



# Correction for Rosales et al., “Global Multilocus Sequence Typing Analysis of *Mycoplasma bovis* Isolates Reveals Two Main Population Clusters”

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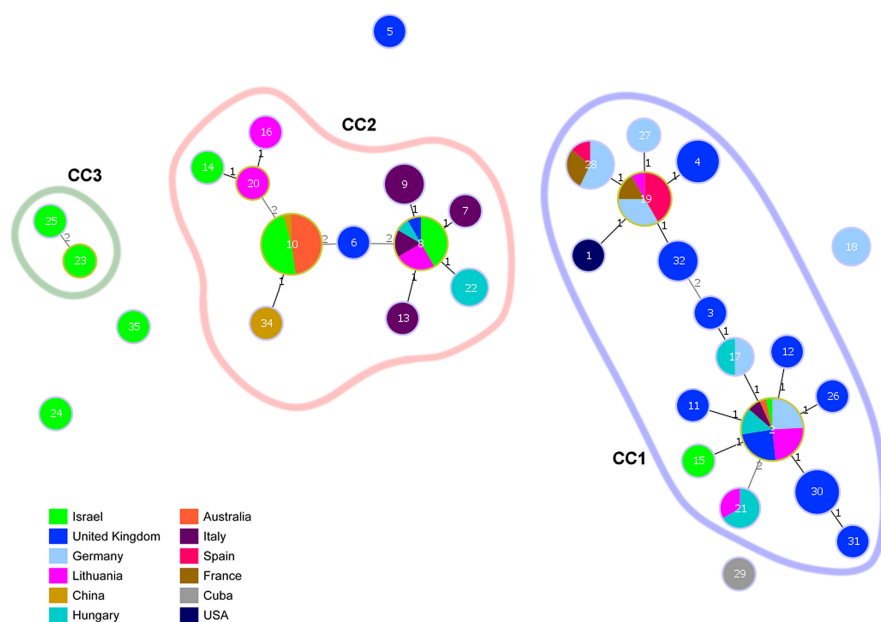
Volume 53, no. 3, p. 789–794, 2015, <https://doi.org/10.1128/JCM.01910-14>.

Pages 789–794 and supplemental material: Data from the *Mycoplasma bovis* Hubei-1 whole-genome sequence were used in this multilocus sequence typing analysis; in subsequent work based on Sanger sequencing, some sequence differences were observed in this strain in comparison with the published whole-genome sequence data. Therefore, to avoid any data mismatch, Hubei-1 data (including references to ST33) should be removed from the article. Therefore, 136 *M. bovis* isolates, not 137, were used, and 34 sequence types, not 35, were identified. These changes do not alter the overall basic results or conclusions of the published article.

Page 790, Table 1: For the “No. of alleles” entry in the row corresponding to the *rpoD* gene, “11” should read “10.”

Page 790, Table 1: For the “No. of polymorphic sites” entry in the row corresponding to the *rpoD* gene, “21” should read “20.”

Page 791: Figure 1 should appear as shown below.



**Citation** Rosales RS, Churchward CP, Schnee C, Sachse K, Lysnyansky I, Catania S, Iob L, Ayling RD, Nicholas RAJ. 2017. Correction for Rosales et al., “Global multilocus sequence typing analysis of *Mycoplasma bovis* isolates reveals two main population clusters.” *J Clin Microbiol* 55:1596–1597. <https://doi.org/10.1128/JCM.00230-17>.

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Page 791, column 2, paragraph headed "Evolutionary relationships and population structure," line 8: "53.28% of the total" should read "53.67% of the total."

Page 792, column 1, lines 13–14: "CC2 included 56 of the 137 analyzed isolates (40.88% of the total)" should read "CC2 included 55 of the 136 analyzed isolates (40.44% of the total)."

Page 792, column 1, line 18: "1.46% of the total" should read "1.47% of the total."

Page 792, column 1, line 22: "4.38% of the total" should read "4.41% of the total."

Table S1 in the supplemental material: Values in the "ST" and "*rpoD*" columns in the rows corresponding to EZ-2, HB0801, JXXY, KF, KLQ, XM, YL2086, ZhX, and ZMD were changed, and the value in the "*rpoD*" column in the row corresponding to SZ was changed. Revised supplemental material is posted at <http://jcm.asm.org/content/53/3/789/suppl/DCSupplemental>.

Figure S1 in the supplemental material: Elements related to ST33 and Hubei-1 have been removed. Revised supplemental material is posted at <http://jcm.asm.org/content/53/3/789/suppl/DCSupplemental>.