

Application de la génomique bactérienne en microbiologie diagnostique

Sébastien Aeby, Florian Tagini et Gilbert Greub

Références

1. Blattner FR, Plunkett G, Bloch CA, Perna NT, Burland V, Riley M, et al. The complete genome sequence of *Escherichia coli* K-12. *Science*. 1997 Sep 5;277(5331):1453–62.
2. Kunst F, Ogasawara N, Moszer I, Albertini AM, Alloni G, Azevedo V, et al. The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. *Nature*. 1997 Nov 20;390(6657):249–56.
3. Hood DW, Deadman ME, Allen T, Masoud H, Martin A, Brisson JR, et al. Use of the complete genome sequence information of *Haemophilus influenzae* strain Rd to investigate lipopolysaccharide biosynthesis. *Mol Microbiol*. 1996 Dec;22(5):951–65.
4. Andersson SG, Zomorodipour A, Andersson JO, Sicheritz-Pontén T, Alsmark UC, Podowski RM, et al. The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria. *Nature*. 1998 Nov 12;396(6707):133–40.
5. Cole ST, Eiglmeier K, Parkhill J, James KD, Thomson NR, Wheeler PR, et al. Massive gene decay in the leprosy bacillus. *Nature*. 2001 Feb 22;409(6823):1007–11.
6. Hayashi T, Makino K, Ohnishi M, Kurokawa K, Ishii K, Yokoyama K, et al. Complete Genome Sequence of Enterohemorrhagic *Escherichia coli* O157:H7 and Genomic Comparison with a Laboratory Strain K-12. *DNA Res*. 2001 Jan 1;8(1):11–22.
7. Pizza M, Scarlato V, Masignani V, Giuliani MM, Aricò B, Comanducci M, et al. Identification of vaccine candidates against serogroup B meningococcus by whole-genome sequencing. *Science*. 2000 Mar 10;287(5459):1816–20.
8. Greub G, Kebbi-Beghdadi C, Bertelli C, Collyn F, Riederer BM, Yersin C, et al. High Throughput Sequencing and Proteomics to Identify Immunogenic Proteins of a New Pathogen: The Dirty Genome Approach. Valdivia RH, editor. *PLoS ONE*. 2009 Dec 23;4(12):e8423.
9. Bertelli C, Collyn F, Croxatto A, Rückert C, Polkinghorne A, Kebbi-Beghdadi C, et al. The *Waddlia* genome: a window into chlamydial biology. *PLoS One*. 2010;5(5):e10890.

10. Bertelli C, Cissé OH, Rusconi B, Kebbi-Beghdadi C, Croxatto A, Goesmann A, et al. CRISPR System Acquisition and Evolution of an Obligate Intracellular Chlamydia-Related Bacterium. *Genome Biol Evol.* 2016;8(8):2376–86.
11. Diene SM, Bertelli C, Pillonel T, Jacquier N, Croxatto A, Jatón K, et al. Comparative genomics of *Neisseria meningitidis* strains: new targets for molecular diagnostics. *Clin Microbiol Infect Off Publ Eur Soc Clin Microbiol Infect Dis.* 2016 Jun;22(6):568.e1–7.
12. Shimomura Y, Okumura K, Murayama SY, Yagi J, Ubukata K, Kirikae T, et al. Complete genome sequencing and analysis of a Lancefield group G *Streptococcus dysgalactiae* subsp. *equisimilis* strain causing streptococcal toxic shock syndrome (STSS). *BMC Genomics.* 2011;12:17.
13. Bertelli C, Greub G. Rapid bacterial genome sequencing: methods and applications in clinical microbiology. *Clin Microbiol Infect.* 2013 Sep;19(9):803–13.
14. Lavezzo E, Toppo S, Franchin E, Di Camillo B, Finotello F, Falda M, et al. Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. *BMC Infect Dis.* 2013;13:554.
15. Sherry NL, Porter JL, Seemann T, Watkins A, Stinear TP, Howden BP. Outbreak investigation using high-throughput genome sequencing within a diagnostic microbiology laboratory. *J Clin Microbiol.* 2013 May;51(5):1396–401.
16. Chin C-S, Sorenson J, Harris JB, Robins WP, Charles RC, Jean-Charles RR, et al. The origin of the Haitian cholera outbreak strain. *N Engl J Med.* 2011 Jan 6;364(1):33–42.
17. Mellmann A, Harmsen D, Cummings CA, Zentz EB, Leopold SR, Rico A, et al. Prospective genomic characterization of the German enterohemorrhagic *Escherichia coli* O104:H4 outbreak by rapid next generation sequencing technology. *PLoS One.* 2011;6(7):e22751.
18. Qin J, Cui Y, Zhao X, Rohde H, Liang T, Wolters M, et al. Identification of the Shiga toxin-producing *Escherichia coli* O104:H4 strain responsible for a food poisoning outbreak in Germany by PCR. *J Clin Microbiol.* 2011 Sep;49(9):3439–40.
19. Blanc DS, Gomes Magalhaes B, Abdelbary M, Prod'hom G, Greub G, Wasserfallen JB, et al. Hand soap contamination by *Pseudomonas aeruginosa* in a tertiary care hospital: no evidence of impact on patients. *J Hosp Infect.* 2016 May;93(1):63–7.
20. Jatón L, Pillonel T, Jatón K, Dory E, Prod'hom G, Blanc DS, et al. Common skin infection due to Pantón-Valentine leucocidin-producing *Staphylococcus aureus* strains in asylum seekers from Eritrea: a genome-based investigation of a suspected outbreak. *Clin Microbiol Infect Off Publ Eur Soc Clin Microbiol Infect Dis.* 2016 Jun 6;

21. Bertelli C, Pillonel T, Torregrossa A, Prod'hom G, Fischer CJ, Greub G, et al. Bifidobacterium longum bacteremia in preterm infants receiving probiotics. Clin Infect Dis Off Publ Infect Dis Soc Am. 2015 Mar 15;60(6):924–7.
22. Bertelli C, Aeby S, Chassot B, Clulow J, Hilfiker O, Rappo S, et al. Sequencing and characterizing the genome of Estrella lausannensis as an undergraduate project: training students and biological insights. Front Microbiol. 2015;6:101.