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Modeling pertussis transmission in the Philippines: Insights on epidemic dynamics and vaccination impact

Micko Jay S. Bajamundi[1], Robert Neil F. Leong[2], Mark Lexter D. De Lara[1], Ranzivelle Marianne Roxas-Villanueva[3], Marie Joy Lopez-Relente[4], Allen L. Nazareno*[1]

[1]Institute of Mathematical Sciences, University of the Philippines Los Baños, Laguna, Philippines
[2]Mathematics and Statistics Department, De La Salle University, Manila, Philippines
[3]Institute of Physics, University of the Philippines Los Baños, Laguna, Philippines
[4]Institute of Statistics, University of the Philippines Los Baños, Laguna, Philippines

ABSTRACT

Pertussis, a highly contagious respiratory disease, poses a significant health threat across all ages, with infants younger than one year of age facing the highest risk of hospitalization and death. In the Philippines, pertussis caused 48 deaths among 705 reported cases in 2023. While these numbers appear modest, they likely reflect substantial underreporting given the presumed circulation of the disease, raising concerns about the true extent of the pertussis burden. Modeling efforts can improve our understanding of pertussis transmission dynamics and help assess the impact of vaccination; however, such a comprehensive mathematical analysis has been lacking in the country. We developed a Susceptible-Exposed-Infectious-Recovered-Susceptible (SEIRS)-based model that incorporates varying exposure levels to analyze pertussis transmission dynamics, calibrated using national epidemiological data from 2017 to 2019. Our model captured the observed pertussis epidemic trends and revealed that actual pertussis cases may be 10–40 times higher than reported. The model also demonstrated that maintaining a high level of protection is crucial for preventing case surges, as lower protection levels increase susceptibility and outbreak potential. The substantial underestimation of pertussis incidence and the projected impact of vaccination together highlight the need for enhanced surveillance systems and strengthened pertussis immunization programs. Our study provides important insights into pertussis epidemiology in the Philippines and in the Southeast Asian region, offering a foundation for evidence-based public health policies aimed at achieving more effective pertussis control.

INTRODUCTION

Pertussis or whooping cough, caused by *Bordetella pertussis*, is a highly contagious respiratory disease that remains a significant public health concern. In 2022, an estimated 62,000 cases were reported globally, with more than half occurring in the Western Pacific Region (World Health Organization, Regional Office for the Western Pacific 2025). In the Philippines, 705 cases were recorded in 2023, leading to 48 deaths (Department of Health 2024). Although these figures appear modest, they likely underestimate the true incidence due to underreporting, given the high transmissibility potential of pertussis (Cherry et al. 2013). Despite widespread vaccination efforts (World Health Organization 2025), pertussis continues to circulate, highlighting the need for a better understanding of its transmission dynamics.

Vaccination continues to be the most effective strategy for preventing pertussis (Schuchat 2011). Both natural infection and vaccination provide temporary immunity, with infection-induced protection lasting for 15 to 20 years and vaccination-

KEYWORDS

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*Corresponding author
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induced immunity ranging from 5 to 30 years (Wirsing von König et al. 2002; Wendelboe et al. 2005; Russell et al. 2021). The DTaP (Diphtheria, Tetanus, and Pertussis) and Tdap (Tetanus, Diphtheria, and acellular Pertussis) vaccines protect against pertussis, with DTaP given in five doses to children up to age 7 and Tdap given as a booster for adolescents (11–12 years) and adults every 10 years (Centers for Disease Control and Prevention 2025). In the Philippines, the Department of Health (DOH) offers free diphtheria-tetanus-pertussis immunization beginning at six weeks of age (Department of Health 2025; UNICEF Philippines 2025). In 2019, vaccination coverage for children aged 12–23 months reached 71%, up from 69% in 2017 and 65% in 2018 (World Health Organization 2024).

Accurate disease incidence data are vital for public health decision-making. However, pertussis is often underreported due to factors such as misdiagnosis, inadequate surveillance, and asymptomatic or mild cases going unnoticed (Meadows et al. 2022). In some countries, actual incidence rates may be significantly higher than reported (Bagordo et al. 2023; Guzman-Holst et al. 2023), making it challenging to assess the true impact of the disease and potentially influencing how interventions and resources are prioritized.

Dynamic modeling is a powerful tool for understanding disease transmission and assessing the population-level impact of vaccination programs (Hethcote 2000). These models account for the dynamic nature of infection spread by assuming that the rate at which susceptible individuals become infected depends on the number of infectious individuals in the population (Jit and Brisson 2011), providing a more realistic representation of transmission. Additionally, dynamic models capture nonlinear effects, such as herd immunity, which is crucial for accurately evaluating the impact of vaccination strategies on disease burden (Hethcote 2000).

Several studies have explored the dynamics of pertussis transmission across different geographical contexts. Luz et al. (2006) applied a classic compartmental model assuming complete immunity after recovery, incorporating age structure to simulate transmission in São Paulo, Paraná, and Bahia, Brazil. Safan et al. (2022) extended this framework by incorporating reinfection and vaccination, with reinfection assumed to be less probable than primary infection. Russell et al. (2021) compared four dynamic models, some accounting for lifelong immunity and others allowing repeat infection, and incorporated age structuring to evaluate maternal pertussis immunization in Brazil. Meanwhile, Ameri and Cooper (2019) adopted a network-based approach, introducing an “exposed but not yet infectious” compartment and modeling interactions among individuals within a scale-free network. Building on insights from these prior studies, the present study integrates the possibility of reinfection, accounts for vaccination and underreporting, and distinguishes between exposed non-infective and infectious individuals to develop a pertussis transmission model tailored to the Philippine setting.

To our knowledge, no similar models have been developed for the Philippines to describe pertussis transmission or evaluate the impact of vaccination. Because disease dynamics and vaccination outcomes are influenced by local demographics and healthcare practices, developing a country-specific model is important in providing context-relevant insights that can guide immunization strategies and policy decisions. This baseline study, therefore, characterizes pertussis transmission dynamics in the Philippines using national incidence data from 2017 to 2019. By estimating the degree of underreporting and assessing the overall effectiveness of the vaccination program, it offers preliminary evidence for strengthening pertussis control and management, insights that may also apply to other Southeast Asian countries facing comparable epidemiological challenges.

METHODS

Pertussis Transmission Model

We used a modified SEIRS model that accounts for both reinfection and vaccine-induced protection, following the framework described by Campbell et al. (2015). The Susceptible (S) compartment represents individuals at risk of infection, while the Exposed (E) compartment consists of those in the latent period. Infectious individuals (I) recover into the Recovered (R) compartment, gaining temporary immunity. The Vaccinated (V) compartment includes individuals who have gained protection mainly through vaccination. Immunity wanes over time, returning individuals to susceptibility. Reinfection was assumed to be less likely than primary infection (Campbell et al. 2015; Safan et al. 2022). Figure 1 illustrates the pertussis transmission dynamics, with transitions between epidemiological states governed by the following differential equations:

$$\frac{dS_1}{dt} = -\lambda S_1(I_1 + I_2) - vS_1$$

$$\frac{dS_2}{dt} = \omega_N R + \omega_V V - \theta\lambda S_2(I_1 + I_2) - vS_2$$

$$\frac{dE_1}{dt} = \frac{\lambda}{N} S_1(I_1 + I_2) - \sigma E_1$$

$$\frac{dE_2}{dt} = \theta \frac{\lambda}{N} S_2(I_1 + I_2) - \sigma E_2$$

$$\frac{dI_1}{dt} = \sigma E_1 - \gamma I_1$$

$$\frac{dI_2}{dt} = \sigma E_2 - \gamma I_2$$

$$\frac{dR}{dt} = \gamma I_1 + \gamma I_2 - \omega_N R$$

$$\frac{dV}{dt} = -\omega_V V + vS_1 + vS_2$$

$$\frac{dInc}{dt} = \phi \frac{\lambda}{N} S_1 (I_1 + I_2) + \phi\theta \frac{\lambda}{N} S_2 (I_1 + I_2)$$

