associated with sporadic infections. *J Clin Microbiol* 37:2189–2196.
6. Yu VL, Plouffe JF, Pastoris MC, Stout JE, Schousboe M, Widmer A, Summersgill J, File T, Heath CM, Paterson DL, Cheresky A. 2002. Distribution of *Legionella* species and serogroups isolated by culture in patients with sporadic community-acquired legionellosis: an international collaborative survey. *J Infect Dis* 186:127–128. <http://dx.doi.org/10.1086/341087>.
7. 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. <http://dx.doi.org/10.1186/1471-2164-9-75>.
8. Khan MA, Knox N, Prashar A, Alexander D, Abdel-Nour M, Duncan C, Tang P, Amatullah H, Dos Santos CC, Tijet N, Low DE, Pourcel C, Van Domselaar G, Terebiznik M, Ensminger AW, Guyard C. 2013. Comparative genomics reveal that host-innate immune responses influence the clinical prevalence of *Legionella pneumophila* serogroups. *PLoS One* 8:e67298. <http://dx.doi.org/10.1371/journal.pone.0067298>.
9. Joly JR, Chen YY, Ramsay D. 1983. Serogrouping and subtyping of *Legionella pneumophila* with monoclonal antibodies. *J Clin Microbiol* 18:1040–1046.
10. Helbig JH, Kurtz JB, Pastoris MC, Pelaz C, Lück PC. 1997. Antigenic lipopolysaccharide components of *Legionella pneumophila* recognized by monoclonal antibodies: possibilities and limitations for division of the species into serogroups. *J Clin Microbiol* 35:2841–2845.
11. Helbig JH, Benson RF, Pelaz C, Jacobs E, Lück PC. 2007. Identification and serotyping of atypical *Legionella pneumophila* strains isolated from human and environmental sources. *J Appl Microbiol* 102:100–105. <http://dx.doi.org/10.1111/j.1365-2672.2006.03057.x>.
12. Cazalet C, Jarraud S, Ghavi-Helm Y, Kunst F, Glaser P, Etienne J, Buchrieser C. 2008. Multigenome analysis identifies a worldwide distributed epidemic *Legionella pneumophila* clone that emerged within a highly diverse species. *Genome Res* 18:431–441. <http://dx.doi.org/10.1101/gr.7229808>.