

# Draft Genome Sequence of the Quorum-Sensing and Biofilm-Producing *Pseudomonas aeruginosa* Strain Pae221, Belonging to the Epidemic High-Risk Clone Sequence Type 274

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***Pseudomonas aeruginosa* Pae221 is a clinical isolate from blood culture. Pae221 was found to be a strong quorum-sensing and biofilm-producing strain and also demonstrates a notable production of phenazines. This strain belongs to sequence type 274 (ST274), an epidemic high-risk clone. Here, we report the draft genome sequence of *P. aeruginosa* Pae221.**

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*Pseudomonas aeruginosa* is a ubiquitous Gram-negative bacterium whose metabolic versatility allows it to thrive in diverse ecological niches. In the human body, *P. aeruginosa* is able to transform into a hostile opportunistic pathogen, mainly when there is a breach of host tissue barriers or a suppressed immune system (1).

The successful combination of a number of intrinsic and acquired resistance mechanisms as well as the expression of numerous secreted virulence factors make this bacterium a threatening human pathogen. The expression of virulence genes in *P. aeruginosa* is found to be modulated by a bacterial cell-to-cell signaling mechanism, widely known as quorum sensing (QS) (2). QS bacteria produce and release small signaling molecules that at a high population density interact with associated receptors to induce the expression of various genes, including those related to biofilm production and virulence (2).

Here, we present the draft whole-genome sequence of *P. aeruginosa* Pae221, a QS and biofilm-producing strain isolated from a patient with bacteremia during a multicenter study, which included 10 Spanish hospitals (3). Pae221 also presents an enhanced production of phenazines when cultured in medium supplemented with divalent cations. Pae221 belongs to sequence type 274 (ST274), an epidemic high-risk clone circulating in Spain, which is also found in other European countries and Australia (4–8).

The *P. aeruginosa* Pae221 genome (Pae221\_ST274) was sequenced using an Illumina HiSeq 2000 genome sequencer (with 100-bp paired-end reads) (GATC Biotech, Konstanz, Germany). The total number of paired reads obtained was 7,346,760, providing approximately 226-fold coverage of the genome. The sequences obtained were used for *de novo* assembly using SPAdes version 3.1.0 (9). The quality of the genome assembly was assessed

in QUAST (10). The draft genome sequence consists of 353 contigs, with an  $N_{50}$  contig size of 339,356 nucleotides and a total length of 6,364,167 bp; the G+C content is 66.3%, similar to that of other *P. aeruginosa* sequenced genomes. The assemblies obtained were annotated using the Era7 tool BG7 (11). A total of 5,761 coding sequences (CDS) and 67 tRNA genes were identified in Pae221. Using the Harvest alignment tool (12), we determined that the most similar genome to Pae221 (91%) was that of the Liverpool epidemic strain LESB65, a QS overproducer hypervirulent strain (13). Pae221 possesses 40 CDS that are not present in the LESB65 genome. Among these, 4 genes were related to phenazine biosynthesis, similar to those described in *P. aeruginosa* isolate ATCC 700888 (14). More detailed analyses of the Pae221 strain, including comparative studies with other *P. aeruginosa* strains and transcriptome analysis, are in progress.

**Nucleotide sequence accession numbers.** The draft genome sequence of *P. aeruginosa* Pae221 has been deposited in GenBank/ENA under the accession no. [CDFS01000000](https://www.ncbi.nlm.nih.gov/nuccore/CDFS01000000). The version described in this paper is CDFS01000001.1 and consists of the contig sequences CDFS01000001 to CDFS01000370.

