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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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Epsilonproteobacteria in Humans, New Zealand

To the Editor: Cornelius et al. (*1*) addressed the potential of *Campylobacter ureolyticus* as an emerging pathogen by conducting a molecular study on 128 diarrheal specimens and 49 fecal samples from healthy volunteers**.** Reporting the identification of *C. ureolyticus* in 12 (24.5%) of 49 healthy volunteers, a number that they compared with our finding of 349 (23.8%) from *Campylobacter* spp.–positive samples (*2*), the authors concluded that *C. ureolyticus* species "are unlikely causes of diarrhea," an assertion with which we take issue.

This interpretation does not take into account that our screening involved 7,194 symptomatic patients: a sample size 40× greater than that of Cornelius et al. In this context, the likely carriage rate for *C. ureolyticus* is 1.15%. Also, our assay, which has a limit of detection in the picomolar range, is likely comparable with, if not greater than, that of Cornelius et al. (*1*).

Accounting for variations in geographic location and detection methods, a detection rate of 24.5% in healthy volunteers (overall detection rate 14.7%) is high in contrast to our reported rate of 1.15%. One possible explanation for this discrepancy is that Cornelius et al. "did not specifically exclude volunteers who had had gastrointestinal disturbances in the 10 days before sampling," Campylobacter can be shed in feces for <4 weeks after infection. Also, Cornelius et al. (*1*) noted the possibility of "genetically distinct but phenotypically indistinguishable genomospecies differing in their pathogenic potential" to account for the presence of the emerging pathogen *C. concisus* in healthy volunteers and patients with diarrheal illness. This may also apply for *C. ureolyticus*.

We reported a strong seasonal prevalence of *C. ureolytcius* and a bimodal age distribution (*2*). The lack of any related details from Cornelius et al. may undermine their reported detection rates. These factors strongly suggest that the statement, "these species are unlikely causes of diarrhea," should, at the very least, be taken under advisement.

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In Response: In response to the letter by Bullman et al. (*1*), a major aspect of our study (*2*) was to compare epsilonproteobacterial populations in healthy persons and those who have diarrhea. We have not examined as many diarrheal samples as Bullman et al. (*3*). However, in contrast with their study, we have examined samples from persons with no evident disease manifestations. Because the presence of an agent during disease is not proof of causation, we believed that a baseline for comparison was needed. *Campylobacter ureolyticus* was found in a greater proportion of samples from healthy persons (24%) than samples from persons who had diarrhea (11%) ($p = 0.041$, by χ^2 test).

Samples from healthy persons were tested on 2 occasions: 18 samples in September 2007 (New Zealand spring) at the Institute of Environmental Science and Research, Christchurch, in the workplace, and 31 samples in June 2009 (New Zealand winter), at Christchurch Hospital under the guidance of a clinician. We have no reason to believe any of the workplace samples were provided when volunteers had diarrhea, particularly considering our workplace guidelines and staff characteristics. In each testing round, 6 fecal samples had positive test results for *C. ureolyticus*. These periods equate to the peak and trough periods described by Bullman et al. (*3*). We were unable to provide many details regarding sampling in our paper because of space constraints.

Considering our baseline comparisons of healthy persons with those who had diarrhea, we affirm our con-