PAN AMERICAN JOURNAL OF PUBLIC HEALTH 100 YEARS

Original research

Effects of migration rates and vaccination on the spread of yellow fever in Latin American communities

Sabrina Simon,[1] Marcos Amaku[1] and Eduardo Massad[2]

Suggested citation Simon S, Amaku M, Massad E. Effects of migration rates and vaccination on the spread of yellow fever in Latin American communities. Rev Panam Salud Publica. 2023;47:e86. https://doi.org/10.26633/RPSP.2023.86

ABSTRACT

Objective. To assess how relevant the flow of people between communities is, compared to vaccination and type of vector, on the spread and potential outbreaks of yellow fever in a disease-free host community.
Methods. Using a SEIRV-SEI model for humans and vectors, we applied numerical simulations to the scenarios: (1) migration from an endemic community to a disease-free host community, comparing the performance of *Haemagogus janthinomys* and *Aedes aegypti* as vectors; (2) migration through a transit community located on a migratory route, where the disease is endemic, to a disease-free one; and (3) effects of different vaccination rates in the host community, considering the vaccination of migrants upon arrival.
Results. Results show no remarkable differences between scenarios 1 and 2. The type of vector and vaccination coverage in the host community are more relevant for the occurrence of outbreaks than migration rates, with *H. janthinomys* being more effective than *A. aegypti*.
Conclusions. With vaccination being more determinant for a potential outbreak than migration rates, vaccinating migrants on arrival may be one of the most effective measures against yellow fever. Furthermore, *H. janthinomys* is a more competent vector than *A. aegypti* at similar densities, but the presence of *A. aegypti* is a warning to maintain vaccination above recommended levels.

Keywords Yellow fever; vaccination; human migration; epidemiological models; public health; vector borne diseases; disease outbreaks; Latin America.

Yellow fever (YF) was introduced to the Americas through migration, and today it circulates in 13 Latin American countries, while many others are at risk. Even with an effective and low-cost vaccine, there are about 200 000 cases and 78 000 deaths annually on the African continent alone, where YF is endemic in 34 countries. These figures reveal how underestimated the epidemic potential of this reemerging zoonotic disease is, which, being climate-sensitive, could be driven by the global climate crisis (1–3).

The current areas of highest predicted receptivity to YF transmission outside contemporary risk zones in Latin America are found in Central America, where the geographic distribution of competent vectors, such as *Haemagogus janthinomys* and *Aedes aegypti* mosquitoes (except for Mexico), overlaps with main routes and hotspots of mixed migratory flows on the continent (4). Due to the convergence of these two phenomena, since 2007, the World Health Organization has proposed that migratory patterns be considered in the risk analysis of immunization campaigns (5). Furthermore, the Eliminate Yellow Fever Epidemics Program (EYE) establishes that the allocation of YF vaccines should be defined by modeling methods that include human movements and a One Health approach considering non-human primate vectors and hosts (6).

Epidemiological modeling studies that address the relationship between vector-borne diseases and human movement have the traveler effect as one of the most explored topics, which assesses the risk of virus introduction into a susceptible population by the entry of an infectious individual (7–9). However, a reckless interpretation of these studies may shift the responsibility

[1] University of São Paulo, São Paulo, Brazil ✉ Sabrina Simon, ssimon@alumni.usp.br

[2] Getúlio Vargas Foundation, Rio de Janeiro, Brazil

onto the immigrant for the outcomes of a potential outbreak in a host community, promoting stigma and xenophobic practices. Migrants are often seen as disease carriers, being socially rejected during epidemics (10), while several scientific papers have been found to reduce displaced people to disease vectors in naive populations (11). The association of diseases with a particular ethnic background or place of origin was strongly perceived at the beginning of the COVID-19 epidemic in the United States of America, where immigrants from Mexico and South America were considered the main population that contributed to spreading the disease and therefore faced severe stigma (12).

Intending to enrich the evidence and discussions generated by epidemiological modeling methods applied to infectious diseases in the context of the migratory crisis, we use a SEIRV-SEI deterministic compartmental model for humans and mosquito populations in order to verify how relevant the flow of people between two communities is, compared to the effects of vaccination of migrants upon arrival and the biology of vectors. Using simulations, the aim of this study is to compare the role of *H. janthinomys* and *A. aegypti* as competent vectors and to assess the effects of different migration rates and vaccination coverages on a potential outbreak in hypothetical populations representing Latin American communities.

MATERIALS AND METHODS

Model formulation

We consider scenarios where humans migrate from a source community to a host community. In the system of equations, the source community is assigned as community 1, and the community of destination is assigned as community 2. Each community has its own mosquito populations that can be vectors of the YF virus, which can be either *H. janthinomys* or *A. aegypti*. People migrating from one community to another can be either susceptible (*S*), which means they do not have antibodies for YF, or be exposed (*E*), infected (*I*), or recovered (*R*). Exposed (or latent) people have been in recent contact with the virus but are not transmitting the virus yet, while infected people are in the infective period of the disease, either symptomatic or asymptomatic. Recovered individuals have survived the infection and are no longer transmitting the disease, and, in the case of YF, they are probably immune for life. In community 2, vaccinated people (*V*) are also permanently immune to YF. The exact definition of the compartments *S*, *E*, and *I* are also applied to mosquitoes.

The simulations were based on a SEIRV-SEI deterministic compartmental model based on a classical Ross–Macdonald model. The systems of differential equations were structured for the two distinct communities, whose components and meanings are presented in Table 1. Each letter representing a compartment is subscribed by *h* or *m*, indicating humans or mosquitoes, respectively, while *1* and *2* indicate the community to which they belong; i.e., N_{h1} represents the sum of the compartments of the entire human population of the source community 1 in equation [1], as N_{h2} represents the human population of host community 2 in equation [3]. The same system is used for mosquito populations N_{m1} and N_{m2} and their compartments in the two communities presented in equations [2] and [4].

