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Draft Genome Sequences of Strains of *Pasteurella multocida* Isolated from the United Kingdom and the United States

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*Pasteurella multocida* is a major pathogen of farm animals and has worldwide distribution. Here we report the draft genome sequences of four strains that were isolated from animals in the United Kingdom and the United States and represent pathogenic and commensal presentation of the bacterium.

**TABLE 1** Details of the four sequenced *Pasteurella multocida* strains reported here

<table>
<thead>
<tr>
<th>Strain name</th>
<th>Yr of isolation</th>
<th>Geographical location of isolation</th>
<th>Host species and tissue site of isolation</th>
<th>No. of contigs</th>
<th>Cumulative contig length (bp)</th>
<th>No. of proteins predicted*</th>
<th>% of genome with ≥98% identity to PM70b</th>
</tr>
</thead>
<tbody>
<tr>
<td>2000</td>
<td>2000</td>
<td>United Kingdom, Scotland</td>
<td>Bovine, lung</td>
<td>261</td>
<td>2,210,534</td>
<td>2,141</td>
<td>93.34</td>
</tr>
<tr>
<td>P1933</td>
<td>2004</td>
<td>United States</td>
<td>Bovine, lung</td>
<td>269</td>
<td>2,441,686</td>
<td>2,441</td>
<td>92.65</td>
</tr>
<tr>
<td>R11F</td>
<td>1999</td>
<td>United Kingdom</td>
<td>Bovine, vaginal</td>
<td>243</td>
<td>2,195,634</td>
<td>2,129</td>
<td>98.58</td>
</tr>
<tr>
<td>1500E</td>
<td>2000</td>
<td>United Kingdom, Scotland</td>
<td>Bovine, nasal</td>
<td>265</td>
<td>2,210,576</td>
<td>2,148</td>
<td>93.37</td>
</tr>
</tbody>
</table>

* Number of proteins predicted in the PGAAP (Prokaryotic Genomes Automatic Annotation Pipeline) annotation process.

b Percentage length of each genome that has an identity of 98% or greater to the reference genome PM70.
ACKNOWLEDGMENT
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REFERENCES