

Detection of novel organisms associated with salpingitis, by use of 16S rDNA polymerase chain reaction

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Abstract:

Although *Chlamydia trachomatis* and *Neisseria gonorrhoeae* are established causes of salpingitis, the majority of cases have no known etiology. We used broad-range 16S rDNA polymerase chain reaction to identify novel, possibly uncultivable, bacteria associated with salpingitis and identified bacterial 16S sequences in Fallopian-tube specimens from 11 (24%) of 45 consecutive women with laparoscopically confirmed acute salpingitis (the case patients) and from 0 of 44 women seeking tubal ligations (the control subjects) at Kenyatta National Hospital, Nairobi, Kenya. Bacterial phlotypes most closely related to *Leptotrichia* spp. were detected as the sole phlotypes in 1, and mixed with other bacterial phlotypes in 2, specimens. Novel bacterial phlotypes and those associated with bacterial vaginosis, including *Atopobium vaginae*, were identified in 3 specimens. *N. gonorrhoeae* and *Streptococcus pyogenes* were identified in 2 and 1 specimens, respectively. The finding of novel phlotypes associated with salpingitis has important implications for the etiology, pathogenesis, and treatment of this important reproductive-tract disease syndrome.