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DATA NOTE **Open Access**

Complete genome of single locus sequence typing D1 strain *Cutibacterium acnes* CN6 isolated from healthy facial skin

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Abstract

Objectives *Cutibacterium acnes* is a Gram-positive bacterium commonly found on human skin, particularly in sebaceous areas. While it is typically considered a commensal, specific strain types based on single locus sequence typing (SLST) have been associated with pathogenic conditions or healthy skin. Recently, SLST D1 strains, part of phylotype IA1, have received attention for their potential benefits related to skin health. However, their genetic characteristics remain underexplored. Therefore, the whole genome of *C. acnes* CN6, an SLST D1 strain isolated from the facial skin of a healthy individual, was sequenced to expand the understanding of SLST D1 strains and identify genomic features that may support skin health.

Data description The whole genome sequencing of *C. acnes* CN6 was conducted using MinION reads based on de novo assembly, revealing a single circular complete chromosome. With the length of 2,550,458 bp and G + C content of 60.04%, the genome contains 2,492 genes, including 2,433 CDSs, 9 rRNAs, 46 tRNAs, 4 ncRNAs, and 134 pseudo genes. Previously predicted virulence proteins of *C. ances* were detected in the genome. Genome comparation with 200 *C. acnes* strains isolated from healthy facial skin revealed SLST D1 strain-specific genes and a unique variant of the *znuC* gene in D1 strains.

Keywords *Cutibacterium acnes*, Single-locus sequence typing (SLST), Healthy skin, Whole genome sequencing, *De novo* assembly

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Objective

Cutibacterium acnes is a Gram-positive bacterium that is prevalent across human skin, especially in sebaceous areas [1]. While *C. acnes* is a commensal microbe in skin microenvironment, it can act as an opportunistic pathogen, contributing to various pathological states. It has been associated with acne vulgaris, osteoarticular prosthesis infections, and other clinical conditions when the skin microbiome balanced is disrupted [2–6]. In contrast, certain strains of *C. acnes* play a crucial role in maintaining skin homeostasis and promoting skin barrier function, potentially contributing to overall skin health and resilience [7, 8].

Previous studies have suggested a potential association between specific *C. acnes* strains and particular pathogenic conditions based on molecular typing systems such as single-locus sequence typing (SLST) [9–11]. *C. acnes* is classified into phylotypes (IA1, IA2, IB, IC, II, and III), each containing specific SLST classes [12]. Notably, SLST classes H (phylotype IB) and K (phylotype II) have been linked to healthy skin [13]. Recently, *C. acnes* SLST D1 strains, belonging to phylotype IA1, have garnered attention for its potential benefits to skin health [14–16]. However, the current understanding of *C. acnes* SLST D1 strains remains incomplete, necessitating further research.

To address this, we performed whole genome sequencing of a *C. acnes* SLST D1 strain, named CN6, which was isolated from the facial skin of a healthy individuals without any skin disease. With only a single SLST class D genome classified as "complete" in NCBI GenBank—strain CBS-BPNBT19153, which was isolated from contaminated platelet blood concentrates [17]—we aimed to expand the genetic background of SLST D1 strains through this study. Additionally, we identified unique genomic characteristics of the *C. acnes* SLST D1 strain CN6 by comparing its genomic differences with other *C. acnes* strains isolated from the healthy facial skin, providing insights into facial skin health.

Data description

C. acnes CN6 was isolated from a facial skin swab sample collected from a healthy individual without any skin conditions. The pure isolate of *C. acnes* CN6 was cultivated in Brain Heart Infusion agar for 5 days at 37 °C under anaerobic condition using a GasPak EZ anaerobe pouch system (BD, USA). Genomic DNA was extracted using the Wizard genomic DNA purification kit (Promega, USA), following the manufacturer's instructions. The quality and quantity of the extracted DNA was assessed through Nanodrop One Spectrophotometer (Thermo Fisher Scientific, USA) and Qubit 3.0 fluorometer (Thermo Fisher Scientific, USA).

