**Moraxella catarrhalis, a Human Respiratory Tract Pathogen**

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**Moraxella catarrhalis** is an exclusively human pathogen and is a common cause of otitis media in infants and children, causing 15%–20% of acute otitis media episodes. *M. catarrhalis* causes an estimated 2–4 million exacerbations of chronic obstructive pulmonary disease in adults annually in the United States. *M. catarrhalis* resembles commensal *Neisseria* species in culture and, thus, may be overlooked in samples from the human respiratory tract. The prevalence of colonization of the upper respiratory tract is high in infants and children but decreases substantially in adulthood. Most strains produce β-lactamase and are thus resistant to ampicillin but susceptible to several classes of oral antimicrobial agents. Recent work has elucidated mechanisms of pathogenesis and focused on vaccine development to prevent otitis media in children and respiratory tract infections caused by *M. catarrhalis* in adults with chronic obstructive pulmonary disease.

For most of the past century, *Moraxella catarrhalis* was regarded as an upper respiratory tract commensal organism. However, since the late 1970s it has been clear that *M. catarrhalis* is an important and common human respiratory tract pathogen. *M. catarrhalis* has an interesting and checkered taxonomic history. After having initially been named *Micrococcus catarrhalis*, the organism’s name was subsequently changed to *Neisseria catarrhalis*, because of its similarities in phenotype and ecological niche to commensal *Neisseria* species. The bacterium was transferred to a new genus, *Branhamella*, in 1970, because of limited DNA homology with *Neisseria* species. *Branhamella catarrhalis* was subsequently placed in the genus *Moraxella* on the basis of biochemical and genetic relatedness, and *Moraxella catarrhalis* is now the widely accepted name.

The species *M. catarrhalis* is composed of 2 distinct lineages. One lineage that expanded in humans ~5 million years ago is associated with virulence properties, including serum resistance and adherence to epithelial cells. The recognition of *M. catarrhalis* as a common respiratory tract pathogen in children and adults has stimulated novel investigation over the past 2 decades into the microbiology, molecular epidemiology, pathogenesis, genetics, and host response to *M. catarrhalis*. More recently, the widespread use of pneumococcal conjugate vaccines has altered nasopharyngeal colonization patterns and caused an increased prevalence of colonization and infection by *M. catarrhalis*.

The objective of this review is to outline the clinical manifestations and epidemiology of *M. catarrhalis*, particularly as a causal agent of otitis media in children and exacerbations of chronic obstructive pulmonary disease (COPD) in adults, the 2 most common infectious diseases caused by *M. catarrhalis*. In addition, we will highlight recent work elucidating mechanisms of pathogenesis and update the status of vaccine development.

**M. catarrhalis and Otitis Media**

**Acute otitis media.** Approximately 80% of children experience an episode of otitis media by the age of 3 years. Otitis media is the most common bacterial infectious disease in childhood and the most common reason for which children receive antibiotics [1]. On the basis of culture of middle ear fluid obtained by tympanocentesis, which is the gold standard for determining etiology, *Streptococcus pneumoniae*, nontypeable *Haemophilus influenzae*, and *M. catarrhalis* are the predominant causes of acute otitis media. Overall, on the basis of cultures of middle ear fluid, 15%–20% of acute otitis media episodes are caused by *M. catarrhalis* (figure 1) [2–9].

Acute otitis media due to *M. catarrhalis* and *H. influenzae* are clinically milder than that caused by *S. pneumoniae*, with less fever and a lower likelihood of observing a red bulging tympanic membrane [10]. However, substantial overlap is observed, such that these characteristics do not allow one to pre-
dict etiology in an individual patient. Tympanocentesis is required to make an etiological diagnosis of otitis media, but this procedure is not performed routinely. Therefore, treatment of otitis media is generally empirical.

