

by a dot blot hybridization with a 289-bp digoxigenin-labeled probe internal to the amplified DNA fragment. Aqueous humors from patients investigated for ocular syphilis were used as negative controls. The specific *Leptospira* 16S rRNA gene fragment was detected by dot blot hybridization (figure 1) in the aqueous humor of our patient but not in serum and urine samples. The concentration of leptospires in aqueous humor was estimated at 10^3 /mL.

Bilateral or unilateral uveitis [4], cotton wool spots [5], and necrotic retinitis [6], with or without systemic symptoms, have been related to leptospiral infection. These diagnoses were based on history of systemic illness, evidence of specific antibodies in serum, and exclusion of other possible causes. This first report of PCR diagnosis of ocular leptospirosis demonstrates the possibility of a positive diagnosis of ophthalmologic complications in a disease in which the pathogenesis is still misunderstood.

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The Digestive Tract Is a Major Site for *Acinetobacter baumannii* Colonization in Intensive Care Unit Patients

Colleagues—*Acinetobacter baumannii* is widespread in nature [1] and is carried by many healthy people, especially on the skin [2]. Moreover, the organism is increasingly being associated with human disease, particularly in hospital settings among debilitated patients and in intensive care units (ICU) [3]. It is frequently found in the respiratory tract; however, the digestive tract has not been thought to be a major colonizing site [3]. Recently, in an eight-bed ICU, we were confronted with an outbreak with *A. baumannii* that was sensitive only to ticarcillin, colistin, and imipenem. The index case was a 65-year-old woman, who was referred from another hospital 3 weeks before the outbreak began.

For 32 weeks, we assessed patients for colonization with *A. baumannii* beginning with admission and then weekly with rectal swabs and tracheal aspirates. A total of 170 patients was tested. *A. baumannii* was present on rectal swabs and tracheal aspirates of 41 patients (24%; 45% of ICU patients are hospitalized >7 days). All of the isolates had the same susceptibility to antimicrobials. Sixteen patients were admitted from other units with digestive tract colonization with *A. baumannii* and 25 acquired this organism in the ICU despite traditional infection

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control measures [4] (isolation of colonized and infected patients and improvement of hand washing and asepsis). Among these 25 patients, the digestive tract (as assessed by rectal swabs) was the first site colonized in 17 cases. Of the 8 remaining patients, tracheal colonization occurred at the time of (7 patients) or before digestive colonization (1 patient). Moreover, during the same period, no environmental contamination with *A. baumannii* was found on patient care equipment (assessed during weeks 7 and 18).

A. baumannii infection, according to the Centers for Disease Control definition, [5], occurred in 11 patients and was considered to be directly responsible for the deaths of 3 patients (2 nosocomial pneumonias, 1 catheter-related septicemia). Digestive tract colonization (rectal) with multiresistant *A. baumannii* was present before (12 cases, 9 patients) or at the time of infection (2 cases, 2 patients).

Although we did not determine oropharyngeal and cutaneous colonization, these results suggest that the digestive tract was an important reservoir for *A. baumannii* in ICU patients.

The failure to prevent transmission from patient to patient by careful asepsis and improved hand washing indicates the need for strategies to decrease the numbers of *A. baumannii* in colonized patients. For this purpose, because the digestive tract seemed to be a major colonization site, selective digestive decontamination with topical antimicrobials [6] might be considered as a means to decrease *A. baumannii* cross-colonization, making the routine infection control measures more effective in the management of ICU outbreaks.

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Rapid Identification of *Mycobacterium avium-intracellulare* Complex Strains: Clinical Practice Evaluation of DT6 and DT1 Probes

Colleagues—*Mycobacterium avium* is the most frequent cause of disseminated bacterial disease in the later stages of AIDS. Because of the severity of the infection, the increasing incidence over the last 5 years, and the availability of effective treatment, a rapid and reliable detection method would be helpful. The procedure combining radiometric liquid culture and nonradioactive probe technology greatly contributes to more rapid identification, which is easily used in clinical laboratories. However, commercially available probes specific for rRNA do not allow the detection of all clinical isolates of *M. avium* [1-3]. We recently isolated two sequences, DT6 and DT1, specific for *M. avium* and *Mycobacterium intracellulare*, respectively [4], and developed polymerase chain reaction (PCR) tests based on the amplification of these sequences.

Forty-one mycobacterial strains and 121 various biologic specimens were cultured (Bactec 460 TB; Becton Dickinson, Cockeysville, MD); positive cultures were subsequently identified by conventional methods. When a growth index of >500 was reached, DNA was extracted from 1-mL aliquots from vials and analyzed by PCR using two sets of primers: AV1 (5'-GGCCCGATGCGACGTCGAGA-3')/AV2 (5'-GCGCAACTGCGCTTCGTCGA-3') and IN38 (5'-GAACGCCCGTTGCTGGCCATTCACGAGGAG-3')/IN41 (5'-GCGCAACACGGTCCGACAGGCTTCTCGA-3') derived from DT6 and DT1, respectively. The amplified products were hybridized with acetylaminofluorene-labeled DT6 or DT1 probes.

The 22 strains biochemically identified as members of the *Mycobacterium avium-intracellulare* complex (MAC) were assigned to *M. avium* or *M. intracellulare* on the basis of PCR results (table 1). None of the 19 mycobacterial strains other than MAC (2 *Mycobacterium fortuitum*, 3 *Mycobacterium bovis* [1 was strain bacille Calmette-Guérin], 5 *Mycobacterium chelonae*, 3 *Mycobacterium xenopi*, 2 *Mycobacterium terrae*, 1 *Mycobacterium peregrinum*, and 3 *Mycobacterium kansasii*) reacted with any of the primer pairs.

All 88 MAC-containing specimens were positive by PCR using DT6-derived primers (table 1) as well as 4 additional

Table 1. Comparison of polymerase chain reaction (PCR) with the standard bacteriologic method.

Samples	Biochemical identification (n)	PCR-positive with	
		DT6 probe	DT1 probe
41 strains	MAC (22)	21	1
	Other mycobacteria (19)	0	0
121 specimens*	MAC (88)	88	0
	Mixed cultures (4)	4	0
	Other mycobacteria (29)	0	0

NOTE. MAC, *Mycobacterium avium-intracellulare* complex.

* Blood (82), sputum (9), gastric aspirate (10), bronchial aspirate (6), tissue biopsy (5), urine (3), synovial fluid (1), pleural fluid (1), peritoneal fluid (1), bone marrow (1), lymph node puncture (1), and pus (1).

specimens that contained mixed cultures of MAC associated with *Mycobacterium simiae* (3) or *Mycobacterium scrofulaceum* (1). Such mixed cultures have been reported from AIDS patients [5, 6].

The remaining 29 specimens positive for mycobacterial growth but negative by PCR produced isolates consisting of 19 *Mycobacterium tuberculosis*, 2 *Mycobacterium goodii*, 2 *M. kansasii*, 2 *M. scrofulaceum*, and 4 unidentified strains. These latter isolates were obtained from sequential blood cultures from the same AIDS patient.

In conclusion, we found that the PCR assay based on the use of the DT6- and DT1-derived primers offers a practical method for the rapid identification of *M. avium* and *M. intracellulare* and can be successfully used at an early stage in isolation of primary clinical samples.

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