The whole genome sequencing library was constructed using SQK-LSK109 ligation sequencing kit (Oxford Nanopore Technologies [ONT], UK), along with the NEBNext companion module (New England Biolabs, USA). Sequencing was performed on the ONT MinION platform by loading the library into FLOWMIN111 R10.3 flow cell at the KNU NGS Core Facility (Kyungpook National University, Republic of Korea). To generate FASTQ files of the sequencing data, base calling was performed using Guppy v 6.5.7 [18] in high- accuracy mode, followed by using NanoStat v 1.6.0 [19] to calculate sequence statics. A total of 203,933 reads with mean read quality score of 12.5 and N_{50} of 4,114 bp was obtained (Data file 1). After removing low-quality reads with Filtlong v 0.2.1 (https://github.com/rrwick/Filtlong), *de novo* assembly was performed using Flye v 2.9.1 [20] with the modification for the genome size option (–genome-size 2.5 m). The SLST strain type was classified using the online typing tool available at http://medbac.dk/slst_server_script.html [11], and gene annotation was performed using NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v 6.8 [21] and Prokka v 1.14.6 [22] which facilitated the identification of coding sequences (CDSs), rRNAs, tRNAs, and other genomic features.

The complete genome of *C. acnes* CN6 has a total length of 2,550,458 bp with G+C content of 60.04% and coverage of 183x. It encodes a total of 2,492 genes, including 2,433 CDSs, 9 rRNAs, 46 tRNAs, 4 ncRNAs, and 134 pseudo genes (Data file 2).

Predicted virulence proteins were detected using BLASTX based on previously predicted virulence factors in *C. acnes* KPA171202 [23, 24], except for hyaluronate lyase (HYL). Since KPA171202 (phylotype IB) possesses the HylB variant, we identified HYL using the HylA variant from *C. acnes* HL043PA1 (phylotype IA1) [25, 26] (Data file 3). Additionally, a comparative genome analysis was conducted using Roary [27] with 200 *C. acnes* strains isolated from healthy facial skin, including two SLST D1 strains, available on NCBI GenBank database as of August 2024 (Data file 4). A total of 9 genes, excluding unknown genes, were identified as unique to D1 strains among the 4,952 genes in the pan-genome of 201 *C. acnes* strains (Data file 5). Furthermore, a unique variant of the *znuC* gene, which is associated with bacterial survival and virulence under zinc-limited conditions [28, 29], was found to be conserved among the D1 strains. This variant is 822 bp in length, compared to the 804 bp length observed in other SLST types (Data file 6).

Limitations

To fully capture the genetic diversity and potential functional variations within SLST D1 strains of *C. acnes*, further studies involving a larger and more diverse collection of SLST D1 strains, as well as strains from other

Table 1 Overview of data files/data sets

Label	Name of data file/data set	File types (file extension)	Data repository and identifier (DOI or accession number)
Data file 1	Sequence statistics of *C. acnes* CN6	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.26831356.v1) [30]
Data file 2	Genome features of *C. acnes* CN6	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.26892115.v1) [31]
Data file 3	Predicted virulence protein profile of *C. acnes* CN6	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.26892160.v4) [32]
Data file 4	List of *C. acnes* strains used in this study	MS Excel file (.xlsx)	Figshare (https://doi.org/10.6084/m9.figshare.26892166.v2) [33]
Data file 5	SLST D1 strain-specific genes in *C. acnes* CN6	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.26892178.v1) [34]
Data file 6	Multiple sequence alignment of *znuC* gene of different *C. acnes* SLST strain types	Portable Document Format file (.pdf)	Figshare (https://doi.org/10.6084/m9.figshare.26892202.v1) [35]
Data set 1	Sequencing reads of *C. acnes* CN6	Fastq file (.fastq)	NCBI Sequence Read Archive (http://identifiers.org/ncbi/insdc.sra:SRR30894777) [36]
Data set 2	Genome assembly of *C. acnes* CN6	Fasta file (.fna)	NCBI Genome assembly (http://identifiers.org/ncbi/insdc.gca:GCA_041410355.1) [37]

SLST types, are recommended to validate and broaden these findings.

Abbreviations

SLST	Single Locus Sequence Typing
HYL	Hyaluronate Lyase
CDS	Coding Sequences
ONT	Oxford Nanopore Technology
NCBI	National Center for Biotechnology Information
PGAP	Prokaryotic Genome Annotation Pipeline

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Author contributions
Conceptualization: JHS.; Methodology: IK.; Formal analysis: IK.; Investigation: IK.; Resources: YJ, EKL, and YSC.; Data curation: RHK and DL.; Writing-original draft: IK.; Writing-review & editing: DR and JHS.; Project administration: YJ, JHH, JYK, and JHJ.; Funding acquisition: JMK, JTB, YSC, and JHS.; Supervision: YSC and JHS.

