

2015-05-14

Draft Genome Sequences of Six Different Staphylococcus epidermidis Clones, Isolated Individually from Preterm Neonates Presenting with Sepsis at Edinburgh's Royal Infirmary

Paul Walsh

Department of Computer Science; Cork Institute of Technology; Cork, Ireland. NSilico Ltd, Rubicon Innovation Center, Cork, Ireland, Paul.Walsh@cit.ie

M. Bekaert

NSilico Ltd, Rubicon Innovation Center, Cork, Ireland

J. Carroll

NSilico Ltd, Rubicon Innovation Center, Cork, Ireland

T. Manning

NSilico Ltd, Rubicon Innovation Center, Cork, Ireland

B. Kelly

NSilico Ltd, Rubicon Innovation Center, Cork, Ireland

Follow this and additional works at: <https://sword.cit.ie/dptbiosciart>



Part of the [Bacteria Commons](#), [Biology Commons](#), [Biotechnology Commons](#), [Diseases Commons](#), [Genomics Commons](#), [Immunology and Infectious Disease Commons](#), [Infectious Disease Commons](#), [Microbiology Commons](#), and the [Public Health Commons](#)
See next page for additional authors

Recommended Citation

Walsh, P. et al., 2015. Draft Genome Sequences of Six Different Staphylococcus epidermidis Clones, Isolated Individually from Preterm Neonates Presenting with Sepsis at Edinburgh's Royal Infirmary: TABLE 1 . Genome Announcements, 3(3). Available at: <http://dx.doi.org/10.1128/genomeA.00471-15>.

This Article is brought to you for free and open access by the Biological Sciences at SWORD - South West Open Research Deposit. It has been accepted for inclusion in Department of Biological Sciences Publications by an authorized administrator of SWORD - South West Open Research Deposit. For more information, please contact sword@cit.ie.

Authors

Paul Walsh, M. Bekaert, J. Carroll, T. Manning, B. Kelly, A. O'Driscoll, X. Lu, C. Smith, P. Dickinson, K. Templeton, P. Ghazal, and Roy D. Sleator

Draft Genome Sequences of Six Different *Staphylococcus epidermidis* Clones, Isolated Individually from Preterm Neonates Presenting with Sepsis at Edinburgh's Royal Infirmary

P. Walsh,^a M. Bekaert,^a J. Carroll,^a T. Manning,^a B. Kelly,^a A. O'Driscoll,^b X. Lu,^a C. Smith,^c P. Dickinson,^c K. Templeton,^{c,d} P. Ghazal,^c R. D. Sleator^e

nSilico, Cork, Ireland^a; Department of Computing, Cork Institute of Technology, Bishopstown, Cork, Ireland^b; Division of Pathway Medicine, University of Edinburgh, Edinburgh, United Kingdom^c; Microbiological Diagnostic Unit, Royal Infirmary, University of Edinburgh, Edinburgh, United Kingdom^d; Department of Biological Sciences, Cork Institute of Technology, Bishopstown, Cork, Ireland^e

Herein, we report the draft genome sequences of six individual *Staphylococcus epidermidis* clones, cultivated from blood taken from different preterm neonatal sepsis patients at the Royal Infirmary, Edinburgh, Scotland, United Kingdom.

Received 6 April 2015 Accepted 7 April 2015 Published 14 May 2015

Citation Walsh P, Bekaert M, Carroll J, Manning T, Kelly B, O'Driscoll A, Lu X, Smith C, Dickinson P, Templeton K, Ghazal P, Sleator RD. 2015. Draft genome sequences of six different *Staphylococcus epidermidis* clones, isolated individually from preterm neonates presenting with sepsis at Edinburgh's Royal Infirmary. *Genome Announc* 3(3):e00471-15. doi:10.1128/genomeA.00471-15.

Copyright © 2015 Walsh et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to R. D. Sleator, roy.sleator@cit.ie.

