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Detection of *Mycoplasma genitalium* by PCR Amplification of the 16S rRNA Gene

Jørgen Skov Jensen[1],*, Martin B. Borre[2] and Birthe Dohn[1]

+ Author Affiliations

ABSTRACT

In order to develop a species-specific PCR for the detection of *Mycoplasma genitalium*, the sequence of 1,490 bases of the 16S rRNA gene was determined for *M. genitalium* G37 (type strain) and four Danish isolates of *M. genitalium*. The sequences of the four Danish strains, mutually different with respect to their MgPa gene, were 100% homologous, although they carried a single common base substitution compared to the type strain. Among members of the *Mycoplasma pneumoniae* phylogenetic cluster, *M. genitalium* showed the most-prominent homology to the 16S rRNA sequence of *M. pneumoniae* (98% homology). From regions showing the least homology to the *M. pneumoniae* 16S rRNA gene sequence, primers were chosen to amplify DNA from *M. genitalium* only. Two sets of primers were selected for their ability to detect <10 to 50 *M. genitalium* genome copies without cross-reactions with *M. pneumoniae*. The performance of these primers was compared to the performance of two pairs of primers amplifying parts of the MgPa adhesin gene; 1,030 randomly selected specimens submitted for *Chlamydia trachomatis* culture were screened with one of the 16S rRNA gene primer sets. A total of 41 specimens were found to be positive for this gene; 40 of these could be confirmed by one of the MgPa primer sets, whereas the other MgPa primer set detected only 21 positive specimens out of 40. These results indicate that estimates of the prevalence of *M. genitalium* in various populations using

MgPa PCR primers could be incorrectly low if the PCR primers are located in variable regions of the MgPa gene.

FOOTNOTES

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*Corresponding author. Mailing address: Mycoplasma Laboratory, Statens Serum Institut, Artillerivej 5, DK-2300 Copenhagen S, Denmark. Phone: 45 3268 3636. Fax: 45 3268 3152. E-mail: **jsj@ssi.dk**.

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