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Analysis of Strategies for Preventing and Controlling the Chikungunya Virus*

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Abstract: alternatives to stop chikungunya outbreaks are oriented to vector control and developing a specific treatment and a preventive vaccine. Environmental control and mosquito bite prevention are undoubtedly essential to decrease the disease burden, but *Aedes* vectors continue to expand geographically and re-emerge. So, vaccination is proposed to respond to this etiology and recognized as a pressing need for affected countries. A mathematical host-vector model, including asymptomatic population, vector control, and vaccination (assuming the existence of a safe protective vaccine against the chikungunya virus), is suggested to analyze the effects of these efforts. Poisson distribution is applied to interpret the basic reproduction number. Then vaccination and vector control thresholds are established to prescribe the most effective protection measures against exposure to the chikungunya virus. In conclusion, it is advisable to continue with integrated control to reduce the economic impact of relevant public health responses and mitigate other infections since *Aedes* is a transmitter of other arboviruses such as dengue, Zika, and Mayaro. Furthermore, vaccinating all individuals in a community could be a costly and gradual process.

Keywords: CHIKV; *Aedes*; vaccination; mosquito control; mathematical model; basic reproduction number

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* Research article

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Análisis de estrategias para prevenir y controlar el virus Chikunguña

Resumen: las alternativas para detener los brotes de Chikunguña están orientadas, primero, al control del vector y, segundo, al desarrollo de un tratamiento específico y una vacuna preventiva. Es indudable la importancia del control ambiental y la prevención de la picadura de mosquitos para disminuir la carga de la enfermedad, pero sus vectores *Aedes* continúan expandiéndose geográficamente y resurgiendo, por lo que la vacunación se plantea como la respuesta a esta etiología y se reconoce como una necesidad prioritaria para los países afectados. Con el fin de analizar los efectos de los esfuerzos antes mencionados, se propone un modelo matemático hospedero-vector que incluye población asintomática, control de vectores y vacunación (se supone la existencia de una vacuna segura y protectora contra el virus Chikunguña). Se aplica el proceso de Poisson en epidemiología para interpretar el número básico de reproducción, y luego se establecen umbrales de vacunación y control vectorial que prescriben las medidas más efectivas para proteger contra la exposición al virus Chikunguña. Se concluye que para reducir el impacto económico de las respuestas de salud pública correspondientes es recomendable continuar con el control integrado, ya que *Aedes* es transmisor de otros arbovirus como dengue, Zika y Mayaro, lo que ayudaría también a la mitigación de estas otras infecciones. Además, proporcionar la vacuna a todos los individuos de una comunidad podría ser un proceso paulatino y costoso.

Palabras clave: CHIKV; *Aedes*; vacunación; control del mosquito; modelo matemático; número reproductivo básico

Análise de estratégias para prevenir e controlar o vírus Chikungunya

Resumo: as alternativas para deter os surtos de chikungunya estão orientadas, em primeiro lugar, ao controle do vetor e, em segundo, ao desenvolvimento de um tratamento específico e de uma vacina. São inegáveis a importância do controle ambiental e a prevenção da picada de mosquitos para diminuir a carga da doença, mas seus vetores *Aedes* continuam se expandindo geograficamente e ressurgindo, razão pela qual a vacinação se apresenta como resposta a essa etiologia e se reconhece como necessidade prioritária para os países afetados. A fim de analisar os efeitos dos esforços antes mencionados, é proposto um modelo matemático hospedeiro-vetor que inclui população assintomática, controle de vetores e vacinação (é suposta a existência de uma vacina segura e protetora contra o vírus chikungunya). É aplicado o processo de Poisson em epidemiologia para interpretar o número básico de reprodução e logo estabelecidos os parâmetros para a vacinação e o controle vetorial que as medidas mais efetivas prescrevem para proteger da exposição ao vírus chikungunya. Conclui-se que, para reduzir o impacto econômico das respostas de saúde pública correspondentes, é recomendável continuar o controle integrado, já que *Aedes* é transmissor de outros arbovírus como dengue, zika e mayaro, o que ajudaria também para mitigar essas outras infecções. Além disso, proporcionar a vacina a todos os indivíduos de uma comunidade poderia ser um processo paulatino e caro.

