Colonization of healthy children by *Moraxella catarrhalis* is characterized by genotype heterogeneity, virulence gene diversity and co-colonization with *Haemophilus influenzae*

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The colonization dynamics of *Moraxella catarrhalis* were studied in a population comprising 1079 healthy children living in Rotterdam, The Netherlands (the Generation R Focus cohort). A total of 2751 nasal swabs were obtained during four clinic visits timed to take place at 1.5, 6, 14 and 24 months of age, yielding a total of 709 *M. catarrhalis* and 621 *Haemophilus influenzae* isolates.

Between January 2004 and December 2006, approximate but regular 6-monthly cycles of colonization were observed, with peak colonization incidences occurring in the autumn/winter for *M. catarrhalis*, and winter/spring for *H. influenzae*. Co-colonization was significantly more likely than single-species colonization with either *M. catarrhalis* or *H. influenzae*, with genotypic analysis revealing no clonality for co-colonizing or single colonizers of either bacterial species. This finding is especially relevant considering the recent discovery of the importance of *H. influenzae–M. catarrhalis* quorum sensing in biofilm formation and host clearance. Bacterial genotype heterogeneity was maintained over the 3-year period of the study, even within this relatively localized geographical region, and there was no association of genotypes with either season or year of isolation. Furthermore, chronological and genotypic diversity in three immunologically important *M. catarrhalis* virulence genes (*uspA1*, *uspA2* and *hag/mid*) was also observed. This study indicates that genotypic variation is a key factor contributing to the success of *M. catarrhalis* colonization of healthy children in the first years of life. Furthermore, variation in immunologically relevant virulence genes within colonizing populations, and even within genotypically identical *M. catarrhalis* isolates, may be a result of immune evasion by this pathogen. Finally, the factors facilitating *M. catarrhalis* and *H. influenzae* co-colonization need to be further investigated.

**INTRODUCTION**

*Moraxella catarrhalis* is part of the normal bacterial flora in the nasopharynx of children, although over the past two decades, it has emerged as a significant bacterial pathogen and not simply a commensal colonizer (Verduin *et al.*, 2002). Studies have shown that the bacterium rapidly colonizes the nasopharynx soon after birth and that the carriage rate of *M. catarrhalis* in healthy children varies between 7 and 36% (Verhaegh *et al.*, 2010). However, in children with upper respiratory tract infections (URTI), including acute otitis media (AOM), the carriage rate increases to approximately 50% (Berner *et al.*, 1996; Konno *et al.*, 2006; Pettigrew *et al.*, 2008). Otitis media itself is a particularly important URTI during early
childhood and the primary reason for children to visit a physician (Freid et al., 1998; Plasschaert et al., 2006). Furthermore, in many countries, AOM is the most common reason for prescribing antibiotics (Gonzales et al., 2001; Leibovitz, 2003; Pichichero, 2000; Plasschaert et al., 2006) or for undergoing surgery (for the placement of grommets) (Vlastarakos et al., 2007). The most common bacterial species cultured from the nasopharynx of children during otitis media episodes are Streptococcus pneumoniae, Haemophilus influenzae, M. catarrhalis and Staphylococcus aureus, either as single pathogens or as co-cultures (Berner et al., 1996; Pettigrew et al., 2008), with the patterns of nasopharyngeal colonization by micro-organisms being important determinants for otitis media disease (Faden et al., 1991, 1997; Murphy & Parameswaran, 2009).

