Assessing pneumococcal meningitis association with viral respiratory infections and antibiotics: insights from statistical and mathematical models

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Pneumococcus is an important human pathogen, highly antibiotic resistant and a major cause of bacterial meningitis worldwide. Better prevention requires understanding the drivers of pneumococcal infection incidence and antibiotic susceptibility. Although respiratory viruses (including influenza) have been suggested to influence pneumococcal infections, the underlying mechanisms are still unknown, and viruses are rarely considered when studying pneumococcus epidemiology. Here, we propose a novel mathematical model to examine hypothetical relationships between Streptococcus pneumoniae meningitis incidence (SPMI), acute viral respiratory infections (AVRIs) and antibiotic exposure. French time series of SPMI, AVRI and penicillin consumption over 2001–2004 are analysed and used to assess four distinct virus–bacteria interaction submodels, ascribing the interaction on pneumococcus transmissibility and/or pathogenicity. The statistical analysis reveals strong associations between time series: SPMI increases shortly after AVRI incidence and decreases overall as the antibiotic-prescription rate rises. Model simulations require a combined impact of AVRI on both pneumococcal transmissibility (up to 1.3-fold increase at the population level) and pathogenicity (up to threefold increase) to reproduce the data accurately, along with diminished epidemic fitness of resistant pneumococcal strains causing meningitis (0.97 (0.96–0.97)). Overall, our findings suggest that AVRI and antibiotics strongly influence SPMI trends. Consequently, vaccination protecting against respiratory virus could have unexpected benefits to limit invasive pneumococcal infections.

1. Introduction

Streptococcus pneumoniae is a Gram-positive coccobacillus that commonly colonizes the human nasopharynx, and is a leading cause of infectious disease and deaths worldwide, responsible for 1.6 million deaths per year.
[1,2]. In developed countries, \textit{S. pneumoniae} is the main cause of bacterial meningitis at any age [3]. In the USA, it is responsible for 50 per cent of meningitides in infants three months to 2 years old and more than 70 per cent of adults more than 40 years old [4]. Lethality fluctuates between 10 and 33 per cent depending on age, with neurological relapses for 30 per cent of cases all ages combined [4,5].

Over the past decades, the spread of antibiotic-resistant pneumococcal strains has made meningitis treatment more difficult, and generally increased the morbidity and mortality associated with severe pneumococcal infections [6]. The high antibiotic-resistance rates in these bacteria have led to policies of limiting antibiotic use and encouraging anti-bacterial vaccination, resulting in important changes of pneumococcal infection ecology [7–9].

Although much attention has been focused on pneumococcal meningitis, its epidemiological dynamics are not fully understood. For example, the seasonal fluctuations of \textit{S. pneumoniae} meningitis incidence (SPMI) that peak during the winter remain poorly understood [10]. Understanding factors driving these dynamics is crucial to optimize public health programmes devoted to their prevention, for example, anti-pneumococcus vaccine programmes or limiting antibiotic prescriptions.

From an ecological point of view, the dynamics of transmission and evolution of \textit{S. pneumoniae} in host populations are likely to be influenced by the bacteria’s environment. The latter includes population drug exposure [11–13] and co-circulating species [14,15]. Potential interaction mechanisms between community respiratory viruses and \textit{S. pneumoniae} have been proposed, based on incidence time-series analysis and animal \textit{in vivo} studies [16,17]. The underlying hypotheses rely on within-host pathophysiological respiratory virus–bacterium interactions that could influence \textit{S. pneumoniae} colonization, transmission and disease [10,16,18–21]. However, the underlying \textit{in vivo} biological mechanisms are still unclear and cannot be directly inferred [10].

In this study, we propose a new mathematical model of pneumococcal colonization and meningitis infection to explore the hypotheses that community respiratory virus infections influence the epidemiology of pneumococcal meningitis by increasing strain transmissibility or pathogenicity. To assess these hypotheses, we first analysed chronological association between community respiratory virus infections and colonization, transmission and disease [10,16,18–21]. How- ever, the underlying \textit{in vivo} biological mechanisms are still unclear and cannot be directly inferred [10].

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2. Methods

(a) Data

We used three distinct datasets over the 2001–2004 period in France: the SPMI, the incidence of acute viral respiratory infection (AVRI) and antibiotic-exposure rates (ATB; figure 1). Those data were provided by three different surveillance systems.