TABLE 1. Variables and parameters, their respective meanings, and assigned values

Variable*	Biological meaning	Initial value	
N_h	Total population of humans in each community	Variable	
S_h	Susceptible human individuals	Variable	
E_h	Exposed (latent) human individuals	Variable	
I_h	Infected human individuals	Variable	
R_h	Recovered human individuals	Variable	
V_{h2}	Vaccinated human individuals in the community 2	Variable	
N_m	Total population of mosquitoes	Variable	
S_m	Susceptible mosquitoes	Variable	
E_m	Exposed (latent) mosquitoes	Variable	
I_m	Infected mosquitoes	Variable	
Parameter	**Biological meaning**	**Daily rates**	**Source**
μ_h	The natural mortality rate of humans	3.77×10^{-5} day^{-1}	(7)
Λ	The birth rate of humans	μ	
γ_h	Human recovery rate	0.1428 day^{-1}	(8)
ε_h	Latency rate in humans	0.167 day^{-1}	(29)
α_h	Disease-induced mortality rate	8.0×10^{-4} day^{-1}	(7)
δ_{h1}	Human migration rate to the community of origin (from outside the system)	Variable	
δ_{h12}	Human migration rate from the community of origin to the host community	Variable	
w	Vaccination rate	Variable	
a	Average biting rate (*Haemagogus* and *Aedes*)	0.33 day^{-1}	(7)
b	Fraction of infective bites (*Haemagogus* and *Aedes*)	0.25	(8)
c	Susceptibility of *Haemagogus* to the virus	0.4	(8)
	Susceptibility of *Aedes* to the virus	0.25	(8)
ε_m	Latency rate in mosquitoes	0.1428 day^{-1}	(8)

Source: Table prepared by the authors.

$$N_{h1}(t) = S_{h1}(t) + E_{h1}(t) + I_{h1}(t) + R_{h1}(t) \quad [1]$$
$$N_{m1}(t) = S_{m1}(t) + E_{m1}(t) + I_{m1}(t) \quad [2]$$
$$N_{h2}(t) = S_{h2}(t) + E_{h2}(t) + I_{h2}(t) + R_{h2}(t) + V_{h2}(t) \quad [3]$$
$$N_{m2}(t)=S_{m2}(t)+E_{m2}(t)+I_{m2}(t) \quad [4]$$

In terms of natural dynamics, populations [1], [2], [3], and [4] are stable: the number of births equals the total number of deaths in a way that the size of the population remains the same over time if there was no migration:

$$\frac{dN}{dt} = \Lambda N - \mu N \quad [5]$$

So that, for:

$$\frac{dN}{dt} = 0, \text{ then:} \quad [6]$$

$$\Lambda N = \mu N \quad [7]$$

This way, as we consider that both humans and mosquitoes are born susceptible to YF (assuming that vertical transmission is not relevant for the results), the birth rate is present only in the susceptible compartment but is canceled by the death rate of susceptible individuals. However, as YF is endemic in the source population 1, the mortality due to the disease (α) is added to the total amount of deaths to be compensated by the birth rate:

$$\frac{dN_{h1}}{dt} = \Lambda N_{h1} - N_{h1}(\mu + \alpha) \quad [8]$$

So that, for:

$$\frac{dN_{h1}}{dt} = 0, \text{ then:} \quad [9]$$

$$\Lambda N_{h1} = N_{h1}(\mu + \alpha) \quad [10]$$

Even considering that both populations are stable and equal at first, they can grow with migration (host community), shrink (source community), or remain stable (transit community). The movement of individuals across communities may affect the dynamics of a potential outbreak, depending on which compartment they currently are in at the time they move (*S*, *E*, *I*, *R*, or *V*). The direction and rates of the movement and the change of states will determine the outcomes (Table 1).

Systems coupling

The classical Ross–Macdonald model for vector-borne diseases combines the host and vector populations by the term of transmission based on the transmission coefficients between hosts and vectors (b and c) multiplied by the biting rate (a) and by the number of infected hosts (I_h) and infected mosquitoes (I_m).

In this paper, the movement of individuals between them also couples both human populations, and people from every compartment can migrate equally. The migration rate δ_h represents the human movements across populations being subscribed by 12 when designating the movement from community 1 to community 2 (δ_{h12}), and subscribed by 1 when referring to the entry of people from outside the system to community 1 (δ_{h1}).

System 1: Community of origin

Human hosts:

$$\frac{dSh_1}{dt} = -a \cdot b \cdot Im_1 \cdot \left(\frac{Sh_1}{Nh_1}\right) + \mu_h \cdot (Eh_1 + Ih_1 + Rh_1) + \alpha_h \cdot Ih_1 - \delta h_{12} \cdot Sh_1 + \delta h_1 \cdot Sh_1 \quad [11]$$

$$\frac{dEh_1}{dt} = a \cdot b \cdot Im_1 \cdot \left(\frac{Sh_1}{Nh_1}\right) - \varepsilon_h \cdot Eh_1 - \mu_h \cdot Eh_1 - \delta h_{12} \cdot Eh_1 \quad [12]$$

$$\frac{dIh_1}{dt} = \varepsilon_h \cdot Eh_1 - \gamma_h \cdot Ih_1 - \mu_h \cdot Ih_1 - \alpha_h \cdot Ih_1 - \delta_{h12} \cdot Ih_1 \quad [13]$$

$$\frac{dRh_1}{dt} = \gamma_h \cdot Ih_1 - \mu_h \cdot Rh_1 - \delta_{h12} \cdot Rh_1 \quad [14]$$

Mosquito vectors:

$$\frac{dSm_1}{dt} = -a \cdot c \cdot Sm_1 \cdot \left(\frac{Ih_1}{Nh_1}\right) + \mu_m \cdot (Em_1 + Im_1) \quad [15]$$

$$\frac{dEm_1}{dt} = a \cdot c \cdot Sm_1 \cdot \left(\frac{Ih_1}{Nh_1}\right) - \varepsilon_m \cdot Em_1 - \mu_m \cdot Em_1 \quad [16]$$

$$\frac{dIm_1}{dt} = \varepsilon_m \cdot Em_1 - \mu_m \cdot Im_1 \quad [17]$$

System 2: Host community

Human hosts:

$$\frac{dSh_2}{dt} = -a \cdot b \cdot Im_2 \cdot \left(\frac{Sh_2}{Nh_2}\right) + \mu_h \cdot (Eh_2 + Ih_2 + Rh_2 + Vh_2) + \delta_{h12} \cdot Sh_1 - Sh_2 \cdot w \quad [18]$$

$$\frac{dEh_2}{dt} = a \cdot b \cdot Im_2 \cdot \left(\frac{Sh_2}{Nh_2}\right) + \varepsilon_h \cdot Eh_2 - \mu_h \cdot Eh_2 + \delta_{h12} \cdot Eh_1 \quad [19]$$

$$\frac{dIh_2}{dt} = \varepsilon_h \cdot Eh_2 - \gamma_h \cdot Ih_2 - \mu_h \cdot Ih_2 - \alpha_h \cdot Ih_2 + \delta_{h12} \cdot Ih_1 \quad [20]$$