With respect to M. catarrhalis, it has been shown that many factors affect nasopharyngeal carriage of this human-specific pathogen, including, for example, the presence of siblings, day care attendance and respiratory illness (Faden et al., 1997; Hendley et al., 2005; Peerbooms et al., 2002; Principi et al., 1999; Verhaegh et al., 2010). Furthermore, there is increasing information regarding the biological mechanisms facilitating M. catarrhalis-mediated colonization and disease development, with most publications stressing the importance of bacterial adherence as an essential first step in this process. To date, several important M. catarrhalis adhesins have been described, including the ubiquitous surface proteins UspA1 and UspA2, and the haemagglutinin/Moraxella IgD-binding protein Hag/MID (Bullard et al., 2005; Helminen et al., 1994). UspA1 and UspA2 acquire their adherence characteristics through multifunctional binding sites, which include domains that have the ability to attach to epithelial cells via cell-associated fibronectin, laminin and vitronectin (Tan et al., 2006b). Furthermore, UspA1 includes a critical binding site for carcinoembryonic antigen-related cell adhesion molecules, which are expressed in various human tissues including respiratory epithelia (Hill & Virji, 2003; Slevogt et al., 2008). The Moraxella IgD-binding protein, also referred to as Hag (human erythrocyte agglutinin), is also important for host attachment. MID is an outer-membrane protein (OMP) with specific affinity for soluble and cell-bound human IgD and is the only IgD-binding protein in Moraxella (Forsgren et al., 2001).

Several other virulence-associated genes have been identified that may be associated with colonization and infection of M. catarrhalis, including the OMPS CopB, OMPCD, McaP, MhaB, MhaC, Msp22, Msp75, Msp78 and lipoooligosaccharide (LOS) (Akimana & Lafontaine, 2007; Balder et al., 2007; Lipski et al., 2007; Liu et al., 2007; Riesbeck et al., 2006; Ruckdeschel et al., 2008, 2009; Tan et al., 2006a). Furthermore, several of these virulence genes have also been associated with the induction of the humoral immune response, making them potential vaccine candidate genes. However, relatively little is known about the frequency and the extent of genotypic variation within these virulence genes, and in particular how this variation may be associated with colonization over time.

The aim of this study was to investigate the seasonal and yearly prevalence patterns of longitudinal colonization, genotypic variation and variation in virulence-associated genes of M. catarrhalis isolates colonizing children within a single and distinct geographical region. Using these data, we hoped to discover whether distinct isolate genotypes and/or identical putative vaccine candidate gene types circulated during specific time periods in healthy colonized children. We also investigated the longitudinal prevalence of M. catarrhalis and H. influenzae within our cohort of children, looking for co-colonization trends within this age group. These results will further help our understanding of M. catarrhalis population dynamics and provide insights into the chronological diversity and functionality of virulence-associated genes for this bacterial pathogen.

METHODS

Study population. This study was embedded within the Generation R Focus cohort, part of a population-based prospective cohort study from fetal life until young adulthood based in Rotterdam, The Netherlands (The Generation R Study) (Jaddoe et al., 2007, 2008). Within the Generation R Focus cohort, detailed assessments of fetal and postnatal growth and development were performed on 1232 pregnant Dutch women. The mothers gave birth to 1244 infants between February 2003 and August 2005, in Rotterdam, The Netherlands, of whom 138 were excluded from the study analysis because consent was withdrawn after birth. Twins were also excluded from the analysis because of genetic relatedness, leaving a total of 1079 infants. The medical ethics committee of the Erasmus Medical Center approved the study. Written informed consent was obtained from the parents of all the participants.

Infants visited the Generation R Focus cohort research centre at 1.5, 6, 14 and 24 months after birth, resulting in 630 swabs being taken at 1.5 months, 787 swabs at 6 months, 717 swabs at 14 months and 617 swabs at 24 months between November 2003 and September 2007. From 623 children, at least three swabs were available for bacterial culturing.

Bacterial isolates. Bacterial isolates were cultured from nasal swabs taken from infants at 1.5, 6, 14 and 24 months of age by a trained research nurse, using a sterile transport swab immersed in Amies transport medium. Swabs were cultured within 6 h of sampling, using blood agar plates containing 5% sheep blood, chocolate agar and Haemophilus-selective agar at an incubation temperature of 35 °C in 5% CO₂ for 48 h. Plates were examined daily for the growth of M. catarrhalis and/or H. influenzae.