(i) Pneumococcal meningitis

Weekly SPMIs came from surveillance within the French National Centre of Reference for Pneumococi (CNRP) [22], which systematically collects data on pneumococcal meningitis in collaboration with 22 regional observatories for pneumococci, covering around 60 per cent of French cases [24]. \textit{Streptococcus pneumoniae} isolates with minimal inhibitory concentrations (MICs) more than 0.06 \(\mu\)g ml\(^{-1}\) were considered to be penicillin-non-susceptible strains. In this study, both terms ‘non-susceptible’ or ‘resistant’ were used to design equally these strains. In France, during the 2001–2004 period, 85–95 per cent of the penicillin-non-susceptible strains responsible for diseases were also macrolide-resistant [25].

(ii) Winter viruses

Weekly AVRI incidence rate was acquired from the Euroflu Network (http://www.euroflu.org/cgi-files/graphs_public.cgi). French data were collected through the Groupe Regional d’Observation de la Grippe (GROG), a network of more than 500 general practitioners reporting for AVRI all over the country (see http://grog.org/presentation.html for more information on the GROG network). Data were extracted from the web page using GraphClick\(^\circledR\) (http://www.arizona-software.ch/graph-click). The Euroflu AVRI data are available only during winter season for epidemiological weeks 1–15 and 40–52. Additionally, no data were available at the country level for the 2000–2001 winter season. In total, 97 weeks of observation were available over the 2001–2004 period.

(iii) Antibiotics

In France, the National Health Insurance refunds medical care provided by physicians in private practice, community clinics and hospitals to everyone. The antibiotic data used consisted of all ambulatory \(\beta\)-lactam prescribed, dispensed by outpatient pharmacies and reimbursed by two main French National Health Insurance agencies (CNAM-TS and RSI, covering 85% of the French population) from 2001 to 2004 [23]. Because antibiotics are prescription drugs in France, these data are nearly exhaustive. In the following, \(\beta\)-lactam, penicillin and antibiotics were used equally to design this dataset.

(iv) Population


(b) Statistical analysis of the data

Weekly SPMIs were modelled using a generalized estimating equations (GEE) approach, with a Poisson distribution [26]. This model enables specification of overdispersion, and a first-order autoregressive structure that accounts for the autocorrelation of the weekly SPMI within each year and assumes the independence of the years. Data were subjected to univariate and multivariate analyses. For all weekly time lags \(k\) in \([-10,10]\), regressions were defined by:

\[
\ln(E[M(w)]) = \log(\text{pop}) + \text{season}(w) + r \times RX(w - k),
\]

where \(M(w)\) represents the SPMI at week \(w\); ‘pop’ is the population estimate for the considered year; ‘season’ is a periodic trigonometric function and \(RX(w - k)\) represents antibiotic use or AVRI, at week \((w - k)\), after removing seasonality using a trigonometric function of period 52 weeks:

\[
X(w) = a + b \times \sin\left(2\pi \frac{w}{52}\right) + c \times \cos\left(2\pi \frac{w}{52}\right) + RX(w)
\]

for week \(w\), where \(X(w)\) represents the antibiotic use (ATB) or AVRI time series, \(RX(w)\) their weekly respective residuals and \(a, b, c\) the regression coefficients.

To determine which time-delay range has the strongest association, separate lagged Poisson regressions between \(E[M(w)]\) and RATB\((w - k)\) or RAVRI\((w - k)\) were estimated for different \(k\)-values, \(-10 \leq k \leq 10\), and t-test for the regression coefficients was performed [27].

Multivariate Poisson regressions were also performed and compared using the quasi-likelihood information criterion (QIC) [28].
The GEE model was successively tested for total, susceptible and resistant SPMI, using ATB and AVRI as covariates. The regressions were computed using the GENMOD procedure in SAS.

(c) Mathematical modelling

We developed a new mathematical model of pneumococcal colonization and meningitis infection, and used it to identify the mechanisms responsible for the chronological associations among AVRI, antibiotic use and SPMI. A series of dynamic submodels in which pneumococcal transmissibility and pathogenicity could change as a function of earlier AVRI were formulated. The models were then fitted to SPMI data to assess their explanatory power.


