

**Table 1. Primer sequences, size of fragment, and percent coverage of complete coding sequence for *Ureaplasma* spp. MLST and eMLST schemes.**

<b>Gene</b>	<b>Annotation</b>	<b>Size (bp) of fragments Analyzed</b>	<b>PCR and sequence primers (5'-3') (F/R)<sup>a</sup></b>
<i>ftsH</i>	Cell division protein FtsH	463-469	TAAAAAAGACGACTTAACTCAACC (F) AATAAAGAGTCGCTTTGTGCT (R)
<i>rpL22</i>	50S ribosomal protein L22	453-456	TCCAACAATGAAAAGAACACT (F) TTTCCTTCATAGTAAGCATC (R)
<i>valS</i>	Valyl-tRNA synthetase	326	GTCTCAAGAATGATGAACTTTAGCC (F) GCAACAACACTAGATTATATTTATCC (R)
<i>thrS</i>	Threonyl-tRNA synthetase	598	TGATACTGTTATTACGCCTATA (F) AGCGGTAAAATACCTTTAGTTTGTT (R)
<i>ureG</i>	Urease complex component	470	TTAATTATTGGTGTAGGTGGACCTG (F) TCAATTCAATCAGCAACAGAT (R)
<i>mba-np1</i>	MBA N-terminal paralog	474	TAGCGGATTTATCGGTTGAACTATA (F) TTAGTTTCAGCACGCCAACCATC (R)

<sup>a</sup> F indicates forward primer and R indicates reverse primer.