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Campylobacter fetus subsp. venerealis is an important venereal pathogen. We sequenced the genomes of Campylobacter fetus subsp. venerealis bv. venerealis strain B6 and bv. intermedius strain 642-21. The genetic variability of these Australian strains will facilitate the study of mechanisms of geographical adaptation of these pathogens that impact livestock.

**C**ampylobacter fetus is an important veterinary pathogen worldwide. This species comprises two closely related subspecies, *C. fetus* subsp. *fetus* and *C. fetus* subsp. *venerealis* (1). The former is a generalist subspecies that colonizes the intestinal and genital tracts of multiple host including sheep, cattle, birds, and humans (2). The latter subspecies, *C. fetus* subsp. *venerealis*, is normally restricted to colonization of the genital tract in ruminants (3). *C. fetus* subsp. *venerealis* is the causative agent of bovine genital campylobacteriosis; asymptomatic in bulls, the disease is spread to female cattle and causes infertility and epidemic abortions (4). In a recent study, *C. fetus* subsp. *venerealis* was shown to contain unique lipopolysaccharide production and type IV secretion machinery as compared to *C. fetus* subsp. *fetus* (5). Targeted mutational inactivation demonstrated the role of lipopolysaccharide biosynthesis genes in the modulation of virulence and host range (5). The evolutionary interplay between microbial pathogens and their hosts is a continual process of adaptation, manifested by genomic variation of host adaptation factors, and by the gain and loss of genes via horizontal gene transfer. Thus, further understanding of local and regional adaptations of these pathogens is necessary to capture the genetic diversity of pathogens isolated from distinct geographic locations worldwide.

Here we report the sequencing of two *C. fetus* subsp. *venerealis* biovar genomes isolated in Australia, *C. fetus* subsp. *venerealis* bv. venerealis strain B6 and *C. fetus* subsp. *venerealis* bv. intermedius strain 642-21. Sequencing was performed on an Illumina/GAII platform and generated 23,021,027 and 22,819,299 paired-end reads with an insert size of 320 bp for both biovar strains. We also acknowledge Bioplates Australia and iVEC for providing access to their computational pipelines and computational resources used in this study.

**REFERENCES**

1. Hum S, Quinn K, Brunner J, On SLW. 1997. Evaluation of a PCR assay for identification and differentiation of Campylobacter fetus subspecies. Aust. Vet. J. 75:827–831. http://dx.doi.org/10.1111/j.1751-0813.1997.tb15665.x.
2. van Bergen MAP, Dingle KE, Maiden MCJ, Newell DG, van der Graaf-Bastyns K, Chapelle S, Vandamme P, Goossens H, Dewachter R. 2005. Clonal nature of *Campylobacter fetus* as defined by multilocus sequence typing. J. Clin. Microbiol. 43:5888–5898. http://dx.doi.org/10.1128/JCM.43.12.5888-5898.2005.
3. Moolhuijzen PM, Lew-Tabor AE, Blixt A, Agüero FG, Comerci DJ, Ugaldé RA, Sanchez DO, Appels R, Bellgard M. 2009. Genomic analysis of *Campylobacter fetus* subspecies: identification of candidate virulence determinants and diagnostic assay targets. BMC Microbiol. 9:86. http://dx.doi.org/10.1186/1471-2180-9-86.
4. Bystyns K, Chapelle S, Vandamme P, Goossens H, Dewachter R. 1995.
Species-specific detection of campylobacters important in veterinary medicine by PCR amplification of 23S rDNA areas. Syst. Appl. Microbiol. 17: 563–568. http://dx.doi.org/10.1016/S0723-2020(11)80077-9.

5. Kienesberger S, Sprenger H, Wolfgruber S, Halwachs B, Thallinger GG, Perez-Perez GI, Blaser MJ, Zechner EL, Gorkiewicz G. 2014. Comparative genome analysis of Campylobacter fetus subspecies revealed horizontally acquired genetic elements important for virulence and niche specificity. PLoS One 9:e85491. http://dx.doi.org/10.1371/journal.pone.0085491.

6. Robertson G, Schein J, Chiu R, Corbett R, Field M, Jackman SD, Mungall K, Lee S, Okada HM, Qian JQ, Griffith M, Raymond A, Thiessen N, Cezard T, Butterfield YS, Newsome R, Chan SK, She R, Varhol R, Kamoh B, Prabhu AI, Tam A, Zhao YJ, Moore RA, Hirst M, Marra MA, Jones SJ, Hoodless PA, Birol I. 2010. De novo assembly and analysis of RNA-seq data. Nat. Methods 7:U909–U962. http://dx.doi.org/10.1038/nmeth.1517.

7. Hunter AA, Maagregor AB, Szabo TO, Wellington CA, Bellgard MI. 2012. Yabix: an online research environment for grid, high performance and cloud computing. Source Code Biol. Med. 7:1. http://dx.doi.org/10.1186/1751-0473-7-1.

8. Gorkiewicz G, Kienesberger S, Schober C, Scheicher SR, Gully C, Zechner R, Zechner EL. 2010. A genomic island defines subspecies-specific virulence features of the host-adapted pathogen Campylobacter fetus subsp. venerealis. J. Bacteriol. 192:502–517. http://dx.doi.org/10.1128/JB.00803-09.