Absence of Mycoplasma species DNA in chronic fatigue syndrome

People with chronic fatigue syndrome (CFS) suffer from multiple symptoms that include fatigue, problems with memory, concentration, sleep and musculoskeletal pain. The association of any one infectious agent with CFS has been difficult to establish and is complicated further by the lack of a known lesion or diseased tissue to sample. Peripheral blood, by its nature of systemic circulation, serves as an ideal specimen in CFS, as it samples the entire body and could thus serve as a sentinel for diverse lesions. Plasma, the liquid portion of peripheral blood that is devoid of cells, is known to contain remnants of numerous physiological and disease processes. We used plasma DNA to detect and characterize bacterial 16S rDNA sequences in a group of individuals with CFS and a group of non-fatigued controls (Vernon et al., 2002). Whilst a variety of bacterial sequences were detected in both fatigued and non-fatigued groups, no Mycoplasma sp. 16S rDNA sequences were found. A few studies have reported the detection of several Mycoplasma species in peripheral blood cells of CFS patients by using Mycoplasma species-specific PCR (Nasralla et al., 1999; Nijs et al., 2002). In this study, we used Mycoplasma species-specific primer pairs for direct amplification of these microbes from plasma DNA.

As part of a population-based study of CFS in Wichita, Kansas, USA (Reyes et al., 2003), peripheral blood was collected during the clinical evaluation of 34 subjects, classified according to the 1994 international case definition for CFS, and a random selection of 55 non-fatigued subjects. Blood was collected in sodium citrate Vacutainer tubes (Beckton Dickinson) and shipped by overnight courier to the Centers for Disease Control (CDC), where plasma was collected by separation on lymphocyte separation medium (LSM; ICN Biomedicals). Plasma (1 ml) was concentrated to approximately 250 μl in a Centricon centrifugal filter unit YM-100 (Millipore). Cell-free plasma DNA was extracted by using a QIAamp DNA Mini kit (Qiagen) according to the manufacturer’s instructions and quantified by using a DyNA Quant 200 fluorometer (Amersham Biosciences).

Primer pairs for Mycoplasma fermentans, Mycoplasma hominis, Mycoplasma penetrans and Mycoplasma pneumoniae were synthesized according to published sequences. Conditions for each primer pair were optimized and shown to amplify 0.3–2 pg genomic equivalents of Mycoplasma DNA (Fig. 1). Despite these optimized conditions and the high level of sensitivity of this amplification method, no Mycoplasma products were amplified from any of the 89 cell-free plasma DNA samples.

There have been a few reports of an association between infection with Mycoplasma species and CFS. One study has shown M. fermentans to be the mycoplasma detected most commonly by PCR in the blood of CFS patients from the USA (Nasralla et al., 1999). However, a serological survey of people diagnosed with CFS (as defined by the 1994 CFS case definition) was negative for antibodies to M. fermentans (Komaroff et al., 1993). Our demonstration of the absence of Mycoplasma DNA by a sensitive amplification approach supports the negative serology study. Although cell-free plasma DNA may have limitations for monitoring the presence of Mycoplasma species, we believe this is unlikely, as numerous other cell-associated microbial pathogens can be detected readily in cell-free plasma DNA (Vernon et al., 2002). As it has been shown that Mycoplasma species exist at relatively high rates in the peripheral blood of CFS patients in both the USA (Nasralla et al., 1999) and Europe (Nijs et al., 2002), it seems plausible that these microbial sequences should have been detected in plasma, reflecting death and lysis of infected cells.

Our goal was to reproduce the results of Nasralla et al. (1999) and Nijs et al. (2002) in a systematic way by using well-defined CFS subjects and non-fatigued controls. These authors detected the presence of four species of Mycoplasma DNA in patients with CFS and fibromyalgia. These studies used patients in tertiary care clinics rather than the general population and the results may reflect recruitment bias. Our study tested persons with CFS identified in the general population. Previous studies did not include appropriate controls, thus reported associations may be spurious. Our study enrolled non-fatigued controls from the same population as CFS cases. Finally, neither previous studies that reported an association nor our study, which shows no association, have been replicated independently. Independent reproducibility of PCR-based detection methods for infectious agents by other laboratories is an important factor for establishing an infectious cause of disease. Unfortunately, it is not uncommon to see variations in the rate of positivity in similar types of clinical sample from different laboratories that are engaged in PCR-based detection methods.
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