Genotyping. Genotyping of M. catarrhalis isolates was performed using PFGE and multilocus sequence typing (MLST). PFGE was also performed on H. influenzae isolates.

PFGE for M. catarrhalis was performed as detailed by Verduin et al. (2000). Briefly, M. catarrhalis plug digestions were performed using SphI at 20 U per reaction and an electrophoresis protocol comprising a first block with a constant voltage of 6 V cm⁻¹ and a pulse time from 3.5 to 25 s during the first 12 h, followed by a second block of 8 h where the pulse time increased linearly from 1 to 5 s. The PFGE protocol for H. influenzae was adapted from the work of Moor et al. (1999). Digestions were performed using Smal at 30 U per reaction and an electrophoresis protocol comprising a first block with a constant voltage of 6 V cm⁻¹ and a pulse time from 6 to 8 s during the first 7 h, followed by a second block of 17 h where the pulse time
increased linearly from 1 to 38 s. All PFGE patterns were analysed using BioNumerics (Applied Maths), with gel lanes normalized against a lambda DNA ladder (Bio-Rad) and band tolerance set at 1.5%. PFGE products between 48.5 and 339.5 kb for *M. catarrhalis* and 48.5 and 485 kb for *H. influenzae* were included in the band matching analysis.

MLST genotyping was performed to determine whether *M. catarrhalis* genotypes circulating in the Rotterdam area were similar to *M. catarrhalis* genotypes worldwide and to establish genetic relationships with other internationally recognized clones available in the *M. catarrhalis* MLST database. MLST was performed on 12 *M. catarrhalis* isolates that had been cultured serially on three separate occasions from four children. Briefly, PCR was performed to detect and sequence the *abcZ, adk, efp, funC, glyRS, mutY, ppa* and *trpE* genes as described in the guidelines available at the MLST website (http://mlst.ucc.ie/). A touchdown thermocycling programme was used for *glyRS* and *adk*. The touchdown protocol used an initial annealing temperature of 70 °C, which was reduced by 1 °C per cycle over 15 PCR cycles. The following 20 cycles of amplification used an annealing temperature of 55 °C. For *ppa, efp, abcZ* and *trpE*, a standard PCR protocol comprising an annealing temperature of 52 °C and an elongation time of 2 min at 72 °C for 25 cycles was used, whilst for *funC* and *mutY* an annealing temperature of 55 °C was used. PCR primer pairs were used for amplicon sequencing, except for the genes *glyRS, funC* and *mutY*, which required separate sequencing primers (primers are available at http://mlst.ucc.ie/). Allelic profiles were defined and compared with the MLST types of isolates from different geographical regions available at http://mlst.ucc.ie/.

**PCR screening of virulence genes.** *M. catarrhalis* isolates were grown from the glycerol stock overnight at 37 °C on blood agar plates. DNA was extracted using the MagNA Pure LC System (Roche Applied Science). PCR was performed to detect the *uspA1, uspA2, uspA2H, hag/mid* and *ompl1* genes and 16S rRNA and LOS types as described previously (Verhaegh et al., 2008). A touchdown thermocycling programme was used for all PCRs except for *hag/mid* and LOS PCRs. The touchdown protocol used an initial annealing temperature of 70 °C, which was reduced by 1 °C per cycle over 15 cycles of PCR. The following 20 cycles of amplification used an annealing temperature of 55 °C. All isolates negative for both *uspA2* and *uspA2H* genes were tested using primers *uspA2end.f* and *uspA2end* (Verhaegh et al., 2008), which amplify a conserved region found at the 3′-end of both *uspA2* and *uspA2H* genes.

For the *hag/mid* gene PCR, a standard PCR protocol comprising an annealing temperature of 55 °C and an extension time of 8 min at 68 °C for 25 cycles was used. The LOS-typing PCR protocol was performed as described by Edwards et al. (2005).

