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, gyrB 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 the markers described oryx bacillus as a separate taxon. Thus, we thought it pertinent to provide additional information that would be useful in speciating isolates of the oryx bacillus.

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. africanaum 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).

Nicolaas C. Gey van Pittius, Paul D. van Helden, and Robin M. Warren

Author affiliations: Stellenbosch University Faculty of Medicine and Health Sciences, Tygerberg, South Africa

References

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. ureolyticus 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.

Susan Bullman, Daniel Corcoran, James O’Leary, Deirdre Byrne, Brigid Lucey, and Roy. D. Sleator
Author affiliations: Cork Institute of Technology, Cork, Ireland (S. Bullman, B. Lucey, R.D. Sleator); and Cork University Hospital, Cork (D. Corcoran, J.O’Leary, D. Byrne, B. Lucey)
DOI: http://dx.doi.org/10.3201/eid1810.120369

References

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 χ² 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-