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Complete Genome Sequences of *Streptococcus mitis* Strains Isolated from the Oral Cavity and Urogenital Tract of a Woman and Her Male Sexual Partner

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ABSTRACT *Streptococcus mitis* is a member of the mitis group of the genus *Streptococcus*, which includes commensal species of the oral cavity and upper respiratory tract. Here, we report 39 complete genome sequences of *S. mitis* strains isolated from the oral cavity and urogenital tract of a woman and her male sexual partner.

Streptococcus mitis is an abundant member of the commensal microbiota of the upper respiratory tract and oral cavity (1, 2). Although it is considered to be a commensal species, *S. mitis* can cause a variety of invasive diseases in human (3). In order to increase our knowledge of this commensal bacterium, we isolated multiple strains of *S. mitis* from a woman and her male sexual partner. These strains were isolated from different anatomical sites and on different days. Here, we present the genome sequences for a subset of this collection.

Samples were collected from oral swabs, vaginal swabs, periurethral swabs, penile swabs, and voided urine samples from one female and her male sexual partner as part of an institutional review board (IRB)-approved study (LU 209830). Swabs were collected using the BD liquid Amies elution swab (ESwab) collection system. Urine samples were collected as clean-catch midstream voided urine. (Note that the participant was given instructions for obtaining the voided urine samples, and the periurethral swab and urine samples differed significantly [4].) Strains were isolated using a modified version of the expanded quantitative urine culture (EQUC) protocol (5) and stored at -80°C . From these samples, 39 *S. mitis* strains, identified by matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry, were selected for whole-genome sequencing. Each *S. mitis* isolate was grown on Columbia colistin-naladixic acid agar with 5% sheep blood plates incubated under 5% CO_2 conditions at 37°C for 48 h. Pure cultures of *S. mitis* were transferred to brain heart infusion (BHI) broth with 10% fetal bovine serum (FBS) and incubated under 5% CO_2 conditions at 37°C for 48 h and pelleted. DNA was extracted from pellets using a phenol-chloroform method and quantified using a Qubit 2.0 fluorometer and an Agilent Bioanalyzer. DNA libraries were created using the Illumina Nextera kit and sequenced using the MiSeq reagent kit v2, producing, on average, 336,117 pairs of 250-bp reads. Quality control and demultiplexing of sequence data were done with onboard MiSeq Control software and MiSeq Reporter v3.1. Raw reads were trimmed using Sickle v1.33 (<https://github.com/najoshi/sickle>) and assembled using SPAdes v3.13.0 (6) with the “only-assembler” option for k values of 55, 77, 99, and 127. Genome coverage was calculated using BMap v38.47 (<https://sourceforge.net/projects/bbmap/>). The NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.8 (7) was used to annotate the genome sequences. Unless previously noted, default parameters were used for each software tool.

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TABLE 1 Genome assembly and annotation statistics

