Answer to Photo Quiz: Helically Coiled Clostridium sp. Closely Related to Clostridium ramosum

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A manual anaerobic identification panel was performed (RapID ANA II system; Remel, Lenexa, KS), which identified the organism as Clostridium septicum with 99% probability. Although the identification was of high probability, the identification was questioned because the Gram stain and colony morphology were not consistent with C. septicum. Commercial anaerobe kits are not consistently reliable in correctly identifying Clostridium to the species level (1). This is largely due to difficulties in interpreting biochemical reactions and the absence of profile numbers for some species (1). To aid in further identification of the isolate in this case, a sample taken from a colony growing on brucella agar with hemin and vitamin K was interrogated by matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry (Bruker Daltonics, Billerica, MA). Mass spectrum analysis identified the bacterium as Clostridium ramosum. The isolate was also forwarded to the Centers for Disease Control and Prevention (CDC) via the Georgia Public Health Laboratory, where 16S rRNA sequence analysis identified the bacterium as closely related to C. ramosum.

C. ramosum was originally named Bacillus ramosus in 1898 and has a long history of name changes, including Nocardia ramosa (1931), Actinomyces ramosus (1934), Fusiformis ramosus (1936), Bacteroides ramosus (1937), and Ramibacterium ramosum (1938). It was finally placed in the genus Clostridium in 1971, when the bacterium was shown to form spores. Organisms originally named Catenabacterium filamentosum are now also classified as C. ramosum. C. ramosum and the helically coiled clostridia are described as having some features in common (2). All are obligately anaerobic, nonmotile, Gram-positive rods with rounded ends. Spore formation is notoriously difficult to detect and typically requires selection and/or prolonged incubation (e.g., 2 weeks). Unlike most other clostridia, they do not produce butyric acid as a product of glucose fermentation. All are commonly found as normal flora of the intestinal tracts of humans and some animals. They are divided into five groups based on cell morphology, carbohydrate fermentation, and the guanine-plus-cytosine (G+C) content of their DNA (2). Group I is C. ramosum, which consists of straight rods that may develop long filamentous forms under certain growth conditions. Groups II to V are a heterogenous collection of clostridia that are distinguished by their coiled morphology. Group II is Clostridium coeleatum, group III is Clostridium spiroforme, and groups IV and V are not yet named.

While C. ramosum strains are usually described as straight rods, coiling morphology has been reported to occur in some strains identified as C. ramosum (2, 3). Historically, some of these C. ramosum strains were renamed based solely on the coiled morphology seen on the Gram stain (3). It may be desirable to find more-accurate phenotypic and genetic characteristics that distinguish the taxonomic genera of C. ramosum and the heterogeneous non-group I clostridia (4).

Bacteremia caused by Clostridium sp. is rare and is occasionally polymicrobial. Clostridium perfringens, C. septicum, C. tertium, and C. sordelli are the species most commonly recovered from blood cultures. C. ramosum has also been reported, but bacteremia due to the coiled clostridia is very rare (3). The clinical significance of Clostridium species in the bloodstream is frequently unclear. Clostridial bacteremia usually has a gastrointestinal source and occurs most frequently in the setting of underlying medical conditions (e.g., intra-abdominal sepsis, other gastrointestinal disorders, pregnancy, malignancies, and alcoholism with aspiration) and, less commonly, following trauma or surgery (5, 6). Clostridia are often regarded as contaminants or as unimportant causes of transient bacteremia since their presence appears to be unrelated to the clinical condition (5). The clinical significance of Clostridium bacteremia should be interpreted with caution, however, regardless of species, because of the high risk of associated mortality in some patients, particularly those with underlying liver cirrhosis who do not receive appropriate therapy (5).

Our patient was covered with broad-spectrum antibiotics (vancomycin and piperacillin-tazobactam) prior to receiving notification of the positive blood culture and Gram stain results. After the Gram stain results were reviewed and it was noted that no other blood cultures were positive, therapy was switched to ceftriaxone for spontaneous bacterial peritonitis prophylaxis since the patient had long-standing ascites but no recent taps indicating infection.

REFERENCES