Model compartments were structured with respect to colonization status and antibiotic exposure (figure 2a). Uncolonized individuals (NC) could become colonized at rate \(\beta\) through contacts with colonized individuals. Two stages of \textit{S. pneumoniae} penicillin susceptibility, corresponding to different levels of MIC, were modelled: susceptible (S) for strains with MIC \(< 0.06 \mu\text{g ml}^{-1}\); and intermediate or resistant (R) for strains with MIC \(\geq 0.06 \mu\text{g ml}^{-1}\). Emergence of resistance or increase of its level was not considered in the model. Independently of their carriage status, individuals could be unexposed \((U_{\text{NC}}, U_{S}, U_{R})\) or exposed \((P_{\text{NC}}, P_{S}, P_{R})\) to antibiotics.

Because antibiotic exposure varies over the year, we used the observed time series ATB(\(w\)) to parametrize the rates of exposure each week \(w\) of the period considered: \(a_{\text{ATB}}(w) = \text{ATB}(w)\). In the absence of antibiotic use, natural immunity was defined as inducing carriage clearance in colonized individuals with an average of three weeks in the population [29–32]. The impact of antibiotic exposure, characterized by \(\sigma\), depended on the colonizing strain's levels of resistance: antibiotics cleared susceptible bacteria in one week on average (\(\sigma_{S} = 0\)), but had no effect on colonization with resistant bacteria (\(\sigma_{R} = 1\)).

Figure 1. Observed \textit{S. pneumoniae} meningitis reported cases (SPMI), acute viral respiratory infections (AVRI) and antibiotic use over seasons 2001–2004. (a) Weekly total (black curve), antibiotic-susceptible (blue) and -resistant SPMI (red), from surveillance within the CNRP [22]. Isolates with MICs more than 0.06 \(\mu\text{g ml}^{-1}\) were considered to be penicillin-non-susceptible, designated herein by ‘non-susceptible’ or ‘resistant’. (b) Weekly AVRI incidence rate during winter seasons, acquired from Euroflu Network (collected only from October to March, epidemiological weeks 1–15 and 40–52 of each year). (c) Weekly antibiotic prescription rate per individual. Antibiotic use was based on \(\beta\)-lactam reimbursement data from the French National Health Insurance [23]. The datasets covered 208 weeks for SPMI and antibiotic use, and 97 weeks of AVRI observation. Weeks ending in a new month are indicated on the x-axis.
Antibiotic exposure duration was assumed to have a mean of \( \frac{1}{\gamma_p} = 8 \) days.

The duration of colonization by susceptible strains was fixed (\( \frac{1}{\gamma_S} = 3 \) weeks on average). Possible epidemic fitness differences between penicillin-susceptible and -resistant pneumococcal strains were included in the model by introducing different clearance rates for each strain. Resistance-associated fitness cost was defined as the mean ratio of carriage durations between resistant and susceptible strains: \( f_{R/S} = \lambda_S/\lambda_R \). Other parameters being equal, this quantity is equivalent to the ratio of resistant to susceptible pneumococci reproductive numbers. \( f_{R/S} \) was numerically estimated to maximize the log-likelihood of the model to reproduce observed susceptible and resistant SPMI data.

Meningitis infection (I) could occur in all pneumococcal carriers. We assumed that the natural probability \( p_0 \) of developing meningitis was constant throughout carriage duration and was independent of
antibiotic susceptibility. In France, vaccination with a pneumococcal conjugate vaccine (PCV) was introduced for children in 2003. Because vaccination recommendations were restrictive before 2005 [33], immunization was considered to be marginal during the period of study, and PCV was not considered in the model.

Four interaction submodels were derived, assuming different mechanisms of virus-induced modified transmissibility and pathogenicity (figure 2):

— MOD[Ø], in which AVRI has no impact on SPMI
— MOD[T], for which we assumed that, during AVRI epidemic periods, transmission of pneumococcal strains to non-carriers could be promoted when either these non-carriers or the pneumococcal carriers were infected with the virus. The pneumococcal transmission rate at week \( w \) was modelled as
\[
\beta(w) = \beta_0 \times (1 + \xi \times \text{AVRI}(w)),
\]
where \( \beta_0 \) is the intrinsic pneumococcal transmission rate, AVRI(\(w\)) is the virus-infection incidence in the population at week \( w \) and \( \xi \) is a factor representing the impact of a respiratory virus infection on pneumococcal strains transmission, reflecting either a modification of the chance of transmission, or of the rate of acquisition.

