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Exploring the role of competition induced by non-vaccine serotypes for herd protection

G.L. Masala<sup>1</sup>, M. Lipsitch<sup>2</sup>, C. Bottomley<sup>1</sup>, S. Flasche<sup>1</sup>

Affiliations: <sup>1</sup>London School of Hygiene and Tropical Medicine, London, UK;

<sup>2</sup>Harvard University, Boston, US

Corresponding author: Stefan Flasche, London School of Hygiene and Tropical Medicine,  
Keppel Street, WC1E 7HT London, UK, [Stefan.Flasche@lshtm.ac.uk](mailto:Stefan.Flasche@lshtm.ac.uk), +44 (0)20 7958 8272

Key words: Pneumococcus, vaccination, serotype competition, herd protection

12 **Abstract**

13 The competitive pressure from non-vaccine serotypes may have helped pneumococcal conjugate vaccines  
14 (PCVs) to limit vaccine serotype (VT) prevalence. We aim to investigate if, consequently, the indirect protection  
15 of higher valency vaccines could fall short of the profound effects of current formulations.

16 We compare three previously described pneumococcal models harmonized to simulate 20 serotypes with a  
17 combined pre-vaccination prevalence in <5y old children of 40%. We simulate vaccines of increasing valency by  
18 adding serotypes in order of their competitiveness and explore their ability to reduce VT carriage by 95% within  
19 10 years after introduction.

20 All models predict that additional valency will reduce indirect vaccine effects and hence the overall vaccine  
21 impact on carriage both in children and adults. Consequently, the minimal effective coverage (efficacy against  
22 carriage \* vaccine coverage) needed to eliminate vaccine type carriage increases with increasing valency. One  
23 model predicts this effect to be modest while the other two predict that high-valency vaccines may struggle to  
24 eliminate VT pneumococci unless vaccine efficacy against carriage can be substantially improved. Similar  
25 results were obtained when settings of higher transmission intensity and different PCV formulations were  
26 explored.

27 Failure to eliminate carriage as a result of increased valency could lead to overall decreased impact of  
28 vaccination if the disease burden caused by the added serotypes is low. Hence a comparison of vaccine  
29 formulations of varying valency, and pan-valent formulations in particular, should consider the invasiveness of  
30 targeted serotypes, as well as efficacy against carriage.

31

## 32 **Background**

33 In 2000 the first pneumococcal conjugate vaccine (PCV), which provided protection against seven of the most  
34 pathogenic pneumococcal capsular serotypes, was licensed and recommended for immunization of infants in  
35 the US [1]. Subsequently, 10- and 13-valent formulations have been licensed and are now being used to  
36 prevent pneumococcal disease in more than 130 countries worldwide [2–11]. The incidence of carriage and  
37 disease associated with vaccine type serotypes (VT) declined in vaccinated children, and also in unvaccinated  
38 children and adults, after PCVs were introduced into national immunization programmes [12]. However, the  
39 overall prevalence of pneumococcal carriage remained approximately constant as non-vaccine serotypes  
40 (NVT), i.e., serotypes not targeted by the vaccine, filled the ecological niche [13]. The increased disease from  
41 these serotypes has partially offset the benefit of pneumococcal vaccination. As a result pneumococcal  
42 vaccines that target more or all serotypes are being developed [14].

43 Previous work has suggested that the competition between vaccine type (VT) and non-vaccine type (NVT)  
44 serotypes plays an important role in the herd protection observed in the post PCV era [15–17]. In particular, by  
45 reducing acquisition of VT carriage, pneumococcal conjugate vaccines give NVTs a competitive advantage over  
46 VTs in the nasopharynx. Thus, in vaccinated populations the presence of NVT in vaccinated hosts provides  
47 additional competitive pressure, which combines with the immune protection afforded by the vaccine, to  
48 suppress VT colonization. Moreover, at the population level, there is competition between VT and NVT in non-  
49 vaccinated hosts, and the spread of VT is likely inhibited by competition from NVT in non-vaccinated people as  
50 well. In each of these cases, the mechanisms of competition might include direct competition in the  
51 nasopharynx [18], induction of innate immune effectors by NVT that also inhibit VT [19], and induction of forms  
52 of acquired immunity that also inhibit VT, such as Th17-based and antibody-based immunity to conserved  
53 antigens [20–22]. For higher valent pneumococcal vaccines, including those that target proteins common to  
54 most pneumococci [14], this hypothesis implies that, by effectively losing the benefit of NVT competition, even  
55 with similar vaccine efficacy against pneumococcal carriage and disease, levels of indirect protection in  
56 unvaccinated individuals could fall short of the profound effects that have been observed with the routine use  
57 of conjugate vaccines.

