**Draft Genome Sequence of *Streptococcus anginosus* BVI, a New Vaginal Pathogen Candidate**

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**Streptococcus anginosus** is a pathogen implicated in urogenital and gastrointestinal tract infections. Here, we report the draft genome sequence of *S. anginosus* BVI, isolated from a bacterial vaginosis patient attending a prenatal care unit in Cali, Colombia. The genome sequence of BVI consists of 2,014,025 bp, encoding 2,088 predicted proteins.

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REFERENCES

1. Asam D, Spellerberg B. 2014. Molecular pathogenicity of Streptococcus anginosus. Mol Oral Microbiol 29:145–155. http://dx.doi.org/10.1111/omi.12056.

2. Ruoff KL. 1988. Streptococcus anginosus (Streptococcus milleri): the unrecognized pathogen. Clin Microbiol Rev 1:102–108. http://dx.doi.org/10.1128/CMR.1.1.102.

3. Jensen A, Hoshino T, Kilian M. 2013. Taxonomy of the Anginosus group of the genus Streptococcus and description of Streptococcus anginosus subsp. whileyi subsp. nov. and Streptococcus constellatus subsp. viborgensis subsp. nov. Int J Syst Evol Microbiol 63:2506–2519. http://dx.doi.org/10.1099/ijs.0.043232-0.

4. Grinwis ME, Sibley CD, Parkins MD, Eshaghurshan CS, Rabin HR, Surette MG. 2010. Macrolide and clindamycin resistance in Streptococcus milleri group isolates from the airways of cystic fibrosis patients. Antimicrob Agents Chemother 54:2823–2829. http://dx.doi.org/10.1128/AAC.01845-09.

5. Whiley RA, Beighton D, Winstanley TG, Fraser HY, Hardie JM. 1992. Streptococcus intermedius, Streptococcus constellatus, and Streptococcus anginosus (the Streptococcus milleri group): association with different body sites and clinical infections. J Clin Microbiol 30:243–244.

6. Siegman-Igra Y, Azmon Y, Schwartz D. 2012. Milleri group streptococcus—a stepchild in the viridans family. Eur J Clin Microbiol Infect Dis 31:2453–2459. http://dx.doi.org/10.1007/s10096-012-1589-7.

7. Lambert JA, John S, Sobel JD, Akins RA. 2013. Longitudinal analysis of vaginal microbiome dynamics in women with recurrent bacterial vaginosis: recognition of the conversion process. PLoS One 8:e82599. http://dx.doi.org/10.1371/journal.pone.0082599.

8. Romero R, Hassan SS, Gajer P, Tarca AL, Fadrosh DW, Nikita L, Galuppi M, Lamont RF, Chaemsaithong P, Miranda J, Chaiworapongsa T, Ravel J. 2014. The composition and stability of the vaginal microbiota of normal pregnant women is different from that of non-pregnant women. Microbiome 2:4. http://dx.doi.org/10.1186/2049-2618-2-4.

9. MacIntyre DA, Chandiramani M, Lee YS, Kindinger L, Smith A, Angelopoulou N, Lehne B, Arulkumaran S, Brown R, Teoh TG, Holmes E, Nicolohson JK, Marchesi JR, Bennett PR. 2015. The vaginal microbiome during pregnancy and the postpartum period in a European population. Sci Rep 5:8988. http://dx.doi.org/10.1038/srep08988.

10. Pearce MM, Hilt EE, Rosenfeld AB, Zillioux MJ, Thomas-White K, Fok C, Kliethermes S, Schreckenberger PC, Brubaker L, Gai X, Wolfe AJ. 2014. The female urinary microbiome: a comparison of women with and without urgency urinary incontinence. mBio 5:e01283-14. http://dx.doi.org/10.1128/mBio.01283-14.

11. Nath K, Galdi J. 1995. Rapid salt-based mini-scale Gardnerella vaginalis DNA isolation procedure. Biotechniques 19:738–740.

12. Kim M, Oh HS, Park SC, Chun J. 2014. Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. Int J Syst Evol Microbiol 64:346–351. http://dx.doi.org/10.1099/ijs.0.059774-0.

13. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. http://dx.doi.org/10.1093/bioinformatics/btu153.

14. Meyer F, Goesmann A, McHardy AC, Bartels D, Bekel T, Clausen J, Kalinowski J, Linke B, Rupp O, Giegerich R, Pühler A. 2003. GenDB—an open source genome annotation system for prokaryote genomes. Nucleic Acids Res 31:2187–2195. http://dx.doi.org/10.1093/nar/gkg212.

15. Chen L, Zheng D, Liu B, Yang J, Jin Q. 2016. VDDB 2016: hierarchical and refined dataset for big data analysis—10 years on. Nucleic Acids Res 44:D694–D697. http://dx.doi.org/10.1093/nar/gkv1239.