| Strain | Partner sex | Isolation source | Coverage (×) | No. of contigs | N_{50} (bp) | Genome length (bp) | No. of CDS | No. of rRNAs | No. of tRNAs | GenBank WGS accession no. ^a | SRA accession no. |
|--------|-------------|---------------------|--------------|----------------|---------------|--------------------|------------|--------------|--------------|--|-------------------|
| SM05 | Female | Voided urine sample | 59.22 | 23 | 194,401 | 2,001,354 | 1,950 | 3 | 44 | WIKE000000000 | SRR10341581 |
| SM07 | Female | Periurethral swab | 64.74 | 27 | 199,509 | 2,002,948 | 1,956 | 3 | 44 | WIKD000000000 | SRR10341580 |
| SM09 | Female | Oral swab | 68.4 | 15 | 187,601 | 1,973,655 | 1,962 | 3 | 43 | WIKC000000000 | SRR10341605 |
| SM12 | Male | Oral swab | 33.68 | 46 | 105,495 | 2,095,125 | 2,043 | 3 | 42 | WIKB000000000 | SRR10341594 |
| SM20 | Female | Vaginal swab | 50.33 | 55 | 82,209 | 2,008,422 | 1,969 | 3 | 43 | WIKA000000000 | SRR10341584 |
| SM26 | Female | Oral swab | 58.51 | 27 | 251,708 | 2,060,956 | 1,982 | 3 | 41 | WIJZ000000000 | SRR10341583 |
| SM27 | Female | Voided urine sample | 53.29 | 27 | 174,586 | 2,001,505 | 1,957 | 3 | 44 | WIJY000000000 | SRR10341582 |
| SM30 | Female | Periurethral swab | 51.27 | 28 | 199,508 | 2,007,955 | 1,965 | 3 | 44 | WIJX000000000 | SRR10341577 |
| SM33 | Male | Oral swab | 15.19 | 55 | 74,863 | 2,093,429 | 2,047 | 3 | 39 | WIJW000000000 | SRR10341576 |
| SM39 | Female | Oral swab | 46.12 | 127 | 27,218 | 2,015,490 | 2,042 | 3 | 47 | WIJV000000000 | SRR10341575 |
| SM45 | Female | Voided urine sample | 44.13 | 25 | 148,327 | 2,002,001 | 1,953 | 3 | 44 | WIJU000000000 | SRR10341579 |
| SM48 | Male | Oral swab | 19.61 | 45 | 105,607 | 2,094,194 | 2,038 | 3 | 42 | WIJT000000000 | SRR10341578 |
| SM04 | Female | Voided urine sample | 51.52 | 21 | 225,775 | 2,000,773 | 1,956 | 3 | 44 | WIJS000000000 | SRR10341613 |
| SM06 | Female | Voided urine sample | 59.03 | 27 | 188,320 | 2,002,707 | 1,957 | 3 | 44 | WIJR000000000 | SRR10341612 |
| SM08 | Female | Periurethral swab | 51.75 | 18 | 205,523 | 1,996,012 | 1,960 | 3 | 44 | WIJQ000000000 | SRR10341611 |
| SM10 | Female | Oral swab | 51.35 | 49 | 132,942 | 2,168,718 | 2,121 | 4 | 39 | WIJP000000000 | SRR10341610 |
| SM11 | Female | Oral swab | 56.8 | 113 | 30,148 | 2,014,391 | 2,031 | 4 | 47 | WIJO000000000 | SRR10341609 |
| SM13 | Male | Oral swab | 48.15 | 120 | 97,578 | 2,152,221 | 2,150 | 3 | 43 | WIJN000000000 | SRR10341608 |
| SM14 | Male | Oral swab | 47.22 | 58 | 64,862 | 2,094,407 | 2,055 | 3 | 42 | WIJM000000000 | SRR10341607 |
| SM15 | Male | Penile swab | 44.11 | 21 | 155,584 | 2,016,502 | 2,018 | 3 | 52 | WIJL000000000 | SRR10341606 |
| SM16 | Male | Penile swab | 53.16 | 67 | 72,040 | 2,017,910 | 1,886 | 2 | 40 | WIJK000000000 | SRR10341604 |
| SM28 | Female | Voided urine sample | 59.9 | 30 | 186,870 | 2,007,541 | 1,963 | 3 | 44 | WIJJ000000000 | SRR10341603 |
| SM29 | Female | Voided urine sample | 47.58 | 24 | 199,508 | 2,005,875 | 1,961 | 3 | 44 | WIJI000000000 | SRR10341602 |
| SM34 | Male | Oral swab | 18.72 | 46 | 105,662 | 2,091,923 | 2,047 | 3 | 43 | WIJH000000000 | SRR10341601 |
| SM40 | Female | Oral swab | 53.86 | 124 | 27,218 | 2,015,048 | 2,039 | 3 | 47 | WIJG000000000 | SRR10341600 |
| SM41 | Female | Oral swab | 46.7 | 27 | 177,356 | 2,032,459 | 2,058 | 3 | 44 | WIJF000000000 | SRR10341599 |
| SM46 | Female | Voided urine sample | 52.34 | 28 | 187,795 | 2,027,642 | 1,964 | 3 | 44 | WIJE000000000 | SRR10341598 |
| SM47 | Female | Voided urine sample | 46.19 | 31 | 147,586 | 2,006,587 | 1,965 | 3 | 44 | WIJD000000000 | SRR10341597 |
| SM49 | Male | Oral swab | 64.52 | 30 | 141,856 | 1,996,076 | 1,958 | 2 | 44 | WIJC000000000 | SRR10341596 |
| SM50 | Male | Oral swab | 49.28 | 18 | 208,384 | 1,894,166 | 1,859 | 4 | 49 | WIJB000000000 | SRR10341595 |
| SM17 | Female | Voided urine sample | 33.99 | 450 | 7,154 | 1,984,878 | 1,944 | 2 | 37 | WIJA000000000 | SRR10341593 |
| SM18 | Female | Voided urine sample | 137.48 | 30 | 147,586 | 2,000,922 | 1,954 | 3 | 44 | WIIZ000000000 | SRR10341592 |
| SM19 | Female | Voided urine sample | 111.07 | 27 | 186,870 | 2,006,191 | 1,965 | 3 | 44 | WIY000000000 | SRR10341591 |
| SM35 | Female | Voided urine sample | 100.62 | 25 | 187,601 | 2,007,565 | 1,963 | 3 | 44 | WIIX000000000 | SRR10341590 |
| SM36 | Female | Voided urine sample | 106 | 25 | 186,870 | 2,005,820 | 1,964 | 3 | 44 | WIIW000000000 | SRR10341589 |
| SM37 | Female | Voided urine sample | 76.02 | 29 | 188,320 | 2,006,041 | 1,963 | 3 | 44 | WIIV000000000 | SRR10341588 |
| SM42 | Female | Voided urine sample | 115.16 | 33 | 131,530 | 2,007,726 | 1,962 | 3 | 44 | WIIU000000000 | SRR10341587 |
| SM43 | Female | Voided urine sample | 94.02 | 26 | 147,586 | 2,000,668 | 1,954 | 3 | 44 | WIIT000000000 | SRR10341586 |
| SM44 | Female | Voided urine sample | 115.16 | 23 | 186,871 | 2,000,125 | 1,953 | 3 | 44 | WIIS000000000 | SRR10341585 |

