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Genome Sequence of *Corynebacterium pseudotuberculosis* MB20 bv. equi Isolated from a Pectoral Abscess of an Oldenburg Horse in California

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The genome of *Corynebacterium pseudotuberculosis* MB20 bv. equi was sequenced using the Ion Personal Genome Machine (PGM) platform, and showed a size of 2,363,089 bp, with 2,365 coding sequences and a GC content of 52.1%. These results will serve as a basis for further studies on the pathogenicity of *C. pseudotuberculosis* bv. equi.

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Recent advances have been made in the genomic analysis of *Corynebacterium pseudotuberculosis*, a species of veterinary and biotechnological interest. Molecular diagnosis of several diseases caused by this species was achieved using multiplex PCR (PCR) (1), and a description of its pangenome was published using 15 strains of *C. pseudotuberculosis* bv. ovis and equi (2). *C. pseudotuberculosis* bv. equi comprises strains that infect horses and cattle and cause infection of cutaneous lymphatic vessels, termed ulcerative lymphangitis, which is characterized by the development of multiple waxy ulcerative lesions. The incidence of this disease in horses has been reported in the literature since the 1910s (3) and remains prevalent in animals worldwide (4, 5); moreover, this infection is likely underreported and has been characterized as a neglected zoonosis (6).

The host-pathogen interaction in this disease has been studied using omics approaches (7). For instance, the differential gene expression of a *C. pseudotuberculosis* bv. ovis strain was analyzed using RNA-seq, and genes involved in the molecular responses of the bacterium to different stresses during infection were identified (8). A study of reverse vaccinology reported by Soares et al. (9) identified 49 possible antigens from the genome of the *C. pseudotuberculosis* bv. equi strain 258 that may serve as targets for the development of effective vaccines. In addition, a new *C. pseudotuberculosis* bv. equi strain was isolated and sequenced, which will aid in future broader studies. These new data combined with those already reported will serve as a basis for the development of studies aimed at a better understanding of the pathogenic potential of *C. pseudotuberculosis* bv. equi.

The MB20 strain was isolated from a pectoral abscess of a 4-year-old horse of the breed Oldenburg, raised in the city of Vacaville, CA, USA. Genomic DNA was sequenced from a fragment library on a 318 chip of the Ion Torrent Personal Genome Machine (PGM) platform (Life Technologies). A total of 2,331,864 reads were generated with an average length of 420 bp, which were used for genome assembly using the software Mira (10). The contigs generated with Mira were analyzed using the SeqMan Pro tool of the software Lasergene 11 Core Suite (DNASTAR) to remove redundant sequences. This approach resulted in 3 contigs, which were sorted with the Artemis Comparison tool (11) using the genome of *C. pseudotuberculosis* 316 as a reference. The scaffold produced at the end of the assembly was 2,363,089 bp in size and underwent automatic annotation using Rapid Annotation using Subsystem Technology (RAST) (12). As a result, 2,365 coding sequences (CDSs), 11 rRNA genes, 51 tRNA genes and a 52.1% GC content were identified. Of the 2,365 CDSs, 790 (33.4%) were classified as hypothetical proteins.

Nucleotide sequence accession numbers. The genomic sequence obtained in this study was deposited in the DDBJ/EMBL/GenBank under accession number JPUV00000000. The version described in this paper is version JPUV01000000.

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REFERENCES

1. **Pacheco LGC, Pena RR, Castro TLP, Dorella FA, Bahia RC, Carminati R, Frota MNL, Oliveira SC, Meyer R, Alves FSF, Miyoshi A, Azevedo V.** 2007. Multiplex PCR assay for the identification of *Corynebacterium pseudotuberculosis* from pure cultures and for rapid detection of this pathogen in clinical samples. J. Med. Microbiol. **56**:480–486. http://dx.doi.org/10.1099/jmm.0.46997-0.
2. **Soares SC, Silva A, Trost E, Blom J, Ramos R, Carneiro A, Ali A, Santos AR, Pinto AC, Diniz C, Barbosa EG, Dorella FA, Aburjaile F, Rocha FS, Nascimento KK, Guimarães LC, Almeida S, Hassan SS, Bakhtiar SM,**

Pereira UP, Abreu VA, Schneider MP, Miyoshi A, Tauch A, Azevedo V. 2013. The pan-genome of the animal pathogen *Corynebacterium pseudotuberculosis* reveals differences in genome plasticity between the biovar ovis and equi strains. PLoS One **8:**e53818. http://dx.doi.org/10.1371/journal.pone.0053818.