Palavras-chave: CHIKV; *Aedes*; vacinação; controle do mosquito; modelo matemático; número reprodutivo básico

Introduction

The chikungunya virus (CHIKV) is an RNA virus belonging to the alphavirus genus of the *Togaviridae* family that causes chikungunya fever. It was first detected in Tanzania in 1952 [1]; the first outbreaks of the epidemic occurred in the Makonde tribe (Tanzania, 1950). The name chikungunya derives from a word of this tribe that means "person that bends up" and describes the contorted posture of people who suffer from intense pain in their joints (arthralgia) [2].

Since 2004, CHIKV has expanded its global geographic distribution, causing sustained epidemics of unprecedented magnitude in Asia and Africa, although some areas of these continents are considered endemic for this disease. The virus produced outbreaks in many new territories of the islands in the Indian Ocean in 2006 and Italy in 2007 when autochthonous transmission by a viremic traveler returning from India was detected. At the end of 2013, the Pan American Health Organization (PAHO)/World Health Organization (WHO) received confirmation of the first autochthonous cases in the Americas, with cases identified on the island of Saint Martin [3], [4].

CHIKV is not transmitted orally, sexually, or via the respiratory tract but through the bite of female *Aedes* mosquitoes, predominantly *A. aegypti* and *A. albopictus*, which must have previously bitten a viremic (a term that describes the presence of the virus in the blood) person to get infected [5]. The influx of people infected with CHIKV is higher than other arboviruses, and they develop clinical symptoms that require medical attention.

Although not all infected people develop symptoms (asymptomatic), the sick person in the acute phase may have a high fever, severe joint pain, headache, nausea, and vomiting; these symptoms remain for 3–10 days. The persistence of symptoms for more than three months, even years, characterizes the disease in its chronic phase. The most frequent symptom is severe joint pain. However, it is believed that, once exposed to the virus, individuals acquire prolonged immunity that protects them against reinfection [6].

The disease is only fatal in 0.4 % of those affected when patients cannot overcome the infection because of a weak immune system. The most vulnerable are the elderly, newborns, and those suffering from heart failure, diabetes, high blood pressure, cancer, autoimmune diseases, among others. In most infections during pregnancy, the virus is not transmitted to the fetus; however, there are occasional reports of spontaneous abortions after a CHIKV infection in the mother [7]. Although the infection appears to induce long-lasting protective immunity, serological studies indicate that between 3 and 28 % of people with antibodies to the virus have asymptomatic infections [8].

Regarding disease control, governments of affected countries have expended considerable efforts and invested millions of dollars in mosquito control, the mainstay of prevention and control [9]–[11]. Mosquito control measures that have been used to reduce CHIKV transmission may be broadly categorized into three types: chemical control, biological control, and habitat control [12]–[14]. Chemical control consists of the gamut of commercial synthetic chemical insecticides, including pyrethroids and organophosphates. Biological control consists of measures that are derived from plants (*e.g.*, essential oils), animals (*e.g.*, predatory fishes), or microorganisms (*e.g.*, *Bacillus thuringiensis* israelensis (Bti)). Habitat control consists of landfill cleaning and source reduction by removing water from receptacles, household containers, and even large leaves. These measures were researched in several studies. On Mayotte Island in 2009, the prevalence of CHIKV was found to be higher in individuals who did not remove breeding habitat [15]; another study from India reported a decrease in the incidence of cases following removal of breeding habitat [16], which was also associated with a decrease in larval densities in three studies [17]–[18].

There is no specific antiviral or commercial vaccine approved by the WHO against chikungunya fever. Then, prevention and mitigation rely on personal protective measures and community-level interventions, including vector control such as the use of repellents (applied to the skin and in the form of diffusers); physical barriers such as long clothing, bed nets, and screens; removal of vector breeding habitat, and mosquito avoidance [19]–[21]. Patient

treatment consists of alleviating the symptoms, including joint pain, with antipyretics, optimal analgesics, and fluids [22].