After amplification, 16S rRNA PCR products were digested using the enzymes *FspBI* (10 U) and *HhaI* (10 U) according to Verhaegh et al. (2008), to identify the 16S rRNA types (Verhaegh et al., 2008).

**Virulence gene variation.** Virulence gene variation was assessed using PCR–RFLP typing on three major *M. catarrhalis* virulence genes. These genes comprised the ubiquitous surface protein genes *A1* and *A2* (*uspA1* and *uspA2*), and the haemagglutinin/IgG-binding protein gene *hag/mid*. PCR products of these genes were digested using the restriction enzyme *HaeIII* (*BsuRI*), using 10 U per reaction mix, and incubated overnight at 37 °C. The *HaeIII* restriction enzyme was chosen because its recognition site(s) is found within immunologically important regions of the *uspA1, uspA2* and *hag/mid* genes.

PCR–RFLP patterns were analysed using BioNumerics (Applied Maths), with gel lanes normalized against a 1 kb (*uspA2* and *hag/mid*) and 100 bp (*uspA1*) ladder and band tolerance set at 1.5%.

**RESULTS**

**Bacterial isolates**

A total of 709 *M. catarrhalis* isolates and 621 *H. influenzae* isolates were cultured from a total of 2751 nasal swabs obtained during the 3-year study period. The ages of the subjects when the cultures were taken are given in Table 1.

**Population dynamics**

Approximate, but regular, 6-monthly cycles of peak colonization prevalence were observed over the 3-year study period for *M. catarrhalis*, with a less regular pattern observed for *H. influenzae*. Peak seasonal prevalence differed between *M. catarrhalis* and *H. influenzae*, with *M. catarrhalis* prevalence highest in autumn and winter [odds ratio (OR) = 1.3–2.0 compared with spring or summer with *P* < 0.03 for each comparison] and *H. influenzae* prevalence highest in winter and spring (OR = 1.5–1.9; *P* < 0.01). Each species seasonal peak represented a significantly higher risk of carriage compared with non-peak seasons and the odds of a child being colonized by one of the two pathogens were significantly increased if

<p>| Table 1. Number of <em>M. catarrhalis</em> and <em>H. influenzae</em> cultures used in this study |</p>
<table>
<thead>
<tr>
<th>Age at collection (months)</th>
<th><em>M. catarrhalis</em></th>
<th><em>H. influenzae</em></th>
</tr>
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<tbody>
<tr>
<td>1.5</td>
<td>73</td>
<td>44</td>
</tr>
<tr>
<td>6</td>
<td>240</td>
<td>194</td>
</tr>
<tr>
<td>14</td>
<td>212</td>
<td>227</td>
</tr>
<tr>
<td>24</td>
<td>184</td>
<td>156</td>
</tr>
<tr>
<td>n=709</td>
<td>n=621</td>
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the other species was present (OR = 1.5; \( P < 0.0001 \)). The peak in joint occurrences occurred in autumn. If the product of the individual species occurrence proportions is considered an indicator of the expected proportion of joint occurrences, chi-squared analyses showed significant excesses over expectations of joint occurrences for spring (\( P < 0.01 \)), summer (\( P < 0.01 \)) and autumn (\( P = 0.04 \)). Both pathogens were at or near their peak prevalence in 2006 and so the joint prevalence was highest that year at 10.8 %. Conversely, the combined absence of both species in children was at its lowest in 2006 at 49.3 %. For \textit{M. catarrhalis}, there were significantly higher risks in 2006 and 2007 compared with 2004 and 2005 (OR = 1.5–2.1; \( P < 0.01 \)). In contrast, the risk for \textit{H. influenzae} was highest in 2006 compared with other years (OR = 1.3–1.7; \( P < 0.03 \)) (Fig. 1).

