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Attributing Cause of Death for Patients with *Clostridium difficile* Infection

To the Editor: Hota et al. report that for deceased patients who had *Clostridium difficile* infection (CDI), agreement is poor between causes of death reported on death certificates and those categorized by a review panel (*1*). Our data support the difficulty of attributing cause of death for patients with CDI.

In 2004 in Quebec, Canada, a mandatory CDI surveillance program was implemented. Deaths that occurred within 30 days after CDI diagnosis were classified as 1) directly attributable to CDI (e.g., toxic megacolon, septic shock), 2) having a CDI contribution (e.g., acute decompensation of chronic heart failure), or 3) unrelated to CDI (e.g., terminal cancer) (*2*). To determine accuracy of the surveillance classifications, we compared cause-of-death classification of 22 deceased CDI patients reported to surveillance by 1 hospital in 2007 with causes of death reported by 13 external reviewers who examined summaries of medical files of the deceased patients. Reviewers were 11 infectious disease and 2 public health physicians involved with CDI surveillance at their respective hospitals but not this hospital. The median (minimal, maximal) κ statistics for comparison of external reviews with surveillance classification were 0.495 (0.252, 0.607) for directly attributable, 0.182 (–0.091, 0.182) for contributed, and 0.321 (0.124, 0.614) for unrelated. Comparison within external reviewers yielded 0.697 (0.394, 1.0), 0.233 (–0.294, 0.703), and 0.542 (0.154, 0.909), respectively. Complete agreement was found for only 6 cases (4 directly attributable and 2 unrelated) (Figure).

Variation among reviewers suggested that categorizations reported to surveillance were inaccurate. Number of deaths among patients with CDI, regardless of the cause of death, seemed to better indicate CDI severity. Since 2008, only the crude numbers of deaths, not subjected to individual interpretation, have been reported to surveillance. A questionnaire addressing concurrent medical conditions, prognosis, level of care, and circumstances of death is being implemented in Quebec hospitals participating in CDI surveillance and should help determine the role of CDI in deaths.

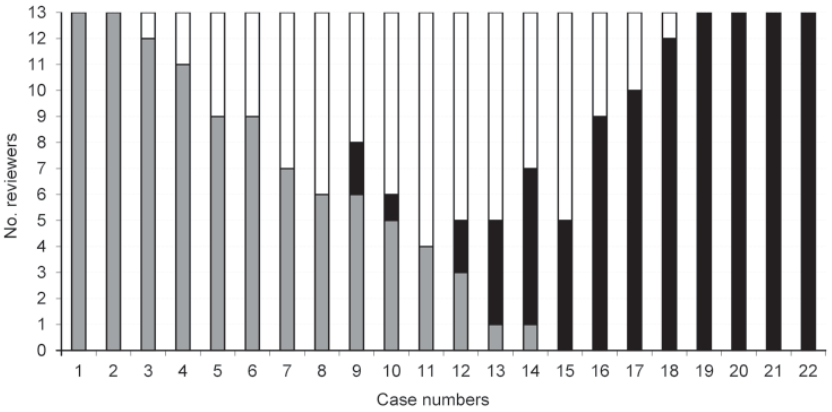

Figure. Classification of cause of death among 22 patients with *Clostridium difficile* infection (CDI), by 13 external reviewers, Quebec, Canada, 2007. Bars indicate the number of reviewers who assigned each category. Gray bars indicate that CDI was unrelated to death, white bars indicate that CDI contributed to death, and black bars indicate that death was directly attributable to CDI.

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Characterization of *Mycobacterium orygis*

To the Editor: In a recently published study, van Ingen et al. (*1*) described the molecular characterization and phylogenetic position of the oryx bacillus, a member of the *Mycobacterium tuberculosis* complex, and proposed a long overdue name for the organism: *Mycobacterium orygis*. The authors described oryx bacillus as a separate taxon; the aim was for this description to be used in the future to identify the subspecies. Thus, we thought it pertinent to provide additional information that would be useful in speciating isolates of the oryx bacillus.

In a recent study, we genotyped an isolate of oryx bacillus obtained from an African buffalo in South Africa (*2*). This isolate was typed by using 16S rDNA, *M. tuberculosis* complex–specific multiplex-PCR, regions-of-difference analyses, *gyrase B* gene single nucleotide polymorphism (SNP) analysis, spoligotyping, and mycobacterial interspersed repetitive units–variable number tandem repeat typing. We showed that, in addition to the markers described by van Ingen et al. (*1*), regions of difference 701 and 702 were also intact in *M. orygis*.

In addition, van Ingen et al. identified the *Rv2042*^{38} GGC mutation as a novel, useful genetic marker to identify *M. orygis*. However, such a marker already exists in the form of the very specific *gyrB*^{oryx} G to A SNP at position 1113, which was described by Huard et al. (*3*). On its own, SNP detection in the *gyrB* gene allows differentiation of at least 6 of the 9 *M. tuberculosis* complex species from each other (*M. canettii*, *M. tuberculosis*, *M. orygis*, *M. microti*, *M. caprae*, and *M. bovis*) (*3*). Thus, the SNP at position 1113 is more useful than the Rv2042^{38} mutation as a novel and distinct genetic marker to identify *M. orygis*.

Apart from this, we found that the sequence type (ST) 587 was not the only spoligotype specific for *M. orygis*. In our study, the variant type ST701 (annotated as *M. africanum* in the spolDB4 database) (*4*) is also an *M. orygis*–specific type and exactly matches that of a previous isolate of the oryx bacillus (SB0319) from the *M. bovis* spoligotype database (*5*). This spoligotype differs from ST587 by the presence of spacer 18, and the spoligotype was not found in the extensive sample set of van Ingen et al. (*1*).

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