American Journal of Engineering Research (AJER) 2016
American Journal of Engineering Research (AJER)
e-ISSN: 2320-0847 p-ISSN : 2320-0936
Volume-5, Issue-2, pp-182-188
www.ajer.org
Research Paper Open Access

Analysis of an Improved SIRS Epidemic Model with Disease Related Death Rate and Emigration Rate

Shivram Sharma[1], V.H. Badshah[1], Vandana Gupta[2]
[1]*School of Studies in Mathematics, Vikram University, Ujjain (M.P.), India*
[2]*Govt. Kalidas Girls' College, Ujjain (M.P.), India*
[1]shivramsharmajnu85@gmail.com,[1]vhbadshah@gmail.com,
[2]drvg1964@gmail.com

Abstract: *In this paper, we consider an SIRS epidemic model with an asymptotically homogeneous transmission function, disease related death rate and emigration rate. We obtain the disease free and endemic equilibrium. We also establish the conditions for the global stability of the equilibriums. An example is also furnished which demonstrates validity of main result.*

Keywords*: SIRS model, Transmission function, Basic reproductive number, disease-free equilibrium, endemic equilibrium, Stability.*
2010 AMS Subject Classification: 34D23; 93A30; 93D20.

I. Introduction

A mathematical model is a description of a system using mathematical concept and language. Mathematical models are used not only in the natural sciences and engineering disciplines but also in the social sciences. The first SIR epidemic model was proposed by Kermack and Mckendrick [23] in the year 1927. The SIRS epidemic model has been studied by many authors (see [1-5], Hethcote [16, 17], Capasso and Serio [9], Mena-Lorca [29]) and the different epidemic models have been proposed and studied in the literature (see Hethcote and Tudar [19], Lie et al. [25, 26], Hethcote et al. [20], Hethcote and Van den Driessche [21], Derrick and Vanden Driessche [12], Berretta and Takeuchi [6, 7], Beretta et al. [8], Ma et al. [27, 28], Ruan and Wang [32],Song and Ma [33], Song et al. [34], D'onofno et al. [13], Xiao and Ruan [35]).

Bilinear and standard incidence rates have been frequently used by many authors [18, 10, 29, 30, 24, 14 and 22]. Disease transmission is a dynamical process driven by the interaction between the susceptible and the infective. The behaviour of the SIRS models are greatly affected by the way in which transmission between infected and the susceptible individuals are modelled. Many models of epidemiology are based on the so called "mass action" assumption for transmission. During the last few decades, such assumptions have faced some questions and consequently a number of realistic transmission functions have become the focus of considerable attention (Capasso and Serio [9], Lie et al. [25, 26], Hethcote et al. [20], Hethcote and Van den Driessche [21], Ruan and Wang [32], Xiao and Ruan [35]). Pathak et al. [31] have considered an SIR epidemic model with an asymptotically homogeneous transmission function.

In this paper we consider an SIRS epidemic model with an asymptotically homogeneous transmission function, disease related death rate and emigration rate. In the next section, we give basic definitions. In the third section, we present the model and derive the disease free equilibrium and the endemic equilibrium. In the fourth section, we prove some theorems for the global stability of the disease free and endemic equilibrium. The fifth section contains an example which demonstrates validity of main result. In the last section, we give conclusion.

II. Preliminaries

Definition 2.1 The incidence in an epidemiological model is the rate at which susceptible become infectious. If the unit time is days, then the incidence is the number of new infection per day.

Definition 2.2 The average number of secondary infections produced by one infected individuals during the mean course of infection (infectious period) in a completely susceptible population is called a basic reproductive number or simply the reproductive number σ .

Definition 2.3 SIRS means the recovered individuals have only temporary immunity after they recovered from infection.

III. The mathematical model

The proposed model is the nonlinear ordinary differential equations:

$$\begin{aligned}
\frac{dX}{dt} &= (A - B) - \frac{\beta XY}{1 + aX + bY} - dX + \delta Z \\
\frac{dY}{dt} &= \frac{\beta XY}{1 + aX + bY} - (\gamma + \alpha + d)Y \qquad (3.1) \\
\frac{dZ}{dt} &= \gamma Y - (\delta + d)Z \\
\frac{dN}{dt} &= (A - B) - dN - \alpha Y
\end{aligned}$$

Where $N(t)$ is the total varying population size as a function of time t, and $X(t), Y(t), Z(t)$ denote the number of individuals who are susceptible, infectious and recovered at time t, respectively and $X(t) + Y(t) + Z(t) = N(t)$, A is the constant immigration rate of the population, B is the emigration rate of the population, d is the natural death rate of the population, β is the transmission coefficient, α is the disease-related death rate constant, γ is the natural recovery rate of the infective individuals, δ is the loss of immunity rate constant, a and b are the parameters which measure the effects of sociological, psychological or other mechanisms. We assume that d, α and δ are nonnegative and that A, B, β, γ and $\delta + d$ are positive.

