International Journal of Mathematics and Physical Sciences Research ISSN 2348-5736 (Online)
Vol. 9, Issue 2, pp: (97-101), Month: October 2021 - March 2022, Available at: www.researchpublish.com

MODELLING THE EFFECT OF VACCINATION ON THE DYNAMICS OF INFECTIOUS DISEASES

Dr. Ime Okonna

Dept. of Gen. Studies, Akwa Ibom State Polytechnic, Ikot Osurua, Akwa Ibom State, Nigeria.

Author Email: imeokonna2004@yahoo.com

Abstract: **In this paper, we analyze the effect of vaccination on the dynamics of infectious diseases using a simplified SIR model with a vaccination compartment. We have obtained results about the stability of the disease-free and endemic equilibria of the model. Analytical and numerical simulations show that when the basic reproduction number (R_0) is less than one, the disease free equilibrium is stable and becomes unstable when $R_0 > 1$ giving rise to a stable endemic equilibrium. The importance of vaccination to a susceptible population is highlighted.**

Keywords: **Vaccination, Epidemic model, Basic Reproduction number, Stability, Disease free equilibrium, Endemic equilibrium.**

1. INTRODUCTION

Vaccination models like the one we propose in this paper is a veritable tool in the fight against infectious diseases. A susceptible population timely vaccinated will usually develop immunity against the disease for which the vaccine is developed. In the WHO bulletin, Andre et al [1] acknowledges that only clean water performs better than vaccination in the reduction of the burden of infectious disease in a population. An estimated 20.3 million deaths were prevented by the measles vaccine alone between 2000 and 2015[2].

Modelling the effect of vaccination on the transmission dynamics of infectious diseases in a population can help interpret the trial result and generalize the findings to the long term impact of vaccination on the population at various coverage levels (see [3 - 10]).

In this paper, we have adapted a classical SIR epidemiological model consisting of the infectives (I), the susceptibles (S) and recovered (R) by adding a vaccination compartment (V) to have an SIVR model. We have shown that if $R_0 < 1$ then the disease free equilibrium is locally asymptotically stable and when $R_0 > 1$, then the endemic equilibrium is locally asymptotically stable. Numerical simulations support our analytical calculations and also show that we have global asymptotic stability of the disease free equilibrium for $R_0 < 1$ and the endemic equilibrium for $R_0 > 1$. The paper is organized as follows: The model is described in Section 2. The basic reproduction number and relevant results for the stabilities of the disease free and endemic equilibria could be found in Section 3. We have numerical simulations in 4 and conclusion in Section 5.

2. DERIVATION OF THE MODEL

We consider a deterministic model that incorporates a vaccination compartment to the classical SIR epidemic model. Individuals are assumed to be in one of the following epidemiological states: Susceptibles (at risk of contracting the disease), Infectives (infected and capable of transmitting the disease), Vaccinated (population vaccinated and are immune to the infection) and Recovered (those that have recovered from the infection). All recruitment is into the susceptible class, and occurs at a constant rate β. A susceptible individual has an average ϕI contacts that would be sufficient to

transmit the disease. Thus, the rate at which susceptibles in the population are infected is ϕSI. Susceptible individuals are vaccinated at a constant rate κ and are removed to the vaccination compartment. We present the model as follows:

$$\begin{aligned}\frac{dS(t)}{dt} &= \beta - \mu S(t) - \kappa S(t) - \phi \mathrm{S(t)I(t)} + \sigma \mathrm{V(t)} \\ \frac{dI(t)}{dt} &= \phi \mathrm{S(t)I(t)} - (\mu + \Upsilon) I(t) \\ \frac{dV(t)}{dt} &= \kappa S(t) - (\mu + \sigma) V(t) \\ \frac{dR(t)}{dt} &= \Upsilon \mathrm{I(t)} - \ \mu R(t)\end{aligned} \tag{1}$$

The rate of infection is represented by ϕ, while recovery rate is represented by ϒ. This model has the death rate, μ which represent death rate as a result of natural causes. In developing the model, we have taken into consideration the fact that vaccinated individuals lose the effect of the vaccine at a constant rate σ to become susceptible again. Since this model is for human population, we assume that all its state variables and parameters are nonnegative for all t $\geq$ 0. The region biologically relevant is given by

$$\Omega = \left\{(S, I, V, R) \in \mathcal{R}_+^4 : 0 \leq S + I + V + R \leq \frac{\beta}{\mu}\right\} \tag{2}$$