58 In this paper we explored three previously developed dynamic modelling approaches for pneumococcal  
59 ecology as to whether they predict a similar contribution of NVT competition to the indirect effects of  
60 pneumococcal vaccination. We harmonized key model parameters that govern vaccine efficacy and  
61 pneumococcal epidemiology in the absence of vaccination and explored various vaccine scenarios to better  
62 understand the role of competition in providing protection.

63

## 64 **Methods**

### 65 Models

66 The model by Bottomley et al [16] (M\_B) is a deterministic model that represents the pre-PCV steady state of  
67 pneumococcal infections in the Gambia and was used to predict the impact of introduction of PCV13 into the  
68 childhood vaccination program. It is fitted to local longitudinal pre-vaccination carriage data. Serotypes are  
69 grouped into three classes of transmissibility (low, medium, high) and clearance rate (high, medium, low).

70 Serotypes within the same group share the same properties. Pneumococcal carriers are assumed to gain partial  
71 immunity against acquisition of new serotypes during the episode of carriage, which represents the mechanism  
72 of serotype competition, and a proportion of clearances leads to life-long immunity against the cleared  
73 serotype, which balances competitive advantages to sustain serotype diversity. The default model  
74 parameterization is the same as reported in the original manuscript.

75 The model by Cobey & Lipsitch [23] (M\_CL) is an individual-based model that represents a generic high-income  
76 setting. Serotypes differed by their intrinsic duration of carriage and their in vivo competitive ability.  
77 Pneumococcal carriers are assumed to gain partial protection, quantified by the competitive ability of the  
78 resident type, against acquisition of additional serotypes during the episode of carriage, which represents the  
79 mechanism of competition. Following clearance, the host's susceptibility to any subsequent homologous  
80 acquisition as well as the duration of any subsequent carriage episode is reduced. The serotype-specific  
81 immunity accentuates within-serotype competition thus providing balancing selection on serotypes, and  
82 acquired immunity independent of capsule reduces fitness differences. The simulations presented in this work  
83 rely on the default model parameterization, i.e. homogeneous mixing, the default rate of acquisition of  
84 capsular immunity ( $\sigma = 0.3$ ) and the default rate of acquisition of nonspecific immunity assuming non-linear  
85 reduction in carriage duration ( $\epsilon = 0.25$ ).

86 The model by Flasche et al [15] (M\_F) is an individual based model that generalizes the most commonly used  
87 deterministic pneumococcal model [17,24,25]. It represents a generic high income country setting. Serotypes  
88 differ by their intrinsic duration of carriage. Duration of carriage and susceptibility to acquisition decline with  
89 age but are exposure independent. The acquisition of a pneumococcus triggers both a transient homologous  
90 immune response, which represents serotype competition, and a transient heterologous immune response,  
91 which represents the mechanism to ensure serotype coexistence. Both immune responses are assumed to  
92 prevent additional acquisition of respective serotypes. Unless mentioned otherwise the simulations presented  
93 in this work rely on the default model parameterization, i.e. the duration of specific and non-specific immunity  
94 was 9 and 18 weeks respectively.

95 While there was no formal model selection process we included models that span most of the range of  
96 alternative dynamic pneumococcal model assumptions on serotype competition and natural immunity. An  
97 overview of the different modelling approaches in this study is shown in Table 1. The main differences between  
98 models in regards to this work are the assumptions on acquired immunity and the resulting mechanisms for  
99 competition and serotype coexistence.

100

## 101 Analyses

102 We harmonized models to simulate 20 artificial serotypes with a combined pre-vaccination prevalence in <5y  
103 old children of 40%, approximating a high income setting with moderate transmission, or 70%, approximating a  
104 low income setting with high transmission intensity. In M\_B serotypes were evenly distributed between the  
105 three classes, i.e. 7, 7, 6 serotypes of low, mid and high transmission intensity. For each model, parameters  
106 governing transmission intensity were scaled to achieve the desired prevalence. In M\_F changing the  
107 transmission intensity alone was insufficient to achieve the targeted 70% prevalence (compare discussion in  
108 Flasche et al [15]). Hence, once the effects of increasing the transmission intensity saturated it was kept  
109 constant and the duration of specific and non-specific immunity were subsequently decreased to 6 and 12

110 weeks respectively to achieve the targeted prevalence. As M<sub>B</sub> was not age structured we split all  
111 compartments into an <5y old and a 5 years and older compartment retaining all original parameters and  
112 constant rate of transition between the strata such that the mean time spent in the <5 stratum was 5 years. To  
113 minimize the effects of stochasticity M<sub>CL</sub> was run 10 times and mean values are presented. Stochastic  
114 variability on presented outcomes was too small to visualize in the Figures so it was omitted. The Simpson  
115 Index was calculated as a measure of serotype diversity [26].