Because *A. aegypti* and *A. albopictus* mosquitoes persist, enormous efforts have been made to develop a commercial vaccine for CHIKV as a preventive control tool. Several technologies have been used to develop candidate vaccines for preclinical testing in animal models and phase I and II clinical trials in humans [23], including inactivated viral vaccines, live-attenuated viruses (LAV), alphavirus chimeras, recombinant viral vaccines, consensus-based DNA vaccines, recombinant subunit vaccines and, more recently, a virus-like particle (VLP) vaccine [22]. Four vaccine candidates have been tested in humans in a phase I clinical trial (inactivated virus, LAV, VLP, and the measles-vectored vaccine), and at present, only the recombinant measles virus expressing CHIKV VLPs has entered phase II clinical trials [24].

At the theoretical level, in 2016, Requena and Segovia formulated a mathematical model to simulate an outbreak of chikungunya in a local population, transmitted from a neighboring infected population [25]. Martínez *et al*. propose a predictive mathematical model of chikungunya diffusion in Colombia to obtain the necessary sanitary responses and evaluate the effectiveness of control actions against mosquito vectors [26].

Model formulation

We considered an epidemic model with two transmission routes and a single vector (*Aedes aegypti*) for the CHIKV, whose assumptions are 1) there are no alternative hosts as sources of food; 2) the latent population can fall into two classes, symptomatic and asymptomatic, before moving on to the infectious class; 3) vaccinated people acquire permanent immunity against infection; 4) the virus continues to replicate inside the vector until the mosquito dies; 5) vectors are homogeneously mixed in the human population; 6) vector and host can transmit the virus only during the infectious state; 7) there is no transovarial transmission of the virus either in the vector or the host; 8) the birth and mortality rates of humans are equal.

Model variables. $x_1 \equiv x_1(t)$: average number of susceptible people at time t; $x_2 \equiv x_2(t)$: average number of latent people at time t; $x_3 \equiv x_3(t)$: average number of symptomatic people at time t; $x_4 \equiv x_4(t)$: average number of asymptomatic people at time t; $x_3 \equiv x_3(t)$: average number of immune people at time t; $y_1 \equiv y_1(t)$: average number of non-carrier female mosquitoes at time t; $y_2 \equiv y_2(t)$: average number of carrier female mosquitoes at time t; $M \equiv M(t)$: variable total population of mosquitoes; $N \equiv N(t)$: constant total population of humans.

Model parameters. β: probability of CHIKV transmission from infected persons to non-carrier mosquitoes; σ: probability of CHIKV transmission from carrier mosquitoes to susceptible people; f : fraction of people of the exposed class who become symptomatic; μ: per-head mortality rate equal to the per-head birth rate for humans; ϵ: mortality rate of the adult mosquito; γ: common transfer rate of humans from the exposed class to the symptomatic and asymptomatic classes; θ: recovery rate of infected people; ω: pre-infection vaccination rate; π: rate of mosquito elimination through adulticides, lethal traps, among others; ρ: constant increment rate of non-carrier mosquitoes.

The transmission dynamics is interpreted according to the compartmental diagram in Fig. 1 and governed by the system of nonlinear ordinary differential equations (1):

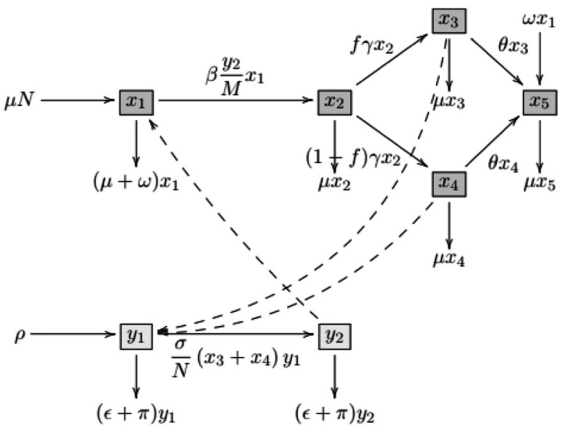


Fig. 1. Flow diagram of the model (1); dashed lines represent the interactions between new infections.

