



Corrigendum

Corrigendum to ‘Multilocus sequence typing of *Mycoplasma bovis* reveals host-specific genotypes in cattle versus bison’ Vet. Microbiol. 175 (1) (2015) 92–98

Karen B. Register^{a,*}, Luke Thole^b, Ricardo F. Rosenbush^b, F. Chris Minion^b

^a USDA, Agricultural Research Service, National Animal Disease Center, Ruminant Diseases and Immunology Research Unit, 1920 Dayton Avenue, Ames, IA 50010, United States

^b Department of Veterinary Microbiology and Preventive Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA 50011, United States

The authors regret that bison isolate NADC30, which is ST2, was erroneously reported as ST3. Thus, there was a total of 21 ST2 isolates identified in our study. Three of the 32 STs reported are associated exclusively with bison isolates while 28 STs were found only in cattle isolates. Further, isolate KRB8, an ST3 isolate cultured from the lung of a white-tailed deer in Minnesota, was inadvertently omitted from Table 1, Fig. 2 and the supplementary table. Accordingly, a total of 137 isolates was evaluated, 94 from cattle, 42 from bison and one from a white-tailed deer. Corrected versions of Table 1 and Fig. 2 appear below. The addition of isolate KRB8 results in a discrimination index of 0.922, with 70.8% of all isolates found in Clade I. These changes do not alter the overall conclusions of the paper. The authors would like to apologise for any inconvenience caused.

Fig. 2 Unrooted Neighbor-Joining tree inferred from *M. bovis* MLST sequences, representing 32 STs. The percentages of replicate trees in which the associated taxa cluster together in the bootstrap test (10,000 replicates) are indicated at each node; branches with bootstrap values less than 50% have been condensed. The number of isolates identified for each ST is indicated in parenthesis. STs identified exclusively in bison isolates are denoted by shaded circles. The geographic origin of bracketed subclades and undifferentiated branches is given to the right of the tree.

Table 1
M. bovis isolates used in this study.

Host	Anatomic origin	Geographic origin	No. of isolates
bison (n = 42)	lung	United States	13
		Canada	13
	larynx/pharynx	United States	4
	lymph node	United States	1
	subcutaneous tissue	United States	1
	joint	United States	2
	mammary gland	United States	2
	uterus	United States	1
		Canada	1
	placenta	Canada	1
	fetus	Canada	3
cattle (n = 94)	lung	United States	30
		China	3
		Israel	2
		Lithuania	3
		Australia	1
		Hungary	2
	milk	United States	18
		Israel	1
	nasopharynx	United States	5
	joint	United States	4
		Israel	3
	ear	United States	6
		Israel	1
	trachea	Israel	1
vulva	Israel	1	
unknown	United States	11	
	United Kingdom	2	
white-tailed deer (n = 1)	lung	United States	1

DOI of original article: <https://doi.org/10.1016/j.vetmic.2014.11.002>

* Corresponding author.

E-mail address: Karen.Register@ars.usda.gov (K.B. Register).

<https://doi.org/10.1016/j.vetmic.2018.11.012>