116 We explored two vaccines with alternative compositions each. Firstly, we compared generic vaccines of  
117 increasing valency where serotypes are included in order of their competitiveness. Serotype “1” is the  
118 strongest competitor, indicated in all models by the highest prevalence in the pre vaccine era, and “20” the  
119 lowest. Note that the serotype names do not correspond to the numbering conventionally used for  
120 pneumococcal serotypes. Secondly, to approximate PCV7, PCV10, PCV13 and PCV15 we modelled inclusion of  
121 serotypes into the vaccine in respect to their observed paediatric prevalence rank among carriage globally. For  
122 example PCV7 targets serotypes 4,6B,9V,14,18C,19F and 23F which are the 18<sup>th</sup>, 2<sup>nd</sup>, 6<sup>th</sup>, 5<sup>th</sup>, 11<sup>th</sup>, 1<sup>st</sup>, 3<sup>rd</sup> most  
123 prevalent serotypes globally; hence the PCV7-like vaccine in this work targets model serotypes 1,2,3,5,6,11 and  
124 18 (Table 2) [27]. Serotypes of a lower rank than 20 were not included since the models only consisted of 20  
125 serotypes.

126 M<sub>B</sub> and M<sub>F</sub> assume that both immunity, including vaccine induced immunity act as all-or-nothing while the  
127 Cobey and Lipsitch model assumes it is leaky. The models were run to predict 1) the impact of vaccination  
128 against each targeted serotype [28] (assuming 100% coverage and 55% efficacy) and 2) the effective coverage  
129 needed to achieve elimination of VT carriage. We defined effective coverage as vaccine efficacy times vaccine  
130 coverage (N.B. in the two models that assume all-or nothing vaccine protection this is equivalent to the fraction  
131 of the population that is protected by vaccination), and elimination of VT carriage as a reduction of VT carriers  
132 of 95% or more. The impact of vaccination is measured as either the percentage reduction in the number of VT  
133 carriers, or alternatively with any serotype, in year 10 after the start of vaccination if compared to the year  
134 before vaccination (steady state).

135

136

## 137 **Results**

138 Models differed in the proportion of children among the simulated population. M<sub>B</sub> assumed an age  
139 distribution based on the Gambia and hence that children younger than 5 years old make up 20% of the total  
140 population. In both other models that represent high income countries the corresponding proportion was 5%  
141 (Figure 1). Pneumococcal carriage prevalence was almost evenly distributed across serotypes in M<sub>F</sub> and  
142 dominated by fewer serotypes in M<sub>CL</sub>. The Simpsons index in children was 0.871, 0.845, 0.885 in the  
143 moderate transmission scenario for M<sub>B</sub>, M<sub>CL</sub> and M<sub>F</sub> and 0.925, 0.862, 0.927 in the high transmission  
144 scenario. The models differed how the targeted prevalence in children translated into prevalence in older  
145 individuals (Figure 1). Carriage prevalence decreases with age except for M<sub>B</sub> which was originally designed to  
146 be age independent and hence uses the same parameters for both age groups.

147 In the moderate transmission scenario, the vaccine impact against vaccine type carriage 10 years after the start  
148 of vaccination of a vaccine with 55% effective coverage decreased with increasing vaccine valency in all three  
149 models (Figure 2). The effect of including more VTs was least visible in M\_CL where only inclusion of almost all  
150 serotypes (15 or more) reduced the impact on VT carriage to allow VT circulation. The M\_B predicted the  
151 steepest decrease in vaccine impact on VT prevalence as a result of inclusion of highly and moderately  
152 competitive serotypes, however, further inclusion of weakly competitive serotypes which were hardly carried  
153 in this scenario did not change the impact of vaccination. Similar dynamics were observed for older individuals  
154 and the high transmission scenario, however, M\_F predicted a small initial increase in vaccine impact on VT  
155 carriage before the impact decreased for higher valencies.

156 The impact of vaccination on all serotype carriage measured 10 years after the start of vaccination with a  
157 vaccine with 55% effective coverage generally increased with increasing valency. However, for the high  
158 transmission scenario M\_CL predicted a negative vaccine impact, i.e. an increase in overall pneumococcal  
159 carriage through the inclusion of almost all serotypes into the vaccine formulation and only for valencies of 19  
160 and higher predicted a positive impact of vaccination, i.e. a reduction in all serotype carriage prevalence.

