




Genome Sequence of a *Providencia stuartii* Strain Isolated from *Lucilia sericata* Salivary Glands

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ABSTRACT We present here the draft genome sequence of a *Providencia stuartii* strain, derived from the salivary glands of larval *Lucilia sericata*, a common blow fly important to forensic, medical, and veterinary science. The genome sequence will help dissect coinfections involving *P. stuartii* and *Proteus mirabilis*, as well as blow fly–bacteria interactions.

Providencia stuartii is a Gram-negative bacillus bacterium (1) that frequently causes urinary tract infections in hospital patients and has intrinsic resistance to antibiotics (2). Infections have been reported to progress to bacteremia (3), diarrhea (4), peritonitis (5), meningitis (6), infective endocarditis (7), and often co-occur with *Proteus* infections (8). Additionally, *Providencia* species were reported to associate with blow flies (9, 10), stable flies (11), Mexican fruit flies (12), vinegar flies (13), as well as house flies (14). *Providencia* can cause variable infections and different levels of mortality in their hosts (13) and have been shown to impact blow fly attraction to resources (15).

The *P. stuartii* strain Crippen was isolated from *Lucilia sericata*, a green bottle fly, which is of importance to decomposition ecology (18) as related to the medical and forensic sciences (16, 17). Our strain was coisolated along with *Proteus mirabilis* strain WOOD (19), which can affect *L. sericata* attraction to, and colonization of, resources (20, 21). Mixed microbial communities, including *Proteus-Providencia* coinfections, which increase the incidence of bacteremia and urolithiasis (8), can have properties distinct from those of their individual components (22, 23). This property of mixed cultures has also been shown to impact fly behavior and life history (24). Therefore, knowledge of this genome will help elucidate fly–microbe interactions that are important to forensic science and ecology, as well as coinfections relevant to medicine.

Here, we present a draft genome of *P. stuartii* strain Crippen. The genomic sequence was isolated from a colony derived from maggot salivary glands of *L. sericata* third instars raised on beef liver. DNA sequencing was performed using an Ion Torrent personal genome machine (Life Technologies, Inc., Carlsbad, CA, USA) after preparation with a NEBNext fast DNA fragmentation library prep set. The sequencing data comprise 1,383,989 reads, with an average length of 212 bp, totaling 294 Mb. Sequence assembly using the PATRIC full assembly service (25) produced 243 contigs, with an N_{50} of 191,375 bp and a total of 4.72 million nucleotides, resulting in approximately 62-fold coverage. This strain is comparably similar to three previously sequenced *P. stuartii* strains: MRSN 2154 (GenBank accession no. CP003488.1), ATCC 33672 (GenBank acces-

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sion no. CP008920.1), and FDAARGOS_145 (GenBank accession no. CP014024.1). Further genome assemblies based on CONTIGuator (26) indicate that the longest 37 contigs were mapped to the reference strain, with 93.8% of the assembled nucleotides aligned to the *P. stuartii* MRSN 2154 genome. No evidence of plasmids was found based on analysis with the PlasmidFinder version 1.3 server (27).

Whole-genome annotation was generated using the NCBI Prokaryotic Genome Annotation Pipeline (28) using the PATRIC assembly draft genome. The annotated genome contains 4,534 genes, including 4,428 protein-coding regions, eight 5S rRNAs, 14 16S rRNAs, 15 23S rRNAs, 60 tRNAs, and nine ncRNAs. There were also 600 pseudogenes annotated. A total of eight prophage regions were identified with PHAST (29), of which five regions predicted to be intact, two regions incomplete, and one region that is of questionable functionality. Strain-specific gene functions and phage insertions will be useful in elucidating the interactions among *L. sericata*, *P. mirabilis*, and *P. stuartii*.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [LVIE00000000](https://doi.org/10.1093/nar/gkz000). The version described in this paper is the first version, LVIE01000000.