Table 1 shows the summary of the model parameter values, which were either fitted, assumed, or sourced from the literature, along with the initial conditions for the state variables. The equation $\frac{dInc}{dt}$ denotes the rate of change in the incidence of infection per unit time, which was used to derive the weekly cumulative incidence. To capture reinfection dynamics, we modeled two levels of exposure: individuals with no prior infection (represented by subscript 1) and those who were previously infected or vaccinated (represented by subscript 2). Subsequent reinfections were not explicitly represented to maintain model tractability and reduce parameter uncertainty. For individuals with a history of pertussis infection, susceptibility was assumed to be reduced by a factor of θ. The parameters λ, σ, γ, ω, and v denote the transmission, latent, recovery, immunity loss, and vaccine-induced protection or simply protection rates, while ϕ serves as a scaling factor to account for the underreporting of the incidence of pertussis. It was assumed that the population (N) was constant throughout the simulation period.

Table 1: Summary of model parameters and initialization for the state variables.

Definition	Parameter	Value	Reference
Transmission rate	λ	See Table 2	Fitted
Reporting factor	ϕ	See Table 2	Fitted
Vaccine-induced protection rate	v	See Table 2	Fitted
Latent period	$\frac{1}{\sigma}$	1.14 weeks	(Centers for Disease Control and Prevention, 2024)
Infectious period	$\frac{1}{\gamma}$	3 weeks	(von König et al. 2002; Centers for Disease Control and Prevention 2024)
Waning immunity duration after infection	$\frac{1}{\omega_N}$	782.7 weeks	(Wendelboe et al. 2005)
Waning immunity duration after vaccination	$\frac{1}{\omega_v}$	381.4 weeks	(von König et al. 2002)
Reduced susceptibility factor due to prior infection*	θ	0.5	Assumed
Population	N	106.7,108.6,110.4 million	(World Bank 2025)
Initial susceptible population (naïve)*	$S_1(0)$	97.9999% of N	Assumed
Initial susceptible population (with history of infection)*	$S_2(0)$	0	Assumed
Initial exposed population (naïve)	$E_1(0)$	0	Assumed
Initial exposed population (with history of infection)	$E_2(0)$	0	Assumed
Initial infectious population (naïve)*	$I_1(0)$	0.0001% of N	Assumed
Initial infectious population (with history of infection)	$I_2(0)$	0	Assumed
Initial recovered population	$R(0)$	0	Assumed
Initial vaccine-protected population*	$V(0)$	2% of N	Derived from WHO-reported vaccine coverage data for infants and young children (2017–2019) (World Health Organization 2024), adjusted for population demographics

Notes: *Varied in the sensitivity analysis; WHO, World Health Organization.

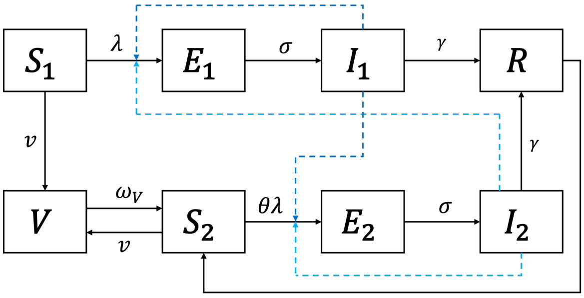


Figure 1: Schematic representation of pertussis transmission. *S*, susceptible; *E*, exposed; *I*, infectious; *R*, recovered; and *V*, vaccinated. The subscript "2" indicates prior infection or vaccination. The susceptibility of previously infected or vaccinated individuals is reduced by a factor of θ relative to naïve susceptibles. Parameters λ, σ, γ, ω, and v represent transmission, latent, recovery, immunity loss, and vaccine-induced protection rates, while ϕ accounts for underreporting. Solid lines indicate movement between compartments, while dashed lines denote indirect influences on transitions. Table 1 shows the summary of the model parameter values and initial conditions.

Mathematical Analysis of the Pertussis Transmission Model

To gain insight into the qualitative behavior of the system, we performed a mathematical analysis of the model. We derived the disease-free equilibrium (DFE) and the basic reproduction number R_0 via the next-generation matrix approach (van den Driessche and Watmough 2002). Stability of the DFE was analyzed using the computed R_0 and the condition for the existence of the endemic equilibrium was determined.

Model Calibration

We solved the model using MATLAB's built-in solver *ode45* (The MathWorks Inc. 2024). The parameters λ, v, and ϕ were estimated by fitting the model to the national weekly cumulative pertussis case reports for each year (from 2017 to 2019), obtained from the Department of Health (DOH) published data (Department of Health 2024). More details regarding the dataset are provided in the *Supporting Information*. Parameter estimation was performed using the least squares approach implemented via the *lsqcurvefit* function in MATLAB. Based on the WHO-reported vaccine coverage data for infants and young children during 2017–2019 (World Health Organization 2024), we estimated that approximately 2% of the population was protected by vaccination. Seroprevalence data suggest substantial underreporting of pertussis, with incidence estimated to be 100–3000 times higher than reported in Italy (Bagordo et al. 2023) and about 100 times higher among older adults in five Latin American countries (Guzman-Holst et al. 2023). Guided by this evidence and adopting a less conservative approach, we constrained v to 0.005–0.05 and ϕ to 0.0003–0.10. Initial parameter values for λ, v, and ϕ were generated using Latin Hypercube Sampling (LHS), with 1000 parameter combinations sampled.

Model Outputs and Sensitivity Analysis

From the best-fit model, we estimated yearly pertussis incidence and compared it with reported cases over the study period. Uncertainty in both incidence and parameter estimates was quantified using a nonparametric bootstrapping approach (Efron and Tibshirani 1993), wherein 1000 resampled datasets were generated from the original cumulative time series. Since the cumulative incidence represents an aggregated model input derived from limited empirical data rather than individual-level observations, its underlying distribution is uncertain. Therefore, a nonparametric bootstrapping approach was employed to estimate uncertainty without assuming any specific probability distribution.

The partial rank correlation coefficient (PRCC) method was carried out to analyze the sensitivity of the model output to individual parameters. Each parameter was assigned a uniform distribution and sampled independently. Parameter ranges were set as either ±50% of the base case values or according to the 95% confidence intervals of the fitted parameters. A total of 1000 simulations were performed to examine how the model output changes over time.

To assess the impact of vaccination (v) across varying levels of pertussis transmission (λ), we estimated the cumulative incidence for each pair of parameter values. The protection and transmission rates were varied from 0.9 to 1.1 times their base case values. Additionally, we evaluated the model sensitivity by analyzing incidence estimates across different scenarios, including the initial infectious proportions (10^{-2}, 10^{-4}, 10^{-6}, 10^{-8}, 10^{-10}). We also varied the proportions of naïve susceptibles and previously infected susceptible individuals (0.5 and 0.5, 0.6 and 0.4, and 0.4 and 0.6), and the initial proportion of protected individuals (ranging from 0.1 to 0.9 in increments of 0.1), to assess how differences in baseline susceptibility and immunity influence the fitted parameters.