Where $N = X + Y + Z$. In the absence of disease i.e. $\alpha = 0$ the population size approaches the constant size $\frac{A - B}{d}$. For the asymptotically transmission function the contact number or basic reproduction number is

$$\sigma = \frac{\beta(A - B) - (A - B)a(\gamma + \alpha + d)}{d(\gamma + \alpha + d)}. \qquad (3.2)$$

For the system (3.1) the first octant in XYZ space is positively invariant. Because $\frac{dN}{dt} < 0$ for $N > \frac{A - B}{d}$, all paths in the first octant approach, enter or stay inside the subset $T = \left\{(X, Y, Z) : X + Y + Z \le \frac{A - B}{d}\right\}$. The continuity of the right side of (3.1) and its derivatives implies that unique solutions exits on a maximal time interval. Since solutions approach, enter or stay in T, they are eventually bounded and hence exist for all positive time [11]. We first consider the existence of equilibrium of system (3.1).

For any values of parameter, model (3.1) always has a disease-free equilibrium $P_o = \left(\frac{A - B}{d}, 0, 0\right)$. To find the positive equilibria, set

$$\begin{aligned}
(A - B) - \frac{\beta XY}{1 + aX + bY} - dX + \delta Z &= 0 \\
\frac{\beta XY}{1 + aX + bY} - (\gamma + \alpha + d)Y &= 0 \qquad (3.3) \\
\gamma Y - (\delta + d)Z &= 0 \\
(A - B) - dN - \alpha Y &= 0
\end{aligned}$$

IV. Main results

Theorem 4.1. From the system (3.2) it follows that

(i) if $\sigma \le 1$, then there is no positive equilibrium;

(ii) if $\sigma > 1$, then there is a unique positive equilibrium $P_e = (X_e, Y_e, Z_e)$ of the system (3.1), called the "endemic equilibrium", given by

$$X_e = \frac{(\gamma + \alpha + d)(1 + bY_e)}{\beta - a(\gamma + \alpha + d)}$$

$$Y_e = \frac{(\delta + d)[(A - B)\beta - (\gamma + \alpha + d)\{(A - B)a + d)\}]}{bd(\gamma + \alpha + d)(\delta + d) + [\alpha(\delta + d) + d(\gamma + \alpha + d)][\beta - a(\gamma + \alpha + d)]}$$

$$Z_e = \frac{\gamma Y_e}{\delta + d} \qquad (4.1)$$

$$N_e = \frac{(A - B) - \alpha Y_e}{d}$$

It is clear that the limit set of system (3.1) is on the plane $X + Y + Z = \frac{A - B}{d}$. Thus we focus on the reduced system

$$\frac{dY}{dt} = \frac{d\beta Y}{(d + aA) + (b - a)dY - adZ}\left(\frac{A - B}{d} - Y - Z\right) - (\gamma + \alpha + d)Y \equiv P(Y, Z)$$

$$\frac{dZ}{dt} = \gamma Y - (\delta + d)Z \equiv Q(Y, Z) \qquad (4.2)$$

Theorem 4.2. System (4.2) does not have nontrivial periodic orbits if $(2d + \gamma + \delta + \alpha)(b - a) > a\gamma$.

Proof. Since $Y > 0$ and $Z > 0$. Take a Dulac function

$$D(Y, Z) = \frac{\{d + a(A - B)\} + (b - a)dY - adZ}{d\beta Y}.$$

We have

$$\frac{\partial(DP)}{\partial Y} + \frac{\partial(DQ)}{\partial Z} = -1 - \frac{(\delta + d)\{d + a(A - B)\}}{d\beta Y} - \left[(2d + \gamma + \delta + \alpha)(b - a) - a\gamma\right] < 0$$

if $(2d + \gamma + \delta + \alpha)(b - a) > a\gamma$

In order to study the properties of the disease-free equilibrium P_0 and the endemic equilibrium P_e.

Theorem 4.3. The equilibrium $P_o = \left(\frac{A - B}{d}, 0, 0\right)$ is locally asymptotically stable if $\sigma \le 1$ and P_o is saddle point if $\sigma > 1$.