**Recurrent otitis media and otitis media with effusion.**

Otitis media with effusion refers to the presence of middle ear fluid without clinical signs of acute otitis media. Children who have ≥4 episodes of acute otitis media in a year or who experience at least 8 months of middle ear effusion in a year are defined as otitis prone [11]. Otitis prone children may experience conductive hearing loss, with resultant delays in speech and language development [12].

When middle ear fluid samples from children who have otitis media with effusion are analyzed using sensitive methods such as polymerase chain reaction, up to 80% contain bacterial DNA from *H. influenzae*, *M. catarrhalis*, or *S. pneumoniae*, suggesting that bacteria play a role in the disease [13–16]. Indeed, *M. catarrhalis* DNA is detected in a larger proportion of cases of otitis media with effusion than of acute otitis media. Although the presence of bacterial DNA may indicate the presence of viable but nonculturable bacteria, the significance of these observations is not yet fully known.

The role of biofilms in otitis media has received an increasing amount of attention recently, particularly in the setting of recurrent otitis media and otitis media with effusion. A biofilm is a community of bacteria enveloped in a self-produced matrix that adheres to a surface. Bacteria in the form of biofilms are relatively resistant to antibiotics and to host immune mechanisms. Biofilms of *M. catarrhalis* are present in the middle ears of children with otitis media and may account, in part, for recurrent and chronic otitis media [17]. However, the role of biofilms in the pathogenesis of otitis media is not yet fully elucidated.

**M. CATARRHALIS AND COPD**

The course of COPD is characterized by intermittent worsening of symptoms, called exacerbations. Exacerbations are associated with lost work time, emergency room visits, hospital admissions, respiratory failure, and sometimes death. The best estimates indicate that approximately one-half of exacerbations are caused by bacterial infection, with the remainder being caused by viral infection and noninfectious causes [18]. The clinical features of an exacerbation due to *M. catarrhalis* are similar to those of exacerbations due to other pathogenic bacteria, including *H. influenzae* and *S. pneumoniae*. The cardinal symptoms of COPD exacerbations are increased sputum production, sputum purulence, and dyspnea, compared with baseline symptoms. Other features may include fever and fatigue. There is much variability in the combination of symptoms that occurs with each exacerbation. Examination of the chest usually reveals rhonchi and generalized decreased air entry. Localized crackles should prompt chest radiography to exclude pneumonia. A Gram-stained smear of sputum reveals neutrophils and abundant gram-negative diplococci, including intracellular bacteria (figure 2).

Point-prevalence studies suggest that *M. catarrhalis* is an important cause of exacerbations of COPD [19–21]. However, because *M. catarrhalis* is isolated from the sputum of adults with COPD even during clinically stable periods, one cannot conclude that the presence of the bacterium in the sputum of an adult with an exacerbation of COPD indicates that *M. catarrhalis* is the cause of the exacerbation. Four main lines of
evidence support the conclusion that \textit{M. catarrhalis} causes exacerbations of COPD.

**Lower respiratory tract bacteriology.** Bacterial pathogens are present in the airways in concentrations associated with respiratory tract infection in approximately one-half of adults with exacerbations of COPD when the distal airways are sampled using bronchoscopy with the protected specimen brush or transtracheal aspiration. \textit{M. catarrhalis} is among the bacterial species that are isolated from the distal airways in such studies [20, 22–24].

**Acquisition of new strains.** Molecular typing of longitudinally collected strains reveals that, rather than increases in the numbers of a persistent colonizing strain, the acquisition of a new bacterial pathogen plays a central role in the pathogenesis of bacterial exacerbations [25]. In approximately one-half of the instances when an adult with COPD acquires a new strain of \textit{M. catarrhalis}, clinical symptoms of exacerbation are observed [25, 26]. This rate is similar to that observed for exacerbations after acquisition of new strains of \textit{H. influenzae} and \textit{Pseudomonas aeruginosa} and somewhat higher than that observed for \textit{S. pneumoniae}.

