Draft Genome Sequences of Mycoplasma alkalescens, Mycoplasma arginini, and Mycoplasma bovigenitalium, Three Species with Equivocal Pathogenic Status for Cattle

Lucia Manso-Silván, Florence Tardy, Eric Baranowski, Aurélien Barré, Alain Blanchard, Marc Breton, Carole Couture, Christine Citti, Emilie Dordet-Frisoni, Virginie Dupuy, Patrice Gaurivaud, Daniel Jacob, Claire Lemaître, Macha Nikolski, Laurent-Xavier Nouvel, François Poumarat, Patricia Thébaut, Sébastien Theil, François Thiaucourt, Pascal Sirand-Pugnet

CIRAD, URMC 3926, Montpellier, France; INRA, URMR 309 CMAEE, Montpellier, France; Anses, Laboratoire de Lyon, UMR Mycoplasmoses des Ruminants, Lyon, France; Université de Lyon, VetAgro Sup, UMR Mycoplasmoses des Ruminants, Marcy l’Etoile, France; INRA, UMR 1225, IHAP, Toulouse, France; Université de Toulouse, INP, ENVT, UMR 1225, IHAP, Toulouse, France; Université de Bordeaux, Centre de Bioinformatique et Génomique Fonctionnelle, Bordeaux, CBIB, Bordeaux, France; INRA, UMR 1332 de Biologie du Fruit et Pathologie, Villenave d’Ornon, France; Université de Bordeaux, UMR 1332 de Biologie du Fruit et Pathologie, Villenave d’Ornon, France; Université Bordeaux, LaBRI, UMR 5800, Talence, France

* Present address: Daniel Jacob and Sébastien Theil, INRA, UMR 1332 de Biologie du Fruit et Pathologie, Villenave d’Ornon, France, and Université de Bordeaux, UMR 1332 de Biologie du Fruit et Pathologie, Villenave d’Ornon, France; Claire Lemaître, INRIA Rennes – Bretagne Atlantique/IRISA, EPI GenScale, Rennes, France.

We report here the draft genome sequences of Mycoplasma alkalescens, Mycoplasma arginini, and Mycoplasma bovigenitalium. These three species are regularly isolated from bovine clinical specimens, although their role in disease is unclear.

Received 26 April 2013 Accepted 1 May 2013 Published 13 June 2013


Copyright © 2013 Manso-Silván et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Lucia Manso-Silván, lucia.manso-silvan@cirad.fr.

Mycoplasma alkalescens, Mycoplasma arginini, and Mycoplasma bovigenitalium are bacteria of the class Mollicutes clustered within the hominis phylogenetic group. They have been associated with disease in cattle, but their contribution to pathogenesis remains unclear. M. alkalescens, described in 1973 (1), has been reported from mastitis in cattle and from arthritis, otitis, and pneumonia in calves (2–5). In pneumatic calves, M. alkalescens is often associated with Mycoplasma bovis, but recent recurrent isolation in the United Kingdom in the absence of other pathogens suggests it may constitute an emerging mycoplasma (6). M. arginini, characterized in 1968 (7), is a much more ubiquitous species isolated from a broad collection of mammalian hosts (8). It has been associated with various pathologies in ruminants and is often found in association with M. bovis in cattle (3). However, its pathogenicity has never been established (9), and this species is best known as a frequent contaminant of eukaryotic cell cultures (10). M. bovigenitalium, characterized in 1955 (11), comprises the strains of the Mycoplasma ovine/caprine serogroup 11, reassigned in 2008 (12). It has been associated with reproductive disorders in ruminants (2, 13, 14) and has proven to induce pneumonia in gnotobiotic calves (9).

Genome sequences of the most relevant mycoplasmal bovine pathogens (Mycoplasma mycoides subsp. mycoides and M. bovis) have already been published. To widen the availability of genome data from mycoplasmas of bovine origin, we present here the genome sequences of M. alkalescens, M. arginini, and M. bovigenitalium.

Selected strains were isolated in France from lung tissue samples from calves with pneumonia. M. alkalescens strain 14918 and M. arginini strain 7264 were isolated in 2007, the latter being

### TABLE 1 General properties of the three genome sequences

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>M. alkalescens 14918</th>
<th>M. arginini 7264</th>
<th>M. bovigenitalium 51080</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of contigs &gt;500 bp</td>
<td>20</td>
<td>18</td>
<td>42</td>
</tr>
<tr>
<td>Median coverage</td>
<td>126×</td>
<td>158×</td>
<td>44×</td>
</tr>
<tr>
<td>GenBank accession no.</td>
<td>AMWK000000000</td>
<td>AORG000000000</td>
<td>AORH000000000</td>
</tr>
<tr>
<td>Genome size (bp)</td>
<td>771,939</td>
<td>615,621</td>
<td>862,247</td>
</tr>
<tr>
<td>G+C (%)</td>
<td>25.56</td>
<td>26.22</td>
<td>28.96</td>
</tr>
<tr>
<td>Gene density (%)</td>
<td>85.18</td>
<td>90.24</td>
<td>88.5</td>
</tr>
<tr>
<td>No. of CDSs</td>
<td>601</td>
<td>513</td>
<td>677</td>
</tr>
<tr>
<td>No. of pseudogenes</td>
<td>33</td>
<td>9</td>
<td>24</td>
</tr>
<tr>
<td>No. of structural RNA genes</td>
<td>37</td>
<td>36</td>
<td>36</td>
</tr>
</tbody>
</table>

* CDSs, coding sequences.

May/June 2013 Volume 1 Issue 3 e00348-13 Genome Announcements genomea.asm.org
found in association with Mannheimia haemolytica. M. bovigenitalium strain 51080 was isolated in 2009 from a septicemic calf, again concomitantly with M. haemolytica. Whole-genome sequences were obtained using a combination of Illumina (single reads) and 454 (mate paired with 8-kb insert size). Assembly was performed using Newbler 2.3, and annotation was conducted using a customized version of the CAAT-Box platform (15), with automatic preannotation for coding sequences followed by expert validation, as detailed previously (16). Genome analysis and comparisons were mainly conducted using the MolliGen 3.0 platform (17).

The general properties of the three genomes are shown in Table 1. Sequences related to integrative conjugative elements were found in both M. alkalescens and M. bovigenitalium, whereas a prophage, similar to that previously described in the small ruminant pathogen Mycoplasma agalactiae (18), was identified in M. bovigenitalium. These mobile genetic elements constitute an important driving force of genome plasticity and may be associated with horizontal gene transfer among Mycoplasma species sharing the same habitat (16, 19).

Comparative genome analysis of mycoplasmas of bovine origin displaying diverse pathogenicity, as well as host and tissue tropism, will improve our understanding of the evolution of bovine mycoplasmas and will pave the way for unraveling the genetic basis of mycoplasma pathogenicity and host specificity.

Nucleotide sequence accession numbers. Draft genome sequences of M. alkalescens, M. arginini, and M. bovigenitalium were deposited as Whole-Genome Shotgun projects at GenBank under the accession no. AMWK00000000, AORG00000000, and AORH00000000, respectively.

ACKNOWLEDGMENTS

Financial support was provided by the EVOLMYCO project (ANR-07-GMGE-001) from ANR to Alain Blanchard (Principal Investigator [PI]), François Thiaucourt (Co-PI), François Poumarat (Co-PI), and Christine Citti (Co-PI).

REFERENCES