Source: Own elaboration

$$\begin{cases} \dot{x}_1 = \mu N - \dfrac{\beta y_2 x_1}{M} - (\mu + \omega)x_1 \\ \dot{x}_2 = \dfrac{\beta y_2 x_1}{M} - (\mu + \gamma)x_2 \\ \dot{x}_3 = f\gamma x_2 - (\mu + \theta)x_3 \\ \dot{x}_4 = (1-f)\gamma x_2 - (\mu + \theta)x_4 \\ \dot{x}_5 = \theta x_4 + \theta x_3 + \omega x_1 - \mu x_5 \\ \dot{y}_1 = \rho - (\epsilon + \pi)y_1 - \left(\dfrac{\sigma x_3 y_1}{N} + \dfrac{\sigma x_4 y_1}{N}\right) \\ \dot{y}_2 = \left(\dfrac{\sigma x_3 y_1}{N} + \dfrac{\sigma x_4 y_1}{N}\right) - (\epsilon + \pi)y_2 \end{cases} \quad (1)$$

subject to: $x_m(0) \geq 0$ ($m = 1, 2, 3, 4, 5$) and $y_n(0) \geq 0$ ($n = 1, 2$) ; $\mu > 0$, $\epsilon > 0$, $\theta > 0$, $\omega > 0$, $\pi > 0$, $0 < \beta < 1$, $0 < \sigma < 1$, $0 < f < 1$, $0 < \gamma < 1$.

It is possible to verify that the system (1) satisfies the conditions of existence and uniqueness of solutions in $\mathbb{R}^7_{\geq 0}$ [27]–[28]. Furthermore, the system (1) is defined in the positively invariant set (2):

$$\Pi = \left\{(x_1, x_2, x_3, x_4, x_5, y_1, y_2) \in \mathbb{R}^7_{\geq 0} : 0 < \sum_{k=1}^{5} x_k = N \ \wedge 0 < y_1 + y_2 \leq \frac{\rho}{\epsilon + \pi}\right\}. \quad (2)$$

Indeed,

$$\left.\frac{dx_1}{dt}\right|_{x_1=0} = \mu N \geq 0, \left.\frac{dy_1}{dt}\right|_{y_1=0} = \rho \geq 0$$

for all $\mu > 0$, $\rho > 0$, and $N > 0$. So, $x_1(t)$ and $y_1(t)$ are non-negative, particularly if $t \longrightarrow +\infty$. Now, adding all equations of the system, we can see that

$$\frac{dN}{dt} = \sum_{k=1}^{5} \frac{dx_k}{dt} = 0.$$

So, the value of N is constant. Similarly, considering the domain defined for the parameters and the initial non-negative conditions, we have

$$\left.\frac{dy_2}{dt}\right|_{y_2=0} = \frac{\sigma}{N}(x_3 + x_4)y_1 = \frac{\sigma}{N}(N - x_1 - x_2)y_1 \geq 0,$$

$$\left.\frac{dx_2}{dt}\right|_{x_2=0} = \frac{\beta y_2 x_1}{M} \geq 0, \left.\frac{dx_3}{dt}\right|_{x_3=0} = f\gamma x_2 \geq 0,$$

$$\left.\frac{dx_4}{dt}\right|_{x_4=0} = (1-f)\gamma x_2 \geq 0, \left.\frac{dx_5}{dt}\right|_{x_5=0} = \theta x_4 + \theta x_3 + \omega x_1 \geq 0.$$

The next set establishes a domain where the system is mathematically and epidemiologically reasonable since it guarantees that the state trajectories are always positive, continuous, and do not escape infinity.

Table 1 contains the hypothetical values that will be used later in the simulations with the Maple software.