^aWGS, whole-genome shotgun.

Table 1 lists all of the 39 *S. mitis* strains and their source, as well as their genome assembly statistics. The average GC content is 41%, similar to that reported in GenBank for other strains of the species. Annotations identified an average of 1,985 coding sequences (CDS) (Table 1). The strains varied in their numbers of rRNA operons and tRNAs. The addition here of 39 genome sequences greatly increases our knowledge of the genetic diversity of this bacterial species within the oral and lower urinary tract microbiota.

Data availability. This whole-genome shotgun (WGS) project has been deposited in GenBank, and the accession numbers for each genome assembly are listed in Table 1. The versions described in this paper are the first versions. Raw sequence data are publicly available in SRA for the 39 *S. mitis* strains; the accession numbers are listed in Table 1. The WGS and SRA records are associated with BioProject number [PRJNA316969](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA316969).

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REFERENCES

1. Aas JA, Paster BJ, Stokes LN, Olsen I, Dewhirst FE. 2005. Defining the normal bacterial flora of the oral cavity. *J Clin Microbiol* 43:5721–5732. <https://doi.org/10.1128/JCM.43.11.5721-5732.2005>.
2. Frandsen EV, Pedrazzoli V, Kilian M. 1991. Ecology of viridans streptococci in the oral cavity and pharynx. *Oral Microbiol Immunol* 6:129–133. <https://doi.org/10.1111/j.1399-302x.1991.tb00466.x>.
3. Mitchell J. 2011. *Streptococcus mitis*: walking the line between commensalism and pathogenesis. *Mol Oral Microbiol* 26:89–98. <https://doi.org/10.1111/j.2041-1014.2010.00601.x>.
4. Wolff BJ, Price TK, Joyce CJ, Wolfe AJ, Mueller ER. 2019. Oral probiotics and the female urinary microbiome: a double-blinded randomized placebo-controlled trial. *Int Urol Nephrol* 51:2149–2159. <https://doi.org/10.1007/s11255-019-02282-3>.
5. Price TK, Dune T, Hilt EE, Thomas-White KJ, Kliethermes S, Brincat C, Brubaker L, Wolfe AJ, Mueller ER, Schreckenberger PC. 2016. The clinical urine culture: enhanced techniques improve detection of clinically relevant microorganisms. *J Clin Microbiol* 54:1216–1222. <https://doi.org/10.1128/JCM.00044-16>.
6. 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. <https://doi.org/10.1089/cmb.2012.0021>.
7. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44: 6614–6624. <https://doi.org/10.1093/nar/gkw569>.