

Whole-Genome Sequencing of *Mycoplasma mycoides* subsp. *mycoides* Italian Strain 57/13, the Causative Agent of Contagious Bovine Pleuropneumonia

M. Orsini,^a I. Krasteva,^a M. Marcacci,^a M. Ancora,^a A. Ciammaruconi,^b B. Gentile,^b F. Lista,^b A. Pini,^a M. Scacchia,^a F. Sacchini,^a C. Cammà^a

Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise G. Caporale, Teramo, Italy^a; Army Medical and Veterinary Research Center, Rome, Italy^b

***Mycoplasma mycoides* subsp. *mycoides* is generally considered one of most pathogenic *Mycoplasma* species, and it is the etiologic agent of contagious bovine pleuropneumonia (CBPP). Here, we present the annotated genome sequence of *M. mycoides* subsp. *mycoides* Italian strain 57/13, isolated in 1992 during CBPP outbreaks in Italy.**

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Address correspondence to C. Cammà, c.camma@izs.it.

Mycoplasma mycoides subsp. *mycoides* is the etiological agent of contagious bovine pleuropneumonia (CBPP) (1), which is considered by the World Organisation for Animal Health (Office International des Epizooties [OIE]) to be one of most severe infectious animal diseases affecting sub-Saharan-African countries, causing major losses of animals with subsequent socio-economic repercussions, with a particular emphasis in international trades (2).

Here, we present the whole-genome sequence of the *M. mycoides* subsp. *mycoides* strain 57/13 that was isolated from the lung of a cow showing CBPP pathological lesions in 1992, during a CBPP outbreak in northern Italy. The strain was identified by PCR as *M. mycoides* subsp. *mycoides* (3). The biochemical and proteomic characterizations of the strain have been reported, but none of the Italian strains, which are considered less pathogenic than are the African strains, have been fully sequenced so far (4, 5).

The strain was grown as previously described (6). Genomic DNA was extracted from culture using the Maxwell 16 cell DNA purification kit (Promega) and sequenced by the PGM Ion Torrent platform, obtaining 427,523 single-end reads spanning from 20 to 400 nucleotides. The quality-filtered reads were assembled into contigs and annotated using a dedicated workflow available at the OriGene website (7), which uses SPAdes (8) and Prokka, respectively (9). Finishing and annotation were manually curated.

The *M. mycoides* subsp. *mycoides* strain 57/13 genome contains a 1,192,498-nucleotide chromosome with 2 rRNA operons, 30 tRNAs, and 1,077 protein-coding genes, of which 332 encode hypothetical proteins conserved among other *M. mycoides* subsp. *mycoides* isolates. Compared to the *M. mycoides* subsp. *mycoides* PG1 type strain (GenBank accession no. BX293980), the *M. mycoides* subsp. *mycoides* strain 57/13 showed an overall identity of 99% and one major insertion. Genome organization highlighted a high degree of overlapped genes. As with other European strains, this isolate lacks the *gtsC* and *lppB* genes (10).

Nucleotide sequence accession number. The whole-genome assembly has been deposited at GenBank under accession no. CP010267.

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The mention of trade names or commercial products in this article is only for the purpose of providing specific information and does not imply recommendation or endorsement by the OIE Reference Laboratory for Contagious Bovine Pleuropneumonia in Teramo, Italy.

REFERENCES

- Westberg J, Persson A, Holmberg A, Goesmann A, Lundeberg J, Johansson KE, Pettersson B, Uhlén M. 2004. The genome sequence of *Mycoplasma mycoides* subsp. *mycoides* SC type strain PG1^T, the causative agent of contagious bovine pleuropneumonia (CBPP). *Genome Res* 14: 221–227. <http://dx.doi.org/10.1101/gr.1673304>.
- World Organisation for Animal Health. 2014. Contagious bovine pleuropneumonia, p 1–16. *In* Manual of diagnostic tests and vaccines for terrestrial animals, 6th ed. Office International des Epizooties, Paris, France.
- Bashiruddin JB, Nicholas RA, Santini FG, Ready RA, Woodward MJ, Taylor TK. 1994. Use of the polymerase chain reaction to detect mycoplasma DNA in cattle with contagious bovine pleuropneumonia. *Vet Rec* 134:240–241. <http://dx.doi.org/10.1136/vr.134.10.240>.
- Houshaymi BM, Miles RJ, Nicholas RA. 1997. Oxidation of glycerol differentiates African from European isolates of *Mycoplasma mycoides* subspecies *mycoides* SC (small colony). *Vet Rec* 140:182–183. <http://dx.doi.org/10.1136/vr.140.7.182>.
- Rice P, Houshaymi BM, Abu-Groun EA, Nicholas RA, Miles RJ. 2001. Rapid screening of H(2)O(2) production by *Mycoplasma mycoides* and differentiation of European subsp. *mycoides* SC (small colony) isolates. *Vet Microbiol* 78:343–351. [http://dx.doi.org/10.1016/S0378-1135\(00\)00305-9](http://dx.doi.org/10.1016/S0378-1135(00)00305-9).
- Krasteva I, Liljander A, Fischer A, Smith DG, Inglis NF, Scacchia M, Pini A, Jores J, Sacchini F. 2014. Characterization of the *in vitro* core surface proteome of *Mycoplasma mycoides* subsp. *mycoides*, the causative agent of contagious bovine pleuropneumonia. *Vet Microbiol* 168: 116–123. <http://dx.doi.org/10.1016/j.vetmic.2013.10.025>.

7. Cuccuru G, Orsini M, Pinna A, Sbardellati A, Soranzo N, Travaglione A, Uva P, Zanetti G, Fotia G. 2014. Orione, a Web-based framework for NGS analysis in microbiology. *Bioinformatics* 30:1928–1929. <http://dx.doi.org/10.1093/bioinformatics/btu135>.
8. 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. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <http://dx.doi.org/10.1089/cmb.2012.0021>.
9. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <http://dx.doi.org/10.1093/bioinformatics/btu153>.
10. Vilei EM, Abdo EM, Nicolet J, Botelho A, Gonçalves R, Frey J. 2000. Genomic and antigenic differences between the European and African/Australian clusters of *Mycoplasma mycoides* subsp. *mycoides* SC. *Microbiology* 146:477–486.