Proof. The Jacobian of system (3.1) at P_o is

$$J(P_o) = \begin{pmatrix} -d & -\frac{\beta(A - B)}{d + a(A - B)} & \delta \\ 0 & \frac{\beta(A - B)}{d + a(A - B)} - (\gamma + \alpha + d) & 0 \\ 0 & \gamma & -(\delta + d) \end{pmatrix}$$

The characteristic equation is

$$(d+t)(\delta+d+t)\left[\frac{\beta(A-B)}{d+a(A-B)}-(\gamma+\alpha+d)-t\right]=0 \qquad (4.3)$$

The roots of (4.3) are

$$-d,\ -(\delta+d) \text{ and } \frac{\beta(A-B)}{d+a(A-B)}-(\gamma+\alpha+d)$$

The first two roots having negative real parts and third root $\frac{\beta(A-B)}{d+a(A-B)}-(\gamma+\alpha+d)$ will have negative real part if $\sigma \le 1$. Thus all roots of (4.3) have negative real parts so P_o is locally asymptotically stable if $\sigma \le 1$ and the root $\frac{\beta(A-B)}{d+a(A-B)}-(\gamma+\alpha+d)$ will have positive real part if $\sigma > 1$ so P_o is saddle point.

Theorem 4.4. The equilibrium $P_o=\left(\frac{A-B}{d},0,0\right)$ is globally asymptotically stable if $\sigma \le 1$.

Proof. Since the set $T=\left\{(X,Y,Z): X+Y+Z \le \frac{A-B}{d}\right\}$ is attractive and positive invariant.

To prove that all paths in T approach $P_o=\left(\frac{A-B}{d},0,0\right)$ for $\sigma \le 1$, define the Liapunov function $L=Y$ in T with

$$\frac{dL}{dt}=\frac{dY}{dt}=\left[\frac{\beta X}{1+aX+bY}-(\gamma+\alpha+d)\right]Y \le 0. \qquad (4.4)$$

The Lasalle-Liapunov theory [15] implies that all paths in T approach the largest positively invariant subset of the set T where $\frac{dL}{dt}=0$.

Here $\frac{dL}{dt}=0$ only if $Y=0$ or $(X,Y,Z)=P_o$. The positively invariant subset of the plane $Y=0$ is the point P_o so P_o is globally asymptotically stable for $\sigma \le 1$. To study the properties of the endemic equilibrium P_e. Let us define

$$x=\frac{\beta}{\delta+d}Y,\quad y=\frac{\beta}{\delta+d}Z,\quad \tau=(\delta+d)t$$

We obtain

$$\frac{dx}{d\tau}=\frac{px}{1+qx-ry}(K-x-y)-mx,$$
$$\frac{dy}{d\tau}=sx-y, \qquad (4.5)$$

Where

$$p=\frac{d}{d+a(A-B)},\quad q=\frac{(\delta+d)d(b-a)}{\beta\{d+a(A-B)\}},\quad r=\frac{a(\delta+d)d}{\beta\{d+a(A-B)\}},$$
$$K=\frac{(A-B)\beta}{d(\delta+d)},\quad m=\frac{\gamma+\alpha+d}{\delta+d},\quad s=\frac{\gamma}{\delta+d}.$$

For equilibrium point set,

$$\frac{dx}{d\tau} = 0 \text{ and } \frac{dy}{d\tau} = 0$$

We obtain, two equilibrium point $(0,0)$ and (x_e, y_e) where

$$x_e = \frac{Kp - m}{p(1+s) + m(q - rs)}, \quad y_e = sx_e$$

The trivial solution $(0,0)$ of system (4.5) is the disease-free equilibrium P_o of model (3.1) and the unique positive equilibrium (x_e, y_e) of system (4.5) is the endemic equilibrium P_e of model (3.1) if and only if $Kp - m > 0$ and $q - rs > 0$.

Theorem 4.5. Suppose $m - Kp < 0$, then there is a unique endemic equilibrium (x_e, y_e) of model (4.5) which is a stable node.

