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# Effectiveness of Dengue Leaky Vaccine: A Modeling Approach

Robert G. S. de Araujo[1], Suani T. R. de Pinho[2]
Universidade Federal da Bahia, Salvador, BR.
Lourdes Esteva[3], Gustavo C. Pacheco[4]
Universidad Nacional Autónoma de México, Ciudad de México, MX.
Ana T. C. Silva[5]
Universidade Estadual de Feira de Santana, Feira de Santana, BR.

Dengue, an endemic disease transmitted by the Aedes aegypti mosquito, affects millions of people annually across various regions worldwide, as reported by the World Health Organization (WHO). The control of dengue transmission is challenging due to the complex dynamics of its vector. However, the advent of vaccines presents a significant opportunity to alter the epidemiological landscape. In this context, the use of mathematical models to assess the impact of interventions in epidemics becomes an essential tool for understanding how vaccine introduction can influence the current scenario. This study employs stochastic modeling to analyze different scenarios in a partially vaccinated population, considering the leaky nature of the vaccine and its association with a reduction in the transmission rate. We derive the master equation for a vector-borne disease model, as in [2], including the presence of vaccinated individuals, obtaining the probability of transition between states

$$\omega_i(n) = \Big[\frac{\beta}{\xi}\delta(n_i, S_H) + \frac{\beta}{\xi}(1-\epsilon)\delta(n_i, S_{HV})\Big]\sum_{\Delta}\delta(n_{i+\Delta}, I_M) + \frac{\beta}{\xi}\delta(n_i, S_M)\Big[\sum_{\Delta}\delta(n_{i+\Delta}, I_H) + (1-\alpha)\delta(n_{i+\Delta}, I_{HV})\Big] + \gamma\Big[\delta(n_i, I_H) + \delta(n_i, I_{HV})\Big] + \mu\delta(n_i, I_M) \quad (1)$$

where $\delta(n_i, \chi)$ is the Kronecker's delta function indicating the $i-th$ site in the state $\chi$. The possible states represent different stages of an individual related to the infectious process, following the table

[1]robert.gabriel@ufba.br
[2]suanipinho@ufba.br
[3]lesteva@ciencias.unam.mx
[4]gcruzpacheco@gmail.com
[5]tereza@uefs.br

Table 1: Possible states.

| Symbol | Description |
|---|---|
| $S_H$ | Susceptible unvaccinated human |
| $I_H$ | Infected unvaccinated human |
| $R_H$ | Recovered unvaccinated human |
| $S_{HV}$ | Susceptible vaccinated human |
| $I_{HV}$ | Infected vaccinated human |
| $R_{HV}$ | Recovered vaccinated human |
| $S_M$ | Susceptible mosquito |
| $I_M$ | Infected mosquito |

By calculating the basic reproduction number $\mathcal{R}_0$, using one-site and pair-site mean-field approximations, and the vaccine effectiveness, using the method presented in [1], we performed simulations of epidemic scenarios to evaluate various control measures. Our results highlight the role of transmission rate, vaccine efficacy, vector control, and the proportion of vaccinated individuals in the epidemic's dynamic process and the vaccine's effectiveness in population protection. Furthermore, we demonstrate non-linear behaviors that can be compared to vaccination programs implemented for recently adopted vaccines in Brazil, such as Qdenga, produced by Takeda Pharmaceutical, and Butantan-DV, produced by Instituto Butantan.

## References

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