RESULTS

The model was shown to be both nonnegative and bounded, indicating that all the state variables stay biologically feasible at all t>0. The basic reproduction number was derived as $R_0 = \frac{\lambda\theta}{\gamma}\left(\frac{\omega_V}{\omega_V + v}\right)$, representing the average number of secondary infections produced by a single infectious individual. The DFE is locally asymptotically stable when $R_0 < 1$ and becomes unstable when $R_0 > 1$ that leads to the existence of an endemic equilibrium. Detailed proofs and derivation of R_0, equilibrium points, and their stability are provided in the *Supporting Information*.

The pertussis transmission model fit well to the cumulative all-age incidence of pertussis infection in the Philippines from 2017 to 2019 (Figure 2). The model closely aligned with the observed data, indicating that it effectively captured the overall trend in pertussis transmission. The estimated parameters, summarized in Table 2, include the transmission rate (λ), protection rate (v), and reporting factor (ϕ). The estimated protection rates for 2017, 2018, and 2019 were approximately 0.002, 0.03, and 0.002, respectively. The corresponding transmission rates were around 0.40, 0.70, and 0.40. The reporting factor varied from 0.02 to 0.09. The estimated incidence rates per 100,000 population were approximately 4 (95% CI: 1, 29) in 2017, 10 (95% CI: 3, 427) in 2018, and 2 (95% CI: 1, 7) in 2019, which were substantially higher than the reported incidence rates. The estimated basic reproduction numbers for the period were less than 0.3. The highest proportion of infectious individuals was observed in 2018, whereas the lowest was recorded in 2019. Similarly, the proportion of protected individuals peaked in 2018, while substantially lower proportions were observed in 2017 and 2019 (Figure S3 in the *Supporting Information*).

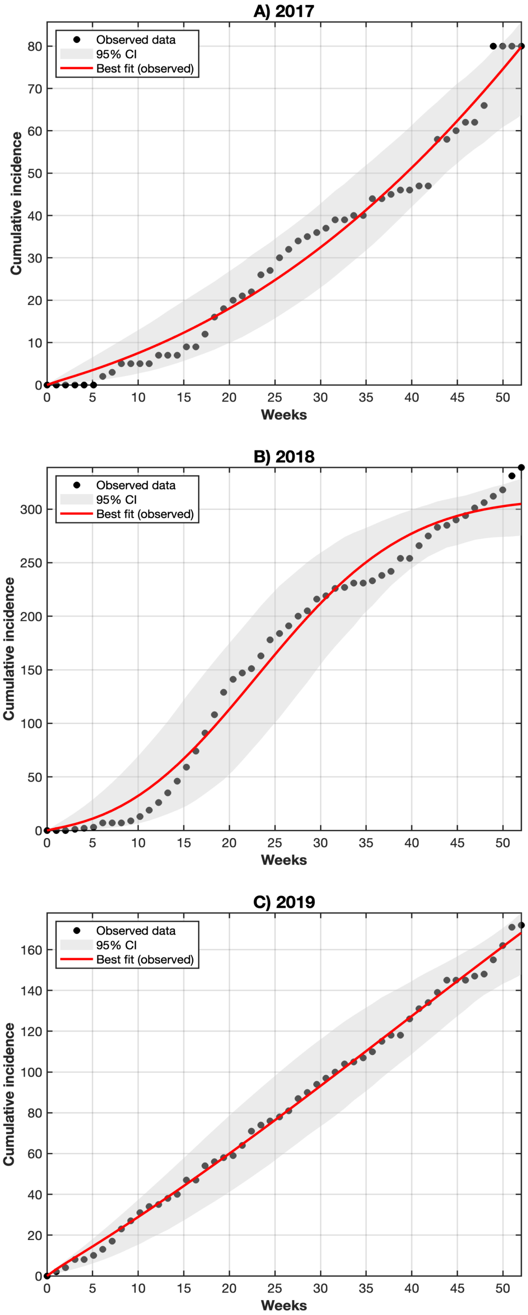


Figure 2: Observed weekly all-age cumulative incidence of pertussis in the Philippines and the fitted pertussis model from 2017 (A) to 2019 (C). The shaded areas indicate the 95% confidence intervals derived from the nonparametric bootstrap simulations.

Table 2: Best-fit model parameters estimate and corresponding modeled incidence rates in the Philippines, 2017–2019, with 95% confidence intervals from bootstrap simulations.

Year	λ	v	ϕ	Estimated incidence rate*
2017	0.403 (95% CI: 0.396, 0.680)	0.002 (95% CI: 0.0005, 0.021)	0.020 (95% CI: 0.002, 0.0348)	4 (95% CI: 1, 29)
2018	0.695 (95% CI: 0.479, 1.336)	0.028	0.027 (95% CI: 0.0007, 0.1)	10 (95% CI: 3, 427)

		(95% CI: 0.013, 0.05)		
2019	0.362 (95% CI: 0.348, 0.545)	0.002 (95% CI: 0.000, 0.017)	0.094 (95% CI: 0.023, 0.1)	2 (95% CI: 1, 7)

Notes: *per 100,000 population and adjusted; The parameters λ, v , and ϕ represent the transmission rate, protection rate, and reporting rate, respectively (see Figure S2 for the distribution); CI, confidence interval.

Sensitivity analysis showed that the model's incidence estimates were highly sensitive to the initial proportion of infectious individuals, with higher initial values resulting in substantially higher incidence (Figure 3). This pattern was associated with a reduction in the estimated transmission rate, reporting rate, and protection rate with increasing initial values. Note that extreme values of the initial proportion of infectious individuals resulted in a poor model fit.