The total human population is given by N = S + I + V+ R, so that $dN/dt \leq \beta - \mu N$, thus $N \to \beta/\mu$ as $t \to \infty$. The first three equations of system (1) do not depend on the last equation, it suffice to analyse the following system:

$$\begin{aligned}\frac{dS(t)}{dt} &= \beta - \mu S(t) - \kappa S(t) - \phi \mathrm{S(t)I(t)} + \sigma \mathrm{V(t)} \\ \frac{dI(t)}{dt} &= \phi \mathrm{S(t)I(t)} - (\mu + \Upsilon) I(t) \\ \frac{dV(t)}{dt} &= \kappa S(t) - (\mu + \sigma) V(t)\end{aligned} \tag{3}$$

3. STABILITY ANALYSIS

The basic reproduction number for the model is given as

$$R_0 = \frac{\phi\beta(\mu + \sigma)}{\mu(\mu^2 + \mu\Upsilon + \mu\kappa + \mu\sigma + \Upsilon\kappa + \Upsilon\sigma)} \tag{4}$$

The disease-free equilibrium given by $E^0 = (S^0, I^0, V^0)$ is the only equilibrium for $R_0 \leq 1$, where

$$S^0 = \frac{\beta(\mu + \sigma)}{\mu(\mu + \kappa + \sigma)}, \quad I^0 = 0, \qquad V^0 = \frac{\beta\kappa}{\mu(\mu + \kappa + \sigma)}$$

If $R_0 > 1$, then there is also a unique endemic equilibrium given by E*= (S*, I*, V*), where

$$\begin{aligned}S^* &= \frac{\Upsilon + \mu}{\phi} \\ I^* &= -\frac{\mu^3 + \mu^2\Upsilon + \mu^2\kappa + \mu^2\sigma - \mu\phi\beta + \mu\Upsilon\kappa + \mu\Upsilon\sigma - \phi\beta\sigma}{\phi(\mu^2 + \mu\Upsilon + \mu\sigma + \Upsilon\sigma)} \\ V^* &= \frac{\kappa(\Upsilon + \mu)}{\phi(\mu + \sigma)}\end{aligned} \tag{5}$$

3.1 Local Stability of the Disease Free Equilibrium.

The characteristics equation after linearizing (1) about the disease free equilibrium E^0 gives

$$(\lambda + \mu)(\lambda + \mu + \kappa + \sigma)(\mu^2\lambda + \mu\kappa\lambda + \mu\sigma\lambda + \mu^3 + \mu^2\Upsilon + \mu^2\kappa + \mu^2\sigma - \mu\phi\beta + \mu\Upsilon\kappa + \mu\Upsilon\sigma - \phi\beta\sigma) = 0 \tag{6}$$

This gives

$$\lambda_1 = -\mu, \qquad \lambda_2 = -(\mu + \kappa + \sigma), \text{ and } \lambda_3 = \mu\{\mu + \Upsilon\}(\mu^2 + \mu\Upsilon + \mu\kappa + \mu\sigma + \Upsilon\kappa + \Upsilon\sigma)(R_0 - 1)$$

The first two eigenvalues λ_1 and λ_2 are negative and if $R_0 < 1$, λ_3 is also negative giving us the following theorem.

Theorem 1.

The disease-free equilibrium point of the system is :

(i) locally asymptotically stable when $R_0 < 1$,

(ii) marginally stable when $R_0 = 1$ and

(iii) unstable when $R_0 > 1$.