— MOD[P], for which we assumed that the probability of colonized individuals developing meningitis at week \( w \), \( p(w) (=\text{PMeningitis|colonized}) \) could be increased in people with AVRI:
\[
p(w) = p_0 \times (1 + \pi \times \text{AVRI}(w)),
\]
where \( \pi \) is a factor representing the impact of a respiratory virus infection on the pathogenicity of pneumococcal strains and \( p_0 \) the natural pneumococcal pathogenicity.

— MOD[T + P], which combined the assumed impacts on transmissibility and pathogenicity of models MOD[T] and MOD[P].

The reported time series of AVRI from the GROG were directly used in the model to parameterize the rate of AVRI per individual each week. Reporting fidelity to AVRI was assumed to be equal to 100 per cent.

(d) Statistical inference and model fitting
Model compartments were initialized to describe a population in which penicillin-resistant pneumococcal rates were equivalent to the French 2001 data (CNRP) with more than 50 per cent of penicillin-non-susceptible strains [25]. Global pneumococcal carriage was set to 10 per cent on average, with a rate of non-susceptible strains initialized to 55 per cent. The meningitis infection compartments (I) were initialized by directly using meningitis observed incidence at the beginning of the study period.

The model was numerically simulated over the 2001–2004 period. To study the role of AVRI, the parameters of the four interaction models (MOD[Ø], MOD[T], MOD[P] and MOD[T + P]) were estimated to obtain the best-fitting model with the observed susceptible and resistant SPMI data, using a Markov chain Monte Carlo (MCMC) algorithm. Only the 97 weeks during which AVRI incidence was available were used for the calculation of the likelihood. The Metropolis–Hasting algorithm was used to sample over the parameter space. For each model, parameters were selected to maximize the Poisson log-likelihood for the susceptible and resistant meningitis time series (with expression detailed in electronic supplementary material, §S3). Posterior estimates were obtained using 3 \( \times 10^7 \) MCMC iterations with sampling every 1000 and a burn-in of 100 000 iterations to allow for the chain convergence. Uninformative priors were used, and several starting points were tested. The best-fitting model was determined using the deviance information criterion (DIC; table 2). This criterion has the advantage of taking into account the model complexity associated with the number of parameters. The selected model is the one that presents the lowest DIC.

The model and estimation framework were programmed in C. The R statistical software (www.r-project.org) was used for the statistical analysis of the model outputs and graphics.

### Table 1. Model parameters.

<table>
<thead>
<tr>
<th>parameter</th>
<th>notation</th>
<th>value</th>
</tr>
</thead>
<tbody>
<tr>
<td>birth rate, death rate</td>
<td>( \mu )</td>
<td>0.00025 individual(^{-1}) week(^{-1})</td>
</tr>
<tr>
<td>infectious contact rate:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>intrinsic pneumococcal transmission</td>
<td>( \beta_0 )</td>
<td>estimated</td>
</tr>
<tr>
<td>impact of AVRI on transmission</td>
<td>( \xi )</td>
<td>estimated</td>
</tr>
<tr>
<td>time-varying transmission</td>
<td>( \beta(w) = f(\beta_0, w) )</td>
<td></td>
</tr>
<tr>
<td>colonization duration:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>for susceptible strains</td>
<td>( 1/A_s )</td>
<td>three weeks</td>
</tr>
<tr>
<td>for resistant strains</td>
<td>( 1/A_R )</td>
<td>estimated</td>
</tr>
<tr>
<td>antibiotic exposure duration</td>
<td>( 1/\gamma_f )</td>
<td>8 days</td>
</tr>
<tr>
<td>decolonization after one week of antibiotic use:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>probability for susceptible strains</td>
<td>( 1 - \alpha_s )</td>
<td>1</td>
</tr>
<tr>
<td>probability for resistant strains</td>
<td>( 1 - \alpha_R )</td>
<td>0</td>
</tr>
<tr>
<td>antibiotic exposure rate</td>
<td>( \alpha_t(w) )</td>
<td>( \text{ATB}(w) )</td>
</tr>
<tr>
<td>pathogenicity in colonized individuals:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>natural probability of meningitis</td>
<td>( p_0 )</td>
<td>estimated</td>
</tr>
<tr>
<td>impact of AVRI on pathogenicity</td>
<td>( \pi )</td>
<td>estimated</td>
</tr>
<tr>
<td>time-varying pathogenicity</td>
<td>( p(w) = g(p_0, w) )</td>
<td></td>
</tr>
<tr>
<td>fitness cost for resistant strains</td>
<td>( f_{ks} )</td>
<td>estimated</td>
</tr>
</tbody>
</table>
Table 2. Posterior median estimates (95% credibility interval) for the four fitted models. Four distinct models of SPMI–AVRI interactions were tested: Mod[Ø], AVRI had no influence whatsoever on SPMI; Mod[T], AVRI affected only pneumonia transmission, whereas pathogenicity remained constant; Mod[P], AVRI influenced only pneumococcal pathogenicity; and Mod[T + P], AVRI could affect both pneumococcal pathogenicity and transmission (transmissibility or acquisition). Here, β0 defines natural pneumococcal transmission rate, ξ defines virus impact on pneumococcal transmission, ρ0 defines the natural pathogenicity rate, π defines virus impact on pathogenicity and ρNS defines resistance-associated fitness cost, which was defined as the mean ratio of carriage duration between susceptible and resistant strains ρNS = λS/λR. In the best-fitting model (highlighted in grey), resulting S. pneumoniae transmission β(w) and pathogenicity p(w) ranged, respectively, from 0.36 to 0.47 per week per person and from 6 × 10^{-7} to 1.8 × 10^{-6}.