Table 1. Entomological and epidemiological parameters

Parameter	β	σ	f	μ	ϵ	Γ
Average value	0.977	0.726	0.25	$\frac{1}{78 \times 365}$	7^{-1}	0.75
Parameter	θ	ω	π	N	P	
Average value	0.91	0.6	0.65	299,712	2,500	

Source: Own elaboration

Basic reproduction number

The system (1) presents two stationary points. E_0 represents the CHIKV-free equilibrium state (3):

$$E_0 = \left(\frac{\mu N}{\mu+\omega}, 0,0,0, \frac{\omega N}{\mu+\omega}, \frac{\rho}{\pi+\epsilon}, 0\right) = \left(x_1^{(0)}, 0,0,0, \frac{\omega}{\mu} x_1^{(0)} \frac{\rho}{\pi+\epsilon}, 0\right) \quad (3)$$

Another steady state represents the prevalence of CHIKV and contains the equilibrium state of the latent population in one of its components (4):

$$\hat{x}_2 = \frac{(\mu+\omega)(\mu+\theta)(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)\rho\theta[\mathbf{R}_0(\omega,\pi)-1]}{\beta(\mu^2 f\gamma\sigma + (\mu+\gamma)(\mu+\theta)(\pi+\epsilon)\theta + \mu\gamma\sigma\theta)} \quad (4)$$

Determining R0 is equivalent to answering the question: Under what conditions does the CHIKV-infected population increase, $\frac{dx_2(t)}{dt} > 0$? Suppose an infected individual enters an immunologically virgin population. It is understood that there is no infection in the environment, and the virus is produced by the infected individual entering the population in question. In this case, the controlled reproduction number is given by (5):

$$\mathbf{R}_0(\omega,\pi) = \frac{\beta\mu f\gamma\sigma}{(\mu+\omega)(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)} + \frac{\beta\mu(1-f)\gamma\sigma}{(\mu+\omega)(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)}. \quad (5)$$

Or equivalently,

$$\mathbf{R}_0(\omega,\pi) = \mathbf{R}_1(\pi,\omega) + \mathbf{R}_2(\pi,\omega) \quad (6)$$

where

$$\mathbf{R}_1(\omega,\pi) = \frac{\beta\mu f\gamma\sigma}{(\mu+\omega)(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)}$$

and

$$\mathbf{R}_2(\omega,\pi) = \frac{\beta\mu(1-f)\gamma\sigma}{(\mu+\omega)(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)}.$$

In interpreting the controlled reproduction number, we notice that the term $\mathbf{R}_1$ gives the average number of secondary infections caused by a symptomatic person in an entirely susceptible population of humans during her/his infectious lifespan. Similarly, the term $\mathbf{R}_2$ gives the average number of secondary infections produced by an asymptomatic person in a fully susceptible population during its infectious period. Thus, $\mathbf{R}_0$ gives the average number of secondary infections that an infected individual, mixed in a CHIKV-free population of humans and mosquitoes, will produce during her/his contagion period [29].

If we consider the transition from an infectious state to a state of removal as the Poisson distribution, we can interpret the basic reproduction number in detail. We have:

$$\mathbf{R}_1(\omega,\pi) = \frac{\beta\sigma}{\mu N} E[y_1]P[x_2]P[x_3]x_1^{(0)} \text{ and}$$

$$\mathbf{R}_2(\omega,\pi) = \frac{\beta\sigma}{\mu N} E[y_1]P[x_2]P[x_4]x_1^{(0)},$$

where

$$E[y_1] = \int_0^{+\infty} te^{-(\pi+\epsilon)t}\,dt, E[x_2] = \int_0^{+\infty} te^{-(\mu+\gamma)t}\,dt, E[x_2] = \int_0^{+\infty} te^{-(\mu+\gamma)t}\,dt$$

and

$$E[x_3] = E[x_4] = \int_0^{+\infty} te^{-(\theta+\mu)t}\,dt.$$

The average life and infectious periods can be calculated utilizing this mathematical theory of epidemics (Poisson distribution) in which many life events are the transition from a susceptible state to a latent state, or from a latent state to an infectious state, or from an infectious state to a removal state. Each has a certain probability of occurrence, regardless of how long it has persisted in the initial state [30]–[31]. Hence, $E[x_2] = 1/(\mu+\gamma)$: average duration of the exposed class; $E[x_3] = 1/(\mu+\theta)$: average duration of the symptomatic class equal to the average duration of the asymptomatic class; $E[y_1] = 1/(\epsilon+\pi)$: life expectancy of the female mosquito.