$$\frac{dRh_2}{dt} = \gamma_h \cdot Ih_2 - \mu_h \cdot Rh_2 + \delta_{h12} \cdot Rh_1 \quad [21]$$

$$\frac{dVh_2}{dt} = Sh_2 \cdot w - \mu_h \cdot Vh_2 \quad [22]$$

Mosquito vectors:

$$\frac{dSm_2}{dt} = -a \cdot c \cdot Sm_2 \cdot \left(\frac{Ih_2}{Nh_2}\right) + \mu_m \cdot (Em_2 + Im_2) \quad [23]$$

$$\frac{dEm_2}{dt} = a \cdot c \cdot Sm_2 \cdot \left(\frac{Ih_2}{Nh_2}\right) - \varepsilon_m \cdot Em_2 - \mu_m \cdot Em_2 \quad [24]$$

$$\frac{dIm_2}{dt} = \varepsilon_m \cdot Em_2 - \mu_m \cdot Im_2 \quad [25]$$

Assumptions

The following assumptions were made: (i) there is no seasonality; (ii) both populations are stable and equal at first; (iii) population densities are assumed to be homogeneous for both human and vector populations, with constant spatial distributions; (iv) the disease is endemic in the source community but absent in the host community at the beginning; (v) vectors do not migrate; (vi) there is no reverse migration from the host community to the community of origin.

Basic reproduction number

The Macdonald equation for the basic reproduction number R_0 for vector-borne diseases is the measurement of the potential for transmission of an infection in an outbreak:

$$R_0 = \frac{ma^2 bc\mu_m^{\varepsilon_m}}{(-ln(\mu_m))\gamma_h} \quad [26]$$

The basic reproduction number characterizes how fast an epidemic can grow by the number of secondary cases generated by each case. If $R_0 > 1$, the infection reaches the threshold of community transmission and spreads in the population until no susceptible individuals remain. It is determined by the ratio of mosquitoes to humans $\left(m = \frac{N_m}{N_h}\right)$ and parameters such as biting rate (a), transmission coefficients between hosts and vectors (b and c), the lifespan of the vector (μ_m), and the time at which humans remain infective (γ_h). We consider the number of mosquitoes in each population (m) to be 1.5 times the number of human hosts, as this is the minimum number assumed by Ronald Ross to reach the transmission threshold for vector-borne diseases (13).

As seasonality and climatic factors are not considered in this model, the maximum simulation time was three years, considering that more extended periods may be affected by El Niño–Southern Oscillation (ENSO) climatic events. All scenarios were built based on populations of 1 000 individuals.

The simulations were performed in the R environment, using the "lsoda" (Ordinary Differential Equations) function of the deSolve package (14) and with the "SSA" function (Stochastic Simulation Algorithm) from the Gillespie SSA2 package for stochastic modeling (15). In addition, sensitivity analysis was carried out with the epiR package (16).

RESULTS

Numerical simulations

In the numerical simulations, we consider three annual migration rates: δ_{h12} = (0.1, 0.5, 0.9 year^{-1}). All analyses were performed for every 1 000 people, and at the initial time, we assumed that both populations were entirely susceptible until an infected individual entered the source population (I_{h1} = 1; S_{h1} = 999).

First scenario: One-way migration from endemic community to disease-free community, and performance of *H. janthinomys* versus *A. aegypti*, with no vaccination. In this scenario, YF is endemic in the source community while the host community is still disease-free. Furthermore, there is no reverse migration, so the source community is subject to depletion if the rate of people leaving exceeds the dynamics of the population itself.

Comparing the role of *H. janthinomys* and *A. aegypti* as main vectors in the two communities, we observe in Figure 1 that: 1) at equal densities, *H. janthinomys* is much more efficient than *A. aegypti*; and 2) the effects of different migration rates are smaller compared to different types of the vector. For this reason, the following simulations will be based on *H. janthinomys* as the predominant vector.

The R_0 number in the host community having *A. aegypti* as the main vector was R_0 = 1.57, while *H. janthinomys* established an R_0 = 6.83. Based on this, the effective vaccination coverage in the host community must be above 85.36%, where *H. janthinomys* is the primary vector.

Second scenario: One-way migration through the endemic community to a disease-free host community, with no vaccination. To transform the source community into a transit community, a susceptible entry term $\delta_{h1} \cdot Sh_1$ was added to equation [18]. The addition of the term $(+\ \delta_{h1} \cdot Sh_1)$ in equation [18] cancels the term $(-\delta_{h12} \cdot Sh_1)$ and eliminates the risk of population depletion, since the entry of new migrants, in this simulation, is equal to the exit rate of people ($\delta_{h1} = \delta_{h12}$).

In this scenario shown in Figure 2, migrants are exposed to the virus when they pass through the endemic community toward the host community, a context that characterizes many border communities in northern South America and much of Central America.

Third scenario: Effects of vaccination in the host community. Figure 3 presents the comparative results of the simulation of three vaccine coverages: 0.1, 0.5, and 0.9 year^{-1} in the two scenarios presented above. In all cases, the annual migration rate was fixed at 0.5 year^{-1}: by starting in parallel with the outbreak, the vaccination reduced 31.98% of cases in the first and 31.15% in the second scenario.

Stochastic modeling

The stochastic simulation is sensitive to the size of the population, presenting more noise when the population is small. Thus, to evaluate the performance of the model, we compared the dynamics of the disease in a population of 1 000 people ($I_{h(t=0)}$ = 1; $S_{h(t=0)}$ = 999) and the same dynamics in a population of 10 000 people, with the introduction made by 10 individuals ($I_{h(t=0)}$ = 10; $S_{h(t=0)}$ = 9 990). Despite the background noise, the results are similar, as shown in Figure 4.