Proof. The Jacobian of system (4.5) at (x_e, y_e) is

$$J = \begin{pmatrix} \frac{px_e[sx_e(r+q) - (1+Kq)]}{(1+qx_e - rsx_e)^2} & \frac{px_e[(Kq-1) - x_e(r+q)]}{(1+qx_e - rsx_e)^2} \\ s & -1 \end{pmatrix}$$

$$\det J = \frac{px_e[(1+s) + K(q - rs)]}{(1+qx_e - rsx_e)^2}$$

Since $q > rs, \det(J) > 0$ when $m - Kp < 0$ and

$$tr(J) = \frac{[ps(r+q)x_e - p(1+Kq)]x_e - [x_e(rs - q) - 1]^2}{(1+qx_e - rsx_e)^2}$$

The sign of $tr(J)$ is determined by

$S = [ps(r+q)x_e - p(1+Kq)]x_e$. Substituting $x_e = \frac{Kp - m}{p(1+s) + m(q - rs)}$ into S, We have

$$S = \frac{p[-K(p+mq)(q-rs) - (mqs + mq + p + ps)](Kp - m)}{[p(1+s) + m(q-rs)]^2}.$$

Since $q > rs$, $[p(1+s) + m(q-rs)]^2 > 0$ and, $[-K(p+mq)(q-rs) - (mqs + mq + p + ps)] < 0$

hence $S < 0$ if $m - Kp < 0$. However, when $m - Kp < 0$, we have $tr(J) < 0$.

This completes the proof.

Theorem 4.6. The equilibrium $P_e = (X_e, Y_e, Z_e)$ is globally asymptotically stable if $\sigma > 1$.

Proof. The proof can be obtained by theorem 4.5.

V. Example

In this section, we give an example to demonstrate the results obtained in the previous sections.

Example 5.1. We take the parameters of the system as $d = 2.37, a = 3.5, b = 3, A = 6.5, B = 3, \delta = 1.2, \alpha = 0.19, \beta = 10, \gamma = 0.20$. Then $P_O = (1.4768, 0, 0)$ and $\sigma = 0.1819 < 1$. Therefore, by theorem 4.4, P_O is a global asymptotically stable in the first octant.

Now we take the parameter of the system as $d = 0.37, a = 3.5,$

$b = 3,\ A = 6.5,\ B = 3,\ \delta = 1.2,\ \alpha = 0.19,\ \beta = 5,\ \gamma = 0.20.$

Then $P_e = (4.8307, 4.6245, 0.5891)$ and $\sigma = 29.1252 > 1$. Therefore, by theorem 4.6, P_e is a global asymptotically stable in the interior of the first octant.

VI. Conclusion

In this paper, we have considered the rich dynamics SIRS epidemic model with an asymptotically homogeneous transmission function, disease related death rate and emigration rate. We have carried out the global qualitative analysis of a realistic SIRS model. Our main results shows that when $\sigma \leq 1$, the disease-free equilibrium P_O is globally asymptotically stable. When $\sigma > 1$, the endemic equilibrium $P_e = (X_e, Y_e, Z_e)$ exists and is globally asymptotically stable.

References

[1] Anderson, R.M., May, R.M., "Population biology of infectious diseases. I", Nature, 280: 361-367, (1979).

[2] Anderson, R.M., May, R.M., "Population dynamic of micro-parasites and their invertebrate hosts", Phil. Trans. Roy. Soc. London B., 291: 451-524, (1981).

[3] Anderson, R.M., Jackson, H.C., May, R.M., Smith, A.D.M., "Population dynamics of fox rabies in Europe", Nature, 289: 765-777, (1981).

[4] Anderson, R.M., "Transmission dynamics and control of infectious disease agents", In: Anderson R.M., May, R.M. (eds.) Population biology of infectious diseases, New York Heidelberg Berlin, Springer, 149-176, (1982a).

[5] Anderson, R.M., "Directly transmitted viral and bacterial infectious of man", In: Anderson R.M. (eds.) Population dynamics of infectious diseases, London New York: Chapman and Hall, 1-37, (1982b).

[6] Beretta, E., Takeuchi, Y., "Global stability of a SIR epidemic model with time delay", J. Math. Biol., 33: 250-260, (1995).

[7] Beretta, E., Takeuchi, Y., "Convergence results in SIR epidemic model with varying population sizes", Nonlinear Anal., 28: 1909-1921, (1997).

[8] Beretta, E., Hara, T., Ma, W., Takeuchi, Y., "Global asymptotic stability of a SIR epidemic model with distributed time delay", Nonlinear Anal., 47: 4107-4115, (2001).

[9] Capasso, V., Serio, G., "A generalization of the Kermack-McKendrick deterministic epidemic Model", Math. Biosci., 42: 43-61, **(**1978**).**

[10] Chamchod, F. and Britton, N.F., "Analysis of vector bias model on malaria transmission", Bulletin of Mathematical Biology, 73(3): 639-657, (2011).

