Absence of Ribosomal RNA of Mycobacterium tuberculosis Complex in Sarcoidosis

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Objective: To determine whether Mycobacterium tuberculosis ribosomal RNA (rRNA) is present in fresh tissue specimens from patients with sarcoidosis.

Design: A prospective study.

Setting: A university-based hospital.

Patients: Thirty-five patients diagnosed as having sarcoidosis at the University Hospital of Bellvitge, Barcelona, Spain, were included in the study. Fresh tissue samples with granulomatous inflammation were prospectively collected between 1997 and 2001 from all patients. For each sample tested, approximately 1 negative control was included.

Main Outcome Measures: Mycobacterium tuberculosis rRNA was detected using an isothermal enzymatic amplification system of target rRNA of M tuberculosis complex via DNA intermediates. Smears for acid-fast staining and mycobacteriological cultures were also obtained.

Results: A total of 78 biopsy specimens (57 skin, 10 lymph node, 3 lacrimal gland, 2 spleen, 2 lung, 2 muscle, 1 bone, and 1 nerve) collected from 74 patients (35 patients with sarcoidosis and 39 control patients) were included in the study. Stains for acid-fast bacilli and mycobacterial cultures were negative for organisms in all cases. Mycobacterium tuberculosis rRNA was not detected in the specimens from any patients with sarcoidosis or in those from control patients whose cultures were negative for organisms. Ribosomal RNA was detected in 6 tissue specimens from patients with cultures that were positive for M tuberculosis and that were processed in parallel to the samples included in the study.

Conclusions: Although previous studies have reported that mycobacterial antigens may play a role in granuloma formation in some patients with sarcoidosis, our results suggest that M tuberculosis cannot be considered to be the etiologic agent of the disease.

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Sarcoidosis is a multisystemic disease that is defined by the formation of noncaseating granulomas in different organs. Although the etiology of sarcoidosis remains uncertain, the apparition of clusters of the disease in some communities and the existence of seasonal variations in incidence suggest that environmental or infectious agents may play a role in its development. Moreover, similarities in the clinical, pathologic, and immunologic abnormalities in patients with sarcoidosis and in certain patients with tuberculosis have raised the suspicion that mycobacterial infection could be associated with the pathogenesis of this disorder.

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The purpose of the present study was to prospectively determine the presence of viable M tuberculosis organisms in fresh tissue samples from patients with sarcoidosis by means of smears for acid-fast staining, mycobacteriological cultures, and the detection of mycobacteria-specific rRNA.

Methods

Patients and Samples

Tissue specimens from patients with sarcoidosis were prospectively collected between 1997 and 2001 at the University Hospital of Bell-
The diagnosis of systemic sarcoidosis was made according to the classic criteria: a compatible clinical and radiologic picture; histologic demonstration of noncaseating granulomas involving 1 or more tissues or a positive Kveim test result; and exclusion of other granulomatous diseases. Half of the specimen from each patient was fixed in 10% buffered formaldehyde and processed for histologic evaluation to determine whether granulomas were present in the samples.

**CONTROLS**

At least 1 negative control was included for each test sample. The negative control samples, which were analyzed in the same manner as the test samples, consisted of fresh specimens of normal tissue obtained from patients without evidence of sarcoidosis or tuberculosis. Most cutaneous specimens were obtained from redundant normal skin acquired during minor surgical procedures.

**SPECIMEN PROCESSING, MICROSCOPY, AND CULTURE**

All biopsy specimens were homogenized in 3 mL of 0.9% sodium chloride solution within 24 hours of specimen collection. Part of this suspension was used for the preparation of smears for acid-fast staining with auramine-rhodamine fluorochrome and for culture. The remaining suspension was stored at -80°C for subsequent use in the genetic amplification procedure. An equal volume (0.5 mL) of the processed specimens was inoculated in 2 culture media: a liquid medium bottle (MB/Bact; bioMérieux SA, Marcy l’Étoile, France) and a Lowenstein-Jensen slant (MAIM, Barcelona, Spain) as a solid medium. All cultures were incubated at 35°C to 37°C for up to 6 weeks. The bottles were registered and processed by means of a nonradiometric system for incubation and continuous monitoring of mycobacterium growth (Bact/ALERT 3-dimensional instrument; bioMérieux SA). The Lowenstein-Jensen media were incubated in 5% carbon dioxide and examined for colonies on the slant once a week.

**EXTRACTION OF NUCLEIC ACIDS**

The material was extracted with a commercially available kit (RNA/DNA Maxi Kit; Qiagen, Hilden, Germany) that allows rapid isolation of RNA and DNA from small numbers of bacteria in clinical samples.