Staphylococcus epidermidis is a Gram-positive bacterium naturally found on human skin (1) and an important opportunistic pathogen linked with neonatal blood sepsis (2–5).

Preterm neonates are a highly susceptible patient group for bacterial infections, due to their naive immune status and the invasive procedures to which they are often subjected to in neonatal ICU settings (2, 6, 7). Rapid detection of blood sepsis and characterization of the causative pathogen are critical first steps to enable appropriate treatment and improved prognostic outcomes (8–10). As part of the ClouDx-i project consortium, we aim to extend our knowledge of currently circulating pathogenic strains linked with neonatal blood sepsis to inform the continued development of new and improved molecular diagnostic assays (11). Herein, we report the draft genome sequences of six individual *Staphylococcus epidermidis* strains, isolated from preterm neonates at the Royal Infirmary, Edinburgh, United Kingdom, in 2014. Positivity for blood sepsis and species of each isolate was confirmed by classical microbiological identification and characterization techniques.

Isolates were grown overnight at 37°C on Luria broth (LB) agar, and genomic DNA was isolated using Qiagen genomic tips (Venlo, Limburg, Netherlands). Genomic DNA fragments, ranging in size from 2 to 10 kb, were generated by sonication. Frag-

ments were subsequently used to produce a non-size-selected genome library using the Nextera mate-pair kit (Illumina, San Diego, CA). The resulting libraries were then sequenced on an Illumina MiSeq using MiSeq Reagent kit v3. Genomic sequence assembly, analysis, and automated reporting were carried out using the Simplicity software pipeline (12). The results of this analysis are summarized in Table 1. Sequence assembly was achieved using a *de-novo* assembly pipeline based on the Spades 3.10 assembly tool, with k-mers K21, K33, K55, K77, K99, and K127 nucleotides in length. Each genome was initially annotated with the Prokka tool (13) and the identified 16S rRNA genes were used to confirm the species as *S. epidermidis* in each case. Each genome was then screened using the Glimmer 3 tool (14). The predicted open reading frames (ORFs) were compared to the Uniprot Trembl database (15) using BLASTp.

Samples were handled in accordance with local ethical approval by the ethics committees of the NHS Lothian SAHSC Bioresource and NHS R&D office (project 2011/R/NE/01) and the HSS BioResource (request 13/ES/0126).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers listed in Table 1.

TABLE 1 Genomic sequence assembly overview

Strain	Total no. of reads	Fold coverage	G+C content (%)	Total contigs (>1,000 bp)	Largest contig (bp)	No. of ORFs	Accession no.
NGS-ED-1107	2,599,368	135.2	32.0	53	207,733	2,570	JZUK00000000
NGS-ED-1109	2,436,309	114.6	32.0	51	360,587	2,252	JZUL00000000
NGS-ED-1110	4,476,721	223.5	32.0	45	207,733	2,515	JZUM00000000
NGS-ED-1111	5,197,793	163.5	32.0	44	250,293	2,583	JZUN00000000
NGS-ED-1117	1,607,705	76.0	32.0	48	206,303	2,459	JZUO00000000
NGS-ED-1118	1,681,207	94.1	31.9	48	206,303	2,444	JZUP00000000

ACKNOWLEDGMENT

This work was supported by the ClouDx-i IAPP EU FP7 project, coordinated by RDS.