3. **Hall IC, Stone RV.** 1916. The diphtheroid bacillus of Preisz-Nocard from equine, bovine, and ovine abscesses: ulcerative lymphangitis and caseous lymphadenitis. J. Infect. Dis. **18:**195–208. http://dx.doi.org/10.1093/infdis/18.2.195.
4. **Hepworth-Warren KL, Sponseller BT, Wong DM, Kinyon JM.** 2014. Isolation of *Corynebacterium pseudotuberculosis* biovar equi from a horse in central Iowa. Case Rep. Vet. Med. **2014:**1–3. http://dx.doi.org/10.1155/2014/436287.
5. **Spier SJ, Leutenegger CM, Carroll SP, Loye JE, Pusterla JB, Carpenter TE, Mihalyi JE, Madigan JE.** 2004. Use of a real-time polymerase chain reaction-based fluorogenic 5′ nuclease assay to evaluate insect vectors of *Corynebacterium pseudotuberculosis* infections in horses. Am. J. Vet. Res. **65:**829–834. http://dx.doi.org/10.2460/ajvr.2004.65.829.
6 **Join-Lambert OF, Ouache M, Canioni D, Beretti JL, Blanche S, Berche P, Kayal S.** 2006. *Corynebacterium pseudotuberculosis* necrotizing lymphadenitis in a twelve-year-old patient. Pediatr. Infect. Dis. J. **25:**848–851.
7. **Dorella FA, Gala-Garcia A, Pinto AC, Sarrouh B, Antunes CA, Ribeiro D, Aburjaile FF, Fiaux KK, Guimarães LC, Seyffert N, El-Aouar R, Silva R, Hassan SS, Castro TLP, Marques WS, Ramos R, Carneiro A, Sá P, Miyoshi A, Azevedo V, Silva A.** 2013. Progression of "OMICS" methodologies for understanding the pathogenicity of *Corynebacterium pseudotuberculosis*: the Brazilian experience. Comput. Struct. Biotechnol. J. **6** e201303013. http://dx.doi.org/10.5936/csbj.201303013.
8. **Pinto AC, Sá PH, Ramos RT, Barbosa S, Barbosa HP, Ribeiro AC, Silva WM, Rocha FS, Santana MP, Castro TL, Miyoshi A, Schneider MP, Silva A, Azevedo V.** 2014. Differential transcriptional profile of *Corynebacterium pseudotuberculosis* in response to abiotic stresses. BMC Genomics **15:**14. http://dx.doi.org/10.1186/1471-2164-15-14.
9. **Soares SC, Trost E, Ramos RT, Carneiro AR, Santos AR, Pinto AC, Barbosa E, Aburjaile F, Ali A, Diniz CA, Hassan SS, Fiaux K, Guimarães LC, Bakhtiar SM, Pereira U, Almeida SS, Abreu VA, Rocha FS, Dorella FA, Miyoshi A, Silva A, Azevedo V, Tauch A.** 2013. Genome sequence of *Corynebacterium pseudotuberculosis* biovar equi strain 258 and prediction of antigenic targets to improve biotechnological vaccine production. J. Biotechnol. **167:**135–141. http://dx.doi.org/10.1016/j.jbiotec.2012.11.003.
10. **Chevreux B, Pfisterer, Drescher B, Driesel AJ, Müller WEG, Wetter T, Suhai S.** 2004. Using the miraEST assembler for reliable and automated mRNA transcript assembly and SNP detection in sequenced ESTs. Genome Res. **14:**1147–1159. http://dx.doi.org/10.1101/gr.1917404.
11. **Carver TJ, Rutherford KM, Berriman M, Rajandream MA, Barrell BG, Parkhill J.** 2005. ACT: the Artemis comparison Tool. Bioinformatics **21:**3422–3423. http://dx.doi.org/10.1093/bioinformatics/bti553.
12. **Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R.** 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res. **42:**D206–D214. http://dx.doi.org/10.1093/nar/gkt1226.