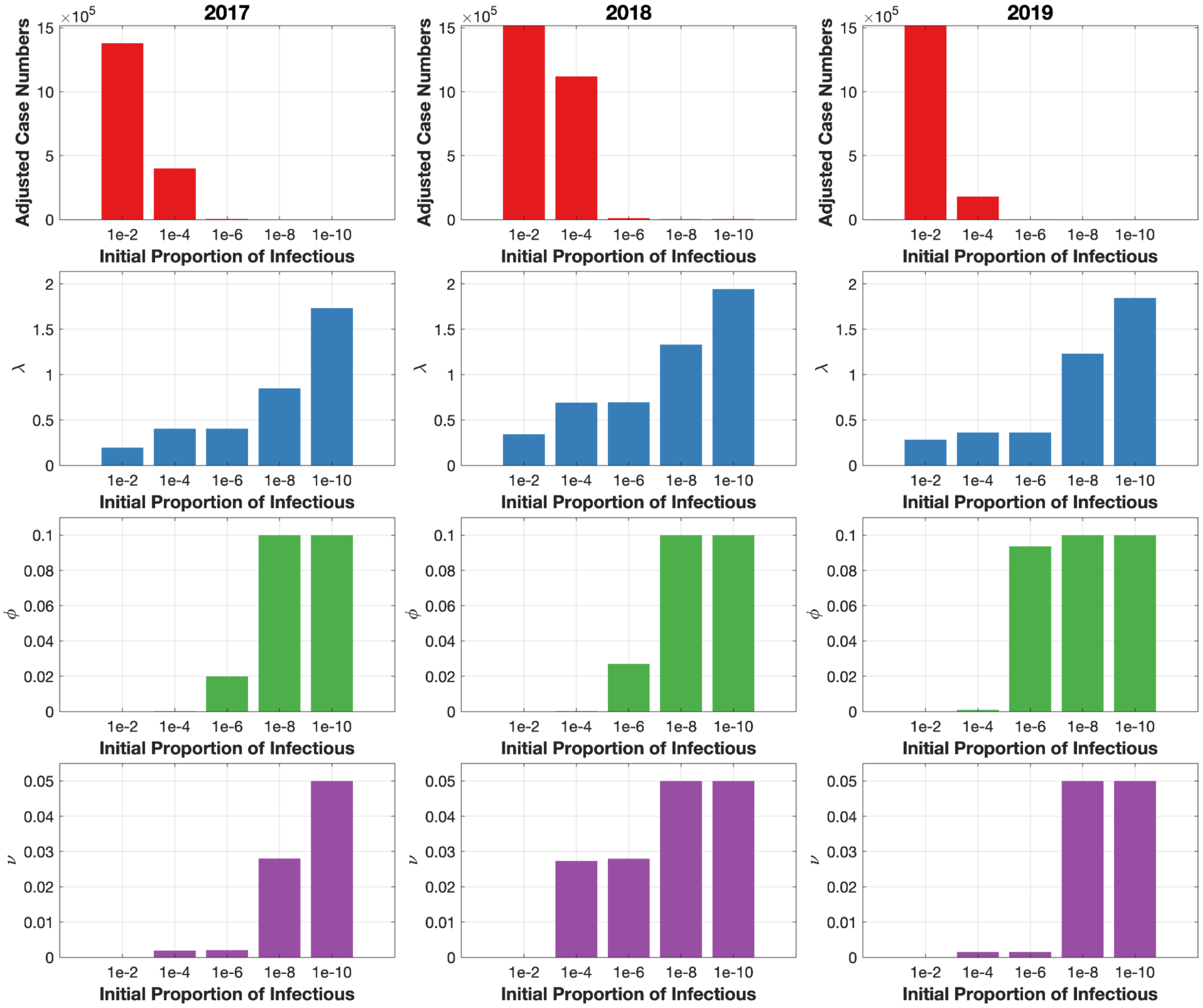
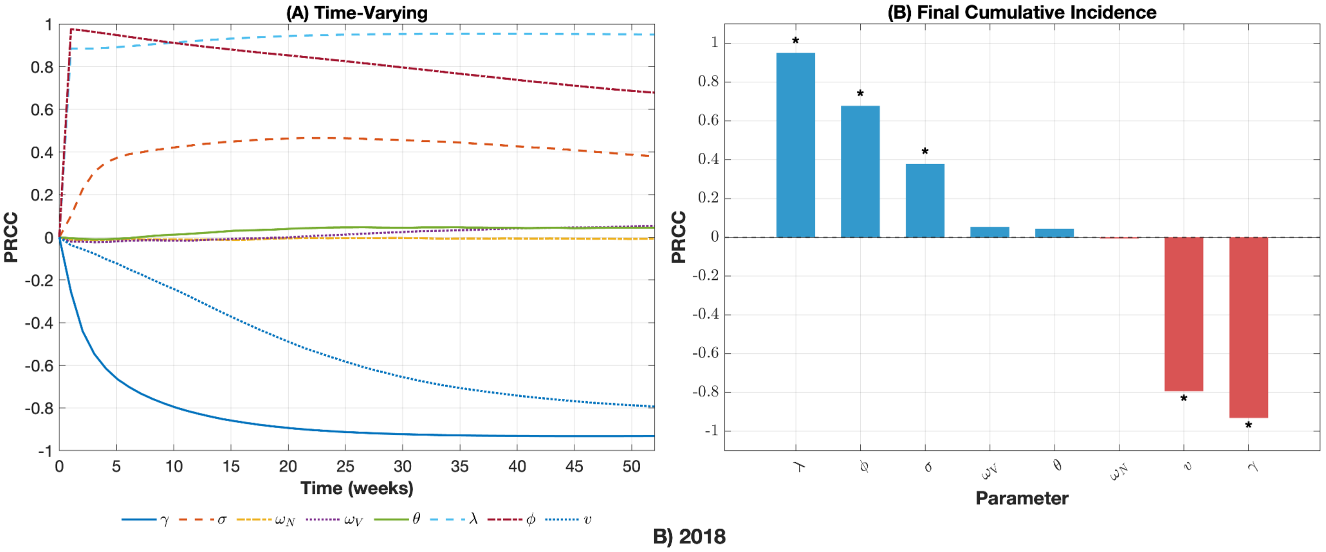


Figure 3: Estimated number of pertussis cases (adjusted) and values of transmission rates (λ), reporting rates (ϕ), and protection rates (ν) for varying initial proportions of infectious individuals, across 2017 to 2019.

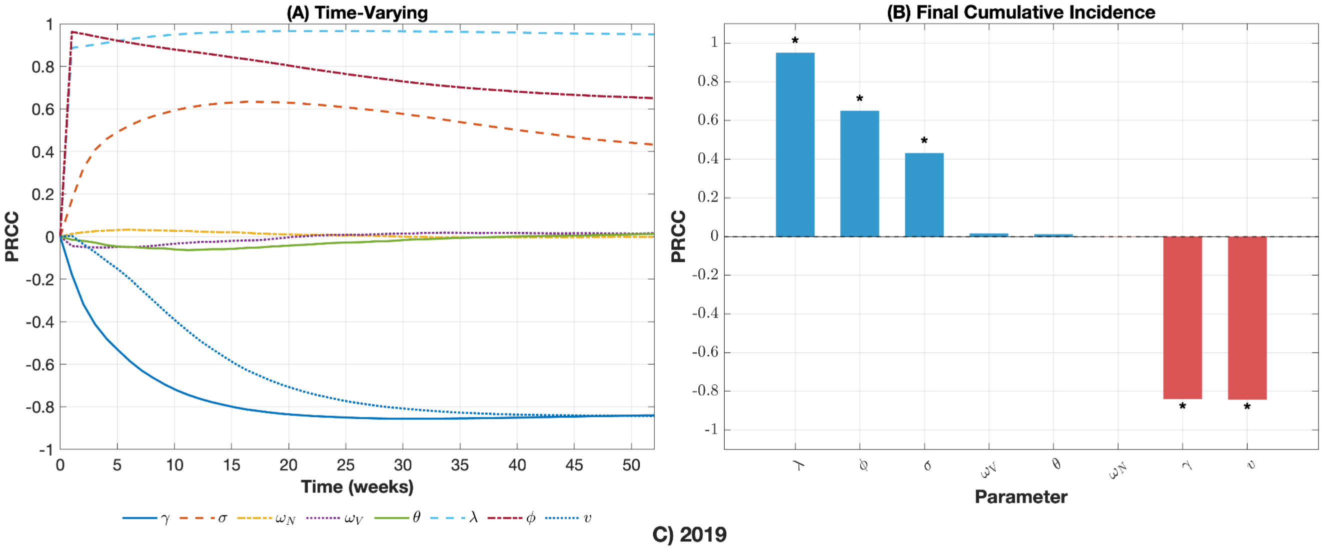
Varying the proportions of naïve and previously infected susceptible populations resulted in only small changes in the fitted parameter estimates across all years. The parameters ϕ and v remained nearly unchanged, reflecting low sensitivity to assumptions about the initial distribution of susceptibility. Moreover, increasing the proportion of previously infected individuals resulted in lower estimates of λ, indicating reduced effective transmission potential with greater partial immunity. Across all years, the reporting rate parameter was the least sensitive, while the other fitted parameters were largely unchanged at lower values of the initial protected proportion but increased as this proportion rose. Details of the results are provided in Tables S1 and S2 of the *Supporting Information*.