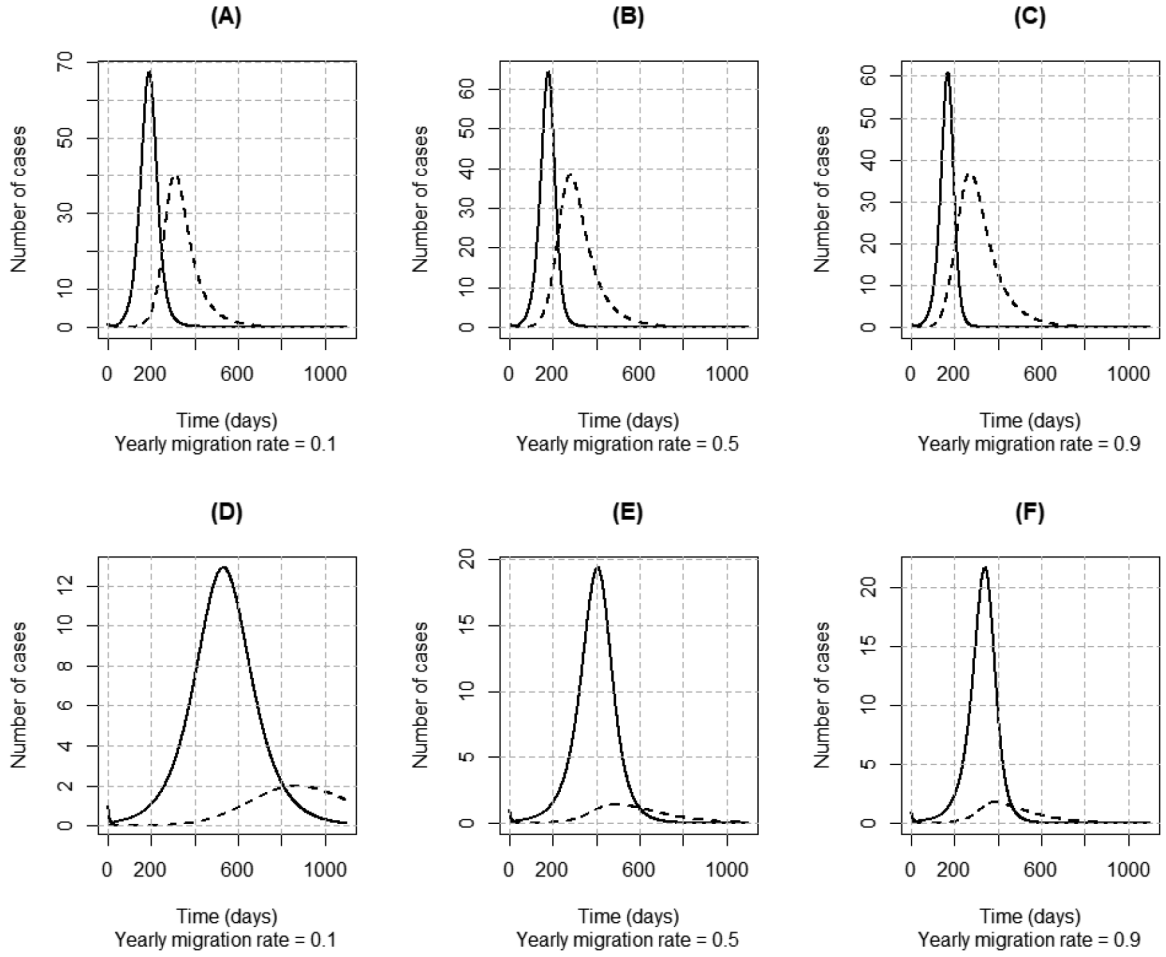
Sensitivity analysis

Finally, the result of the Partial Rank Correlation Coefficient Analysis that evaluates the relevance of parameters to the model outputs is shown in Figure 5.

DISCUSSION

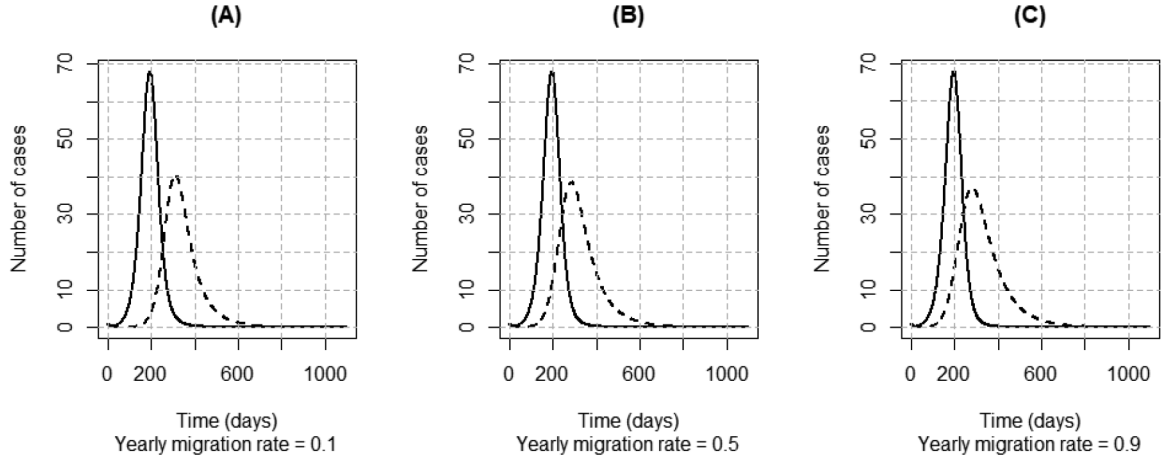
The distinction between origin, transit, or host community depends on the length of stay and other subjective assessments. Countries like El Salvador, Honduras, and Nicaragua are points of origin of migration and, simultaneously, are transit communities for South American migrants heading toward Mexico. In contrast, Costa Rica and Panama are transit and destination communities for groups that migrate in opposite directions

FIGURE 1. Role of *H. janthinomys* (A, B, C) and *A. aegypti* (D, E, F) as vectors, at the same population size, without vaccination, three different migration rates