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REFERENCES

- O'Hara CM, Brenner FW, Miller JM. 2000. Classification, identification, and clinical significance of *Proteus*, *Providencia*, and *Morganella*. *Clin Microbiol Rev* 13:534–546. <https://doi.org/10.1128/CMR.13.4.534-546.2000>.
- Warren JW. 1986. *Providencia stuartii*: a common cause of antibiotic-resistant bacteriuria in patients with long-term indwelling catheters. *Rev Infect Dis* 8:61–67. <https://doi.org/10.1093/clinids/8.1.61>.
- Woods TD, Watanakunakorn C. 1996. Bacteremia due to *Providencia stuartii*: review of 49 episodes. *South Med J* 89:221–224. <https://doi.org/10.1097/00007611-199602000-00013>.
- Yoh M, Matsuyama J, Ohnishi M, Takagi K, Miyagi H, Mori K, Park KS, Ono T, Honda T. 2005. Importance of *Providencia* species as a major cause of travellers' diarrhoea. *J Med Microbiol* 54:1077–1082. <https://doi.org/10.1099/jmm.0.45846-0>.
- Ünverdi S, Akay H, Ceri M, Inal S, Altay M, Demiroz AP, Duranay M. 2011. Peritonitis due to *Providencia stuartii*. *Perit Dial Int* 31:216–217.
- Sipahi OR, Bardak-Ozdemir S, Ozgiray E, Aydemir S, Yurtseven T, Yamazhan T, Tasbakan M, Ulusoy S. 2010. Meningitis due to *Providencia stuartii*. *J Clin Microbiol* 48:4667–4668. <https://doi.org/10.1128/JCM.01349-10>.
- Krake PR, Tandon N. 2004. Infective endocarditis due to *Providencia stuartii*. *South Med J* 97:1022–1023.
- Armbruster CE, Smith SN, Yep A, Mobley HL. 2014. Increased incidence of urolithiasis and bacteremia during *Proteus mirabilis* and *Providencia stuartii* coinfection due to synergistic induction of urease activity. *J Infect Dis* 209:1524–1532. <https://doi.org/10.1093/infdis/jit663>.
- Ahmad A, Broce A, Zurek L. 2006. Evaluation of significance of bacteria in larval development of *Cochliomyia macellaria* (Diptera: Calliphoridae). *J Med Entomol* 43:1129–1133. <https://doi.org/10.1093/jmedent/43.6.1129>.
- Singh B, Crippen TL, Zheng L, Fields AT, Yu Z, Ma Q, Wood TK, Dowd SE, Flores M, Tomberlin JK, Tarone AM. 2015. A metagenomic assessment of the bacteria associated with *Lucilia sericata* and *Lucilia cuprina* (Diptera: Calliphoridae). *Appl Microbiol Biotechnol* 99:869–883. <https://doi.org/10.1007/s00253-014-6115-7>.
- Mramba F, Broce A, Zurek L. 2006. Isolation of *Enterobacter sakazakii* from stable flies, *Stomoxys calcitrans* L. (Diptera: Muscidae). *J Food Prot* 69:671–673. <https://doi.org/10.4315/0362-028X-69.3.671>.
- Kuzina LV, Peloquin JJ, Vacek DC, Miller TA. 2001. Isolation and identification of bacteria associated with adult laboratory Mexican fruit flies, *Anastrepha ludens* (Diptera: Tephritidae). *Curr Microbiol* 42:290–294. <https://doi.org/10.1007/s002840110219>.
- Galac MR, Lazzaro BP. 2011. Comparative pathology of bacteria in the genus *Providencia* to a natural host, *Drosophila melanogaster*. *Microbes Infect* 13:673–683. <https://doi.org/10.1016/j.micinf.2011.02.005>.
- Gupta AK, Nayduch D, Verma P, Shah B, Ghate HV, Patole MS, Shouche YS. 2012. Phylogenetic characterization of bacteria in the gut of house flies (*Musca domestica* L.). *FEMS Microbiol Ecol* 79:581–593. <https://doi.org/10.1111/j.1574-6941.2011.01248.x>.
- Hobson EP. 1935. Sheep blowfly investigations. II. *Ann Appl Biol* 22: 294–300. <https://doi.org/10.1111/j.1744-7348.1935.tb07164.x>.
- Cazander G, Pritchard DI, Nigam Y, Jung W, Nibbering PH. 2013. Multiple actions of *Lucilia sericata* larvae in hard-to-heal wounds: larval secretions contain molecules that accelerate wound healing, reduce chronic inflammation and inhibit bacterial infection. *Bioessays* 35:1083–1092. <https://doi.org/10.1002/bies.201300071>.
- Sze SH, Dunham JP, Carey B, Chang PL, Li F, Edman RM, Fjeldsted C, Scott MJ, Nuzhdin SV, Tarone AM. 2012. A *de novo* transcriptome assembly of *Lucilia sericata* (Diptera: Calliphoridae) with predicted alter-

