Text S1

Measurement of progression risk

For the i^{th} pneumococcal serotype in the j^{th} ethnic group (Jewish/Bedouin) and k^{th} age category (<12 or 12-35m), and corresponding to the pre- or post-licensure period (t), we defined progression rate $D_{iik}(t)$ as

$$D_{ijk}(t) = \frac{\rho_{ijk}(t)\lambda_{jk}(t)}{\phi_{ijk}(t)\pi_{jk}(t)},$$

thereby scaling total pneumococcal OM incidence rates (λ) and carriage prevalence (π) by serotype-specific proportions in disease (ρ) and carriage (ϕ).

We modeled the total rate of pneumococcal OM incidence, $\lambda_{jk}(t)$, as Gamma-distributed with shape and rate parameters taken as the number of pneumococcal MEF isolates and total child-years at risk, respectively.

The total prevalence of pneumococcal carriage within a stratum was $\pi_{jk}(t)$. It is possible that age and season predict variation in carriage prevalence within strata, which could bias comparisons of carriage prevalence calculated from pre-PCV7 and post-rollout studies. Therefore, we used Poisson regression models to test within strata for an association between carriage prevalence and age (log, linear, and quadratic transformations of age in months) and calendar month. We compared values of the Bayesian information criterion (BIC) to identify if accounting for these variables improved model fit. While calendar month did not improve model fit, we identified improvements in the <12m age group when accounting for age in log months. We therefore used the regression models to predict carriage prevalence at age 6 months when generating samples of $\pi_{ik}(t)$.

The proportion $\rho_{ijk}(t)$ of pneumococcal OM episodes ascribed to each serotype i in 1,...,S was

$$\rho_{jk}(t) \sim \text{Dir}(S, \alpha_{jk}(t) = 1 + \mathbf{x}_{jk}^{OM}(t)),$$

where each element $x_{ijk}^{\rm OM}(t)$ was the observed number of OM cases caused by serotype *i*. In the absence of observations, α =1 conferred a flat prior across serotypes. By the same intuition, the serotype distribution in carriage

$$\phi_{jk}(t) \sim \text{Dir}(S, \alpha_{jk}(t) = 1 + \mathbf{x}_{jk}^{\text{Car}}(t)),$$

where each $x_{ijk}^{\mathrm{Car}}(t)$ was the number of carriage isolates observed for serotype i.

We measured the change in rate of progression for each serotype within age- and ethnic strata after vaccine rollout via the relative progression rate (RPR):

$$RPR_{ijk} = \frac{D_{ijk}(PCV13 \text{ era})}{D_{ijk}(Pre-PCV7 \text{ era})}.$$

The effect size presented in the main text is equivalent to $1 - RPR_{ijk}$.

Estimation of pan-serotype effects

We used a Bayesian random effects model to estimate the mean change in progression rate across vaccine-targeted and non-vaccine serotypes within each age and ethnic stratum ($d_{jk}^{\rm VT}$ and $d_{jk}^{\rm NVT}$, respectively). Defining Y_{ijk} and V_{ijk} as the sample mean and variance of $\log(RPR_{ijk})$, as defined above, we modeled

$$Y_{ijk} \sim \mathcal{N}(\mu = \delta_{ijk}, \sigma^2 = V_{ijk}),$$

for observed values of Y_{ijk} and V_{ijk} , where serotype-specific effects δ_{ijk} are distributed according to

$$\delta_{ijk} \sim \mathcal{N}(d_{jk}^{\text{VT}}, \sigma_{jk}^{\text{VT}^2})$$

for i belonging to the vaccine serotypes, and

$$\delta_{ijk} \sim \mathcal{N}(d_{jk}^{\text{NVT}}, \sigma_{jk}^{\text{NVT}^2})$$

for i belonging to the non-vaccine serotypes. We assumed flat priors for population parameters, with each $d_{jk}^{\ell} \sim \mathcal{N}(0,\!10^6)$ and $\sigma_{jk}^{\ell}^2 \sim \mathcal{U}(0,\!10^6)$. We recovered the posterior distribution of the parameters defined above parameters via Markov Chain Monte Carlo sampling, coded de novo, using the Metropolis-Hastings algorithm to update proposals. We drew samples over one million iterations, saving the state of the chain at every 1,000th step to reduce autocorrelation.