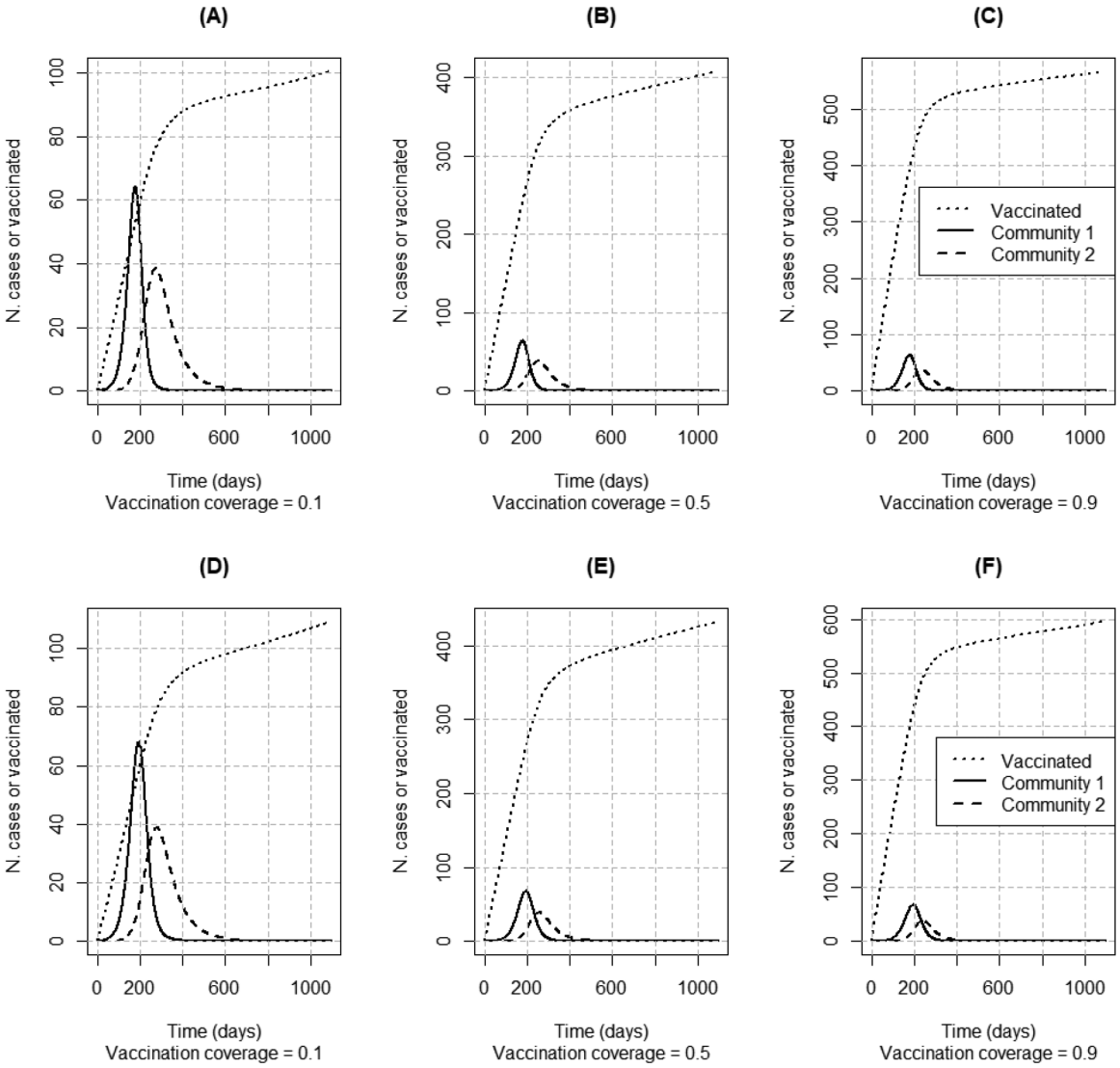
Note: Role of *H. janthinomys* (A, B, C) and *A. aegypti* (D, E, F) as vectors at the same population size without vaccination in three different migration rates: δ_{h12} = 0.1 year^{-1} (A and D); δ_{h12} = 0.5 year^{-1} (B and E); δ_{h12} = 0.9 year^{-1} (C and F). *H. janthinomys* and *A. aegypti* differ in susceptibility to the virus and natural mortality (see Table 1). Every solid line indicates the community of origin (1), and the dashed line corresponds to the host community (2). All cases were simulated for every 1 000 people.
Source: Prepared by authors from the study results.

FIGURE 2. Number of cases in the host community, three years of simulation



Note: The number of cases in the host community is (A) 937; (B) 1 014, and (C) 1 067 in three years of simulation. The solid line indicates the source community, and the dashed line corresponds to the host community. All simulations are for every 1 000 people.
Source: Prepared by authors from the study results.

FIGURE 3. Cases and vaccinated people upon arrival, scenario 1 (A, B, C) and scenario 2 (D, E, F)

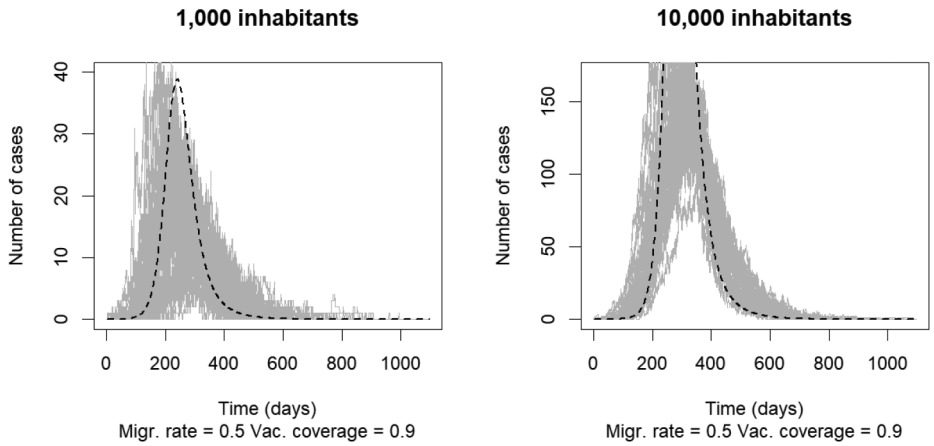


Note: Cases and vaccinated people (dotted lines) upon arrival in scenario 1 (A, B, C) and scenario 2 (D, E, F). Solid lines indicate the community of origin, and the dashed lines correspond to the host community. All simulations are for every 1 000 people.
Source: Prepared by authors from the study results.

(17). The municipality of Necoclí in northern Colombia is a transit community, but migrants can stay from a few nights to several months and therefore be considered a host community (18). The community receives around 70 000 migrants yearly, equivalent to the city's current estimated resident population, with an annual migration rate near 1.0 (19). From 2017 to 2019, YF vaccination coverage of the one-year-old resident population has been maintained at between 85% and 89% in Antioquia department, and these numbers need to increase consistently (20, 21).