<table>
<thead>
<tr>
<th>model</th>
<th>β0</th>
<th>ξ</th>
<th>ρ0</th>
<th>π</th>
<th>ρNS</th>
<th>LL</th>
<th>DIC^a</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mod[Ø]</td>
<td>0.38 (0.37–0.39)</td>
<td>—</td>
<td>1.37 × 10^{-6} (1.06–1.72 × 10^{-6})</td>
<td>—</td>
<td>0.97 (0.969–0.975)</td>
<td>455 (452–456)</td>
<td>—906</td>
</tr>
<tr>
<td>Mod[T]</td>
<td>0.05 (0.02–0.20)</td>
<td>654 (109–1831)</td>
<td>2.67 × 10^{-7} (2.27–3.37 × 10^{-7})</td>
<td>—</td>
<td>0.97 (0.968–0.974)</td>
<td>475 (472–477)</td>
<td>—947</td>
</tr>
<tr>
<td>Mod[P]</td>
<td>0.38 (0.37–0.40)</td>
<td>—</td>
<td>2.2 × 10^{-7} (1.06–5.53 × 10^{-7})</td>
<td>208 (65–495)</td>
<td>0.97 (0.969–0.975)</td>
<td>476 (472–477)</td>
<td>—948</td>
</tr>
<tr>
<td>Mod[T + P]</td>
<td>0.34 (0.31–0.36)</td>
<td>8.7 (46–14.4)</td>
<td>3.6 × 10^{-7} (1.3–7.0 × 10^{-7})</td>
<td>92 (28–361)</td>
<td>0.97 (0.969–0.975)</td>
<td>485 (480–487)</td>
<td>—964</td>
</tr>
</tbody>
</table>

^aWe used the following expression of the deviance information criterion: DIC = −4 × LL + 2 × max(LL), where LL is the mean of the log-likelihood and max(LL) the mode value for the MCMC sample. Model minimizing the DIC was preferred.

3. Results

The equations of the model are provided in the electronic supplementary material, §S2.

The data from January 2001 to December 2004, corresponding to a total of 788 weeks for AVRI observation, were given in figure 1. A total of 183 SPMI episodes were reported. All three time series (SPMI, AVRI and ATB) present a 52-week seasonality with epidemics peaking during the winter. The electronic supplementary material, §S1, provides the time series of ATB or residual AVRI, computed for all time lags between AVRI or antibiotic and SPMI were positively linked. Total antibiotic-resistant SPMIs were also positively linked to antibiotic-resistant pneumococcal meningitis (b) Mathematical modelling and mechanisms testing

In countries with high antibiotic exposure, such as France, antibiotic use is strongly associated with ARVIs and RAVIs in the multivariate analysis. This could be an artifact of the data, as antibiotic-associated meningitis incidence was negatively significantly linked to penicillin consumption over the preceding five to nine weeks (p < 0.02). We found that, regardless of pneumococcal strain susceptibility, SPMI followed AVRI incidence by up to two weeks. Negative long-term dependency (p < 0.01) was observed for total and susceptible meningitis, but associations were only marginally significant.