Genetic diversity of \textit{M. catarrhalis} and \textit{H. influenzae} isolates

A selection of 112 isolates were arbitrarily chosen for PFGE genotyping from the 709 \textit{M. catarrhalis} isolates cultured in this study, including isolates from children colonized only once during the study period and serial isolates cultured from the same child. A high degree of genotypic heterogeneity was maintained over the entire study period. While 16S rRNA types 2 and 3 (lineage 2) composed a distinct clade, heterogeneity of all markers was independent of year, season and serial colonization status (Fig. 2).

MLST genotyping of 12 \textit{M. catarrhalis} isolates was performed in order to determine the global context of colonizing isolates obtained from Rotterdam, The Netherlands. These 12 isolates originated from four children that were colonized with \textit{M. catarrhalis} on three separate occasions, and represented different PFGE genotypic clusters. The Rotterdam isolates tested were found to be non-clonal in nature with many (8 out of 12) singleton MLST types, further indicating the genetic heterogeneity of \textit{M. catarrhalis} isolates, even within a relatively restricted geographical region (Fig. 3).

Due to the significant association between \textit{M. catarrhalis} and \textit{H. influenzae} colonization, 36 \textit{H. influenzae} isolates (including both co-colonizing and single-species isolations) were chosen for PFGE genotyping to study their genetic diversity. No single \textit{H. influenzae} genotype or clonal cluster was associated with co-colonization events (Fig. 4).

PCR screening of virulence genes

PCR screening of the same 112 \textit{M. catarrhalis} isolates for which PFGE was performed revealed an incidence of 97 % (109/112) for \textit{uspA1}, 80 % (90/112) for \textit{hag/mid}, 83 % (85/102) for \textit{uspA2}, 17 % (17/102) for \textit{uspA2H} and 100 % (112/112) for \textit{ompJ}. Ten isolates were found to be PCR-negative using previously published \textit{uspA2} - and \textit{uspA2H}-specific primers, but positive using primers designed to amplify a conserved region of both \textit{uspA2} and \textit{uspA2H}. These 10 isolates were not included in subsequent \textit{uspA2} and \textit{uspA2H} prevalence calculations, though their inclusion as

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**Fig. 1.** Colonization prevalence of \textit{M. catarrhalis} and \textit{H. influenzae} during 2004–2006. (a) Proportion of \textit{M. catarrhalis} (black line) and \textit{H. influenzae} (dashed line) compared with the total number of swabs per month. The proportion of the joint occurrence of the two pathogens in each month compared with the total number of swabs taken per month is also shown (grey line). Note the approximate 6-monthly colonization cycle (from peak to peak), especially for \textit{M. catarrhalis}. (b) Cumulative percentage of \textit{M. catarrhalis}-positive (black line) and \textit{H. influenzae}-positive (dashed line) swabs recorded during the 3-year study period. Co-culture-positive swabs are also shown (grey line). The cumulative colonization burden in the study population increased at a constant rate both for pathogens and for co-colonization over the 3-year study period.
either uspA2 or uspA2H would not have affected the significance of the results (Table 2).

16S rRNA gene type analysis revealed an incidence of 80% for 16S rRNA type 1 (lineage 1), and a combined 20% for types 2 and 3 (lineage 2). All isolates that belonged to lineage 1 were associated with the presence of the hag/mid gene and OmpJ type 2.

Virulence gene diversity

PCR–RFLP was performed on amplified PCR products of the hag/mid, uspA2 and uspA1 virulence genes of 86 M. catarrhalis isolates to assess virulence gene diversity of colonizing M. catarrhalis. Fig. 5 shows the diverse nature of the PCR–RFLP patterns obtained for hag/mid, uspA2 and uspA1 circulating between 2004 and 2006 in healthy children in Rotterdam, The Netherlands. No distinct clustering of PCR–RFLP patterns was observed during particular months or years, suggesting that many different virulence gene variants circulate within colonizing M. catarrhalis populations at any given time. This indicates that individual gene variation is as extensive as whole-genome polymorphism.