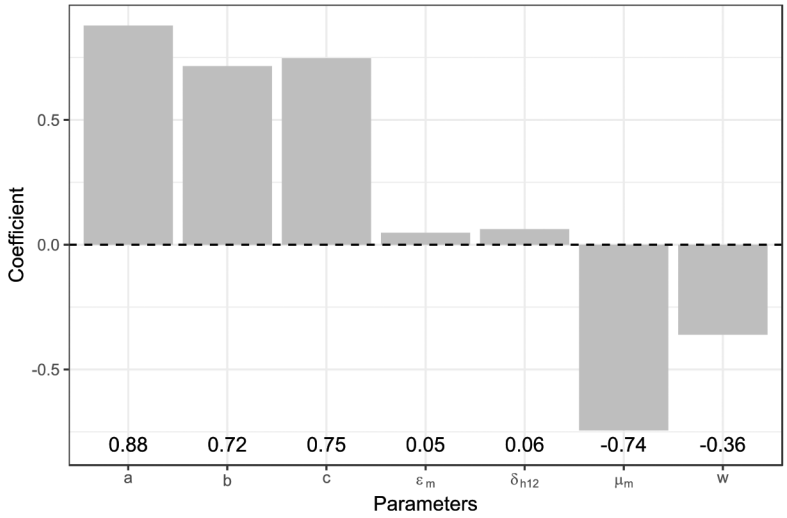
The geographic distribution of the *Haemagogus* and *Aedes* genera covers much of Central America, South America, and the Caribbean, putting the entire region at risk of introducing the YF virus (22). However, there is a considerable difference in their role in the spread of disease at similar densities. The simulations of the first scenario suggest that regions infested by *A. aegypti* would be at a lower risk of outbreaks than regions with a predominance of *H. janthinomys*, but this should be interpreted with caution. First, the proportion of 1.5 mosquitoes for each human is a minimum number to reach the transmission threshold, possibly below what is seen in many locations. *H. janthinomys* occurs predominantly in natural vegetation where ecological factors contribute to its natural control, while *A. aegypti* is well adapted to urban environments in Latin America, where there are no competitors. Therefore, it can be expected that the density of *A. aegypti* could be considerably higher than that of *H. janthinomys* in Latin American cities, and the high population number compensates for the low susceptibility of the mosquito to the virus, increasing its vectorial capacity (23). Second, even at equal densities, both species were able to raise the transmission threshold above the level necessary to cause an epidemic. Thus, we did not exclude *A. aegypti* as a risk factor

FIGURE 4. Stochastic simulation for two host populations with different sizes at the same migration rate and vaccination coverage



Note: Stochastic simulation for two host populations with different sizes at the same migration rate = 0.5 year^{-1} and vaccination coverage = 0.9 year^{-1}. (A) S_{h0} = 999; I_{h0} = 1 while (B) S_{h0} = 9 990; I_{h0} = 10.
Source: Prepared by authors from the study results.

FIGURE 5. Partial rank correlation coefficients for the number of cumulative cases in the host community, scenario 2



Note: Partial rank correlation coefficients for the number of cumulative cases in the host community in scenario 2 as the output variable and the following input variables: biting rate (*a*); the fraction of infective bites (*b*); susceptibility of mosquitoes to the virus (*c*); latency rate in mosquitoes (extrinsic incubation) (ε_m); migration rate (δ_{h12}); natural mortality of mosquitoes (μ_m); and vaccination rate (*w*).
Source: Prepared by authors from the study results.

for introducing YF in disease-free regions or regions with no recent history of cases in the Americas. After all, these two genera were responsible for the outbreaks in Brazil in the first half of the last century (24).

The second scenario shows little difference from the first scenario, which means that a transit community can behave as a source community when applying mathematical models for simulating real-life interventions. Thus, this distinction is an unnecessary complication of the model and can be omitted.

Epidemiological modeling studies commonly assume that people from endemic communities are immune or vaccinated and symptomatic individuals do not travel (25). Migrants may not necessarily be from the endemic community, but they could have been exposed to the virus when passing through it and thus are more likely to be susceptible, acquiring and transmitting the disease. Furthermore, considering that the proportion of asymptomatic cases is approximately 55% of total cases, we choose to maintain the migration of exposed and infective people, both symptomatic and potentially asymptomatic, who may introduce the virus into the target community (26, 27).

The third scenario highlights the impact of vaccination campaigns compared to the previous simulations, but why is vaccination ineffective in preventing 100% of cases? As vaccination starts as the first case arises, it goes in parallel with the epidemic, giving time for new cases. In addition, even if vaccination covers the entire host population and all arriving susceptible migrants, cases will not be avoided entirely due to the entry of exogenous cases. This is why corridors for safe

migration would allow effective measures to take place upon arrival, reducing the entry of exogenous cases, even though it would not hinder the entry of latent and asymptomatic cases already in course. However, 90% vaccination coverage would prevent the vast majority of autochthonous cases, reducing the number of infected by approximately 30%.

In order to affect the dynamics of infectious diseases in the host population, the number of infected immigrants must be sufficient to reach the transmission threshold in the community, whose probability is more significant when the flow is large and continuous (4, 28). However, the sensitivity analysis showed that the migration rate has less influence on the outbreak outcomes in the host community than other components. Although it is evident that the introduction of the first case in the population is due to migration, the outcomes do not depend on the rates of entry, but the vaccination coverage at the host community and vaccination of migrants upon arrival are more relevant in controlling the disease. Naturally, as immigration rates rise, it can overwhelm unprepared health systems, opening the door to health crises, but this is due to a lack of adaptiveness and cannot be used to shift the responsibility onto migrants for spreading disease in a community (10, 12).

As seen, mathematical epidemiologic models can be a powerful tool to design interventions from simulations and raise discussions that shape our approach and communication. By isolating the components of a model, it is possible to understand their relevance as well as the outcomes of the interaction among them, such as the understanding of the relative impact of the migration and vaccination rates over the outcomes of an epidemic in a host community. However, models simplify reality, and we must be cautious to avoid applying generalized conclusions to complex contexts. For example, migratory routes and flow direction are critical components of epidemic diffusion, but these elements are scarce in modeling studies due to intrinsic peculiarities that make it difficult to identify patterns and extrapolate observations.

This study helps to elevate the discussions around the spread of infectious diseases in the context of human migration, putting a spotlight on vaccination as the most effective measure and local responsibility to control the spread of infectious diseases instead of hindering migration or even stigmatizing migrants for spreading them. Furthermore, no matter how the immigration rates increase, vaccination is the most determinant among all the components of the models to the outcome of a potential epidemic, and vaccinating migrants upon arrival is possible when safe corridors replace militarized borders. Lastly, we see how *H. janthinomys* is a more competent vector than *A. aegypti*, but the presence of this latter mosquito still indicates that a community must be prepared for an outbreak, keeping the vaccination levels of the resident population above the recommended threshold.

