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Address for correspondence: Thomas Briese, Center for Infection and Immunity, Mailman School of Public Health, Columbia University – Epidemiology, 722 W 168th St, New York, NY 10032, USA; email: thomas.briese@columbia.edu

## Errata-Vol. 14, No. 9

In Forest Fragmentation as Cause of Bacterial Transmission among Primates, Humans, and Livestock, Uganda (T.L. Goldberg et al.), 2 errors occurred. In Table 3, the numerical values are not in the right positions. The corrected table is available from www.cdc.gov/EID/content/14/09/1375-T3.htm. In the same article, Figures 3 and 4 were inadvertently reversed. This has also been corrected in the online version of the article (available from www.cdc.gov/EID/content/14/9/1375.htm).

In Neurobrucellosis in Stranded Dolphins, Costa Rica (G. Hernández-Mora et al.), the name of co-author Elías Barquero-Calvo was misspelled. Several other editing changes to the online version of the article (available from www.cdc.gov/eid/content/14/9/1430.htm) have also been made upon the authors' request.

In Texas Isolates Closely Related to *Bacillus anthracis* Ames (L.J. Kenefic et al.), 3 author names were inadvertently omitted from the submitted article. They are Carla P. Trim, Jodi A. Beaudry, and James M. Schupp; each is from Northern Arizona University, Flagstaff, Arizona, USA. The complete author list as it should have appeared on the article: Leo J. Kenefic, Talima Pearson, Richard T. Okinaka, Wai-Kwan Chung, Tamara Max, Carla P. Trim, Jodi A. Beaudry, James M. Schupp, Matthew N. Van Ert, Chung K. Marston, Kathy Gutierrez, Amy K. Swinford, Alex R. Hoffmaster, and Paul Keim. The corrected article is available online from www.cdc.gov/EID/content/14/9/1494.htm.

In Clindamycin-Resistant Clone of *Clostridium difficile* PCR Ribotype 027, Europe (D. Drudy et al.), the Figure contained errors. The correct version appears in the online version of this article (available from www.cdc.gov/EID/content/14/9/1485. htm) and is reprinted below.

We regret any confusion these errors may have caused.

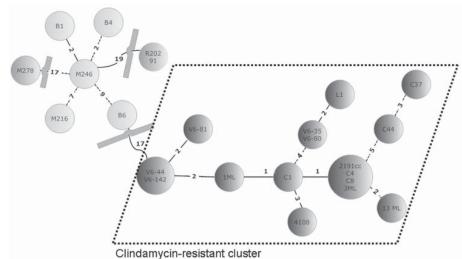


Figure. Minimal spanning tree of 23 Clostridium difficile isolates. In the circles, the individual isolates are mentioned. The numbers between the circles represent the summed tandem repeat differences (STRDs) between multiple-locus variablenumber tandem-repeat analysis types. Straight lines represent single-locus variants, dashed double-locus variants. Curved lines represent triplelocus variants. Two related clusters can be discriminated: the light gray cluster (isolates B1, B4, M246, B6, and M216) and the cluster within dotted lines (isolates V6-44, V6-142, V6-81, 1ML, C1, 4108, V6-35,

V6–80, L1, 2191cc, C4, C8, 3ML, C44, C37, and 13ML) The isolates in the light gray cluster are sensitive to clindamycin; isolates in the cluster surrounded by dashed lines are resistant. Two isolates (M278 and R20291) did not belong to a cluster but were more related to the sensitive cluster than to the resistant cluster. Genetically related clusters were defined by an STRD ≤10.