161 The PCV7-like and PCV10-like as well as the PCV13-like and PCV15-like vaccines were indistinguishable because  
162 the global prevalence rank of the respectively added serotypes were larger than the number of serotypes  
163 considered in this analysis and hence omitted. All three models predict that the impact of vaccination against  
164 pediatric VT carriage is similar (<5% difference) across the PCV-like formulation (Figure 3). However, changes in  
165 vaccine impact on carriage with any serotype were more pronounced but followed the dynamics of the generic  
166 vaccine; i.e. inclusion of more serotypes further reduced carriage prevalence, except in M\_CL in the high  
167 transmission scenario.

168 Consistent with the effect of increasing valency on vaccine impact, increasing the valency of the generic vaccine  
169 formulation was predicted to increase the effective coverage needed to eliminate VT carriage in both children  
170 and older individuals and in both moderate and high transmission intensity settings (Figure 4). In all three  
171 models VT elimination in the general population required less than 10% additional effective coverage to  
172 elimination VT carriage among children. In contrast to the other models M\_CL predicted that addition of up to  
173 half of all serotypes into the generic vaccine formulation would not have a profound effect on the effective  
174 coverage needed for elimination of VT carriage but that only inclusion of at least 10 serotypes or 15 serotypes  
175 in the moderate and high transmission scenario respectively would. Elimination of pneumococci using a pan-  
176 valent vaccine was impossible in M\_F and also for the high transmission scenario in M\_B.

177 For PCV-like vaccines a similar qualitative behavior to the generic vaccine formulations was predicted. The  
178 three models predicted that the effective coverage needed to eliminate VT carriage in the population increases  
179 by 12, 2 and 11% respectively for the moderate transmission intensity setting if a PCV13 or 15 – like vaccine  
180 was used instead of a PCV7 or 10 – like vaccine. In the high transmission intensity setting elimination of VT  
181 carriage for the two modelled vaccine formulations was impossible in M\_F, required effective coverage larger  
182 than 88% and 97% in M\_B and required effective coverage of 34% and 37% in M\_CL.

183

184 **Discussion**

185 Pneumococcal conjugate vaccines have substantially reduced the burden of pneumococcal disease worldwide.  
186 However, through replacement with serotypes not targeted by the vaccines a sizeable burden remains and has  
187 led to ongoing development of vaccines with higher valency. Using qualitative results across three  
188 pneumococcal models that span a variety of assumptions on the acquisition of pneumococcal immunity and  
189 serotype competition, we here show that serotype competition from NVTs aids VT elimination. Accordingly, we  
190 show that targeting an increasing number of serotypes increases the requirements on vaccine efficacy and/or  
191 vaccine coverage to achieve elimination of VT carriage. We predict that the relatively small differences in the  
192 number of serotypes targeted by current PCV formulations are unlikely to be substantial enough to lead to  
193 measurable differences in the ease of VT elimination but that vaccines that target almost all serotypes may  
194 allow continued circulation of the most competitive serotypes even if such vaccine was given at high coverage  
195 and the vaccine efficacy against carriage was improved over the efficacy of PCVs.

196 Given the qualitative nature of this comparison we have only assessed the impact of vaccine valency on the  
197 potential of elimination of pneumococcal carriage. The implications of the results for the disease impact of a  
198 switch from current PCV formulations to a pan valent vaccine are complex. Increasing vaccine valency could  
199 lead to a net increase in pneumococcal disease burden if the highly competitive serotypes are controlled only  
200 through a vaccine with limited valency and are also highly pathogenic while the types not targeted by the  
201 formulation with limited valency rarely cause disease. In this case, the small disease benefit of controlling more  
202 serotypes could be outweighed by the increased circulation of the serotypes in the limited-valency vaccine. The  
203 expansion of PCV formulations thus far to incorporate additional serotypes responsible for significant amounts  
204 of disease has tended to emphasize highly invasive serotypes, thereby minimizing the potential problem we  
205 highlight for expansions of the valency of PCVs. A recent study suggests a method for such that would continue  
206 this beneficial approach [29].

207 In vaccinated persons, these unintended effects might be fully or partially offset through the additional direct  
208 vaccine protection against disease, given that PCV formulations thus far have provided >80% protection against  
209 disease, with lower efficacy against carriage [28,30–32]. This implies that unintended effects of increased  
210 valency of vaccines might be of greatest concern – and thus most deserving of surveillance – in age groups  
211 within a population that have not been vaccinated, such as healthy adults in most countries at present. We  
212 emphasize that the model-comparison exercise here was designed to assess general trends in the behaviors of  
213 the models, rather than to predict specifically how a higher-valency vaccine would act in a particular  
214 population. Setting-specific model parameterization is required to allow quantification of the differential  
215 impact of vaccine of varying valency on pneumococcal disease.