**GENETIC AMPLIFICATION PROCEDURE**

A nucleic amplification test (AMDT; Gen-Probe Inc, San Diego, Calif) was used to detect M tuberculosis rRNA. This test is an isothermal amplification system based on the reverse transcription of mycobacteria-specific rRNA targets via DNA intermediates. It uses 2 enzymes (RNA polymerase and reverse transcriptase) and 2 primers, one of which contains a promoter sequence for RNA polymerase. Detection of RNA amplicons is achieved with an acridinium ester-labeled DNA probe. The entire process (amplification and detection) is performed in a single tube, which helps to reduce the risk of carryover contamination. In the present study, the amplification test was performed and the results were interpreted according to the manufacturer’s recommendations. Six clinical samples (3 lymph node specimens and 1 biopsy specimen each of spleen, liver, and lung) with cultures that were positive for M tuberculosis were used as quality control for extraction and amplification techniques.

A total of 78 specimens obtained from 74 patients (35 patients with sarcoidosis and 39 control patients) were included in the study. The 37 specimens obtained from specific granulomatous lesions of 35 patients with sarcoidosis were skin (n=29), lymph node (n=5), muscle (n=2), lung (n=1), and lacrimal gland (n=1). The 41 specimens obtained from 39 control patients were skin (n=29), lymph node (n=5), spleen (n=2), lacrimal gland (n=2), lung (n=1), bone (n=1), and nerve (n=1).

All the specimens included in the study were negative for acid-fast bacilli. Likewise, all the cultures were negative for M tuberculosis after at least 6 weeks of incubation. The 37 samples from the 35 patients with sarcoidosis and the 41 specimens from the 39 subjects in the control group were all negative for M tuberculosis rRNA. However, rRNA was detected in 6 tissue specimens with cultures that were positive for M tuberculosis and that were processed in parallel to the samples included in the study.

**RESULTS**

In the present study, we were not able to detect the presence of M tuberculosis rRNA in fresh tissue samples of granulomatous lesions prospectively collected from patients with systemic sarcoidosis. The smears for acid-fast bacilli and mycobacteriological cultures were also negative for organisms.

Clinical and pathologic similarities to pulmonary tuberculosis have suggested a potential role of mycobacteria in the etiology of sarcoidosis. The histopathologic features of the granulomas and the occasional presence of caseation necrosis also indicate the possibility of a mycobacterial pathogenesis in sarcoidosis. However, the absence of caseation in most instances, the negativity of mycobacterial cultures, and the absence of a response to antituberculous treatment are factors that contradict this theory. Likewise, over the past century, while there has been a marked reduction in the incidence of tuberculosis, the incidence of sarcoidosis has not decreased.

During the last decade, several studies have used PCR analysis in an attempt to detect mycobacterial DNA in a number of biopsy specimens from patients with sarcoidosis. The findings of these studies have been quite inconsistent, with positive results ranging from 0% to 80%.

The surprising variability of these data may be explained by several technical factors, including the choice of target sequence and DNA-retrieval variability, depending on which technique is used to obtain the DNA. An alternative explanation for these divergent results is inadvertent contamination of samples in some series.

It is noteworthy that the studies showing the highest proportion of positive results for samples from patients with sarcoidosis also reported a relatively high proportion of positive results for samples from control subjects and/or from individuals with prior tuberculous infections. Moreover, most studies about the detection of mycobacterial DNA using PCR in sarcoidosis were performed in formalin-fixed, paraffin-embedded specimens from retrospective pools of pathology departments. In such studies, there is a greater possibility of both contamination of the paraffin-
considered the etiologic agent of sarcoidosis.

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In conclusion, although mycobacterial antigens may appear to be involved in sarcoidosis, the presence of mycobacterial DNA in sarcoidosis lesions has not indicated infection. These points have not been demonstrated consistently to date. Polymerase chain reaction detection of mycobacterial DNA in sarcoidosis does not indicate whether the detected mycobacteria are still viable and susceptible to antituberculous therapy or whether they represent nonviable remnants of prior mycobacterial colonization. The presence of mycobacterial DNA in tissues involved with sarcoidosis only suggests that mycobacterial vestiges may be present in some lesions in a variable proportion of patients. However, the absence of mycobacterial rRNA, despite the higher sensitivity compared with DNA detection, and the negativity of the cultures rules out the presence of viable mycobacteria in the sarcoidosis lesions.

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