Across the period of interest, the PRCC analysis consistently identified transmission (λ), reporting (ϕ), protection (v), and recovery (γ) rates as the most influential parameters affecting cumulative incidence. The parameters λ and ϕ exhibited strong positive correlations, while γ and v demonstrated strong negative correlations (Figure 4). Sensitivity analyses further revealed that the relationship between protection and transmission rates varies across different transmission intensities. Higher transmission levels require proportionally greater vaccination protection to effectively control pertussis incidence, as illustrated in Figure 5 over the three-year period.

A) 2017



B) 2018



C) 2019

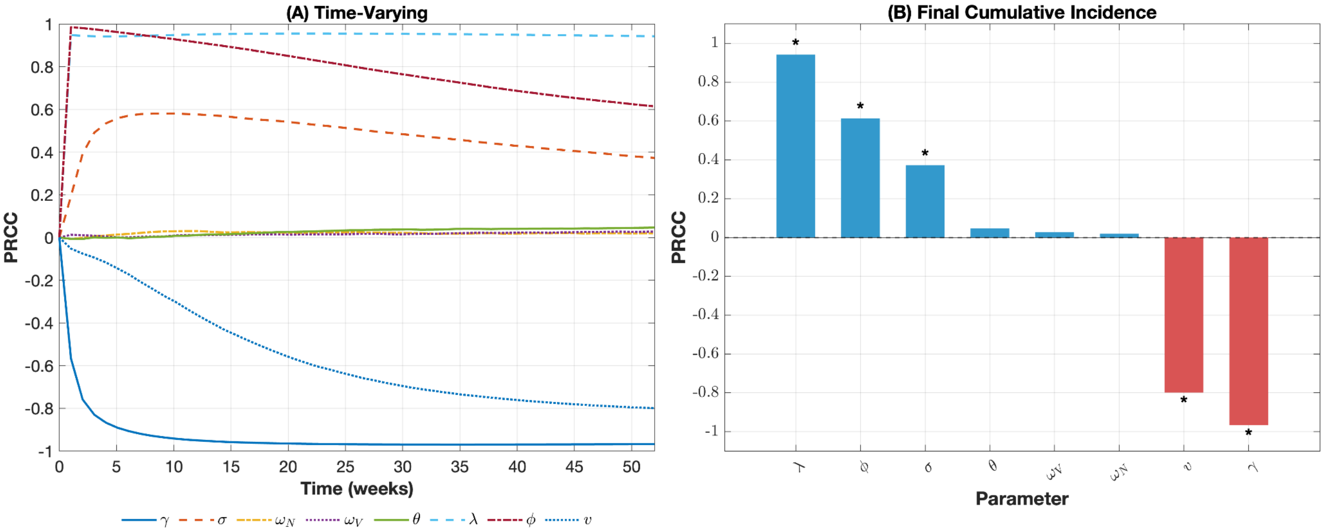


Figure 4: Partial rank correlation coefficients (PRCCs) of model parameters with respect to time-varying and final cumulative incidence for 2017 (A), 2018 (B), and 2019 (C).

In 2017, a period of lower protection and a less severe outbreak, a 0.03 increase in the transmission rate doubled the baseline cumulative incidence. A slight increase of 0.0001 in v produced a similar base case outcome, but only for small changes in the baseline transmission rate. In 2018, with higher protection and a higher baseline transmission rate, a 0.06 increase in transmission doubled the incidence, while a 0.005 increase in v yielded a similar base case outcome under slightly elevated transmission rates. In 2019, when protection levels were comparable but transmission was lower than in 2017, a 0.03 increase in transmission again doubled the baseline incidence, and a 0.0001 increase in v resulted in a similar base case outcome, though at slightly lower transmission levels than in 2017 (Figure 5).

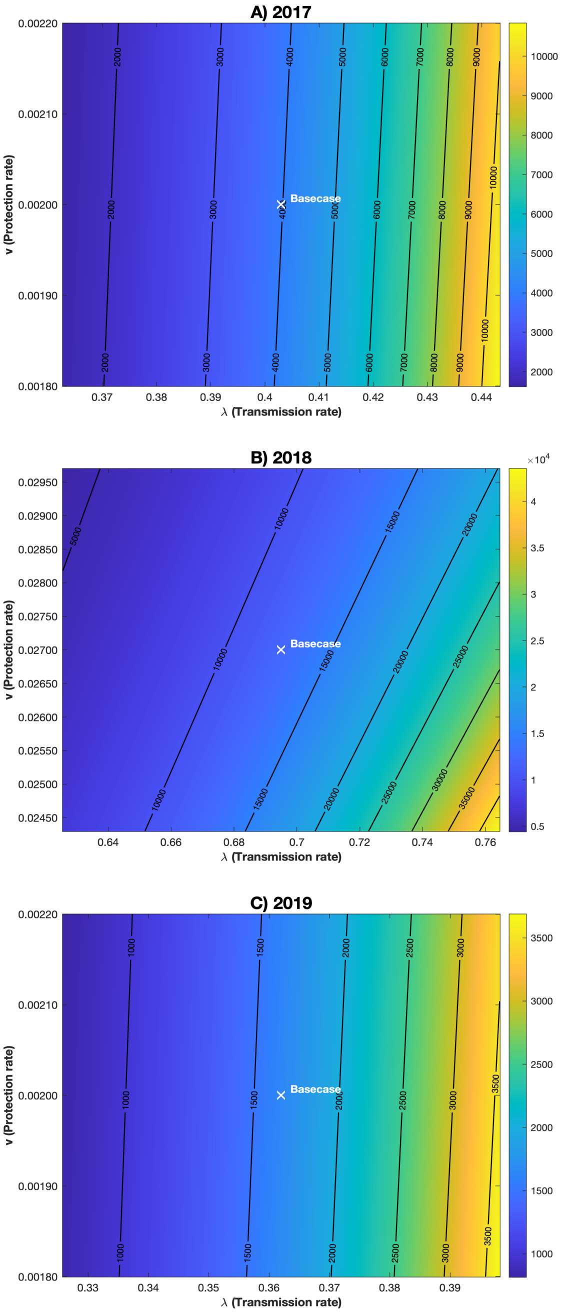


Figure 5: Heatmap with contour overlays of annual cumulative pertussis incidence under varying vaccination and transmission rates from 2017 to 2019.

DISCUSSION

We developed an SEIRS model accounting for the impact of vaccination and potential underreporting of pertussis cases to capture the dynamics of pertussis transmission in the Philippines. The model fit to the cumulative all-age pertussis incidence data from 2017 to 2019 demonstrates that it can reasonably describe observed trends in pertussis epidemiology, despite limited surveillance data. Our findings suggest that the true incidence of pertussis is approximately 10 to 40 times higher than reported cases, with uncertainty estimates suggesting it could be more than 1000-fold higher, underscoring considerable disease surveillance gaps. The transmission rate, protection rate, reporting factor, and recovery rate were found to be the most influential parameters shaping the transmission dynamics.