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## REFERENCES

1. Van Delden C, Iglewski BH. 1998. Cell-to-cell signaling and *Pseudomonas aeruginosa* infections. *Emerg Infect Dis* 4:551–560. [http://dx.doi.org/10.3201/eid0404.980405](https://doi.org/10.3201/eid0404.980405).
2. Lee J, Zhang L. 2014. The hierarchy quorum sensing network in *Pseu-*

- domonas aeruginosa*. Protein Cell <http://dx.doi.org/10.1007/s13238-014-0100-x>.
3. Cabot G, Ocampo-Sosa AA, Tubau F, Macia MD, Rodríguez C, Moya B, Zamorano L, Suárez C, Peña C, Martínez-Martínez L, Oliver A, Spanish Network for Research in Infectious Diseases (REIPI). 2011. Overexpression of AmpC and efflux pumps in *Pseudomonas aeruginosa* isolates from bloodstream infections: prevalence and impact on resistance in a Spanish multicenter study. *Antimicrob Agents Chemother* 55: 1906–1911. <http://dx.doi.org/10.1128/AAC.01645-10>.
  4. García-Castillo M, del Campo R, Morosini MI, Riera E, Cabot G, Willems R, van Mansfeld R, Oliver A, Cantón R. 2011. Wide dispersion of ST175 clone despite high genetic diversity of carbapenem-nonsusceptible *Pseudomonas aeruginosa* clinical strains in 16 Spanish hospitals. *J Clin Microbiol* 49:2905–2910. <http://dx.doi.org/10.1128/JCM.00753-11>.
  5. Cabot G, Ocampo-Sosa AA, Domínguez MA, Gago JF, Juan C, Tubau F, Rodríguez C, Moyà B, Peña C, Martínez-Martínez L, Oliver A, Spanish Network for Research in Infectious Diseases (REIPI). 2012. Genetic markers of widespread extensively drug-resistant *Pseudomonas aeruginosa* high-risk clones. *Antimicrob Agents Chemother* 56: 6349–6357. <http://dx.doi.org/10.1128/AAC.01388-12>.
  6. Fernández-Olmos A, García-Castillo M, Alba JM, Morosini MI, Lamas A, Romero B, Galán JC, del Campo R, Cantón R. 2013. Population structure and antimicrobial susceptibility of both nonpersistent and persistent *Pseudomonas aeruginosa* isolates recovered from cystic fibrosis patients. *J Clin Microbiol* 51:2761–2765. <http://dx.doi.org/10.1128/JCM.00802-13>.
  7. López-Causapé C, Rojo-Molinero E, Mulet X, Cabot G, Moyà B, Figuerola J, Togores B, Pérez JL, Oliver A. 2013. Clonal dissemination, emergence of mutator lineages and antibiotic resistance evolution in *Pseudomonas aeruginosa* cystic fibrosis chronic lung infection. *PLoS One* 8:e71001. <http://dx.doi.org/10.1371/journal.pone.0071001>.
  8. Estepa V, Rojo-Bezares B, Torres C, Sáenz Y. 2014. Faecal carriage of *Pseudomonas aeruginosa* in healthy humans: antimicrobial susceptibility and global genetic lineages. *FEMS Microbiol Ecol* 89:15–19. <http://dx.doi.org/10.1111/1574-6941.12301>.
  9. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <http://dx.doi.org/10.1089/cmb.2012.0021>.
  10. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUASt: quality assessment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <http://dx.doi.org/10.1093/bioinformatics/btt086>.
  11. Pareja-Tobes P, Manrique M, Pareja-Tobes E, Pareja E, Tobes R. 2012. BG7: a new approach for bacterial genome annotation designed for next generation sequencing data. *PLoS One* 7:e49239. <http://dx.doi.org/10.1371/journal.pone.0049239>.
  12. Treangen TJ, Ondov BD, Koren S, Phillippy AM. 2014. Rapid core-genome alignment and visualization for thousands of microbial genomes. *bioRxiv* <http://biorxiv.org/content/early/2014/07/22/007351>.
  13. Carter ME, Fothergill JL, Walshaw MJ, Rajakumar K, Kadioglu A, Winstanley C. 2010. A subtype of a *Pseudomonas aeruginosa* cystic fibrosis epidemic strain exhibits enhanced virulence in a murine model of acute respiratory infection. *J Infect Dis* 202:935–942. <http://dx.doi.org/10.1086/655781>.
  14. Chugani S, Kim BS, Phattarasukol S, Brittnacher MJ, Choi SH, Harwood CS, Greenberg EP. 2012. Strain-dependent diversity in the *Pseudomonas aeruginosa* quorum-sensing regulon. *Proc Natl Acad Sci U S A* 109:E2823–E2831. <http://dx.doi.org/10.1073/pnas.1214128109>.