3.2 Local Stability of the Endemic Equilibrium

We analyse the local stability of the endemic equilibrium point in this section. The characteristics equation at the endemic equilibrium point E* gives

$$\begin{aligned}&\mu^3\lambda^2 - \mu^5 - 2\mu^4\Upsilon - \mu^4\kappa - \mu^4\lambda - 2\mu^4\sigma + \mu^3\phi\beta - \mu^3\Upsilon^2 - 2\mu^3\Upsilon\kappa - 2\mu^3\Upsilon\lambda - 4\mu^3\Upsilon\sigma - \mu^3\kappa\lambda - \mu^3\kappa\sigma - \mu^3\lambda\sigma\\ &- \mu^3\sigma^2 + \mu^2\phi\beta\Upsilon + 2\mu^2\phi\beta\lambda + 2\mu^2\phi\beta\sigma - \mu^2\Upsilon^2\kappa - \mu^2\Upsilon^2\lambda - 2\mu^2\Upsilon^2\sigma - 2\mu^2\Upsilon\kappa\lambda - 2\mu^2\Upsilon\kappa\sigma + \mu^2\Upsilon\lambda^2 - 2\mu^2\Upsilon\lambda\sigma\\ &-2\mu^2\Upsilon\sigma^2 + \mu^2\lambda^3 + 2\mu^2\lambda^2\sigma + \mu\phi\beta\Upsilon\lambda + 2\mu\phi\beta\Upsilon\sigma + \mu\phi\beta\lambda^2 + 3\mu\phi\beta\lambda\sigma + \mu\phi\beta\sigma^2 - \mu\Upsilon^2\kappa\lambda - \mu\Upsilon^2\kappa\sigma - \mu\Upsilon^2\lambda\sigma\\ &- \mu\Upsilon^2\sigma^2 + \mu\Upsilon\lambda^3 + 2\mu\Upsilon\lambda^2\sigma + \mu\kappa\lambda^2\sigma + \mu\lambda^3\sigma + \mu\lambda^2\sigma^2 + \phi\beta\Upsilon\lambda\sigma + \phi\beta\Upsilon\sigma^2 + \phi\beta\lambda^2\sigma + \phi\beta\lambda\sigma^2 + \Upsilon\kappa\lambda^2\sigma + \Upsilon\lambda^3\sigma\\ &+\Upsilon\lambda^2\sigma^2 = 0 \qquad (7)\end{aligned}$$

This simplifies to

$$A_1\lambda^3 + A_2\lambda^2 + A_3\lambda + A_4 = 0 \qquad (8)$$

Where

$$\begin{aligned}A_1 &= \mu^2 + \mu\Upsilon + \mu\sigma + \Upsilon\sigma\\ A_2 &= \mu^3 + \mu^2\Upsilon + 2\mu^2\sigma + \mu\phi\beta + 2\mu\Upsilon\sigma + \mu\kappa\sigma + \mu\sigma^2 + \phi\beta\sigma + \Upsilon\kappa\sigma + \Upsilon\sigma^2\\ A_3 &= \mu^2\phi\beta + 2\mu\phi\beta\sigma + \phi\beta\sigma^2 + \mu(\mu + \Upsilon)(\mu^2 + \mu\Upsilon + \mu\kappa + \mu\sigma + \Upsilon\kappa + \Upsilon\sigma)\{R_0 - 1\}\\ A_4 &= \mu(\mu^2 + \mu\Upsilon + \mu\sigma)(\mu^2 + \mu\Upsilon + \mu\kappa + \mu\sigma + \Upsilon\kappa + \Upsilon\sigma)\{R_0 - 1\}\end{aligned}$$

Lemma 2.

$A_2A_3 > A_1A_4$ whenever $R_0 > 1$.

Proof: $$\begin{aligned}A_2A_3 - A_1A_4 &= \mu^5\phi\beta + \mu^4\phi\beta\Upsilon + 4\mu^4\phi\beta\sigma + \mu^3\phi^2\beta^2 + 4\mu^3\phi\beta\Upsilon\sigma + \mu^3\phi\beta\kappa\sigma + 6\mu^3\phi\beta\sigma^2 + 3\mu^2\phi^2\beta^2\sigma\\ &+\mu^2\phi\beta\Upsilon\kappa\sigma + 6\mu^2\phi\beta\Upsilon\sigma^2 + 2\mu^2\phi\beta\kappa\sigma^2 + 4\mu^2\phi\beta\sigma^3 + 3\mu\phi^2\beta^2\sigma^2 + 2\mu\phi\beta\Upsilon\kappa\sigma^2 + 4\mu\phi\beta\Upsilon\sigma^3 + \mu\phi\beta\kappa\sigma^3\\ &+\mu\phi\beta\sigma^4 + \phi^2\beta^2\sigma^3\phi\beta\Upsilon\kappa\sigma^3 + \phi\beta\Upsilon\sigma^4 + \mu(\mu^2\phi\beta + \mu^2\kappa\sigma + \mu\phi\beta\Upsilon + \mu\phi\beta\sigma + 2\mu\Upsilon\kappa\sigma + \phi\beta\Upsilon\sigma + \Upsilon^2\kappa\sigma)\\ &(\mu^2 + \mu\Upsilon + \mu\kappa + \mu\sigma + \Upsilon\kappa + \Upsilon\sigma)\{R_0 - 1\} \qquad (9)\end{aligned}$$