Our analysis broadly aligns with findings from other settings where pertussis cases were underestimated. Studies across different populations have shown that the true incidence often exceeds reported cases by several orders of magnitude, with estimates ranging from hundreds to thousands of times higher (Bagordo et al. 2023; Guzman-Holst et al. 2023). These apparent discrepancies in the reported incidence of pertussis conceal a much higher level of ongoing transmission. This highlights the limitations of existing surveillance systems and emphasizes the need for improved case detection methods, such as serological surveys and enhanced syndromic surveillance, to obtain more accurate estimates of pertussis burden and to better inform control strategies.

Consistent with previous studies (Safan et al. 2022; Domenech de Cellès et al. 2018; Althouse & Scarpino 2015), we identified the protection rate as a key parameter influencing pertussis transmission. Higher protection levels reduce susceptibility and limit spread, whereas lower protection levels increase the potential for outbreaks. Although estimated R_0 values are modest compared with those reported by Cherry et al. (2013), there remains a risk of outbreak resurgence (Wang et al. 2025), particularly if protection levels decline. The protection rate becomes particularly critical during severe outbreaks, where maintaining high levels of protection is essential, as declines in immunity can trigger increases in case numbers. Alongside the protection rate, the recovery rate was found to be a key factor, with faster recovery shortening the infectious period and curbing onward spread. Collectively, these findings underscore the need for robust public health strategies that promote adherence to recommended immunization schedules and ensure the timely administration of booster doses to maintain durable population immunity against pertussis.

Model results indicate an increase in the protection rate in 2018 that coincides with the nationally reported rise in pertussis cases (World Health Organization 2024), possibly as a result of a stronger public health response during that year. The transmission rate also peaked in 2018, while underreporting remained high but was notably lower than in the previous year. By 2019, the protection rate had returned to the 2017 level, accompanied by a marked improvement in reporting, likely reflecting enhanced surveillance efforts following the rise in 2018. However, these results should be interpreted with caution, given the simplified model structure, potential parameter non-identifiability, and limitations in the quality of the available epidemiological data. Further studies are needed to validate these findings.

This study has several limitations. First, our analysis was based on all-age weekly cumulative incidence data from 2017 to 2019. A more granular, age-stratified dataset spanning a longer timeframe could provide deeper insights into pertussis transmission across different population groups and improve estimates of vaccination impact by age. Moreover, incorporating more localized data (e.g., from specific cities or municipalities) could capture regional variations in transmission dynamics and strengthen the overall analysis. Second, our model does not explicitly distinguish between symptomatic and asymptomatic infections. Since asymptomatic or mild cases often go unreported but may significantly contribute to sustained transmission, incorporating these infections into future models could refine estimates of pertussis spread. Third, we did not account for seasonal variations in transmission. Considering time-varying transmission rates could improve our understanding of temporal fluctuations in pertussis incidence and enhance the accuracy of model predictions. Finally, while we evaluated the overall impact of vaccination, we did not explore specific vaccination strategies. Future research should assess targeted control strategies to identify optimal approaches for reducing pertussis incidence.

CONCLUSION

This study revealed a potential underreporting of pertussis in the Philippines, with the true incidence estimated to be about 10 to 40 times higher than reported, highlighting the need for enhanced surveillance systems and improved case detection to obtain more reliable incidence estimates. While pertussis vaccination has contributed to controlling disease spread, it would be beneficial for future efforts to focus on expanding vaccination coverage, sustaining high population immunity, and strengthening targeted strategies, such as booster campaigns or maternal and adult immunization, to further enhance pertussis control.

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CONFLICT OF INTEREST

All authors reported no known potential conflicts of interest.

CONTRIBUTIONS OF INDIVIDUAL AUTHORS

Author1: Formal analysis, Writing - Original Draft, Methodology, Software, Visualization. **Author2**: Writing-Reviewing and Editing, Methodology, Validation. **Author3**: Methodology, Supervision, Writing-Reviewing and Editing. **Author4**: Writing- Reviewing and Editing, Validation, Visualization. **Author5**: Data Curation, Writing- Reviewing and Editing, Validation. **Author6**: Conceptualization, Methodology, Project administration, Supervision, Writing - Original Draft, Formal analysis, Validation, Writing- Reviewing and Editing. All authors discussed the results and contributed to the final manuscript. All authors have read and agreed to the published version of the manuscript.

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SUPPORTING INFORMATION

Data Description and Preprocessing Techniques

The weekly reported pertussis cases from 2017 to 2019 were obtained from the Weekly Disease Surveillance Report of the Department of Health Epidemiology Bureau. The original dataset consisted of 156 observations, including 16 missing values, which were imputed using the linear interpolation technique (Moritz and Bartz-Beielstein 2017). This method estimates missing values by connecting adjacent observed data points with straight lines and assigning intermediate values proportionally between them, thereby preserving the overall trend and continuity of the time series. The figure below shows the time series of the weekly reported cases from 2017 to 2019. It can be observed that the highest number of pertussis cases was recorded in the 20th week of 2018. It can also be observed that pertussis cases usually spike at the last quarter of the year (September to December).

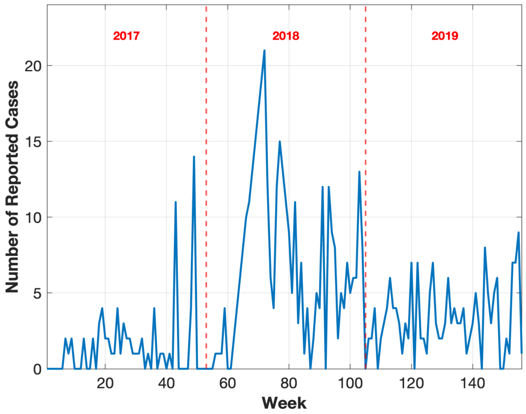

Figure S1: Weekly reported pertussis cases in the Philippines from 2017 to 2019.

Supporting information related to Results

Mathematical Analysis of the Pertussis Transmission Model

Positivity and Boundedness of Solutions

Theorem 1.

If $S_1(0), S_2(0), E_1(0), E_2(0), I_1(0), I_2(0), R(0), V(0) \geq 0$ then $S_1(t), S_2(t), E_1(t), E_2(t), I_1(t), I_2(t), R(t), V(t) \geq 0$ for all $t > 0$ and every solution of the system described starting in $\Omega = \{(S_1, S_2, E_1, E_2, I_1, I_2, R, V) \in R^8_{\geq 0} : N = S_1 + S_2 + E_1 + E_2 + I_1 + I_2 + R + V\}$ remains in Ω for all $t > 0$.

Let the parameters $\lambda, \theta, \sigma, \gamma, \omega\_N, \omega\_V, v \geq 0$ and the initial conditions $S_1(0), S_2(0), E_1(0), E_2(0), I_1(0), I_2(0), R(0), V(0) \geq 0$. The first conclusion is proved by contradiction. Suppose, one of the state variables, say $x_k(t)$, becomes negative at some $t > 0$. Because the variables are continuous, there must exist a first time $t^* > 0$ at which $x_k(t)$ satisfies the following:

1. $x_k(t^*) = 0$, and
2. $x_k(t) < 0$ for some t just after t^*.

At time t^*, all other variables are still nonnegative. We will show that the derivative at the point where the variable reaches zero is nonnegative (i.e., it cannot decrease below 0 after t^*).