DISCUSSION

The colonization dynamics of M. catarrhalis and H. influenzae were studied in a population of 1079 healthy children living in Rotterdam, The Netherlands. Over the 3-year study period, a trend towards a regular 6-monthly M. catarrhalis colonization cycle (peak to peak) was observed for M. catarrhalis (which was less evident for H. influenzae), without a pronounced seasonal peak for either. This observation tends to contrast with other studies reporting a seasonal influence on M. catarrhalis colonization, although these studies also reported that higher detection rates of M. catarrhalis during the colder months could be a side effect of nasal hyper-secretion induced by viral illness or cold weather (Hendley et al., 2005). Marchisio et al. (2001) concluded that the seasonal influence (comparison between spring and autumn) on nasopharyngeal carriage of respiratory tract pathogens in healthy children was negligible (Marchisio et al., 2001). However, their study was limited in describing seasonal variations due to lack of observations in other years, which would have allowed a better understanding of the dynamics
of the individual pathogens. Our results suggest that colonization with *M. catarrhalis* (and to a lesser extent *H. influenzae*) occurs via regular cycles of colonization and clearance, with the apparent increase in *M. catarrhalis* and *H. influenzae* detection during the winter months probably being a consequence of increased viral respiratory infections, e.g. influenza, resulting in increased opportunity for secondary bacterial infection by bacterial pathogens. The link between seasonal virus infections and resultant secondary bacterial infections has been indicated by several publications (Bakaletz, 1995; Pettigrew et al., 2008; Ruuskanen et al., 1991). However, reports by Meijer et al. (2007) and Arkema et al. (2008), who collected clinical and virological data via the European Influenza Surveillance Scheme (EISS), concluded that the 2005–2006 and 2006–2007 influenza seasons in Europe were characterized by moderate clinical activity (Arkema et al., 2008; Meijer et al., 2007), and as a consequence may have resulted in less viral predisposition of the middle ear epithelium to bacterial infection.

At least two studies have suggested that the presence of a particular bacterial species during URTIs may create a more hospitable niche for co-colonization by a second distinct bacterial species (Armbruster et al., 2010; Pettigrew et al., 2008). Armbruster et al. (2010) showed that *H. influenzae* promotes *M. catarrhalis* persistence within polymicrobial biofilms via inter-species quorum signalling, and that co-infection with both species promotes the increased resistance of biofilms to antibiotics and host clearance (Armbruster et al., 2010). In fact, the process of biofilm formation has been demonstrated for numerous pathogens and is clearly an important microbial survival strategy.

In our present study, co-colonization between *M. catarrhalis* and *H. influenzae* was significantly more likely than colonization with either bacterial species alone. This is an interesting result, as (for example) competition for cellular binding sites may be expected to occur in the presence of two distinct bacterial species, although this hypothesis needs further study. In detail, both species can bind to carcinoembryonic antigen-related cell adhesion molecules (CEACAM)-1, which is a receptor for the OMPs UspA1 and P5 of *M. catarrhalis* and *H. influenzae*, respectively.
CEACAM-1 is a specific innate immune receptor and although the CEACAM-binding ligands of respiratory pathogens are structurally diverse, they target a common site on the receptor (Hill et al., 2005; Sarantis & Gray-Owen, 2007). However, competition for binding sites could be outweighed by non-receptor-mediated factors associated with co-colonization events. For example, *M. catarrhalis* releases outer-membrane vesicles (OMVs) or 'blebs' from its surface during growth in several environments, e.g. liquid culture, solid culture and biofilms. The OMVs that are secreted by *M. catarrhalis* carry UspA1 and UspA2, which are known to interfere with the activation of the complement cascade. Tan et al. (2007) showed that blebs carrying UspA1/A2 protected *H. influenzae* from complement-mediated killing, suggesting that *M. catarrhalis* may promote the survival of *H. influenzae* during co-colonization (Tan et al., 2007). Deich & Hoyer (1982) demonstrated the generation and release of DNA-binding vesicles by *H. influenzae* (Deich & Hoyer, 1982), although this study did not mention the effect of *H. influenzae* blebs on the complement cascade. At this time, no other studies have reported the presence of *H. influenzae* blebs and their possible beneficial effect on other bacterial species in co-culture.