Equation (9) is greater than 0 whenever $R_0 > 1$. Hence $A_2A_3 > A_1A_4$. ■

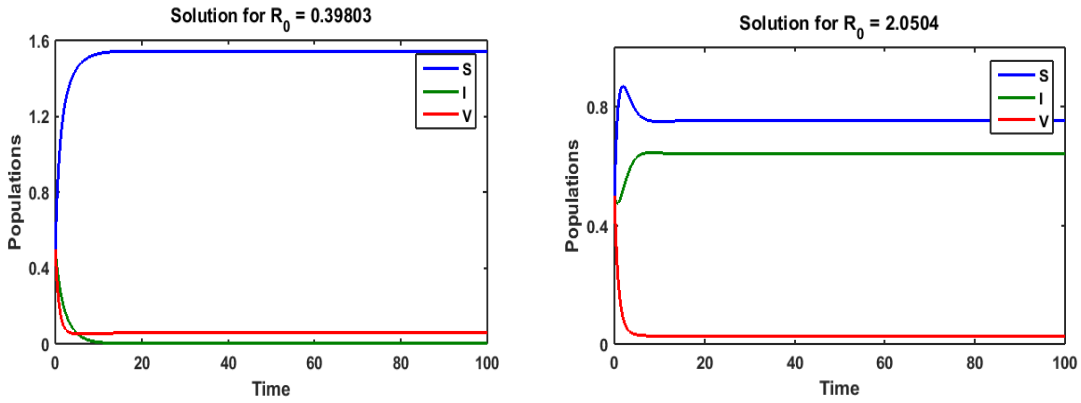
From Lemma 2, (8) satisfy the Routh Hurwitz stability criterion whenever $R_0 > 1$, hence all roots of the characteristic equation (7) have negative real parts. This gives rise to the following theorem.

Theorem 3.

The endemic equilibrium point (E*) of the system is locally asymptotically stable whenever $R_0 > 1$.

4. NUMERICAL SIMULATION

We show numerically the established results in earlier sections about the stability of the disease free and the endemic equilibria of the model as it relates to the basic reproduction number (R_0). The importance of vaccination to a susceptible population is highlighted and the plot of the infectives for different values of the vaccination rate has suggested a minimum vaccination rate and vaccine loss rate to target in a vaccination campaign. We use the ode23 suite in Matlab to simulate system (2) with the parameters as shown below the figures. The parameters are chosen solely for simulation convenience and do not reflect actual collected data.



(a) $R_0 = 0.39803 < 1$, $\phi = 0.165$ (b) $R_0 = 2.0504 > 1$, $\phi = 0.85$

Figure 1: Other parameters are: β = 0.8, μ = 0.5, κ = 0.04, ϒ = 0.14 and σ = 0.6.

In figure 1(a), $R_0 = 0.39803 < 1$, hence the disease free equilibrium becomes stable which shows that the infection dies out of the population. Figure 1(b) shows the stable endemic equilibrium for $R_0 = 2.0504 > 1$, this means that the disease will persist in the population. This simulation agrees with theorems (1) and (3).

In the next figure, we show the effect the vaccination rate (κ) has on the dynamics of system (1) by plotting the vaccination rate against the steady states of the infectives in fig 2(a), and the number of infectives with varying vaccination rate and in fig 2(b).

