dence of colonization by other peritoneal pathogens, and more specifically by gram-negative bacteria (GNB), among PD patients, and to disclose its potential correlation with PD-related infections. During a 3-year period, they prospectively screened 152 PD patients and 99 partners every other month for nasal and pericatheter bacterial colonization (total follow-up for patients, 3,182 months). They performed 1,089 sample assays in patients and 561 in partners.

Although *S. aureus* and coagulase-negative *Staphylococcus* species predominated in both patients and partners, the authors recovered GNB from 15.8% (nares) and 22.4% (pericatheter) of the patients and from 29.3% of the partners. Most isolations of GNB were transient and only 7.2% of the patients and 7.1% of the partners had the same GNB isolated in at least 2 controls from the same sampling. Older age, male gender, longer follow-up on PD, previous immunosuppressive therapy, low socioeconomic status, and a high global incidence of peritonitis were predictive of colonization by GNB.

Previous pericatheter mupirocin therapy was also associated with later colonization by GNB. Nasal or pericatheter colonization by bacteria other than *S. aureus,* particularly GNB, had a poor predictive power for PD-related infections.

The authors concluded that nasal and pericatheter bacterial colonization is variable in PD patients and their partners, and includes the significant presence of potentially pathogenic GNB. Colonization by GNB was not clearly associated with an increased risk of peritonitis or exit-site infection in these patients.

FROM: Perez-Fontan M, Rodriguez-Carmona A, Rosales M, Garcia-Falcon T, Valdes F. Incidence and clinical significance of nasal and pericatheter colonization by Gram-negative bacteria among patients undergoing chronic peritoneal dialysis. *Nephrol Dial Transplant* 2002;17:118-122.

Nosocomial Pathogen: *Moraxella catarrhalis*

Verduin and colleagues from The Netherlands point out that *Moraxella catarrhalis* (formerly known as *Branhamella catarrhalis*) has emerged as a significant bacterial pathogen of humans during the past 2 decades. Microbiological and molecular diagnostic techniques have been developed and improved for *M. catarrhalis*, allowing the adequate determination and taxonomic positioning of this pathogen. Also, studies have revealed its involvement in respiratory (eg, sinusitis, otitis media, bronchitis, and pneumonia) and ocular infections in children and in laryngitis, bronchitis, and pneumonia in adults. The development of (molecular) epidemiologic tools has enabled the national and international distribution of *M. catarrhalis* strains to be established, and has allowed the monitoring of nosocomial infections and the dynamics of carriage. Indeed, such monitoring has revealed an increasing number of ß-lactamase–positive *M. catarrhalis* isolates (now well above 90%), underscoring the pathogenic potential of this organism.

Although several putative *M. catarrhalis* virulence factors have been identified and described in detail, their relationship to actual bacterial adhesion, invasion, and complement resistance (and, ultimately, their role in infection and immunity) has been established in only a few cases. In the past 10 years, various animal models for the study of *M. catarrhalis* pathogenicity have been described, but not all of them are suitable for the study of human infection. Techniques involving the molecular manipulation of *M. catarrhalis* genes and antigens are also advancing our knowledge of the host response to and pathogenesis of this bacterial specie in humans, as well as providing insights into possible vaccine candidates. This review aims to outline our current knowledge of *M. catarrhalis*, an organism that has evolved from an emerging to a well-established human pathogen.

FROM: Verduin CM, Hol C, Fleer A, van Dijk H, van Belkum A. *Moraxella catarrhalis:* from emerging to established pathogen. *Clin Microbiol Rev* 2002;15:125-144.

Antimicrobial Formulary Change and Hospital Resistance Patterns

Empey and colleagues from the University of Kentucky Chandler Medical Center, Lexington, Kentucky, evaluated a university hospital formulary change that was designed to reduce the use of the third-generation cephalosporins ceftazidime and cefotaxime and replace them with the so-called "fourth-generation" cephalosporin cefepime. A retrospective review of antibiotic use and antimicrobial resistance was performed during two 6-month periods before and after the formulary change. All hospitalized patients with vancomycin-resistant *Enterococcus* (VRE), ceftazidime-resistant *Klebsiella pneumoniae* (CRKP), methicillin-resistant *Staphylococcus aureus* (MRSA), piperacillin-resistant *Pseudomonas aeruginosa* (PRPA), and ceftazidime-resistant *P. aeruginosa* (CRPA) infections were included in the study.

Ceftazidime use decreased from 9,600 to 99 g, and cefotaxime use decreased from 6,314 to 732 g, which represented a combined decrease of 89%. Use of cefepime increased from 0 to 5,396 g. Infections from CRKP decreased from 13% to 3%, PRPA infections decreased from 22% to 14%, and CRPA infections decreased from 25% to 15% ($P < .05$ for all). Infections from MRSA dropped insignificantly, and VRE infections increased significantly.

Substituting cefepime for ceftazidime and cefotaxime while reducing the overall use of cephalosporins appears to decrease the rates of CRKP, PRPA, and CRPA.

FROM: Empey KM, Rapp RP, Evans ME. The effect of an antimicrobial formulary change on hospital resistance patterns. *Pharmacotherapy* 2002;22:81-87.