Whatever the exact cause of co-colonization dominance, neither co-colonizing *M. catarrhalis* nor *H. influenzae* belonged to specific genotypic clones, suggesting that a ubiquitous system is facilitating the significant difference in co-colonization (versus single-species colonization) observed in this study. As recently described by Armbruster et al. (2010), the most likely (non-clonal-genotype-related) ubiquitous system driving co-colonization events of these two bacterial pathogens appears to be the quorum sensing system (Armbruster et al., 2010). However, complement-evading systems, e.g. via OMV-mediated protection, may also play a significant role.

Genotypic analysis revealed a high degree of diversity in colonizing *M. catarrhalis* isolates, an observation which is in agreement with previous studies showing that genotypic heterogeneity is typical of worldwide *M. catarrhalis* isolates colonizing both children and adults (Hays et al., 2003; Verhaegh et al., 2008; Wolf et al., 2000). Also, no significant association between genotype (cluster) and season, or year of isolation was observed, which is in contrast with a previous publication by Levy et al. (2009) who reported that winter and spring season was a significant risk factor for clustering. However, Levy et al. (2009) studied transmission between patients within a
relatively confined hospital setting (Levy et al., 2009), whereas the focus of our study was related to community transmission.

The prevalence of the virulence genes uspA1, uspA2 and hag/mid within our Rotterdam isolates was very similar to that previously reported for global M. catarrhalis isolates (Verhaegh et al., 2008). These virulence genes encode OMPs that play an important role in bacterial adherence to human epithelia and complement resistance, as well as being immunogenic (Helminen et al., 1994, 1995; Meier et al., 2003). This finding suggests that equilibrium has been reached with respect to virulence gene distribution in global M. catarrhalis isolates, as local geographical factors do not appear to generate significant differences in virulence gene prevalence.

Finally, a high degree of gene sequence diversity was identified in uspA1, uspA2 and hag/mid virulence genes during the 3-year study period, with no apparent linkage between uspA1, uspA2 and hag/mid banding patterns. Moreover, the PCR–RFLP method used was chosen to target restriction sites associated with immunologically important regions of the corresponding UspA1, UspA2 and Hag/MID proteins. The lack of intra-gene band pattern clustering and lack of inter-gene band pattern linkage indicate that these three immunologically relevant virulence genes may be experiencing immune pressure, each separately adapting to evade the human immune response. The consequence would be immune evasion and an increased ability to colonize human populations over time.

Conclusion

Regular 6-monthly cycles of M. catarrhalis and H. influenzae colonization peaks were observed throughout 2004–2006 in healthy children residing in Rotterdam, The Netherlands. Colonization was characterized by a high degree of M. catarrhalis genotypic diversity that was maintained over the 3-year study period, and was independent of year and season of isolation. Genetic diversity was observed in three immunologically important virulence genes, with no clustering of band pattern types during particular months or years. This high degree of whole-cell genotypic variation, coupled to independent (unlinked) virulence gene variation, is likely to be one of the factors ensuring the success of M. catarrhalis colonization events in the early years of life, facilitating immune evasion and further cycles of colonization.

The fact that the co-colonization prevalence was significantly greater than single-species prevalence alone for these two microbial pathogens adds weight to the recently unlinked virulence gene variation, is likely to be one of the factors ensuring the success of M. catarrhalis colonization events in the early years of life, facilitating immune evasion and further cycles of colonization. Our study provides the first evidence to indicate the importance of this quorum-sensing interaction within the community setting.

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