The probabilities of permanence in each class are $P[x_1] = \mu/(\mu+\omega)$: the probability of staying in the susceptible class; $P[x2] = \mu/(\mu+\gamma)$: the probability of remaining in the class exposed; $P[x_3] = f\gamma/(\mu+\theta)$: the probability of remaining in the symptomatic class; $[x_4] = (1\text{-}f)\ \gamma/\ (\mu+\theta)$: the probability

of remaining in the asymptomatic class; $P[y_i] = (\epsilon)/(\epsilon+\pi)$, $i = 1, 2$: the probability that a female mosquito will remain in the non-carrier class ($i = 1$) or the carrier class ($i = 2$).

Given the definition of $\mathbf{R}_0$ and Equations (3) and (4), if $\mathbf{R}_0 > 1$, the infected individuals at the beginning of the disease will increase the number of new infections, and a CHIKV outbreak will occur. Instead, if $\mathbf{R}_0 < 1$, the sick individuals will be, as a population, inefficient transmitters, and the disease will eventually disappear. Mathematically, this means that if $\mathbf{R}_0 > 1$, the endemic equilibrium will be epidemiologically significant, and the CHIKV-free equilibrium solution will be unstable, but if $\mathbf{R}_0 < 1$, the CHIKV-free equilibrium solution will be the only globally asymptotically stable solution.

Community mitigation strategies

The basic reproduction number (5) deduced from the stability analysis naturally depends on the control strategies. The surfaces of the basic reproduction number as a function of both strategies (vaccination and vector density reduction) are shown in Fig. 2. The reproduction number in the presence of vaccination or vector control is a decreasing function of ω and π; *i.e.*, the higher the vaccination rate or the elimination rate of mosquitoes, the lower the R_0. In this regard, the following question arises: What is the critical proportion of individuals that must be vaccinated or mosquitoes that must be eliminated so that R_0 is less than 1?

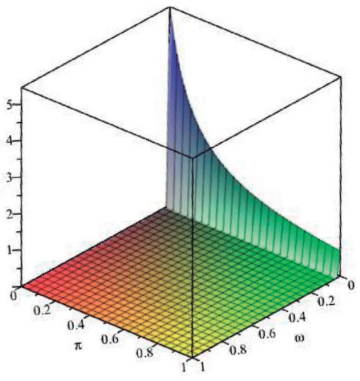


Fig. 2. Basic reproduction number depending on ω and π.
Source: Own elaboration

- In the absence of vaccination and vector control, $\pi = \omega = 0$, the basic reproduction number is

$$\mathbf{R}_0(0,0) = \frac{\beta f \gamma \sigma}{\epsilon(\mu+\gamma)(\mu+\theta)} + \frac{\beta(1-f)\gamma\sigma}{\epsilon(\mu+\gamma)(\mu+\theta)}.$$

- If there is no vaccination ($\omega = 0$), but the vector is controlled ($\pi > 0$), we obtain:

$$\mathbf{R}_0(0,\pi) = \frac{\beta f \gamma \sigma}{(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)} + \frac{\beta(1-f)\gamma\sigma}{(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)}.$$

The graph of the threshold without vaccination is shown in Fig. 3. In this case, the disease is controlled if $\mathbf{R}_0(0, \pi) < 1$; that is, when $\pi > \epsilon(\mathbf{R}_0(0, 0) - 1)$ for $\mathbf{R}_0(0, 0) > 1$. Whenever $\mathbf{R}_0(0, 0) < 1$, it is not necessary to control the vector.