Conclusion

Although human movement is crucial for introducing infectious diseases into naive communities, this study shows that migration rates are one of the components that contribute the least to the unfolding of the epidemic in the host community, while the vaccination rates and measures of vector control prevail as decisive. There is no remarkable distinction between source communities and communities located on a migratory route, but the performance of *H. janthinomys* and *A. aegypti* as main vectors is enormously different. Regularized migration routes can substantially contribute to avoiding a potential epidemic, where vaccination campaigns can be carried out upon arrival, showing that open doors can be more effective for public health than militarized borders and stigma.

Author contributions. All authors were equally engaged in conceiving the original idea, analyzing the data, interpreting the results, and writing the paper. All authors reviewed and approved the final version.

Conflict of interest. None declared.

Financial support. This study was funded by the Coordination for the Improvement of Higher Education Personnel (CAPES) grant 88882.378281/2019-01. The authors declare that they have not entered into an agreement with the funder in a way that could have influenced the design, the data collection, the analysis, the writing, or the decision to publish these results in any way.

Disclaimer. Authors hold sole responsibility for the views expressed in the manuscript, which may not necessarily reflect the opinion or policy of the *RPSP/PAJPH* and/or those of the Pan American Health Organization.

REFERENCES

1. Tabachnick WJ. Climate Change and the Arboviruses: Lessons from the Evolution of the Dengue and Yellow Fever Viruses. Ann Rev Virol. 2016;3(1):125–45. https://doi.org/10.1146/annurev-virology-110615-035630.
2. Gaythorpe KAM, Hamlet A, Cibrelus L, Garske T, Ferguson NM. The effect of climate change on yellow fever disease burden in Africa. Elife. 2020;9:1–27. https://doi.org/10.7554/elife.55619.
3. Pan American Health Organization [Internet]. Washington, DC: PAHO; 2021 [cited 2022 Jul 21]. Yellow fever. Available from: https://www.paho.org/en/topics/yellow-fever.
4. Shearer FM, Longbottom J, Browne AJ, Pigott DM, Brady OJ, Kraemer MUG, et al. Existing and potential infection risk zones of yellow fever worldwide: a modeling analysis. Lancet Glob Health. 2018;6:e270–8. https://doi.org/10.1016/S2214-109X(18)30024-X.
5. World Health Organization. Assessment of yellow fever epidemic risk – a decision-making tool for preventive immunization campaigns. Wkly Epidemiol Rec. 2007;82(18):153–60. Available from: https://apps.who.int/iris/handle/10665/240930.
6. World Health Organization. Eliminate Yellow Fever Epidemics (EYE): strategy partners meeting report: Geneva, Switzerland, 9–10 May 2017. Geneva: WHO; 2018. Available from: https://apps.who.int/iris/handle/10665/279723.
7. Massad E, Amaku M, Coutinho FAB, Struchiner CJ, Lopez LF, Wilder-Smith A, et al. Estimating the size of Aedes aegypti

populations from dengue incidence data: Implications for the risk of yellow fever outbreaks. Infect Dis Model. 2017;2(4):441–54. https://doi.org/10.1016%2Fj.idm.2017.12.001.
8. Esteva L, Vargas C, Yang HM. A model for yellow fever with migration. Comput Math Methods. 2019;1:e1059. https://doi.org/10.1002/cmm4.1059.
9. Chen X, Gao D. Effects of travel frequency on the persistence of mosquito-borne diseases. Discret Contin Dyn Syst – B. 2020;25:4677–701. https://doi.org/10.3934/dcdsb.2020119.
10. Silva TM, Cade MV, Figueiras A, Roque F, Herdeiro MT, Devakumar D. Impact of infectious disease epidemics on xenophobia: A systematic review. J Migr Health. 2022;5:100085. https://doi.org/10.1016/j.jmh.2022.100085.
11. Tasker A, Braam D. Positioning zoonotic disease research in forced migration: A systematic literature review of theoretical frameworks and approaches. PLoS One. 2021;16(7):e0254746. https://doi.org/10.1371/journal.pone.0254746.
12. Saeed F, Mihan R, Mousavi SZ, Reniers RLEP, Bateni FS, Alikhani R, et al. A Narrative Review of Stigma Related to Infectious Disease Outbreaks: What Can Be Learned in the Face of the Covid-19 Pandemic? Front Psychiatry. 2020;11:565919. https://doi.org/10.3389/fpsyt.2020.565919.
13. Smith DL, Battle KE, Hay SI, Barker CM, Scott TW, McKenzie FE. Ross, Macdonald, and a Theory for the Dynamics and Control of Mosquito-Transmitted Pathogens. PLoS Pathog. 2012;8(4):e1002588. https://doi.org/10.1371/journal.ppat.1002588.
14. Soetaert K, Petzoldt T, Setzer RW. Solving Differential Equations in R : Package deSolve. J Stat Softw. 2010;33(9):1–25. https://doi.org/10.18637/jss.v033.i09.
15. Cannoodt R, Saelens W, Deconinck L, Saeys Y. Spearheading future omics analyses using dyngen, a multi-modal simulator of single cells. Nat Commun. 2021;12:3942. https://doi.org/10.1038/s41467-021-24152-2.
16. Stevenson M, Sergeant E. CRAN - Package epiR [Internet]. Melbourne: University of Melbourne; 2022 [cited 2022 Jul 26]. Available from: https://cran.r-project.org/package=epiR.
17. IOM Global Migration Data Analysis Centre [Internet]. Berlin: IOM GMDAC; 2021 [cited 2022 Jul 21]. Migration Data Portal. Migration data in Central America. Available from: https://www.migrationdataportal.org/regional-data-overview/migration-data-central-america.
18. HIAS. Rapid Needs Assessment – Necoclí [Internet]. Silver Spring, MD: HIAS; 2021 [cited 2022 Jul 21]. Available from: https://hias.org/wp-content/uploads/rapid_needs_assessment_report_necocli_eng.pdf.
19. The New Humanitarian [Internet]. Geneva: 2021 Oct 7 [cited 2022 Jul 21]. Dangers in the Darién: Deaths and needs rise on Central American migration route. Available from: https://www.thenewhumanitarian.org/video/2021/10/7/Central-American-migration-route-Darien-Gap-colombia-panama-dangerous.
20. Gobernación de Antioquia [Internet]. [Medellín]: Gobernación de Antioquia; 2018 [cited 2022 Jul 26]. Coberturas de Vacunación con Fiebre Amarilla en Población de 1 Año Según Municipio, Antioquia 2017. Available from: https://www.dssa.gov.co/images/Cobertura_FIEBREAMARILLA_2017_FECHA_08Junio2018.pdf.
21. Gobernación de Antioquia [Internet]. [Medellín]: Gobernación de Antioquia; 2019 [cited 2022 Jul 26]. Anuario Estadístico de Antioquia 2019. Salud y Protección Social. 2. 1. 2-Coberturas de vacunación de niños de un año, por tipo biológico, en los municipios, provincias y subregiones, de Antioquia, acumulado de enero a diciembre de 2019. Available from: https://www.antioquiadatos.gov.co/index.php/biblioteca-estadistica/anuario-estadistico-de-antioquia/anuario-estadistico-de-antioquia-2019/salud-2019/.
22. Obholz G, Diez F, Blas GS, Rossi G. The austral-most record of the genus Haemagogus Williston (Diptera: Culicidae). Rev Soc Bras Med Trop. 2019;53:e20190222. https://doi.org/10.1590/0037-8682-0222-2019.
23. Couto-Lima Di, Madec Y, Bersot MI, Campos SS, Motta MDA, Dos Santos FB, et al. Potential risk of re-emergence of urban transmission of Yellow Fever virus in Brazil facilitated by competent Aedes populations. Sci Rep. 2017;7(1):4848. https://doi.org/10.1038/s41598-017-05186-3.
24. Massad E, Amaku M, Coutinho FAB, Struchiner CJ, Lopez LF, Coelho G, et al. The risk of urban yellow fever resurgence in Aedes-infested American cities. Epidemiol Infect. 2018;146(10):1219–25. https://doi.org/10.1017/s0950268818001334.
25. Kung'aro M, Luboobi LS, Shahada F. Modelling and stability analysis of SVEIRS yellow fever two host model. Gulf J Math [Internet]. 2015 [cited 2022 Jul 21];3(3). https://doi.org/10.56947/gjom.v3i3.152.
26. Johansson MA, Vasconcelos PFC, Staples JE. The whole iceberg: estimating the incidence of yellow fever virus infection from the number of severe cases. Trans R Soc Trop Med Hyg. 2014;108(8):482–7. https://doi.org/10.1093/trstmh/tru092.
27. Sadeghieh T, Sargeant JM, Greer AL, Berke O, Dueymes G, Gachon P, et al. Yellow fever virus outbreak in Brazil under current and future climate. Infect Dis Model. 2021;6:664–77. https://doi.org/10.1016/j.idm.2021.04.002.
28. Cathey JT, Marr JS. Yellow fever, Asia, and the East African slave trade. Trans R Soc Trop Med Hyg. 2014;108(5):252–7. https://doi.org/10.1093/trstmh/tru043.
29. Organización Panamericana de la Salud. Control de la fiebre amarilla: guía práctica. Publicación Científica y Técnica No. 603. Washington, DC: OPS; 2005. Available from: https://iris.paho.org/handle/10665.2/722.