1. If $S_1(t^*) = 0$ then $\frac{dS_1}{dt} = -\frac{\lambda}{N} S_1(I_1 + I_2) - vS_1 = 0$.
2. If $S_2(t^*) = 0$ then $\frac{dS_2}{dt} = \omega_N R + \omega_V V - \theta \frac{\lambda}{N} S_2(I_1 + I_2) - vS_2 = \omega_N R + \omega_V V \geq 0$.
3. If $E_1(t^*) = 0$ then $\frac{dE_1}{dt} = \frac{\lambda}{N} S_1(I_1 + I_2) - \sigma E_1 = \lambda S_1(I_1 + I_2) \geq 0$.
4. If $E_2(t^*) = 0$ then $\frac{dE_2}{dt} = \theta\lambda \frac{\lambda}{N}(I_1 + I_2) - \sigma E_2 = \theta \frac{\lambda}{N} S_1(I_1 + I_2) \geq 0$.
5. If $I_1(t^*) = 0$ then $\frac{dI_1}{dt} = \sigma E_1 - \gamma I_1 = \sigma E_1 \geq 0$.
6. If $I_2(t^*) = 0$ then $\frac{dI_2}{dt} = \sigma E_2 - \gamma I_2 = \sigma E_2 \geq 0$.
7. If $R(t^*) = 0$ then $\frac{dR}{dt} = \gamma(I_1 + I_2) - \omega_N R = \gamma(I_1 + I_2) \geq 0$.
8. If $V(t^*) = 0$ then $\frac{dV}{dt} = -\omega_V V + vS_1 + vS_2 = v(S_1 + S_2) \geq 0$.

We can see that in each case, when a variable first becomes 0, its derivative becomes nonnegative, implying that the variable cannot decrease below zero after t^*. This contradicts our assumption that the variable becomes negative at some $t > 0$. Therefore, $S_1(t), S_2(t), E_1(t), E_2(t), I_1(t), I_2(t), R(t), V(t) \geq 0$ for all $t > 0$.

Now for the second part of the conclusion, let $N(t) = S_1(t) + S_2(t) + E_1(t) + E_2(t) + I_1(t) + I_2(t) + R(t) + V(t)$ be the total number of individuals in all compartments at time t. Differentiating N,

$$\frac{dN}{dt} = \frac{dS_1}{dt} + \frac{dS_2}{dt} + \frac{dE_1}{dt} + \frac{dE_2}{dt} + \frac{dI_1}{dt} + \frac{dI_2}{dt} + \frac{dR}{dt} + \frac{dV}{dt}$$

$$\begin{aligned} &= \left(-\frac{\lambda}{N} S_1(I_1 + I_2) - vS_1\right) \\ &\qquad + (\omega_N R + \omega_V V - \theta\lambda S_2(I_1 + I_2) - vS_2) \\ &\qquad + \left(\frac{\lambda}{N} S_1(I_1 + I_2) - \sigma E_1\right) \end{aligned}$$

$$\begin{aligned} &+ \left(\theta \frac{\lambda}{N} S_2(I_1 + I_2) - \sigma E_2\right) + (\sigma E_1 - \gamma I_1) + (\sigma E_2 - \gamma I_2) \\ &\qquad + (\gamma(I_1 + I_2) - \omega_N R) \\ &\qquad + (-\omega_V V + vS_1 + vS_2) = 0. \end{aligned}$$

Integrating both sides gives $N(t) = N(0), \forall t \geq 0$, implying that the total population remains constant over time. Clearly, every value of each variable lies between 0 and *N(0)*, then the solution $(S_1, S_2, E_1, E_2, I_1, I_2, R, V)$ stays in a bounded region of the nonnegative space for all $t \geq 0$. Hence, the system is bounded.

Local Stability of Disease-Free Equilibrium (DFE)

The disease-free equilibrium (DFE) is a state at which the disease is not present in the population. In other words, $\bar{E}_1 = \bar{E}_2 = \bar{I}_1 = \bar{I}_2 = 0$. The remaining steady-state equations are as follows:

$$\begin{aligned} 0 &= -v\bar{S}_1 && \left(from\ \frac{dS_1}{dt}\right) \\ 0 &= \omega_N \bar{R} + \omega_V \bar{V} - v\bar{S}_2 && \left(from\ \frac{dS_2}{dt}\right) \\ 0 &= -\omega_N \bar{R} && \left(from\ \frac{dR}{dt}\right) \\ 0 &= -\omega_V \bar{V} + v\bar{S}_1 + v\bar{S}_2 && \left(from\ \frac{dV}{dt}\right) \end{aligned}$$

Assuming ω_N, $\omega_V \geq 0$ and $v > 0$ then $\bar{R} = 0$, $\bar{S}_1 = 0$, $\bar{V} = \frac{v}{\omega_V} \bar{S}_2$.

Note that $\bar{S}_2 + \bar{V} = N$; thus giving the DFE: $\bar{S}_1 = \bar{E}_1 = \bar{E}_2 = \bar{I}_1 = \bar{I}_2 = \bar{R} = 0, \bar{S}_2 = \frac{\omega_V}{\omega_V + v} N, \bar{V} = \frac{v}{\omega_V + v} N$.

To establish the local stability of the DFE, we used the basic reproduction number, R_0. Following the next-generation method, we considered the disease-related classes/compartments.
$x = (E_1, E_2, I_1, I_2)$.

We set up new infection vector $F(x)$ and transmission vector $V(x)$. New infections enter only the exposed compartments.

$$F_1 = \frac{\lambda}{N} S_1 (I_1 + I_2)$$

$$F_2 = \frac{\theta\lambda}{N} S_2 (I_1 + I_2)$$

$$F_3 = F_4 = 0.$$

Non-infection transitions are:

$$V_1 = \sigma E_1$$

$$V_2 = \sigma E_2$$

$$V_3 = \gamma\, I_1 - \sigma E_1$$

$$V_4 = \gamma\ I_2 - \sigma E_2$$

Now we compute the Jacobians $F = D_x F$ and $V = D_x V$ evaluated at the DFE.

$$F = \begin{pmatrix} 0 & 0 & \frac{\lambda}{N}\bar{S_1} & \frac{\lambda}{N}\bar{S_1} \\ 0 & 0 & \frac{\theta\lambda}{N}\bar{S_2} & \frac{\theta\lambda}{N}\bar{S_2} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \sigma & 0 & 0 & 0 \\ 0 & \sigma & 0 & 0 \\ -\sigma & 0 & \gamma & 0 \\ 0 & -\sigma & 0 & \gamma \end{pmatrix}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{\sigma} & 0 & 0 & 0 \\ 0 & \frac{1}{\sigma} & 0 & 0 \\ \frac{1}{\gamma} & 0 & \frac{1}{\gamma} & 0 \\ 0 & \frac{1}{\gamma} & 0 & \frac{1}{\gamma} \end{pmatrix}$$

We now form the next generation matrix $K = FV^{-1}$

$$K = \begin{pmatrix} \frac{\lambda\bar{S_1}}{N\gamma} & \frac{\lambda\bar{S_1}}{N\gamma} & \frac{\lambda\bar{S_1}}{N\gamma} & \frac{\lambda\bar{S_1}}{N\gamma} \\ \frac{\theta\lambda\bar{S_2}}{N\gamma} & \frac{\theta\lambda\bar{S_2}}{N\gamma} & \frac{\theta\lambda\bar{S_2}}{N\gamma} & \frac{\theta\lambda\bar{S_2}}{N\gamma} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$R_0 = \rho(K)$ or the spectral radius of K is $\frac{\lambda}{N\gamma}\left(\underline{S_1} + \theta\underline{S_2}\right)$. Substituting the values of $\bar{S_1}$ and $\bar{S_2}$, we have $R_0 = \frac{\lambda\theta}{\gamma}\frac{\omega_V}{\omega_V+v}$.