**Immune responses.** Adults with COPD who experience exacerbations associated with acquisition of new strains of \textit{M. catarrhalis} develop immune responses after infection. In a longitudinal study, we examined monthly sputum cultures from 104 patients with COPD over a period of 81 months and demonstrated that, of the 50 patients who acquired \textit{M. catarrhalis}, 72% generated new systemic or mucosal antibody responses to their homologous isolates [26]. Clearance of the strain from the respiratory tract was associated with strain-specific protection.

**Airway inflammation.** Sputum from patients with exacerbations associated with acquisition of a new strain of \textit{M. catarrhalis} have elevated markers of airway inflammation compared with exacerbations in which no bacterial pathogen is isolated [27, 28]. Because the severity of clinical symptoms of exacerbations closely parallels levels of airway inflammation, these observations strongly implicate \textit{M. catarrhalis} in the etiology of exacerbations, specifically after acquisition of a new strain.

**Prevalence of \textit{M. catarrhalis} as a cause of exacerbations.** As outlined above, results of studies that analyzed lower airway bacteriology, acquisition of new strains, immune responses, and host inflammatory responses represent independent lines of evidence suggesting that \textit{M. catarrhalis} causes exacerbations of COPD (table 1). On the basis of the results of an ongoing prospective study, \textit{M. catarrhalis} is the second most common bacterial cause of exacerbations after \textit{H. influenzae} (figure 3). The best estimate is that \textit{M. catarrhalis} causes \(~10\%\) of exacerbations of COPD, accounting for 2–4 million exacerbations annually in the United States [26].

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### Table 1. Evidence indicating that \textit{Moraxella catarrhalis} causes exacerbations of chronic obstructive pulmonary disease.

<table>
<thead>
<tr>
<th>Evidence</th>
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<tbody>
<tr>
<td>Presence of \textit{M. catarrhalis} in lower airways detected by bronchoscopy with protected specimen brush during exacerbation [20, 22–24]</td>
</tr>
<tr>
<td>Acquisition of new strain associated with exacerbations [25, 26]</td>
</tr>
<tr>
<td>Development of strain-specific protection following clearance [26]</td>
</tr>
<tr>
<td>Development of new systemic and/or mucosal antibody responses following clearance [26, 29–32]</td>
</tr>
<tr>
<td>Increased airway inflammation in \textit{M. catarrhalis} culture-positive exacerbation, compared with culture-negative exacerbation [27, 28]</td>
</tr>
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**Chronic colonization of the airways in persons with COPD.** The respiratory tract of healthy people is sterile below the vocal cords. However, the lower airways of some adults with COPD are colonized by bacteria as a result of impaired mucociliary clearance, even in a clinically stable state. Carefully performed point-prevalence studies that have used bronchoscopy and a protected specimen brush to obtain uncontaminated lower airway cultures have demonstrated that \textit{M. catarrhalis} colonizes the lower respiratory tract in up to 2.5%–10% of adults with COPD while in a stable state [22, 33]. Bacteria in the airways slough highly inflammatory cell wall antigens into the airways, and this process contributes to the airway inflammation that is a hallmark of COPD.

**OTHER INFECTIONS CAUSED BY \textit{M. CATARRHALIS}\**

**Sinusitis.** Bacterial sinusitis occurs after a small percentage of viral upper respiratory tract infections. \textit{M. catarrhalis} is responsible for \(~20\%\) of cases of acute bacterial sinusitis in children and a smaller proportion of cases in adults [34–36]. Sinusitis due to \textit{M. catarrhalis} is clinically indistinguishable from that caused by \textit{S. pneumoniae} or \textit{H. influenzae}.