(iii) Antibiotic versus S. pneumoniae meningitis incidence

We found that, regardless of pneumococcal strain susceptibility, SPMI followed AVRI incidence by up to two weeks. Negative long-term dependency (p < 0.01) was observed for total and susceptible meningitis, but associations were only marginally significant.

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we found that the best fit was obtained when both transmissibility and risk of infection were allowed to depend on observed AVRI (table 2).

For the selected model, the posterior median estimates were $\xi = 8.7$ (95% credibility interval (4.6–14.4)) for virus impact on pneumococcal transmission/acquisition; $\pi = 92$ (28–361) for virus impact on pathogenicity; and $\fr = 0.97$ (0.969–0.975) for the antibiotic-resistance-associated fitness cost estimate. In a typical simulation using the median posterior estimates, pneumococcal transmissibility ranged from 0.36 to 0.47 per week per person (reaching a 1.3-fold increase) and pneumococcal pathogenicity ranged from $6 \times 10^{-7}$ to $1.8 \times 10^{-6}$ (a threefold increase). Although low, the resistance-associated fitness cost was significantly lower than 1, suggesting that resistant strains are slightly less competitive than susceptible ones.

Lastly, one can directly interpret the posterior estimates of $\xi$ and $\pi$ at the individual level (see the electronic supplementary material, §S2 for details on the mathematical development and interpretation). From that point of view, the model predicts that AVRI substantially increases a colonized patient’s absolute risk of meningitis (by a factor of 90) and also increases the individual’s risk of acquisition/transmissibility of pneumococci (by a factor of 9).

The 2001–2004 SPMI simulated using the selected model and the median estimated parameters are depicted in figure 2c (see also the electronic supplementary material, figure S2), along with the observed SPMI over the same period.

4. Discussion

Pneumococcal meningitis incidence (SPMI) was found to be highly associated with the incidence of AVRIs and with antibiotic use: SPMI increased shortly after AVRI incidence (the two following weeks) and decreased overall as the antibiotic-prescription rate rose (six to seven weeks after). In addition, our modelling study discarded the hypothesis of a unique interaction between AVRI and pneumococci. Model simulations required a combined AVRI impact on both pneumococcal transmissibility and pathogenicity to reproduce the data accurately, along with diminished epidemic fitness of resistant pneumococcal strains causing meningitis.

Vaccination with PCV has been shown to widely modify pneumococcal epidemiology [7,9]. In France, PCV vaccination was initiated in 2003, targeting a specific population (at-risk children less than 2 years old), with recommendations extended
in 2006 to every child less than 2 years old. In the same period, a campaign to decrease antibiotic consumption was launched [23]. In this study, we focused on years 2001–2004, in order to obtain stable meningitis ecology, with a limited effect, if any, of vaccination.

For clarity purposes, the model developed here used several simplifications regarding S. pneumoniae epidemiology. First, the model was not age-stratified. Pneumococcal colonization is known to decrease with age [34], and children have generally higher rates of pneumococcal meningitis and antibiotic consumption. Although this simplification should not affect our findings on the association between AVRI and SPMI, extending the model and examining the effect of age on such an association will be of interest in the future. Second, the model included only penicillin resistance, neglecting other drug resistances (and multiresistances). In France, most penicillin-resistant pneumococcal strains also carry a macrolide resistance gene. The inclusion in the model of the 2001–2004 macrolide exposure rates, in addition to the β-lactams ones, would increase the co-selection of resistant strains under antibiotic exposure [35]. Therefore, it is predictable that the estimated epidemic fitness difference between susceptible and resistant S. pneumoniae would be increased to compensate for this selective advantage.

The model and data used here did not allow estimating any reporting fidelity in AVRI. The AVRI reporting rate was therefore assumed to be equal to 100 per cent in the model. In practice, reporting fidelity in AVRI is usually imperfect. This simplification should not impact the significance of our conclusions regarding the role of AVRI on pneumococcal epidemiology. It would, however, affect the amplitude of this effect: a lower reporting rate would reduce the quantitative estimation of ε and π by the same rate. The presented estimates can therefore be interpreted as a maximization of AVRI’s impact on pneumococcal pathogenicity and transmissibility.