216 We show that the observation that serotype competition aids VT elimination and hence that increasing the  
217 valency of pneumococcal conjugate vaccine is likely to increase the herd immunity threshold is insensitive to  
218 different assumptions of paediatric carriage prevalence and vaccine formulation which we consistently  
219 explored across all three models. Most importantly we show that this finding is also insensitive to alternative  
220 model assumptions of pneumococcal ecology, the mechanisms of between serotype competition and  
221 differences in underlying demographics.

222 We made the simplifying assumption that serotype specific direct vaccine effects are the same across vaccines  
223 and targeted serotypes and that they follow those of current PCV formulations; i.e. an approximate 55%  
224 efficacy against carriage acquisition of any targeted serotype [28]. However, because of the complexities

225 involved in the conjugation procedure of PCVs it is unlikely that using current techniques PCVs will be able to  
226 target more than 20 of the over 90 pneumococcal serotypes [33]. Vaccines that target common proteins rather  
227 than specific capsules on the other hand may prevent pneumococcal disease by different mechanisms, e.g.  
228 enhanced IL-17A mediated nasopharyngeal clearance rather than prevention of acquisition [34]. While  
229 inference of the differential population impact of specific pneumococcal vaccines would require a more precise  
230 parameterization including the focus on a specific setting, the qualitative results of this work are likely to  
231 similarly apply.

232 In a few instances the models predicted changes to pneumococcal ecology following vaccination that seem  
233 counter-intuitive at first. In the high transmission scenario, M\_CL predicted that overall pediatric carriage  
234 prevalence would stay relatively constant (less than 5% change) for vaccines that included up to 8 of the most  
235 competitive serotypes, but then increase by up to 40% if more serotypes were targeted by the vaccine to finally  
236 reduce overall carriage by targeting at least 19 serotypes (Figure 2). This is unique to this model because of its  
237 inclusion of a gradient in type-specific ability to prevent additional acquisition: carriers of highly-competitive  
238 serotypes are more protected against acquisition of further serotypes. By protecting against the most  
239 competitive serotypes through vaccination the remaining serotypes are under less pressure from competition  
240 to a point where they act almost independently. For vaccines that target between 9 and 18 of all serotypes in  
241 the high transmission setting the prevalence of untargeted serotype in the virtual absence of competition then  
242 adds up to exceed the overall prevalence before vaccination (Appendix Figure 1). Furthermore, in M\_CL the  
243 impact of vaccination with low valency vaccines is similar in both transmission settings but higher for moderate  
244 to high valency vaccines in high transmission settings than in moderate transmission settings. In contrast, most  
245 models including M\_B and M\_F predict that transmission intensity and the herd immunity threshold are always  
246 positively correlated [35]. In M\_CL that same effect is evident only for vaccines that target all serotypes. For  
247 vaccines that target most but not all pneumococci this model predicts that the relatively weak competitive  
248 pressure from NVTs in combination with a substantial increase in overall pneumococcal prevalence in high  
249 transmission scenarios helps to control VT circulation better than vaccination in a moderate transmission  
250 scenario with less transmissible VTs but also lower NVT carriage prevalence that compete with VTs. M\_F  
251 predicted that, assuming 55% effective coverage in the high transmission scenario, increasing the valency to up  
252 to 15 serotypes leads to a small increase in vaccine impact on VT carriage which is qualitative different from all  
253 other models and scenarios presented here. This is a result of comparing the impact of vaccination on a  
254 different number of serotypes. In particular, reduction in carriage prevalence of e.g. serotype “1” as a result of  
255 vaccination in the high transmission scenario steadily declines with increasing valency in M\_F (Figure 2).  
256 However, the indirect effect of vaccination against serotypes of lower prevalence is greater and hence  
257 comparing the impact of vaccination on all vaccine serotypes includes both the counter-acting trends. Only in  
258 the high transmission setting in M\_F is a net increase in vaccine effects against VTs predicted for low valency  
259 vaccines.

260 While the models agree well on the qualitative relation between vaccine valency and the herd immunity  
261 threshold we have observed stark differences in the quantitative results. For example M\_CL predicted that  
262 much lower effective coverage is required for elimination of VT carriage. Many factors contribute to this  
263 observation and some could be addressed by more detailed harmonization of the models to a specific setting.  
264 However, two intrinsic model assumptions likely drive this behavior: 1) the strength of vaccine protection and  
265 2) the strength of serotype competition. M\_CL assumes a relatively strong vaccine protection by reducing