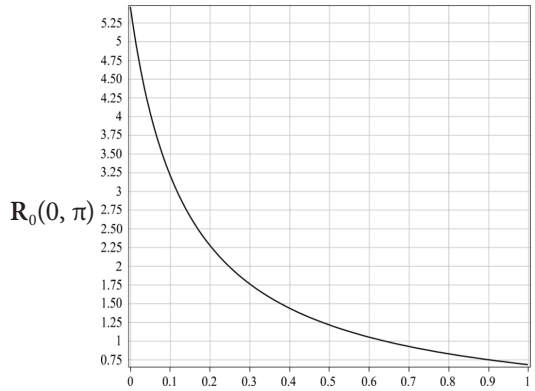
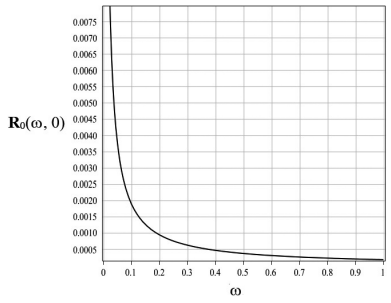


Fig. 3. Basic reproduction number in the function of π.
Source: Own elaboration

- If people are vaccinated ($\omega > 0$), but the vector is not controlled $\pi = 0$, the basic reproduction number is

$$\mathbf{R}_0(\omega,0) = \frac{\beta\mu f\gamma\sigma}{\epsilon(\mu+\omega)(\mu+\gamma)(\mu+\theta)} + \frac{\beta\mu(1-f)\gamma\sigma}{\epsilon(\mu+\omega)(\mu+\gamma)(\mu+\theta)}.$$

The graph of the threshold without vector control is shown in Fig. 4. In this case, the disease is controlled if $\mathbf{R}_0(\omega, 0) < 1$; that is, when $\omega > \mu(\mathbf{R}_0(0,0) - 1)$ for $\mathbf{R}_0(0, 0) > 1$. Whenever $\mathbf{R}_0(0, 0) < 1$, it is not necessary to control the vector.



$\mathbf{R}_0(\omega, 0)$

Fig. 4. Basic reproduction number in the function of ω.
Source: Own elaboration

For a global understanding of the meaning of the basic reproduction number, we disaggregate the expression (6) as follows:

$$\mathbf{R}_0(\omega,\pi) = \left(\frac{1}{\epsilon(\mu+\gamma)}\beta\mu f\right)\left(\frac{1}{(\pi+\omega)(\mu+\theta)}\sigma\gamma\right) + \left(\frac{1}{\epsilon(\mu+\omega)}\beta\mu(1-f)\right)\left(\frac{1}{(\mu+\gamma)(\mu+\theta)}\sigma\gamma\right).$$

Note the additive and multiplicative effects of $\mathbf{R}_0$. Since the mosquito can transmit the infection to unvaccinated susceptible persons, the vector can acquire the virus from the symptomatic or asymptomatic persons infected with CHIKV. The terms $\mu/(\mu + \gamma)$ and $\mu/(\mu + \omega)$ are the fractions of unvaccinated and vaccinated susceptible persons, in the absence of symptomatic and asymptomatic persons but the presence of one or a small number of carrier mosquitoes. The term $\epsilon^{-1}\beta f\mu/(\mu + \gamma)$ indicates the incidence (new cases of chikungunya) in the susceptible population not vaccinated during the lifetime of the mosquito, providing the number of carrier mosquitoes $(\mu+\gamma)^{-1}(\mu+\theta)^{-1}\sigma\gamma$.

Table 2 summarizes the control strategies based on the threshold (5). Although Fig. 4 indicates that a constant low vaccination rate (above 0.016 %) over time is sufficient to stop the spread of chikungunya, in this case, it is possible to prioritize resources towards the immunization of the most vulnerable groups of people or with a higher risk of the disease. According to Fig. 3, vector control seems to be related to a high daily vector mortality rate (above 63.7 %). Furthermore, the situation $\mathbf{R}_0(\omega, 0) < \mathbf{R}_0(0,\pi)$, illustrated in Fig. 5, holds if $\epsilon > \mu$; for $\epsilon > \mu$, a lower burden of chikungunya is expected when an appropriate fraction of the population is immunized.