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Data availability
The genome assembly described in this Data note can be freely and openly accessed on GenBank under accession number GCA_041410355. Associated Data files are available on Figshare (https://figshare.com/). Please see Table 1 and references [30-37] for details and links to the data.

Declarations

Ethics approval and consent to participate
The study and protocol were approved by the Institutional Review Board of Hangang Sacred Heart Hospital (HG 2023-020).

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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References

1. Ahle CM, Feidenhansl C, Brüggemann H. Cutibacterium acnes. Trends Microbiol. 2023;31(4):419–20.
2. Rozas M, Hart de Ruijter A, Fabrega MJ, Zorgani A, Guell M, Paetzold B, Brillet F. From dysbiosis to healthy skin: major contributions of *Cutibacterium acnes* to skin homeostasis. Microorganisms. 2021;9(3):628.
3. Almoughrabie S, Cau L, Cavagnero K, O'Neill AM, Li F, Roso-Mares A, Mainzer C, Closs B, Kolar MJ, Williams KJ, Bensinger SJ. Commensal *Cutibacterium acnes* induce epidermal lipid synthesis important for skin barrier function. Sci Adv. 2023;9(33):eadg6262.
4. Lomholt HB, Kilian M. Population genetic analysis of *Propionibacterium acnes* identifies a subpopulation and epidemic clones associated with acne. PLoS ONE. 2010;5(8):e12277.
5. Horneff JG, Hsu JE, Huffman GR. *Propionibacterium acnes* infections in shoulder surgery. Orthop Clin North Am. 2014;45(4):515–21.
6. Kadler BK, Mehta SS, Funk L. *Propionibacterium acnes* infection after shoulder surgery. Int J Shoulder Surg. 2015;9(4):139–44.
7. Leheste JR, Ruvolo KE, Chrostowski JE, Rivera K, Husko C, Miceli A, Selig MK, Brüggemann H, Torres G. *P. acnes*-driven disease pathology: current knowledge and future directions. Front Cell Infect Microbiol. 2017;7:81.
8. Mayslich C, Grange PA, Dupin N. *Cutibacterium acnes* as an opportunistic pathogen: an update of its virulence-associated factors. Microorganisms. 2021;9(2):303.
9. Liew-Littorin C, Brüggemann H, Davidsson S, Nilsdotter-Augustinsson Å, Hellmark B, Söderquist B. Clonal diversity of *Cutibacterium acnes* (formerly *Propionibacterium acnes*) in prosthetic joint infections. Anaerobe. 2019;59:54–60.
10. Salar-Vidal L, Achermann Y, Aguilera-Correa JJ, Poehlein A, Esteban J, Brüggemann H, ESCMID Study Group for Implant-Associated Infections (ESGIAI). Genomic analysis of *Cutibacterium acnes* strains isolated from prosthetic joint infections. Microorganisms. 2021;9(7):1500.
11. Scholz CF, Jensen A, Lomholt HB, Brüggemann H, Kilian M. A novel high-resolution single locus sequence typing scheme for mixed populations of *Propionibacterium acnes in vivo*. PLoS ONE. 2014;9(8):e104199.
12. Dagnelie MA, Khammari A, Dréno B, Corvec S. *Cutibacterium acnes* molecular typing: time to standardize the method. Clin Microbiol Infect. 2018;24(11):1149–55.
13. Dagnelie MA, Corvec S, Saint-Jean M, Bourdès V, Nguyen JM, Khammari A, Dréno B. Decrease in diversity of *Propionibacterium acnes* phylotypes

in patients with severe acne on the back. Acta dermato-venereologica. 2018;98(2):262–7.