**Bacteremia, pneumonia, and other invasive infections.** Pneumonia due to \textit{M. catarrhalis} occurs infrequently but is well described in elderly persons, especially in those with underlying cardiopulmonary disease [37]. \textit{M. catarrhalis} rarely causes bacteremic illness. A recent review identified only 72 reported cases [38]; these cases included endocarditis, pneumonia with bacteremia, preseptal and periorbital cellulitis, neonatal meningitis, and septic arthritis. No clear association between \textit{M. catarrhalis} infection and a particular immunodeficiency has been identified [39].

**EPIDEMIOLOGY AND DYNAMICS OF RESPIRATORY TRACT COLONIZATION**

**Children.** \textit{M. catarrhalis} is an exclusively human pathogen with an ecological niche in the human respiratory tract. The prevalence of colonization of the upper respiratory tract is
highly dependent on age. Whereas the rate of colonization among adults is low (1%–5%), nasopharyngeal colonization is quite common through infancy [40, 41]. A substantial variation in rates of colonization is observed in different geographic regions. One study in Buffalo, New York, demonstrated that 66% of infants were colonized at least once during the first year of life, whereas a similar study in Goteborg, Sweden, demonstrated colonization at one-half of that rate [42, 43]. Active turnover of different strains is observed. In a study of rural aboriginal infants near Darwin, Australia, 100% of infants were colonized with *M. catarrhalis* by the age of 3 months [44]. Several factors—including living conditions, hygiene, environmental factors (e.g., household smoking), genetics of the population, and others—likely account for differences in colonization rates. The pathogenesis of otitis media involves migration of bacterial pathogens from the nasopharynx to the middle ear via the Eustachian tube; therefore, patterns of nasopharyngeal colonization are important determinants of otitis media.

A change in patterns of nasopharyngeal colonization is occurring in countries where pneumococcal conjugate vaccines are used widely. Colonization by vaccine serotypes of *Pneumococcus* is decreasing, and colonization by the nonvaccine pneumococcal serotypes *H. influenzae* and *M. catarrhalis* is increasing, resulting in a shift in the pathogens that cause otitis media [45, 46]. Revai et al. [47] demonstrated a significantly greater prevalence of *M. catarrhalis* in the nasopharynx during episodes of otitis media in children who had received the vaccine, compared with the prevalence among episodes that occurred before introduction of the pneumococcal conjugate vaccine. Pneumococcal vaccination does not affect the genetic diversity of nasopharyngeal isolates of *M. catarrhalis*, suggesting that the increase in prevalence of colonization will translate to increased rates of otitis media [48]. Similar shifts are being observed among children and adults with sinusitis [36, 49].

**Adults with COPD.** Although clinical trials demonstrate that *M. catarrhalis* is cultured frequently from adults with COPD, point-prevalence studies do not paint a full picture of the dynamics of acquisition, colonization, and clearance in the setting of COPD. Longitudinal analysis, including the molecular typing of strains, demonstrates that once a strain is cleared, protection from reacquisition of the same strain is observed [26]. The median duration of carriage of a strain was relatively short (~1 month). This pattern of colonization is quite distinct from that of *H. influenzae*, in which a subset of strains causes persistent colonization for months to years in adults with COPD.

**Nosocomial transmission.** *M. catarrhalis* is transmitted among patients in hospitals, particularly in multiple-bed wards and during winter months [50, 51]. Clusters of *M. catarrhalis* respiratory tract infections have been reported in hospital units, but one must be cautious in concluding that the bacterium is the cause of infection when it is isolated [52–54].

**MICROBIOLOGICAL DIAGNOSIS**

*M. catarrhalis* is a gram-negative diplococcus that produces nonhemolytic, round, opaque colonies on blood agar. Colonies of *M. catarrhalis* resemble commensal *Neisseria* that are present in the normal human upper airway flora. *M. catarrhalis* colonies can be slid along the agar surface without disruption; this is termed the “hockey puck sign.” In addition, after 48 h of growth *M. catarrhalis* colonies tend to be larger than those of *Neisseria* and take on a pink color. The difficulty in distinguishing colonies of *M. catarrhalis* from those of *Neisseria* explains, in part, why *M. catarrhalis* has been overlooked as a respiratory tract...
Table 2. Adhesins and potential vaccine antigens of Moraxella catarrhalis.