266 susceptibility to VT acquisition permanently after vaccination. M\_F assumes vaccine protection, albeit non-  
267 leaky, to only hold for 10 years while M\_B also assumes lifelong protection from vaccination, although  
268 modelled as all-or-nothing and hence even stronger than in M\_CL. While the evidence suggest PCVs to be leaky  
269 [36] little is known about upcoming pan-valent vaccines. Vaccine protection has been found to remain present  
270 5 years after completion after childhood immunization [37] but there is some evidence that protection declines  
271 over time albeit with a half-life that exceeds 5 years [28]. Further, M\_CL has the weakest serotype competition  
272 of the models by assuming leaky protection against heterologous acquisition of additional colonizing strains  
273 during carriage with the most competitive serotypes providing stronger protection against new acquisition. In  
274 comparison M\_B and M\_F respectively assume competitive exclusion on acquisition and potential co-infection  
275 but only after non-leaky heterologous immunity following acquisition has ended. With the relatively weak  
276 competition of serotypes in M\_CL a targeted pediatric carriage prevalence is achieved with lower transmission  
277 intensity and this in turn will ease elimination of vaccine serotypes in comparison to the other models where  
278 transmission is more intense. Recent advances in molecular serotyping methods have shown the pneumococci  
279 frequently co-colonise [38,39] and while epidemiological studies suggest that carriage induces both  
280 homologous and heterologous protection such protection from a single episode of carriage likely is relatively  
281 weak [20,40,41].

282

## 283 **Conclusion**

284 Using three different modelling approaches for pneumococcal ecology that represent a range of alternative  
285 assumptions on pneumococcal immunity and serotype competition we found that NVT competition helps  
286 vaccines of limited valencies eliminate VT carriage. This implies that new vaccines that targeted the majority of  
287 pneumococcal serotypes will benefit less from NVT competition and are likely to offer less indirect protection  
288 than current PCVs. Head to head comparison of current PCVs with high-valency vaccines should not only be on  
289 the grounds of non-inferiority of direct effects but should also account for indirect effects, and closely monitor  
290 IPD endpoints.

291

## 292 **Funding**

293 This work was supported by the Bill & Melinda Gates Foundation (Investment ID OPP1125745) and the US NIH  
294 (R01 AI048935 ).

295

## 296 **Conflicts of interest**

297 M. Lipsitch has received research funding from PATH and Pfizer, and honoraria/consulting fees from Affinivax,  
298 Pfizer and Antigen Discovery. All other authors declare that they don't have any conflicts of interest.

299

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## Tables and Figures

Table 1: Summary of the main features of each model of pneumococcal transmission

	Bottomley et al	Cobey & Lipsitch	Flasche et al
<b>Model type</b>	Compartmental	Individual based	Individual based
<b>Demographics</b>	Gambia	High income country	High income country
<b>Mixing patterns</b>	Homogeneous	Homogeneous	Age-assortative
<b>Natural immunity as a result of infection</b>	<i>non-specific</i> : transient immunity for the duration of infection <i>anticapsular</i> : chance to develop permanent homologous immunity	<i>non-specific</i> : permanent increase in clearance rate, transient reduction in acquisition rate for the duration of infection <i>anticapsular</i> : permanent reduction in susceptibility to homologous infection	<i>non-specific</i> : transient immunity to heterologous infection <i>anticapsular</i> : additional transient immunity to homologous infection <i>other</i> : exposure independent reduction of susceptibility and carriage duration with age
<b>Vaccine induced immunity</b>	Like anticapsular natural immunity but higher chance for protection	Like anticapsular natural immunity but stronger protection	Like anticapsular natural immunity but longer protection

422

423 Table 2: PCV formulations and the ranks of each serotype in terms of its global prevalence according to a  
 424 review on the global distribution of paediatric pneumococcal carriage

	Serotypes (rank)
<b>PCV7</b>	4 (18), 6B (2), 9V (6), 14 (5), 18C (11), 19F (1), 23F (3)

<b>PCV10</b>	+ 1 (31), 5 (38), 7F (32)
<b>PCV13</b>	+ 3 (9), 6A (4), 19A (7)
<b>PCV15</b>	+ 22F (27), 33F (24)

425

426 Fig. 1 Model demographics and serotypes distribution before the introduction of vaccination. Upper panel: The  
427 cumulative age distribution of the model populations. Lower panel: a stacked barplot to illustrate the  
428 predicted serotype distributions (stacked prevalence of serotype specific carriage episodes scaled to the overall  
429 carriage prevalence) in children and the rest of the population in low and high transmission settings.

430 Fig. 2: Predicted percentage reduction in the prevalence of pneumococcal carriage (bottom row), VT carriage  
431 (middle row) and carriage of the most competitive serotype (top row) 10 years after vaccine introduction,  
432 assuming 55% efficacy against acquisition of pneumococcal VTs and 100% coverage.