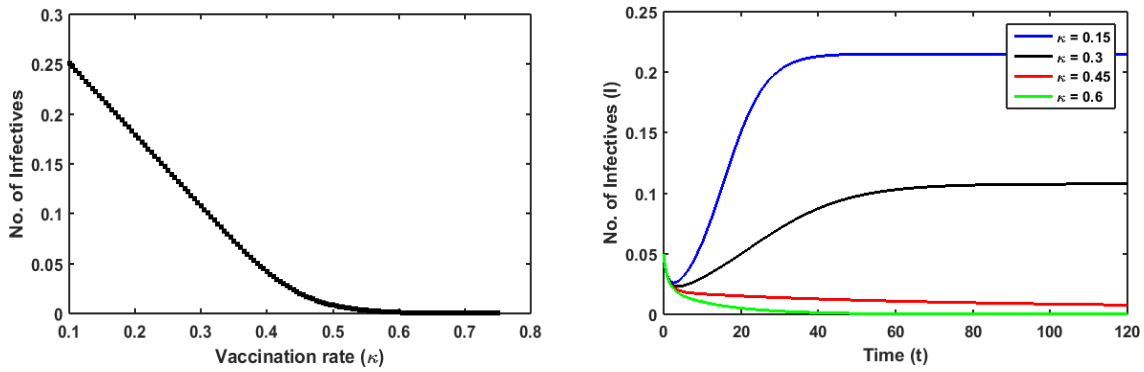


Figure 2: Simulation of the evolution of the infected individuals for different values of vaccination rate *κ*. Other parameters are: β = 0.8, μ = 0.58, ϕ = 0.75, ϒ = 0.15 and σ = 0.5.

5. CONCLUSION

We conclude that the system developed and analysed in this paper give a good mathematical model to study the effect of vaccination in a population and could be used with actual data collected from endemic regions for the purpose of strategic planning and control of infectious diseases. Targeted vaccination on a population could provide an effective tool in the control of an epidemic as could be seen in fig. 2 (a) and (b). The infection was eradicated at the choice of the vaccination rate at a threshold value showing that we need not vaccinate everybody in a given population before controlling an epidemic.

REFERENCES

[1] FE Andre, R Booy, HL Bock, J Clemens, SK Datta, TJ John, BW Lee, S Lolekha, H Peltola, TA Ruff, M Santosham, HJ Schmitt "Vaccination greatly reduces disease, disability, death and inequity worldwide", Bulletin of the World Health Organization, Volume 86, Number 2, February 2008, 81-160

[2] Patel MK, Gacic-Dobo M, Strebel PM, et al. "Progress Toward Regional Measles Elimination — Worldwide, 2000–2015". MMWR Morb Mortal Wkly Rep 2016;65:1228–1233. DOI: http://dx.doi.org/10.15585/mmwr.mm6544a6

[3] C.M. Kribs-Zaleta, J.X. Velasco-Hernández, "A simple vaccination model with multiple endemic states", Math. Biosci. 164 (2000) 183–201.

[4] S.M. Blower, A.R. Mclean, "Prophylactic vaccines, risk behavior change, and the probability of eradicating HIV in San Francisco", Science 265 (1994) 1451.

[5] B. Reade, R. Bowers, M. Begon, R. Gaskell, "A model of disease and vaccination for infection with acute and chronic phases",Journ. Theor. Biol. 190 (1998) 355.

[6] J. MULLER, "Optimal Vaccination Patterns in Age-Structured Populations: Endemic Case", ELSEVIER, Mathematical a Computer Modelling 31 (2000) 149-160

[7] E. C. Yuan, D. L. Alderson, S. Stromberg and J. M. Carlson, "Optimal Vaccination in a Stochastic Epidemic Model of Two Non- Interacting Populations". PLoS ONE 10(2): e0115826. https://doi.org/10.1371/journal (2015)

[8] B. Shulgin, L. Stone and A. Z. Bull, "Pulse vaccination strategy in the SIR epidemic model", Math. Biol. (1998) 60: 1123. doi:10.1006/S0092-8240(98)90005-2

[9] J. Arino, C. Connell McCluskey, and P. van den Driessche, "Global Results for an Epidemic Model with Vaccination that Exhibits Backward Bifurcation", SIAM J. Appl. Math., 64(1), 260–276 (2003).

[10] Fred Brauer "Backward bifurcations in simple vaccination models", ELSEVIER, J. Math. Anal. Appl. 298 (2004) 418–431