<table>
<thead>
<tr>
<th>Adhesin</th>
<th>Molecular mass</th>
<th>Putative function and other features</th>
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<tbody>
<tr>
<td>MID/Hag</td>
<td>200 kDa</td>
<td>Adhesin; binds immunoglobulin D; hemagglutinin</td>
</tr>
<tr>
<td>MchA1, MchA2 (MhaB1, MhaB2)</td>
<td>184 kDa, 201 kDa</td>
<td>Filamentous hemagglutinin-like adhesin</td>
</tr>
<tr>
<td>McmA</td>
<td>110 kDa</td>
<td>Metallopeptidase-like adhesin</td>
</tr>
<tr>
<td>TbpB (OMP B1)</td>
<td>80–85 kDa</td>
<td>Binds transferrin</td>
</tr>
<tr>
<td>UspA1</td>
<td>88 kDa (oligomer)</td>
<td>Adhesin; binds laminin</td>
</tr>
<tr>
<td>UspA2</td>
<td>62 kDa (oligomer)</td>
<td>Binds complement, vitronectin, and laminin</td>
</tr>
<tr>
<td>Msp 75</td>
<td>~75 kDa</td>
<td>Homology to succinic dehydrogenase</td>
</tr>
<tr>
<td>McaP</td>
<td>66 kDa</td>
<td>Adhesin; phospholipase B</td>
</tr>
<tr>
<td>OMP E</td>
<td>50 kDa</td>
<td>Possible fatty acid transport</td>
</tr>
<tr>
<td>OMP CD</td>
<td>45 kDa</td>
<td>OmpA-like protein; binds mucin; adhesin</td>
</tr>
<tr>
<td>M35</td>
<td>36.1 kDa</td>
<td>Porin; conserved with 1 variable loop</td>
</tr>
<tr>
<td>OMP G1a</td>
<td>~29 kDa</td>
<td>Lipoprotein; copper transport protein</td>
</tr>
<tr>
<td>OMP G1b</td>
<td>~29 kDa</td>
<td>Surface molecule; unknown function</td>
</tr>
<tr>
<td>OpA</td>
<td>24 kDa</td>
<td>Homologous with Neisseria Opa adhesins</td>
</tr>
<tr>
<td>Msp 22</td>
<td>~22 kDa</td>
<td>Surface lipoprotein; divalent ion transport</td>
</tr>
<tr>
<td>Type IV pili</td>
<td>16 kDa</td>
<td>Adhesin; transformation; biofilm formation</td>
</tr>
<tr>
<td>OMP J</td>
<td>19 kDa, 16 kDa</td>
<td>Homologous with Neisseria Opa adhesins</td>
</tr>
<tr>
<td>Lipooligosaccharide</td>
<td>2.5–4 kDa</td>
<td>Detoxified form is potential vaccine antigen</td>
</tr>
</tbody>
</table>

Pathogen. Gram-stained smears of sputum samples that contain M. catarrhalis demonstrate gram-negative diplococci as the predominant bacterial form, with bacteria typically observed intracellularly within neutrophils (figure 2). Accurately distinguishing M. catarrhalis from commensal Neisseria in sputum cultures is important to recognize and treat respiratory tract infections caused by M. catarrhalis.

A variety of biochemical tests can distinguish M. catarrhalis from Neisseria. M. catarrhalis produce oxidase, catalase, and DNase (detected using DNase test agar with methyl green); reduce nitrate and nitrite; and hydrolyze tributyrin. M. catarrhalis does not ferment carbohydrates. Kits that use these biochemical reactions are commercially available.

