Molecular Identification of *Pasteurella dagmatis* Peritonitis in a Patient Undergoing Peritoneal Dialysis

FRÉDÉRIC WALLET,1* FATOUMA TOURE,2 ANNIE DEVALKENAERE,1 DOMINIQUE PAGNIEZ,2 AND RENE J. COURCOL1

Laboratoire de Bactériologie-Hygiène1 and Service de Néphrologie B,2 Hôpital A. Calmette, CHRU de Lille, Lille, France

Received 30 June 2000/Returned for modification 18 August 2000/Accepted 21 September 2000

*Pasteurella dagmatis* was identified as the etiologic agent of peritonitis in a continuous ambulatory peritoneal dialysis patient by utilizing a molecular kit in our hospital's clinical laboratory. This method would appear a useful approach to identify a species of *Pasteurella* not included in the existing database of commercial identification kits when discrepancies exist between phenotypic tests.

CASE REPORT

A 43-year-old female patient was admitted to the nephrology unit for evaluation of turbidity of peritoneal fluid. The peritoneal catheter exit site was of normal appearance. Microscopic examination of the fluid revealed 5,800 cells/mm³ with 90% polymorphonuclear cells. Gram staining did not reveal any microorganisms. The white blood cell count was 7.7 × 10⁹/liter with 81% polymorphonuclear cells. Primary antibiotic therapy was started with intraperitoneal administration of piperacillin (2 g, four times a day) and cephalothin (500 mg, four times a day), resulting in rapid improvement. The outcome was uneventful, with the patient being discharged 6 days later on oral ofloxacin (200 mg/day) for 10 days. The patient’s mother drew our attention to the fact that her daughter lived in the company of at least 10 cats. The patient denied accidental animal contact with peritoneal dialysis equipment and the fact that the library of the API 20E system contained only three species of *Pasteurella* prompted us to use the MicroSeq 500 16S ribosomal DNA (rDNA) bacterial sequencing kit (PE Applied Biosystems, Foster City, Calif.). A 527-bp portion of the amplified DNA was sequenced on an automated DNA sequencer (377 ABI Prism; PE Applied Biosystems). These 527 bp were compared with National Center for Biotechnology Information GenBank entries by using the BLAST algorithm, giving 97% homology with *P. dagmatis* and 94% with *P. multocida*. The molecular identification of *P. dagmatis* was the most reliable, corresponding to the phenotypic identification. At the same time, because the colony morphologies of the two *Pasteurella* species are similar, hydrolysis of urea was tested on several colonies of the primary isolate to rule out the possibility of a coinfection with *P. multocida*, as described by Zbinden et al. for cat-bite wounds (8). All the colonies were urease positive. At last, in vitro susceptibility tests, using a disk-diffusion technique on Mueller-Hinton agar with 5% horse blood added, showed that this bacterium was susceptible to ampicillin, piperacillin, cefotaxime, aminoglycosides, trimethoprim-sulfamethoxazole, and fluoroquinolones.

*Pasteurella* species exist as normal upper respiratory and gastrointestinal flora of cats (50 to 90% colonized) and dogs (50 to 66% colonized) and may colonize the human respiratory tract in underlying respiratory tract disease. Among the *Pasteurella* species, *P. multocida* is most frequently reported (3). We report a case of continuous ambulatory peritoneal dialysis (CAPD) peritonitis, which was for the first time attributed to *P. dagmatis* using a combination of phenotypic and molecular methods for identification. CAPD peritonitis is usually caused by a single organism. Coagulase-negative staphylococci are the most commonly identified agents (7). *Pasteurella* species are rarely reported. In the recent literature, the clinical and microbiological features of *P. multocida* cases have been described (4, 5). To prevent peritonitis due to *Pasteurella* spp. in the patient undergoing CAPD, animals should be kept away from the location of exchanges, and animal contact with peritoneal dialysis equipment must be avoided. In the *P. dagmatis* endocarditis case described by Sorbello et al. (6), the bacterium was identified by using two commercial identification kits. Discrepancies were found between these methods, and the identification was eventually made possible by combining phenotypic features obtained with the different identification systems. Using several
commercial kits, it is indeed possible to gather all the necessary substrates to obtain a correct identification, but this approach is time-consuming. Moreover, the commercial identification systems are not useful to differentiate *P. multocida* from *P. dagmatis*, since *P. dagmatis* is not included in the existing database. Fajfar-Whetstone et al. (2) were able to obtain a good identification of *P. dagmatis*, not with the API 20E system but with the test for hydrolysis of urea, thus showing the limits of the commercial kit. Among *Pasteurella* spp., *P. multocida* is the most frequently reported organism (3), particularly in CAPD, but the method of identification is rarely described (4, 5). The molecular approach using 16S rDNA bacterial sequencing is an alternative method to identify the bacterium. The use of the Microseq 500 16S rDNA bacterial sequencing kit allowed us to confirm in 1 day, in a routine diagnostic laboratory, the first reported case of *P. dagmatis* peritonitis in a CAPD patient. This method would appear a useful approach to identify species of *Pasteurella* not included in the existing database of commercial identification kits, as well as subspecies of *P. multocida* which may be difficult to identify using phenotypic tests (1), thus giving more information on the pathogenicity of such bacteria when they are found in clinical samples.

REFERENCES