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PHOTO QUIZ

Photo Quiz: A Bacterium Better Known by Surgical Pathologists than by Clinical Microbiologists

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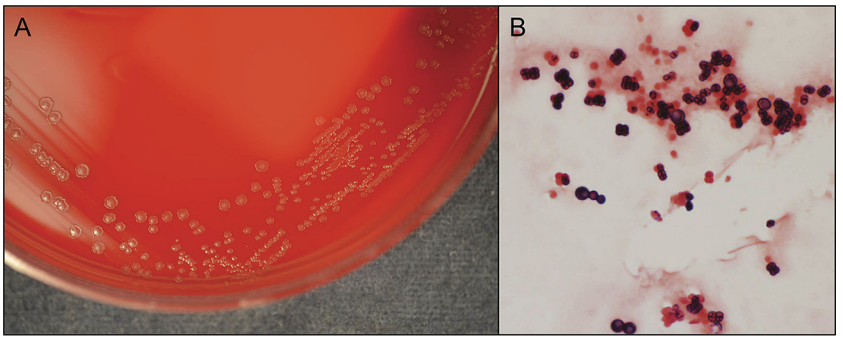

FIG 1 (A) Small, flat, irregular colonies on CDC anaerobe agar with 5% sheep blood. (B) Large, Gram-variable coccoid-like structures on Gram stain demonstrating chaining and internal septations. Magnification, ×1,000.

A 33-year-old woman with medullary sponge kidney associated with kidney stones and recurrent urinary tract infections presented to the clinic with flank pain, dysuria, vomiting, and fever. Her last urinary tract infection was 4 months prior, at which time urine culture was positive for *Enterococcus faecalis* susceptible to ampicillin and vancomycin, and treatment included a 14-day course of cefepime and levofloxacin. At this current presentation, urine cytology showed hematuria and pyuria, and she was admitted with a diagnosis of urosepsis. Two blood culture sets were drawn on admission before antibiotics were started. One set grew *Escherichia coli* in the aerobic bottle only. The anaerobic bottle from the second set was flagged positive for growth after 19 h of incubation and showed large, round, Gram-variable structures clustering on Gram stain (Fig. 1). The aerobic bottle from the second set of blood cultures was negative for growth. After 48 h of incubation under anaerobic conditions, the organism grew on CDC anaerobe agar with 5% sheep blood (BD, Franklin Lakes, NJ) but did not grow on laked kanamycin vancomycin agar or phenylethyl alcohol agar; the isolate did not grow aerobically. The colonies were small, flat, and irregular. Gram stain from the colonies showed large (approximately 3 μm in diameter) coccoid structures which were variably Gram positive. Some cocci were in chains while others showed internal septations. The organism was not identifiable on matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS; Bruker, Billerica, MA) using either FDA or *in vitro* diagnostics (IVD) databases; the closest match was *Aromatoleum evansii* (a Gram-negative betaproteobacterium), with a low score of 1.183 (the cutoff for acceptability is 1.70). 16S rRNA sequencing was performed on the isolate for identification.

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