Sensitive methods, such as polymerase chain reaction, to detect M. catarrhalis and other bacterial pathogens in respiratory secretions are in development. Indeed, M. catarrhalis DNA in middle ear effusions can be detected by polymerase chain reaction in children with otitis media [13–15, 17]. The application of such sensitive assays are likely to contribute important new observations about the epidemiology and disease patterns of M. catarrhalis, but they are not yet commercially available.

PATHOGENESIS OF INFECTION

The pathogenesis of bacterial otitis media involves the migration of bacteria from the nasopharynx to the middle ear via the Eustachian tube, which is often precipitated by a preceding viral infection. The acquisition of a new strain of M. catarrhalis is a key element in the pathogenesis of exacerbations of COPD. Analysis of the genetic relationships among strains indicates that strains of M. catarrhalis differ with regard to virulence [55–57]. The species is composed of 2 distinct lineages; the seroresistant lineage appears to be more strongly associated with virulence [57]. Furthermore, the distribution of virulence-associated genotypes and phenotypes differs in strains found in children, compared with those found in adults [58].

The recognition of M. catarrhalis as an important human pathogen has stimulated active investigation into the molecular mechanisms of pathogenesis, and some of these observations are highlighted briefly here. A critical initial step in colonization and infection is adherence to the respiratory tract epithelium. Table 2 lists the growing number of adhesins that have been identified in M. catarrhalis.

M. catarrhalis was previously thought to be an exclusively extracellular pathogen. However, M. catarrhalis invades multiple cell types, including bronchial epithelial cells, small airway epithelial cells, and type 2 alveolar cells [59]. Furthermore, M. catarrhalis is present intracellularly in human pharyngeal lymphoid tissue, providing a potential reservoir for persistence in the human respiratory tract [60].

One mechanism that M. catarrhalis uses to subvert innate host immune responses is complement inactivation by multiple mechanisms that render strains of M. catarrhalis resistant to killing by human serum [61, 62]. Indeed, seroresistant strains may be more virulent [55, 57].

M. catarrhalis forms biofilms in vitro and have been identified in middle ear samples obtained from children [17, 63]. The role of biofilms in the pathogenesis of otitis media is an area of active investigation. M. catarrhalis induces activation of the mitogen-activated protein kinase and nuclear factor–κB sig-
naling systems in bronchial epithelial cells, with release of interleukin-8 and granulocyte-macrophage colony-stimulating factor from the cells [64]. Three serotypes of M. catarrhalis have been identified based on structural differences in lipooligosaccharide [65]. Serotype A is the predominant type among clinical isolates. The distribution of serotypes appears to differ by patient age, with isolates from adults having a somewhat greater proportion of serotype A, compared with those from children [58, 65]. Lipooligosaccharide is likely a key inducer of the host inflammatory response.

**Animal models.** Studies of the pathogenesis of and host response to M. catarrhalis infection have been limited by the absence of a good animal model of infection. M. catarrhalis does not readily infect or colonize a variety of laboratory animal species, consistent with the observation that M. catarrhalis is an exclusively human pathogen. The chinchilla model of otitis media that has yielded important observations in the case of S. pneumoniae and H. influenzae has not been useful in studying M. catarrhalis, because the organism is cleared readily from the middle ear of chinchillas and other animals. Chinchillas can be colonized in the nasopharynx for several weeks and, thus, may be useful for studies of colonization. A mouse pulmonary clearance model has been useful for assessing putative vaccine antigens (see the Status of Vaccine Development section).

**TREATMENT CONSIDERATIONS**

More than 90% of M. catarrhalis produce a β-lactamase and are, thus, resistant to ampicillin. Two types of β-lactamases have been identified, BRO-1 and BRO-2 [66]. After the rapid acquisition of β-lactamase in the 1970s and 1980s, the antimicrobial susceptibility of M. catarrhalis has remained relatively stable in surveys of worldwide collections of strains [67, 68]. Many infections due to M. catarrhalis can be treated with oral antibiotic therapy. Table 3 lists oral antibiotics that are active against M. catarrhalis. Treatment of otitis media in children and exacerbations of COPD in adults, the 2 most common infectious diseases caused by M catarrhalis, is generally empirical [1, 18]. Therefore, antimicrobial agents that are active against S. pneumoniae and H. influenzae, in addition to M. catarrhalis, are usually administered.