[11] Coddington, E. A., Levinson, N., "Theory of ordinary differential equation", MaGraw-Hill, New York, (1995).

[12] Derrick, W.R., Van den Driessche, P., "A disease transmission model in nonconstant population", J. Math. Biol., 31: 495-512, (1993).

[13] D'Onofrio, A., Manfredi, P., Salinelli, E., "Bifurcation thresholds in an SIR model with information-dependent vaccination", Mathematical Modelling of Natural Phenomena, 2: 23-38, (2007).

[14] Gabriela, M., Gomes, M., White, L.J. and Medley, G.F., "Reinfection threshold", Journal of Theoretical Biology, 236(1): 111-113, (2005).

[15] Hale, J.K., "Ordinary differential equations", Wiley-Interscience, New York, (1969).

[16] Hethcote, H.W., "Qualitative analysis for communicable disease models", Math. Biosci., 28: 335-356, (1976).

[17] Hethcote, H.W., "Three basic epidemiological models", In: Gross, L., Hallam, T.G., Levin, S.A. (eds.) Applied mathematical ecology, Berlin Heidelberg New York, Springer, 119-144, (1989).

[18] Hethcote, H.W. and Van den Driessche, P., "An SIS epidemic model with variable population size and a delay", Journal of Mathematical Biology, 34(2): 177-194, (1995).

[19] Hethcote, H.W., Tudor, D.W., "Integral equation models for endemic infectious diseases", J. Math. Biology, 9: 37-47, (1980).

[20] Hethcote, H.W., Lewis, M.A., Van den Driessche, P., "An epidemiological model with delay and a nonlinear incidence rate", J. Math. Biology, 27: 49-64, (1989).

[21] Hethcote, H.W., Van den Driessche, P., "Some epidemiological model with nonlinear incidence", J. Math. Biology, 29: 271-287, (1991).

[22] Jiang, Z. and Wei, J., "Stability and Bifurcation Analysis in a delayed SIR model", Chaos solitons and Fractals, 35(3): 609-619, (2008).

[23] Kermack, W.O., McKendrick, A.G., "Contribution to mathematical theory of epidemics", P. Roy. Soc.

Lond. A Mat., 115: 700-721, (1927).
[24] Li, Y.M., Graef, J.R., Wang, L. and Karsai, J., "Global dynamics of a SEIR model with varying total population size", Mathematical Bioscience, 160(2): 191-213, (1999).
[25] Liu, W.M., Hethcote, H.W., Levin, S.A., "Dynamical behaviour of epidemiological models with nonlinear incidence rates", J. Math. Biology, 25: 359-380, (1987).
[26] Liu, W.M., Levin, S.A., Iwasa, Y., "Influence of nonlinear incidence rates upon the behaviour of SIRS epidemiological models", J. Math. Biology, 23: 187-204, (1986).
[27] Ma, W., Song, M., Takeuchi, Y., "Global stability of an SIR epidemic model with time-delay", Appl. Math. Lett., 17: 1141-1145, (2004).
[28] Ma, W., Takeuchi, Y., Hara, T., Beretta, E., "Permanence of an SIR epidemic model with distributed time delays", Tohoku Math. J., 54: 581-591, (2002).
[29] Mena-Lorca, J.M., Hethcote, H.W., "Dynamic models of infectious diseases as regulators of population sizes", J. Math. Biology, 30: 693-716, (1992).
[30] Mishra, B.K. and Saini, D.K., "SEIRS epidemic model with delay for transmission of malicious objects in computer network", Applied Mathematics and Computation, 188(2): 1476-1482, (2007).
[31] Pathak, S., Maiti, A., Samanta, G.P., "Rich dynamics of an SIR epidemic model", Nonlinear Analysis: Modelling and Control, 15(1): 71-81, (2010).
[32] Ruan, S., Wang, W., "Dynamical behaviour of an epidemic model with nonlinear incidence rate", J. Differ. Equations, 188: 135-163, (2003).
[33] Song, M., Ma, W., "Asymptotic properties of a revised SIR epidemic model with density dependent birth rate and tie delay", Dynamic of Continuous, Discrete and Impulsive Systems, 13: 199-208, (2006).
[34] Song, M., Ma, W. Takeuchi, Y., "Permanence of a delayed SIR epidemic model with density dependent birth rate", J. Comput. Appl. Math., 201: 389-394, (2007).
[35] Xiao, D., Ruan, S., "Global analysis of an epidemic model with nonmonotone incidence rate", Math. Biosci. 208: 419-429, (2007).