REFERENCES

- Coates R, Moran J, Horsburgh MJ. 2014. Staphylococci: colonizers and pathogens of human skin. *Future Microbiol* 9:75–91. <http://dx.doi.org/10.2217/fmb.13.145>.
- Kaufman D, Fairchild KD. 2004. Clinical microbiology of bacterial and fungal sepsis in very-low-birth-weight infants. *Clin Microbiol Rev* 17:638–680. <http://dx.doi.org/10.1128/CMR.17.3.638-680.2004>.
- Hasman H, Saputra D, Sicheritz-Ponten T, Lund O, Svendsen CA, Frimodt-Møller N, Aarestrup FM. 2013. Rapid whole-genome sequencing for the detection and characterization of microorganisms directly from clinical samples. *J Clin Microbiol* 52:139–146. <http://dx.doi.org/10.1128/jcm.02452-13>.
- Stoll BJ, Hansen N, Fanaroff AA, Wright LL, Carlo WA, Ehrenkranz RA, Lemons JA, Donovan EF, Stark AR, Tyson JE, Oh W, Bauer CR, Korones SB, Shankaran S, Laptook AR, Stevenson DK, Papile L-A, Poole WK. 2002. Changes in pathogens causing early-onset sepsis in very-low-birth-weight infants. *New Engl J Med* 347:240–247. <http://dx.doi.org/10.1056/NEJMoa012657>.
- Stoll BJ, Hansen NI, Sánchez PJ, Faix RG, Poindexter BB, Van Meurs KP, Bizzarro MJ, Goldberg RN, Frantz ID, Hale EC, Shankaran S, Kennedy K, Carlo WA, Watterberg KL, Bell EF, Walsh MC, Schibler K, Laptook AR, Shane AL, Schrag SJ, Das A, Higgins RD, Eunice Kennedy Shriver National Institute of Child Health and Human Development Neonatal Research Network. 2011. Early onset neonatal sepsis: the burden of group B streptococcal and *E. coli* disease continues. *Pediatrics* 127:817–826. <http://dx.doi.org/10.1542/peds.2010-2217>.
- Shah BA, Padbury JF. 2014. Neonatal sepsis: an old problem with new insights. *Virulence* 5:170–178. <http://dx.doi.org/10.4161/viru.26906>.
- Ghazal P, Dickinson P, Smith CL. 2013. Early life response to infection. *Curr Opin Infect Dis* 26:213–218. <http://dx.doi.org/10.1097/QCO.0b013e32835fb8bf>.
- Labib AZ, Mahmoud AB, Eissa N, El Gendy FM, Soliman MA, Aly AA. 2013. Early diagnosis of neonatal sepsis: a molecular approach and detection of diagnostic markers versus conventional blood culture. *Int J Microbiol Res* 4:77–85.
- Mancini N, Carletti S, Ghidoli N, Cichero P, Burioni R, Clementi M. 2010. The era of molecular and other non-culture-based methods in diagnosis of sepsis. *Clin Microbiol Rev* 23:235–251. <http://dx.doi.org/10.1128/CMR.00043-09>.
- Sibley CD, Peirano G, Church DL. 2012. Molecular methods for pathogen and microbial community detection and characterization: current and potential application in diagnostic microbiology. *Infect Genet Evol* 12:505–521. <http://dx.doi.org/10.1016/j.meegid.2012.01.011>.
- Bullman S, Lucey B, Sleator RD. 2012. Molecular diagnostics: the changing culture of medical microbiology. *Bioeng Bugs* 3:1–7. <http://dx.doi.org/10.4161/bbug.3.1.19011>.
- Walsh P, Carroll J, Sleator RD. 2013. Accelerating *in silico* research with workflows: a lesson in simplicity. *Comput Biol Med* 43:2028–2035. <http://dx.doi.org/10.1016/j.compbiomed.2013.09.011>.
- Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <http://dx.doi.org/10.1093/bioinformatics/btu153>.
- Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. 1999. Improved microbial gene identification with Glimmer. *Nucleic Acids Res* 27:4636–4641. <http://dx.doi.org/10.1093/nar/27.23.4636>.
- Boeckmann B, Bairoch A, Apweiler R, Blatter M-C, Estreicher A, Gasteiger E, Martin MJ, Michoud K, O'Donovan C, Phan I, Pilbout S, Schneider M. 2003. The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. *Nucleic Acids Res* 31:365–370. <http://dx.doi.org/10.1093/nar/gkg095>.