**STATUS OF VACCINE DEVELOPMENT**

A vaccine that would prevent otitis media in children, particularly otitis prone children, would have an enormous human and economic impact. Otitis media accounts for >13 million antibiotic prescriptions annually and approximately $6 billion in health care costs in the United States annually [1]. A recent clinical trial assessing a vaccine that is composed of pneumococcal polysaccharide of 11 capsular serotypes conjugated to protein D, a surface protein of H. influenzae, demonstrated partial protection against both pneumococcal and H. influenzae otitis media [69]. The demonstration of induction of a protective response against H. influenzae with a surface protein antigen represents proof of principle for the approach of using a surface protein of a nonencapsulated gram-negative bacterium as a vaccine antigen. A successful vaccine for otitis media should be directed toward preventing infection due to S. pneumoniae, H. influenzae, and M. catarrhalis. A second population that would benefit from a vaccine to prevent M. catarrhalis infections are adults with COPD.

An obstacle for the development of a vaccine against M. catarrhalis is the absence of a good animal model. The most widely used model for assessing M. catarrhalis vaccine antigens is the mouse pulmonary clearance model, which measures clearance of bacteria from the lungs following bacterial challenge directly into the airways. However, this model system does not simulate human respiratory tract infection, because animals do not show evidence of infection but rather clear M. catarrhalis in ~24 h. The identification of a reliable correlate of protection from M. catarrhalis infection, such as an in vitro assay or an animal model, would facilitate vaccine development for M. catarrhalis.

The observation that patients with COPD appear to develop strain-specific protection after clearing M. catarrhalis supports the feasibility of inducing protective responses to M. catarrhalis [26]. The challenge is to design a vaccine that will induce such a protective response against all strains. An approach that has been taken by several research groups has been to identify and assess conserved surface molecules as vaccine antigens. The ideal vaccine antigen would be (1) present on the surface of all strains, (2) antigenically conserved among strains, (3) expressed during infection of the human host, (4) immunogenic in infants, and (5) capable of inducing a protective immune response. Recently, a genome-mining approach has identified additional vaccine antigens for M. catarrhalis [70]. Table 2 summarizes several potential vaccine antigens that are in various stages of development.

**SUMMARY**

M. catarrhalis is an exclusively human pathogen that may be overlooked in culture because of its phenotypic similarity to commensal Neisseria, which are part of the normal flora of the

Table 3. Oral antimicrobial agents to which most strains of Moraxella catarrhalis are susceptible.

<table>
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<th>Drug</th>
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<tr>
<td>Amoxicillin-clavulanic acid</td>
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<tr>
<td>Extended-spectrum cephalosporins (e.g., cefixime, cefpodoxime, cefaclor, loracarbef, and cefuroxime)</td>
</tr>
<tr>
<td>Newer macrolides (e.g., azithromycin and clarithromycin)</td>
</tr>
<tr>
<td>Trimethoprim-sulfamethoxasole</td>
</tr>
<tr>
<td>Tetracyclines</td>
</tr>
<tr>
<td>Fluoroquinolones</td>
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upper respiratory tract. Widespread administration of pneumococcal conjugate vaccines may be causing an increase in *M. catarrhalis* infections by altering patterns of nasopharyngeal colonization. *M. catarrhalis* causes 10%–20% of otitis media episodes in children and is the second most common cause of exacerbations of COPD in adults. The species is composed of 2 distinct genetic lineages that appear to differ with regard to virulence capabilities. A vaccine to prevent *M. catarrhalis* infections would have a substantial human and economic impact. Several potential vaccine antigens are in various stages of development.

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