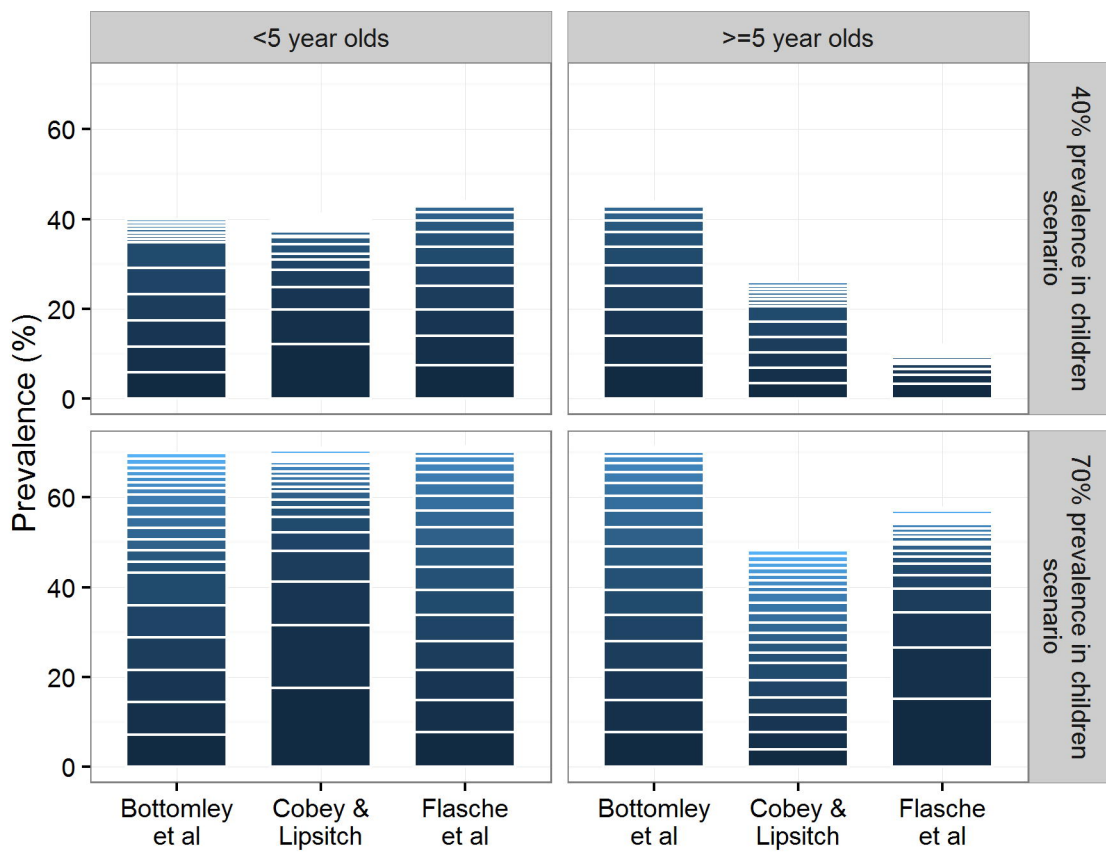
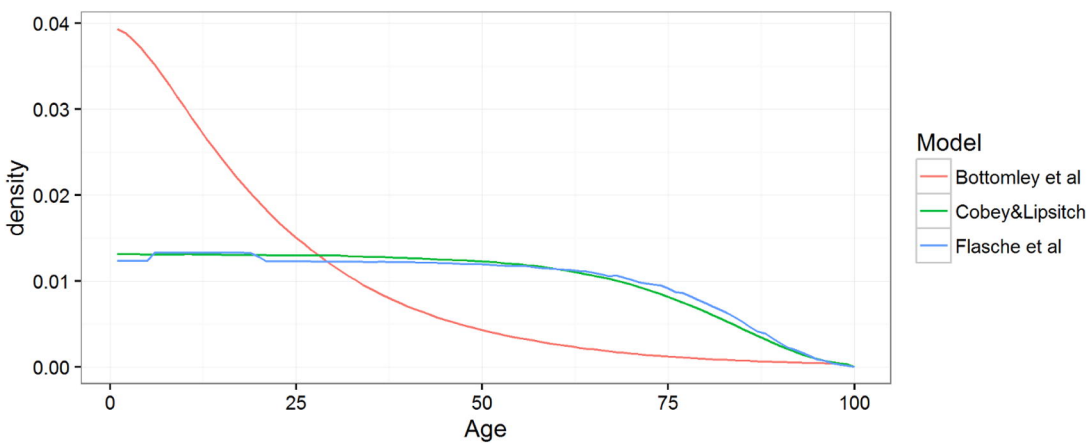
433 Fig. 3: Percentage reduction in the prevalence of pneumococcal carriage 10 years after introduction of a PCV  
434 like vaccine, assuming 55% efficacy against acquisition of pneumococcal VTs and 100% coverage.

