the sample was deposited on an agar plate flooded with a suspension of a antimicrobial susceptible strain of Micrococcus luteus. After 24 h of incubation at 37°C, presence of antimicrobial activity in the sample was evident by a visible area of growth inhibition of M. luteus around the sample. Procedures for DNA extraction and 16S rRNA gene amplification and sequencing have been detailed (4).

Gram staining of the sample showed numerous polymorphonuclear leukocytes and gram-negative bacteria. Culture of the sample remained sterile after 20 days of incubation, and antimicrobial susceptibility was found. The 16S rRNA gene amplification and sequencing determined a 1,493 nucleotide sequence. This sequence had 99.7% nucleotide similarity with that of L. amnionii (GenBank accession no. AY078425), which corresponded to a difference of 4 nucleotide. The 16S rRNA gene sequence of the detected bacterium was deposited under accession no. AY489565. L. amnionii was previously recovered in anaerobic culture of the amniotic fluid of a woman after intrauterine fetal demise (2). It was isolated on blood and chocolate agar under anaerobic conditions and showed very small gray colonies of <1 mm. This slow-growing bacterium was lost after two subcultures, and no isolate is available for further description (2). In that case and in the case reported here, the patients had uneventful recoveries after an amoxicillin plus clavulanic acid antimicrobial regimen was given. This bacterium and our isolate are related to, but different from, L. sanguinegens.

Leptotrichia is a small genus closely related to Fusobacterium and comprises slow-growing, gram-negative, filamentous, anaerobic bacterial flora of the oral cavity and genital tract (5). Species included in the genus are L. buccalis, L. trevisanii, L. sanguinegens, and L. amnionii (2,6).

All Leptotrichia species are extremely fastidious and cannot be grown easily on conventional microbiologic media or by conventional methods. As evidenced by sequences available in the GenBank database, most of the 16S rRNA gene sequences are from cloned DNA from complex flora but not from bacterial isolates. Leptotrichia species has been suspected to play a role in periodontal disease. However, Leptotrichia species have only been associated with serious systemic disease, usually in immunocompromised patients (7,8). Bacteremia caused by L. sanguinegens in pregnant women has also been reported (9). More widespread use of polymerase chain reaction amplification and sequencing of the 16S rRNA gene for identification or detection of fastidious pathogens in humans will likely provide verification of several new pathogens that are now part of normal human flora.

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Cholera in Mozambique, Variant of Vibrio cholerae

To the Editor: Cholera outbreaks caused by toxigenic Vibrio cholerae serogroup O1 frequently occur in many sub-Saharan African countries. The serogroup O1 is classified into two biotypes, classical and El Tor. The seventh and current pandemic of cholera is caused by the El Tor biotype; the classical biotype is believed to be extinct. The classical and El Tor biotypes of V. cholerae O1 are closely related in their O-antigen biosynthetic genes but differ in other regions of the genome. The genomic structure of the CTXΦ filamentous phage (1), in which the cholera toxin genes are contained, differs between the classical and El Tor biotypes. CTX<sup>classΦ</sup> is found in classical strains, CTX<sup>eltorΦ</sup> is
present in El Tor and O139 strains, and CTXΦ is found in resurgent O139 strains. The diversity of CTXΦ among biotypes is mainly due to the variations in the repeat sequence elements, particularly in the \(rstR\) gene region (2).

While conducting surveillance in the cholera treatment center in Beira, the second largest city in Mozambique, we examined 175 rectal swabs or stool samples from January 7 to March 8, 2004, using standard published procedures. During this period, we isolated 58 strains of *V. cholerae* O1. The isolates were transported to the Enteric Microbiology Unit of the International Center for Diarrheal Disease Research in Dhaka, Bangladesh (ICDDR,B), for further phenotypic and genotypic characterization to determine serotype, biotype, and presence of important virulence genes. All 58 strains were identified as *V. cholerae* O1 of the Ogawa serotype. Forty strains selected for detailed characterization were resistant to polymyxin B, agglutinated chicken cells, yielded a positive Voges-Proskauer reaction, were positive for the El Tor hemolysin by the tube agglutination method, and were sensitive to group IV El Tor biotype overall but carried the classical prophage shows evidence of transmission of the classical CTXΦ. The CTX prophages in El Tor strains give rise to infectious phage particles (1), but neither of the two CTX prophages integrated at two different sites of the classical genome give rise to phage particles (4). Subsequent studies have shown that, although the genes of the classical prophages encode functional forms of all of the proteins needed for production of CTXΦ, the CTX prophage does not yield virions because of the atypical arrangement of its prophage arrays (4).

Figure: Amino acid sequence alignment of CT-B subunit of *Vibrio cholerae* O1 classical, El Tor, and Mozambique (B33 and B65) strains. Identical amino acid residues are indicated by a period. Amino acid sequences of CtxB of *V. cholerae* classical (AAL80524.1; AAM47189.1) and El Tor (AAM74192.1; AAM77066.1) are from GenBank.
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Instruction for Emerging Infectious Diseases Authors

Letters

Letters commenting on recent articles as well as letters reporting cases, outbreaks, or original research are welcome. Letters commenting on articles should contain no more than 300 words and 5 references; they are more likely to be published if submitted within 4 weeks of the original article’s publication. Letters reporting cases, outbreaks, or original research should contain no more than 800 words and 10 references. They may have one Figure or Table and should not be divided into sections. All letters should contain material not previously published and include a word count.

Table 2. Orientia tsutsugamushi IgG and IgM antibody titers for six southwest islanders with prolonged fever and abdominal distress

<table>
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<tr>
<th>Patient no.</th>
<th>Antibody type</th>
<th>Acute-phase titer</th>
<th>Convalescent-phase titer</th>
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</tr>
<tr>
<td></td>
<td>IgM</td>
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</tr>
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<td>IgG</td>
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<td>1:32,768</td>
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<tr>
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<td>IgM</td>
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<td>IgM</td>
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<td>1:1,024</td>
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<tr>
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<td>IgM</td>
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</tr>
<tr>
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</tr>
<tr>
<td></td>
<td>IgM</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

*Ig, immunoglobulin; NA, result not available.