Manuscript submitted on 30 August 2022. Revised version accepted for publication on 28 January 2023.

Efectos de las tasas de migración y de la vacunación en la propagación de la fiebre amarilla en comunidades de América Latina

RESUMEN

Objetivo. Evaluar la importancia del flujo de personas entre comunidades, en comparación con la vacunación y el tipo de vector, para la propagación y los posibles brotes de fiebre amarilla en una comunidad de acogida libre de la enfermedad.

Métodos. Con el empleo de un modelo SEIRV—SEI para personas y vectores, aplicamos simulaciones numéricas a las siguientes situaciones hipotéticas: 1) migración desde una comunidad con endemicidad a una comunidad de acogida libre de la enfermedad, en la que se compararon los resultados producidos por *Haemagogus janthinomys* y *Aedes aegypti* como vectores; 2) migración a través de una comunidad de tránsito situada en una ruta migratoria, donde la enfermedad es endémica, hacia otra comunidad libre de la enfermedad; y 3) efectos de tasas de vacunación diferentes en la comunidad de acogida, tomando en consideración la vacunación de las personas migrantes a su llegada.

Resultados. Los resultados no muestran diferencias notables entre las situaciones 1 y 2. En cuanto a la aparición de brotes, tanto la cobertura vacunal en la comunidad de acogida como el tipo de vector tienen más importancia que las tasas de migración; y *H. janthinomys* muestra mayor eficacia que *A. aegypti*.

Conclusiones. Dado que, para determinar la aparición de un posible brote, la vacunación tiene mayor importancia que las tasas de migración, la vacunación de las personas migrantes a su llegada puede ser una de las medidas más eficaces contra la fiebre amarilla. Además, a densidades similares, *H. janthinomys* es un vector más competente que *A. aegypti*, por lo que la presencia de *A. aegypti* constituye una señal de alerta para mantener la vacunación por encima de los niveles recomendados.

Palabras clave Fiebre amarilla; vacunación; migración humana; modelos epidemiológicos; salud pública; enfermedades transmitidas por vectores; brotes de enfermedades; América Latina.

Efeitos das taxas de migração e vacinação na propagação da febre amarela em comunidades latino-americanas

RESUMO

Objetivo. Avaliar a relevância do fluxo de pessoas entre comunidades em comparação com a vacinação e tipo de vetor para a propagação e potenciais surtos de febre amarela em uma comunidade de destino livre da doença.

Métodos. Usando um modelo SEIRV-SEI para humanos e vetores, foram aplicadas simulações numéricas aos seguintes cenários: (1) migração de uma comunidade endêmica para uma comunidade de destino livre da doença, comparando o desempenho de *Haemagogus janthinomys* e de *Aedes aegypti* como vetores; (2) migração através de uma comunidade de trânsito localizada em uma rota migratória, onde a doença é endêmica, para uma comunidade de destino livre da doença; e (3) efeitos de diferentes taxas de vacinação na comunidade de destino, considerando-se a vacinação dos migrantes ao chegarem.

Resultados. Os resultados não revelaram diferenças marcantes entre os cenários 1 e 2. O tipo de vetor e a cobertura vacinal na comunidade de destino são mais relevantes para a ocorrência de surtos do que as taxas de migração; o vetor *H. janthinomys* é mais efetivo do que *A. aegypti*.

Conclusões. Na medida em que a vacinação é mais determinante para um potencial surto que as taxas de migração, a vacinação de migrantes na chegada pode ser uma das medidas mais efetivas contra a febre amarela. Além disso, o *H. janthinomys* é um vetor mais competente do que o *A. aegypti* em densidades similares, mas a presença de *A. aegypti* é um alerta para manter a vacinação acima dos níveis recomendados.

Palavras-chave Febre amarela; vacinação; migração humana; modelos epidemiológicos; saúde pública; doenças transmitidas por vetores; surtos de doenças; América Latina.