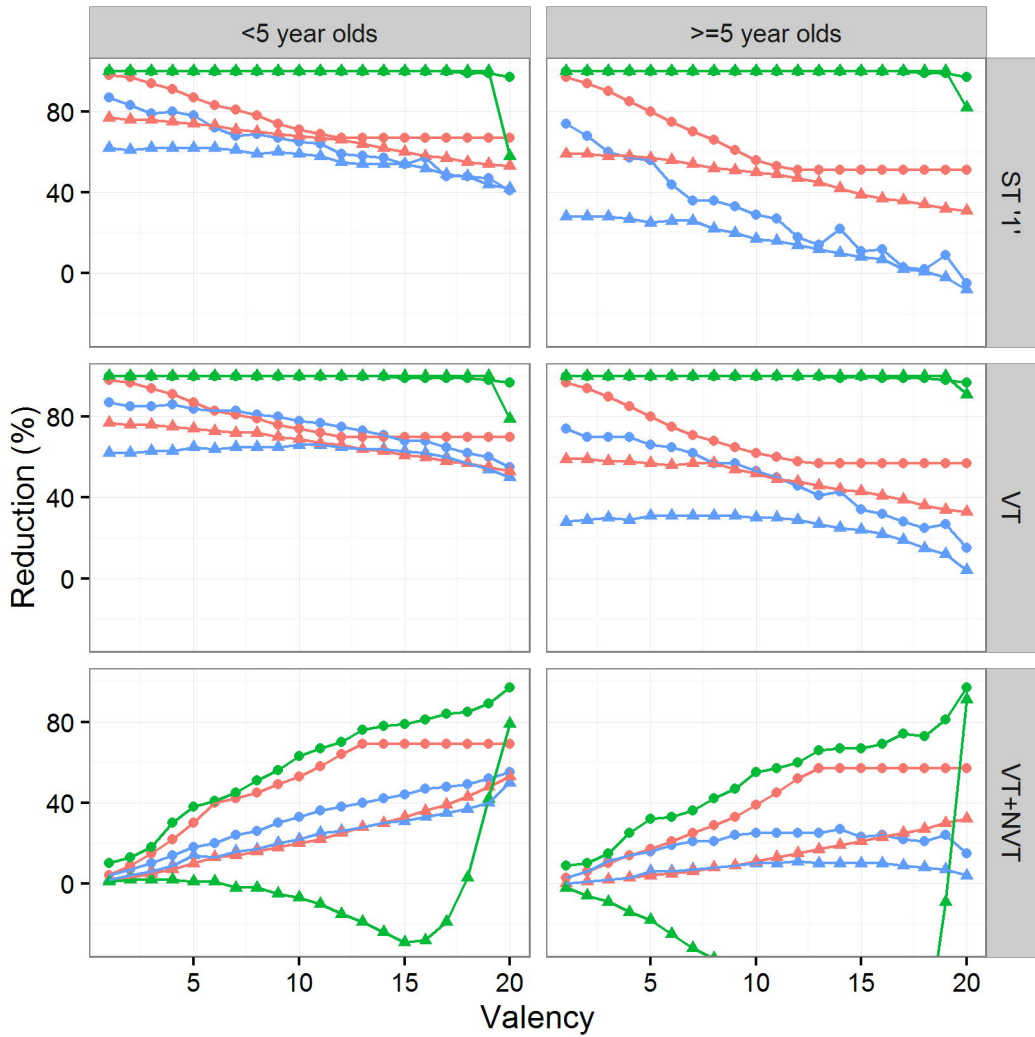
435 Fig. 4: The effective coverage needed to prevent 95% of VT carriage 10 years after the start of vaccination,  
436 assuming serotypes are added to the vaccine in order of their carriage prevalence. At valency 7 and 10 the  
437 respective effective coverage for PCV7/10 – like and PCV13/15 – like vaccines are indicated by large dots and  
438 triangles in respective colors.

439

#### 440 Appendix

441 Appendix Figure 1: The proportion of carriers that carry 1,2...,6 pneumococci at a time following ten years of  
442 vaccination. Rows show different models and columns different transmission intensities indicated by the  
443 prevalence of carriage in less than 5-year-old children before vaccination. In M\_B each host can only carry one  
444 pneumococci at a time and hence the model is not represented here.





### Model

- Bottomley et al
- Cobey&Lipsitch
- ▲— Flasche et al

### Prevalence

- 40
- ▲ 70