- native splices, single nucleotide polymorphisms and transcript expression estimates. *Insect Mol Biol* 21:205–221. <https://doi.org/10.1111/j.1365-2583.2011.01127.x>.
18. Prinkkilä ML, Hanski I. 1995. Complex competitive interactions in four species of *Lucilia* blowflies. *Ecol Entomol* 20:261–272. <https://doi.org/10.1111/j.1365-2311.1995.tb00456.x>.
 19. Yuan Y, Zhang Y, Fu S, Crippen TL, Visi DK, Benbow ME, Allen MS, Tomberlin JK, Sze SH, Tarone AM. 2016. Genome sequence of a *Proteus mirabilis* strain isolated from the salivary glands of larval *Lucilia sericata*. *Genome Announc* 4(4):e00672-16. <https://doi.org/10.1128/genomeA.00672-16>.
 20. Tomberlin JK, Crippen TL, Tarone AM, Singh B, Adams K, Rezenom YH, Benbow ME, Flores M, Longnecker M, Pechal JL, Russell DH, Beier RC, Wood TK. 2012. Interkingdom responses of flies to bacteria mediated by fly physiology and bacterial quorum sensing. *Anim Behav* 84:1449–1456. <https://doi.org/10.1016/j.anbehav.2012.09.013>.
 21. Ma Q, Fonseca A, Liu W, Fields AT, Pimsler ML, Spindola AF, Tarone AM, Crippen TL, Tomberlin JK, Wood TK. 2012. *Proteus mirabilis* interkingdom swarming signals attract blow flies. *ISME J* 6:1356–1366. <https://doi.org/10.1038/ismej.2011.210>.
 22. Schaffer JN, Pearson MM. 2015. *Proteus mirabilis* and urinary tract infections. *Microbiol Spectr* 3:UTI-0017-2013. <https://doi.org/10.1128/microbiolspec.UTI-0017-2013>.
 23. Wie SH. 2015. Clinical significance of *Providencia* bacteremia or bacteriuria. *Korean J Intern Med* 30:167–169. <https://doi.org/10.3904/kjim.2015.30.2.167>.
 24. Tomberlin JK, Crippen TL, Tarone AM, Chaudhury MFB, Singh B, Cammack JA, Meisel RP. 2017. A review of bacterial interactions with blow flies (*Diptera: Calliphoridae*) of medical, veterinary, and forensic importance. *Ann Entomol Soc Am* 110:19–36. <https://doi.org/10.1093/aesa/saw086>.
 25. Wattam AR, Abraham D, Dalay O, Disz TL, Driscoll T, Gabbard JL, Gillespie JJ, Gough R, Hix D, Kenyon R, Machi D, Mao C, Nordberg EK, Olson R, Overbeek R, Pusch GD, Shukla M, Schulman J, Stevens RL, Sullivan DE, Vonstein V, Warren A, Will R, Wilson MJ, Yoo HS, Zhang C, Zhang Y, Sobral BW. 2014. PATRIC, the bacterial bioinformatics database and analysis resource. *Nucleic Acids Res* 42:D581–D591. <https://doi.org/10.1093/nar/gkt1099>.
 26. Galardini M, Biondi EG, Bazzicalupo M, Mengoni A. 2011. CONTIGuator: a bacterial genomes finishing tool for structural insights on draft genomes. *Source Code Biol Med* 6:11. <https://doi.org/10.1186/1751-0473-6-11>.
 27. Carattoli A, Zankari E, García-Fernández A, Voldby Larsen M, Lund O, Villa L, Møller Aarestrup F, Hasman H. 2014. *In silico* detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. *Antimicrob Agents Chemother* 58:3895–3903. <https://doi.org/10.1128/AAC.02412-14>.
 28. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for metagenomic annotation. *OMICS* 12:137–141. <https://doi.org/10.1089/omi.2008.0017>.
 29. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <https://doi.org/10.1093/nar/gkr485>.