Existence of the Endemic Equilibrium (EE)
We set all derivatives to zero at EE and assume that $\bar{I} = \bar{I}_1 + \bar{I}_2 > 0$.

From $E_1' = 0$, $\bar{E}_1 = \frac{\lambda\bar{S_1}}{N\sigma}\bar{I}$. From $\bar{I}_1{}' = 0$, $\bar{I}_1 = \frac{\sigma}{\gamma}\bar{E}_1 = \frac{\lambda\bar{S_1}}{N\gamma}\bar{I}$.
Similarly, $\bar{E}_2 = \frac{\theta\lambda\bar{S_2}\bar{I}}{N\sigma}$ and $\bar{I}_2 = \frac{\theta\lambda\bar{S_2}\bar{I}}{N\gamma}$.
Thus, $\bar{I} = \bar{I}_1 + \bar{I}_2 = \frac{\lambda}{N\gamma}(\bar{S_1} + \theta\bar{S_2})\bar{I}$.
With $\bar{I} > 0$, $\frac{\lambda}{N\gamma}(\bar{S_1} + \theta\bar{S_2}) = 1$, which is the endemic equilibrium condition. From $\frac{dR}{dt} = 0$, $\bar{R} = \frac{\gamma}{\omega_N}\bar{I}$.
From $\frac{dS_1}{dt} = 0$, $\bar{S_1} = 0$. From $\frac{dS_2}{dt} = 0$, $\omega_N\bar{R} + \omega_V\bar{V} = \frac{\theta\lambda}{N}\bar{S_2}\bar{I} + V\bar{S_2}$.
Lastly, with $V' = 0$, $\bar{V} = \frac{V}{\omega_V}(\bar{S_1} + \bar{S_2}) = \frac{V}{\omega_V}\bar{S_2}$. Then, $\bar{S_2} = \frac{N\gamma}{\theta\lambda}$,
$\bar{V} = \frac{V}{\omega_V}\frac{\gamma N}{\theta\lambda}$, $\bar{R} = \frac{\gamma}{\omega_N}\bar{I}$,
$N = \bar{S_2} + \bar{E_1} + \bar{E_2} + \bar{I_1} + \bar{I_2} + \bar{R} + \bar{V}$.
Hence, $\bar{I} = \frac{N - \frac{\gamma N}{\theta\lambda}\left(1 + \frac{V}{\omega_V}\right)}{\frac{\gamma}{\sigma} + 1 + \frac{\gamma}{\omega_N}}$.
For the EE to exist biologically, $N > \frac{N\gamma}{\theta\lambda}\left(1 + \frac{V}{\omega_V}\right)$ or $R_0 > 1$.

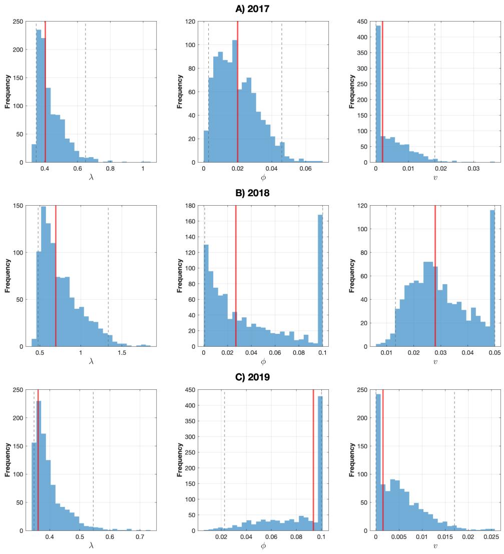

Figure S2: Distributions of the parameter estimates $\boldsymbol{\lambda}$, $\boldsymbol{\phi}$, and $\boldsymbol{v}$ obtained through 1000 bootstrapped resamples generated via nonparametric sampling of cumulative reported incidence of pertussis in the Philippines, from 2017 to 2019.

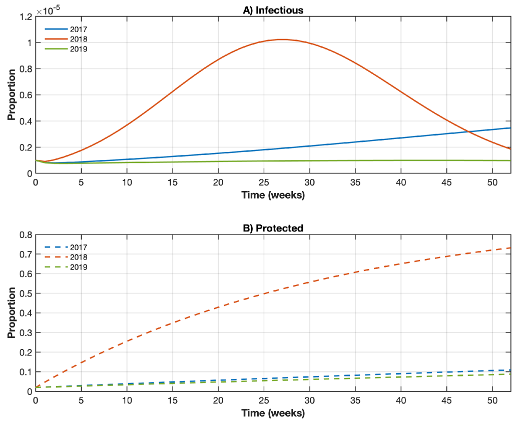

Figure S3: Estimated weekly number of A) infectious and B) protected individuals in the Philippines, from 2017 to 2019.

Table S1: Fitted parameter values when varying the proportions of initial naïve susceptibles ($\boldsymbol{S_1}$) and previously infected individuals ($\boldsymbol{S_2}$).

S1	S2	λ	ϕ	$\boldsymbol{v}$
2017				
0.5	**0.5**	0.5387	0.0198	0.0021
0.6	**0.4**	0.5773	0.0198	0.0021
0.4	**0.6**	0.5049	0.0199	0.0021
2018				
0.5	**0.5**	0.9349	0.0263	0.0286
0.6	**0.4**	1.0043	0.0261	0.0287
0.4	**0.6**	0.8746	0.0264	0.0284
2019				
0.5	**0.5**	0.4825	0.0935	0.0016
0.6	**0.4**	0.4523	0.0936	0.0016
0.4	**0.6**	0.5171	0.0935	0.0016

Table S2: Fitted transmission rate ($\boldsymbol{\lambda}$) when varying the proportion of initial protected individuals ($\boldsymbol{V}$).

Initial proportion of protected individuals	2017	2018	2019
0.1	0.440	0.759	0.394
0.2	0.495	0.856	0.443
0.3	0.566	0.983	0.507
0.4	0.660	1.154	0.591
0.5	0.793	1.397	0.709
0.6	0.992	1.771	0.887
0.7	1.325	2.421	1.183
0.8	1.995	3.853	1.776
0.9	4.045	7.352	3.565

Table S3: Fitted protection rate ($\boldsymbol{v}$) when varying the proportion of initial protected individuals ($\boldsymbol{V}$).

Initial proportion of protected individuals	2017	2018	2019
0.1	0.020	0.027	0.094
0.2	0.020	0.027	0.094
0.3	0.020	0.026	0.094
0.4	0.020	0.026	0.094
0.5	0.020	0.025	0.094
0.6	0.020	0.024	0.093
0.7	0.020	0.023	0.093
0.8	0.019	0.019	0.093
0.9	0.019	0.009	0.093

Table S4: Fitted protection rate ($\boldsymbol{v}$) when varying the proportion of initial protected individuals ($\boldsymbol{V}$).

Initial proportion of protected individuals	2017	2018	2019
0.1	0.002	0.028	0.002
0.2	0.002	0.029	0.002
0.3	0.003	0.029	0.002
0.4	0.003	0.030	0.002
0.5	0.003	0.031	0.003
0.6	0.004	0.033	0.004
0.7	0.005	0.035	0.005
0.8	0.008	0.042	0.007
0.9	0.015	0.068	0.014

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