**INTRODUCTION**

Vaccines can provide recipients with large direct protective effects by priming their immune system before wild exposure to a pathogen. For contagious diseases, indirect protective effects of a vaccine campaign emerge when an individual (vaccinated or unvaccinated) has a lower rate of encountering the pathogen because some fraction of their contacts were vaccinated and are therefore less likely to carry the pathogen themselves. The extent of indirect protection therefore depends on both the degree to which each recipient benefits from the vaccine, often called the vaccine efficacy, and the fraction vaccinated, often called the vaccine coverage.

Over time, the direct effects of some vaccines wane and render the recipient once again susceptible to the disease. Likewise, waning of indirect, or “herd”, protection in a particular population can result from the waning of direct effects, but also through population turnover with a net replacement of vaccinated individuals with unvaccinated individuals.

Although much attention is given to measuring the duration and magnitude of vaccine efficacy, many questions regarding herd protection remain. For instance, vaccines can be a relatively quick means to protect an at-risk population until longer-term solutions can be instituted, but there is a need to know how much time is “bought” by such a vaccination campaign. For routine rather than stopgap vaccination, the decision of when to boost or revaccinate will depend in part on the duration of herd immunity (DHI) following vaccination. Finally, mobility is recognized as an important factor for targeting vaccination, but it remains to be seen how strongly, and in what direction, population mobility should be considered.

We study the model system of oral cholera vaccines to address these questions. Due to reliable vaccine efficacy and high coverage through mass campaigns, cholera vaccines can generate powerful herd protection effects [Ali 2005]. When a sufficient proportion of a population is immunized, the effective reproductive number can be reduced below one, a threshold commonly defined as herd immunity.

In this paper, we estimate the time-varying profile of oral cholera vaccine efficacy and use mathematical models to study the implications of vaccine waning and human mobility on herd protection. We apply our model to three case-study settings of Dhaka, Calcutta, and Juba. Finally, we provide a tool that can help guide decisions regarding time-to-revaccination.

**RESULTS**

Following the method Durham et al [1998], we estimate the time-varying vaccine efficacy using data from a set of published clinical trials, cohorts, and case-control studies [Table TBD]. We find that the whole-cell (WC) and B subunit killed whole-cell (BS-WC) vaccines provide some degree of protective efficacy for XXXX and XXXX years, respectively.

In the simplest setting with no births, deaths, or migration, mass vaccination can provide some herd protection as long as direct vaccine efficacy remains, which we estimate to be 3.7 years for the WC vaccine and 4.2 years for the BS-WC vaccine (Figure AA, dashed grey lines). The inclusion of migration can substantially decrease these durations. In a high-migration setting with an average duration of residence of 2 years, the duration of any herd protection decreases below three years for each (Figure AA, solid lines). Rates of birth and death rates must be unreasonably large in order to substantially alter the waning of herd protection – even conservative estimates of a life expectancy of 40 years only results in an approximately 2% decrease in the duration of herd protection (Figure AA, black lines).

Of higher interest to policy-makers is not just the duration of any herd protection, but specifically the duration of herd immunity (DHI). Our primary metric of DHI is defined as the number of days following a vaccination campaign with an effective reproductive number (R­e) below one. Figure VC shows the strong positive dependence of DHI on high initial vaccine coverage and low R­0­­. Low rates of migration and birth/death will also extend DHI (Supplemental Information).

Although deterministic models exhibit threshold-like behavior once the reproductive number exceeds one, an outbreak in a stochastic world is possible below the threshold and is not guaranteed above the threshold. For instance, if we assume a Poisson distribution of secondary cases and define an outbreak as at least ten transmission events, the probability of an outbreak is 24.6% when the reproductive number equals one (Figure BB, horizontal grey line) and 79.7% when the reproductive number is 2 [Becker 2015]. Holding vaccine coverage at 100%, Figure BB shows that the probability of an outbreak is reduced by mass vaccination, but not eliminated, for a duration of time that depends critically on the vaccine efficacy profile and migration rate. See Supplemental Information for dependence on other factors such as vaccine coverage, seasonality, and birth/death rates.

In settings with strong seasonal variation in the force of infection, the duration of herd immunity can be extended by up to XXXX% via strategic vaccination. The timing of such strategic vaccination is challenging, however, as it depends on the seasonal forcing patterns, the transmission potential of the setting, the migration rate of the setting, and the vaccine coverage and waning profile.