Some data limitations should also be mentioned. Two independent surveillance systems report viral respiratory infections in France: the Sentinelles network, which reports influenza-like syndrome incidence; and the GROG surveillance programme, which combines virological testing and sentinel indicators to report AVRI (including influenza-like illness and respiratory syncytial virus, RSV) [36]. In order to include AVRI with the largest definition, data from the GROG network were used here. As mentioned earlier, during the study period, the GROG network reported only viral infections occurring during winter seasons. As a consequence, our statistical and inference analyses were restricted to these periods, excluding summertime incidences and limiting the power of our analysis. Furthermore, other respiratory viral pathogens, not reported by the GROG, together with other environmental factors, such as air pollution, daily light or temperature, were not included in this study. Despite these limitations, the short-term associations found between AVRI and SPMI are in accordance with previous findings [10,17,37].

High incidences of bacterial respiratory infections during influenza pandemics have been reported in the past [19,36], and an increased incidence of these infections (e.g. pneumonia) in potentially coming pandemics is of concern [39]. The temporal relationship among circulating winter virus infections (influenza virus, RSV) and invasive pneumococcal disease has also been reported in several studies [10,17–20,37]. Herein, we highlight two distinct mechanisms underlying such associations and suggest that the existence of a unique interaction mechanism is very unlikely.

AVRIs are known to increase the risk of invasive bacterial infection [16]. Several biological mechanisms have been suggested to explain such phenomena. First, the idea that daily light and temperature exposure modifications altered host immune responses was advanced to explain the seasonal variations of infection incidences [40]. This hypothesis does not agree with our statistical results. Such a mechanism would tend to influence AVRI and SPMI simultaneously. Herein, the time-series relationships were strongly asymmetric. Second, virus infection might facilitate pneumococcal infection by damaging the airway mucosa and epithelial lining [10,41,42], increasing pneumococcal adherence to epithelia [41,43] and/or impairing innate immune responses to pneumococcal infections [42,44–46].

However, our results suggest that AVRI-induced increased pathogenicity of pneumococci is not enough to explain the observed trends of pneumococcal meningitis. The AVRI should also modify between-host interactions by emphasizing S. pneumoniae’s transmissibility. Such an increased epidemic potential could actually reflect two distinct mechanisms. First, AVRI infection could enhance the transmission probability of the bacteria in colonized individuals (and therefore increase pneumococcus’s reproductive number) by increasing bacterial load in the host or creating new transmission routes. Second, virus infection could increase host susceptibility to pneumococcal colonization (e.g. enhance the acquisition risk) in AVRI-infected individuals. Our model did not allow discriminating between the two. A more complex model, in which the dynamics of virus infection in the population is explicitly modelled, will be necessary in the future to explore in details this enhancing effect on pneumococcal transmissibility. To date, this phenomenon of ‘cloud humans’, in which virus-infected individuals transmit more bacteria, has been little studied in human populations [47,48].

Based on the influenza-like illness incidence reported by the Sentinelles network, it is probable that influenza viruses are responsible for the second winter peak shape of AVRI. Here, the lack of virological information impeded the separate quantification of the role of the distinct viruses on pneumococcal epidemiology. However, assessing the role of the viruses individually will be of great interest in the future.

A distinct but related aspect is that of the significant resistance-associated fitness cost. In this study, antibiotic-driven selection on its own was not sufficient to reproduce the observed trends, and significantly lower fitness for resistant pneumococci was found (estimated resistance-associated fitness cost of 0.97 (0.969–0.975)). Reduced transmissibility of antibiotic-resistant pneumococcal strains has already been suggested [49,50], but biological evidence in humans is still lacking. Although resistance-associated fitness cost was a secondary consideration here, this parameter is of importance in measuring the selective power associated with antibiotic exposure pressure. Our finding provides some insights into the influence of antibiotic exposure on the selection of circulating pneumococcal strains: susceptible strains would be disadvantaged under antibiotic exposure but become more epidemic than resistant strains when antibiotic use declines. A possible consequence of fewer antibiotic prescriptions might be an increased incidence of severe pneumococcal infections caused by antibiotic-susceptible strains.

The results presented here bring to light, at the epidemiological level, the potential means for respiratory viruses and S. pneumoniae interactions. They suggest that respiratory viruses
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