14. Mcdowell A, Brüggemann H, Layton AM. Treatment of acne patients with isotretinoin increases β-diversity of a putative health-associated strain of *Cutibacterium acnes* within the follicular microbiome of responders. Exp Dermatol. 2024;33(1):e14967.
15. Agak GW, Thiboutot DM, Zaenglein AL, Nelson AM. SLST D1 strains may contribute to skin health. Exp Dermatol. 2024;33(1):e14968.
16. Nolan ZT, Banerjee K, Cong Z, Gettle SL, Longenecker AL, Kawasawa YI, Zaenglein AL, Thiboutot DM, Agak GW, Zhan X, Nelson AM. Treatment response to isotretinoin correlates with specific shifts in *Cutibacterium acnes* strain composition within the follicular microbiome. Exp Dermatol. 2023;32(7):955–64.
17. National Center for Biotechnology Information. Genome assembly http://identifiers.org/insdc.gca:GCA_029851525.1 (2023).
18. Wick RR, Judd LM, Holt KE. Performance of neural network basecalling tools for Oxford Nanopore sequencing. Genome Biol. 2019;20:1–0.
19. De Coster W, D'hert S, Schultz DT, Cruts M, Van Broeckhoven C. NanoPack: visualizing and processing long-read sequencing data. Bioinformatics. 2018;34(15):2666–9.
20. Kolmogorov M, Yuan J, Lin Y, Pevzner PA. Assembly of long, error-prone reads using repeat graphs. Nat Biotechno. 2019;37(5):540–6.
21. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, et al. NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res. 2016;44(14):6614–24.
22. Seemann T. Prokka: rapid prokaryotic genome annotation. Bioinformatics. 2014;30(14):2068–9.
23. Cobian N, Garlet A, Hidalgo-Cantabrana C, Barrangou R. Comparative genomic analyses and CRISPR-Cas characterization of *Cutibacterium acnes* provide insights into genetic diversity and typing applications. Front Microbiol. 2021;12:758749.
24. McLaughlin J, Watterson S, Layton AM, Bjourson AJ, Barnard E, McDowell A. *Propionibacterium acnes* and acne vulgaris: new insights from the integration of population genetic, multi-omic, biochemical and host-microbe studies. Microorganisms. 2019;7(5).
25. Nazipi S, Stødkilde K, Scavenius C, Brüggemann H. The skin bacterium *Propionibacterium acnes* employs two variants of hyaluronate lyase with distinct properties. Microorganisms. 2017;5(3):57.
26. Hajam IA, Katiki M, McNally R, Lázaro-Díez M, Kolar S, Chatterjee A, Gonzalez C, Paulchakrabarti M, Choudhury B, Caldera JR, Desmond T. Functional divergence of a bacterial enzyme promotes healthy or acneic skin. Nat Commun. 2023;14(1):8061.
27. Page AJ, Cummins CA, Hunt M, Wong VK, Reuter S, Holden MT, Fookes M, Falush D, Keane JA, Parkhill J. Roary: rapid large-scale prokaryote pan genome analysis. Bioinformatics. 2015;31(22):3691–3.
28. Ammendola S, Pasquali P, Pistoia C, Petrucci P, Petrarca P, Rotilio G, et al. High-affinity Zn2 + uptake system ZnuABC is required for bacterial zinc homeostasis in intracellular environments and contributes to the virulence of *Salmonella enterica*. Infect Immun. 2007;75(12):5867–76.
29. Huang LX, Zuo YF, Qin YX, Zhao LM, Lin M, Yan QP. The zinc nutritional immunity of *Epinephelus coioides* contributes to the importance of *znuC* during *Pseudomonas plecoglossicida* infection. Front Immunol. 2021;12:678699.
30. Kim I. Sequence statistics of *C. acnes* CN6. figshare https://doi.org/10.6084/m9.Figshare.26831356.v1 (2024).
31. Kim I. Genome features of *C. acnes* CN6. figshare https://doi.org/10.6084/m9.figshare.26892115.v1 (2024).
32. Kim I. Predicted virulence protein profile of *C. ances* CN6. figshare https://doi.org/10.6084/m9.figshare.26892160.v4 (2024).
33. Kim I. List of *C. acnes* strains used in this study. figshare https://doi.org/10.6084/m9.figshare.26892166.v2 (2024).
34. Kim I. SLST D1 strain-specific genes in *C. acnes* CN6. figshare https://doi.org/10.6084/m9.figshare.26892178.v1 (2024).
35. Kim I. Multiple sequence alignment of *znuC* gene of different *C. acnes* SLST classes. figshare https://doi.org/10.6084/m9.figshare.26892202.v1 (2024).
36. National Center for Biotechnology Information. Seq Read Archive. 2024. http://identifiers.org/ncbi/insdc.sra:SRR30894777 (2024).
37. National Center for Biotechnology Information. Genome assembly http://identifiers.org/ncbi/insdc.gca:GCA_041410355.1 (2024).

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