A natural extension of this model can be used to explore priority setting for remote versus highly mobile communities. We show that if the risk of cholera introduction is proportional to the rate of population turnover (e.g., the pathogen is introduced only by migrants), vaccine impact may be maximized for intermediate levels of connectedness. That is, highly remote communities may retain herd immunity for a long time, but are unlikely to have cholera introduced and therefore the number of expected cholera cases is low. Conversely, highly mobile communities are more likely to have cholera introduced, but population turnover can quickly cause herd immunity to wane.

**DISCUSSION**

Our results show that even for a population that recently underwent a mass OCV campaign, there is a risk of cholera re-emergence in the near future. Such re-emergence does not imply vaccine failure, but instead can result from population turnover, waning of direct effects, or pernicious seasonal forcing.

Our results can help guide decision-makers on the time window they can expect a population to resist a cholera outbreak even if the pathogen were to be introduced. During this window, WASH interventions can be scaled-up to provide longer-term protection, or a data-driven routine re-vaccination schedule can be determined.

Our results depend on several simplifying assumptions...

Cholera vaccine efficacy has been shown to vary by age of recipient, however for simplicity we do not model this age structure in the main results.

**METHODS**

We developed a SEIR-type compartmental model with individuals fully susceptible to cholera (S), exposed but not yet infectious (E), infectious (I), recovered and immune (R), and vaccinated (V) (Figure CC). Key parameters for each transition are shown in Table TBD.

To extend this model to account for the observation that cholera vaccine direct effects do not tend to wane exponentially, we separate the V compartment into *n* monthly stages, thereby creating an Erlang-distribution for the duration of time in any V compartment [Lloyd 2001, Krylova 2013]. The average time residing in each month compartment is therefore 30.5 days (or, the rate is 0.033 per day). On average, individuals move from compartment S to V1 for months [0,1) post-vaccination, to V2 for months [1,2) post-vaccination, etc. We adapted monthly VE(t) estimates using data from [Clemens 1990] and re-analyzed by [Durham 1998] and define VE(1) to be the VE for months [0,1) post-vaccination, VE(2) to be the VE for months [1,2) post-vaccination, etc. We parameterized the time-varying distribution of vaccine efficacy of Shanchol and Dukoral using tables provided by [Durham 1998] and linear interpellations between 6-month estimates.

We assume a constant rate of emigration from our system that is equal for all compartments. The total system size is held constant by offsetting this emigration with an equal rate of immigration that is entirely into the S compartment, thereby assuming that neighboring areas are not vaccinated. If immunity levels (via vaccination or naturally acquired infection) are nonzero in neighboring locations, migrants from those locations could instead extend herd immunity in the population of interest. The rates of migration in our model range from an average residence time of 2 years in a high-migration setting (similar to the 58% loss to follow up over two years during a recent trial in Dhaka [Qadri 2015 Lancet]) to 20 years in a low-migration setting (similar to the 9% loss to follow up over two years in a trial in Calcutta [Sur 2011 PLOSNTD]).

To account for seasonal forcing, the transmission parameter is allowed to vary with each day (t) according to a sinusoidal function where *f* is the magnitude of seasonal forcing and is a frameshift parameter accounting for the time of initial vaccination campaign (τ=0 if vaccination occurs at the peak transmission season, τ=π if vaccination occurs at the trough of transmission season). Therefore, we assume an annual cycle, but note that some regions such as Dhaka may exhibit biannual cycles [cite].

We define the duration of herd immunity as the number of days following a vaccination campaign with an effective reproductive number (R­e) below one. We calculate

where is the proportion of the population susceptible at time *t*,

where is the total population size at time *t*.

We can use Re(t) to estimate the probability of the community sustaining an outbreak given the introduction of a single case. For this calculation, we assume a Poisson distribution of secondary infections and define an outbreak as at least 10 cases (see supplemental information for overdispersed distributions and different outbreak thresholds) [Becker 2015].

Our primary results assume a “leaky” vaccine mode of action, but analysis using an “all or none” mode of action was repeated using a time-invariant VE estimate and creating paths from each vaccine compartment back to the S compartment so that the duration of time in the V­n ensemble is variable (????). More details on the methods and results from this model can be found in the supplementary information. In summary, the results presented in the main text were robust to the assumed mode of vaccine action.

Furthermore, our primary results assume a direct transmission route of cholera, while some models prefer transmission through an intermediary such as a water reservoir [cite]. Our results regarding the duration of herd protection are insensitive to assumptions regarding transmission route, as they deal with vaccine effects and changes to the population demographic via birth/death or migration.