

1 **Draft Genome Sequence of *Acholeplasma laidlawii* isolated from the conjunctiva of a heifer**  
2 **with Infectious Bovine Keratoconjunctivitis**

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9 **ABSTRACT**

10 *Acholeplasma laidlawii* can be isolated from cattle environments and different body sites of  
11 bovines. It is still under evaluation if *A. laidlawii* may act as a primary pathogen. Here, we  
12 present the whole-genome sequence of *A. laidlawii* isolated from the conjunctiva of a heifer with  
13 Infectious Bovine Keratoconjunctivitis.

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15 **ANNOUNCEMENT**

16 *Acholeplasmas* are cell wall-less bacteria belonging to the class Mollicutes, order  
17 *Acholeplasmatales*, and classified in the family of *Acholeplasmataceae*. *Acholeplasma spp.* are  
18 described as saprophytes found in soil, compost, and wastewater or commensals distributed in  
19 vertebrates, insects, and plants (6).

20 Within the *Acholeplasma* genus, *Acholeplasma laidlawii* is the best-studied species. *A. laidlawii*  
21 is often found in dairy and beef cattle environments. It has been isolated from different body  
22 sites of bovines, including mastitic milk, bulk tank milk, aborted fetus, semen, preputial samples,  
23 nasal secretions, pneumonia, and healthy lungs (7, 4). One trial performed by Pugh et al. in 1976  
24 (8) demonstrated the ability of *A. laidlawii* to establish clinical signs of infectious bovine  
25 keratoconjunctivitis in calves after experimental induction. Other publications exclude the role of  
26 *A. laidlawii* as the causative agent of keratoconjunctivitis. Still, the authors state that the  
27 simultaneous presence of *A. laidlawii* with other major pathogens may contribute to lesion  
28 severity (1).

29 Here, we announce the draft genome sequence of *A. laidlawii* strain QMP CG1-1743 isolated  
30 from the conjunctival swab of a 6-9 months' heifer affected with Infectious Bovine  
31 Keratoconjunctivitis and showing watery eyes and corneal opacities. The heifer under testing

32 was from an organic herd; it was not treated with any antibiotics but was administered plasma  
33 eye drops as treatment. The initial isolation of the strain PG-8A was carried out by standard  
34 procedures for mycoplasma culturing, which include streaking on modified Hayflick agar  
35 medium and incubation for up to 7 days at 37°C with CO<sub>2</sub> enrichment. Well defined positive  
36 colonies showing typical mycoplasma morphology were submitted to an initial speciation test  
37 that includes a PCR amplification of the 16S-23S internal transcribed spacer (ITS) followed by  
38 Sanger sequencing of the amplicons (2).

39 The isolate was then sub-cultured in modified Hayflick medium, incubated for 3 days at 37°C  
40 with CO<sub>2</sub>, and pelleted by centrifugation at 13,000 g for 10 minutes. DNA was directly extracted  
41 from the pellet using MagMAX core nucleic acid purification kit (Applied Biosystems, Foster  
42 City, CA). DNA concentration was measured with a Qubit 3.0 fluorometer (Life Technologies,  
43 MD). The isolate was sequenced on an Illumina MiSeq using 2 x 250 bp reads, and read quality  
44 was assessed using FastQC (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) (5). A  
45 total of 406,301 paired reads were generated with an average Phred score of 37.35 for forward  
46 reads and 37.12 for reverse reads. Raw reads were assembled using SKESA v. 2.3.0 (9),  
47 assembly quality was checked using QUAST v. 5.0.2 (3), and reads were mapped back to the  
48 assembly to identify coverage depth with BMap v. 38.58  
49 (<http://sourceforge.net/projects/bbmap/>). Total assembly length was 1,329,497 bp with 55  
50 contigs, an N50 of 75,018, and 31.74% GC content. The average read depth was 108×. Average  
51 nucleotide identity was computed against all *Acholeplasma* genomes available from GenBank  
52 (accessed July 7, 2020) using fastANI v. 1.3. The highest ANI was 93.8% with *A. laidlawii* strain  
53 MDBK/IPV (GCA\_001730135.1). ANIs in comparison to three assemblies of the *A. laidlawii*  
54 type strain (GCA\_000018785.1, GCA\_900476025.1, and GCA\_003385765.1) were 93.2–93.3%,  
55 indicating that this isolate is divergent from previously sequenced *A. laidlawii* isolates and might  
56 represent a distinct lineage.

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58 **Data availability.** Sequencing data has been submitted to NCBI under BioSample  
59 SAMN16288725.

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