Table 2. Mitigation strategies

Control type	Control criteria
$\mathbf{R}_0(0,0) = \frac{\beta\gamma\sigma}{\epsilon(\mu+\gamma)(\mu+\theta)}$	***Without control***
$\mathbf{R}_0(0,\pi) = \frac{\beta\gamma\sigma}{(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)}$	$\pi > \epsilon(\mathbf{R}_0(0,0) - 1)$
$\mathbf{R}_0(\omega,0) = \frac{\beta\mu\gamma\sigma}{\epsilon(\mu+\omega)(\mu+\gamma)(\mu+\theta)}$	$\omega > \mu(\mathbf{R}_0(0,0) - 1)$
$\mathbf{R}_0(\omega,\pi) = \frac{\beta\mu\gamma\sigma}{(\mu+\omega)(\pi+\epsilon)(\mu+\gamma)(\mu+\theta)}$	$\mathbf{R}_0(\omega,\pi) < 1$

Source: Own elaboration

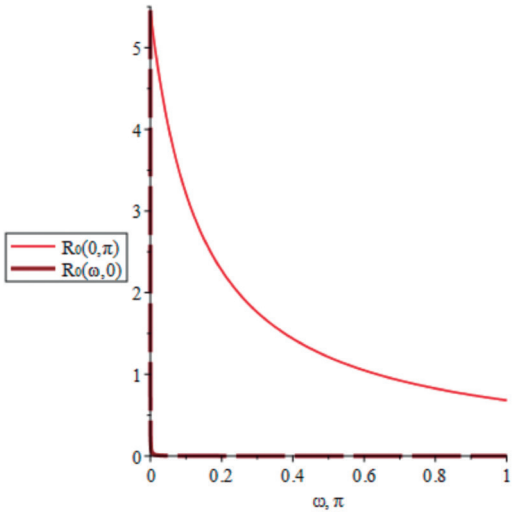


Fig. 5. Comparison of for exclusive control measures.
Source: Own elaboration

Conclusions

This study established mitigation strategies at the community level that contemplate vaccination and vector elimination in its adult or juvenile phase using the basic reproduction number that predicts the temporal dynamics of an outbreak of chikungunya. Evaluation of individual measures suggests greater effectiveness of immunization than reducing vector density when mosquitoes' natural mortality is lower than that of humans, which seems reasonable considering both species' survival scales.

Until now, the PAHO/WHO portals and scientific publications suggest no validated and approved ready-to-use vaccine against CHIKV for humans; however, there are articles on two potential vaccine candidates. One demonstrated complete immunity against CHIKV in mice and non-human primates (NHPS) [32]. The other, a novel LAV candidate, has undergone a phase II clinical trial and is recommended as an option for emergency CHIKV vaccinations, in addition to being a potential vaccine candidate that can be further developed [33]. Indeed, a registered human CHIKV vaccine would help stop virus transmission and alleviate the disease burden in areas where *Aedes* mosquitoes continue to spread CHIKV. This study anticipates that giving a safe and protective vaccine against chikungunya to a community would positively reduce the burden of this disease.

However, if public health authorities agree that an epidemic is susceptible to control, they will seek that programs for mitigation (and then the desirable eradication) be sustainable and economical. In the light of this study, integrated control is recommended; similar research on vector-borne diseases suggests that a combination of interventions is likely more effective than a single intervention [34]–[36].

The proposed model is limited (which is a mathematical simplification), mainly due to the following reasons:

1. It is assumed that all individuals belong to a panmictic population (well mixed) in which mosquitoes and humans have the same probabilities of contacting each other. This model could include a spatial variation of vector concentration.
2. The second aspect is the climatic effect on the vector population dynamics. Locally, temperature, precipitation, and humidity significantly affect the dynamics of vector-borne diseases, including chikungunya. This model could include the unique effects of temperature on vector parameters.

A more realistic model can be developed by incorporating these assumptions. The proposed model allows us to establish the future of the disease in a specific community, as long as the precise information on the specific parameters is available. It is not possible to use the results of this work directly on an outbreak. It must be kept in mind that mathematical models represent reality and help understand how it works under a significant number of assumptions.

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