Simple Model for Respiratory Diseases

Puntani Pongsumpun*

Department of Mathematics, Faculty of Science, King Mongkut's Institute of Technology Ladkrabang, Thailand.

* Corresponding author. Email: kppuntan@kmitl.ac.th

Abstract: Respiratory diseases can easily transmit between people. In this study, we formulate the simple model S-I-R-I (Susceptible-Infectious-Recovered-Infectious) for describing the transmission of this disease. The model is analyzed by using dynamical modeling method. After that, we simulate our equations by using numerical method. The numerical solutions are found to confirm our analytical results. Analysis of parameters are given.

Key words: Dynamical modeling method, model, numerical method, respiratory diseases, simulation.

1. Introduction

Respiratory diseases are caused by several types of viruses such as influenza virus, Para influenza virus, Respiratory syncytial virus etc. Almost cases of respiratory diseases caused by influenza virus [1]. Influenza virus has two types; types A and types B. The emerging infectious disease incidence has increased every year. These diseases are occurred via the respiratory tract. The spread of the disease is rapid and extensive. Emerging diseases have occurred since 1980, as the bird flu in Asia. The outbreak of severe acute respiratory infections (SARS) disease, Ebola, Middle East respiratory syndrome (MERS) caused serious effects on the health system. Most respiratory diseases, ie. SARS and Ebola, there is no vaccine. These diseases has spread rapidly and may infect again. Respiratory Disease Caused by an infection of the respiratory tract. Avian influenza virus has many subtypes but there are only some strains can infect human such as H5N1, H7N3, H7N7, H7N9, and H9N2 [2]. There was one elderly woman from   Jiangxi Province, China, died of pneumonia in December 2013 from the H10N8 strain, the first human was confirmed to be died by that strain [3]. Most avian flu cases are a result of either handling dead infected birds or from contact with infected fluids. It can also be transmitted through contaminated surfaces and droppings. Most birds have only a mild form of the H5N1 strain, once domesticated birds such as chickens or turkeys are infected, it can die because the birds are often in closed contact. Because of low hygiene conditions, there is a large threat of this disease in Asia. This disease can be easily transmitted from birds, human-to-human transmission is more difficult without prolonged contact [4]. Some strains of avian influenza are present in the intestinal tract of large numbers of shore birds and water birds, but these strains are rarely caused infection [5]. SARS is a viral respiratory disease of zoonotic origin caused by the SARS coronavirus (SARS-CoV). The outbreak is occurred between November 2002 and July 2003 in Southern China. There were about 8,096 cases and 774 deaths reported from 37 countries [6]. The most cases from Hong Kong [6] (9.6% fatalityrate) according to the World Health Organization (WHO) [7]. There is no cases of SARS have been reported worldwide since 2004 [8]. In 1968, Rvachev [9] developed the spatial-temporal model by

using SIR model to study the connection of SIR model with the real epidemic situation in Soviet Union. After that, Rvachev *et al.* extended their model by finding the effect of air travel with the transmission of this disease [10]. In 1988, Flahault *et al.* [11] studied and formulated the mathematical model describing the transmission of Influenza in France. After that [12], they studied and constructed mathematical model describing the transmission of influenza in Europe. In 2014, Chowell *et al.* [13], studied the transmission model of Mers by considering the data of Mers during April and October 2013, the basic reproduction number and disease severity.

In this study, we analyze the simple model for describing the transmission of respiratory diseases and numerical results are found to show the behaviors of solutions.

2. Transmission Model

Mathematical model is applied to describe the transmission of the diseases are occurred long time ago. To model the transmission of the disease, we have to know process about the disease and what are its transmission cycles. Respiratory disease can transmit between humanthrough contaminated surfaces and droppings. To construct the mathematical model, we need to define variables and parameters for describing the transmission of this disease. We define the variables as follows:

$S(t)$ is the number of susceptible human ,

$I(t)$ is the number of infectious human,

$R(t)$ is the number of recovered human.
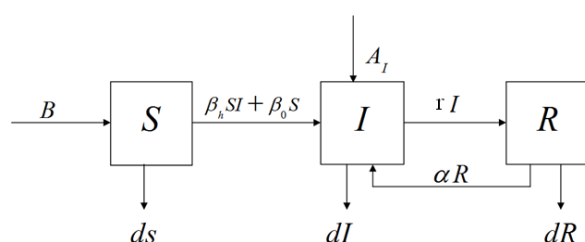
The diagram can be written as

Fig. 1. Diagram of our model equations.

From the above diagram, we can have following equations.

$$S^{'}(t) = B - (\beta_h S(t)I(t) + \beta_o S(t)) - dS(t)$$
$$I^{'}(t) = (\beta_h S(t)I(t) + \beta_o S(t)) + \alpha R(t) + A_I - (r+d)I(t) \qquad (1)$$
$$R^{'}(t) = rI(t) - (\alpha + d)R(t)$$

where *B* is the number of   human population at the beginning time,

β_h is the infection rate of respirator y diseases between human,

β_o is the infection rate of respirator y diseases from the other factors,

r is the recovery rate of cases,

α is the rate at which recovered human become to be infectious human again,

A_i is the initial number of cases,

d is the natural death rate of human.

N is the total human.

2.1. Analytical Results

The steady states can be found from setting (1) to zero, then the steady states are

1) The first steady state (S_1^*, I_1^*, R_1^*)

where

$$S_1^* = \frac{B}{(\beta_0 + d + \beta_h I_1^*)} \tag{2}$$

$$R_1^* = \frac{I_1^* r}{(a + d)} ,$$

and I_1^* is given by

$$I_1^* = \frac{(A_1(A_2\beta_h - A_3d)N - A_3dNr + \sqrt{\begin{array}{c}N^2(4A_1(A_3A_i + B\beta_0)\beta_h(A_1+r)+(A_1A_2\beta_h \\ +A_1A_3d+A_3d_r)^2)\end{array}}}{(2(\alpha\beta_h dN^2 + \beta_h dN(dN+dr)))} \tag{3}$$

where $A_1 = a + d$, $A_2 = A_i + B$, $A_3 = B_0 + d$

2) The second steady state (S_2^*, I_2^*, R_2^*) where

$$S_2^* = \frac{B}{(\beta_0 + d + \beta_h I_2^*)} ,$$

$$R_2^* = \frac{I_2^* r}{(a + d)}$$

and I_2^* is defined by

$$I_2^* = \frac{(A_1(A_2\beta_h - A_3d)N - A_3dNr + \sqrt{\begin{array}{c}N^2(4A_1(A_3A_i + B\beta_0)\beta_h(A_1+r)+(A_1A_2\beta_h \\ +A_1A_3d+A_3d_r)^2)\end{array}}}{(2(\alpha\beta_h dN^2 + \beta_h dN(dN+dr)))} \tag{4}$$

We analyze the stability of the steady states by looking the sign of all eigenvalues. For the first steady state, we found that all eigenvalues have negative signs when $R_0 < 1$.

For $R_0 > 1$, all eigenvalues of the second steady state have negative real parts. R_0 is defined as

$$R_0 = \frac{4A_1(A_3A_i + B\beta_0)\beta_h d(A_1 + r) + (-A_1A_2\beta_h + A_1A_3d + A_3dr)^2}{(-A_1A_2\beta_h + A_1A_3d + A_3d_r)^2} .$$

If all eigenvalues of the steady states have negative real parts, then that steady state will be local stable [14].

2.2. Numerical Results

We simulate our equations by using numerical method. We consider the behaviors of solutions for the different set of parameters as follows:
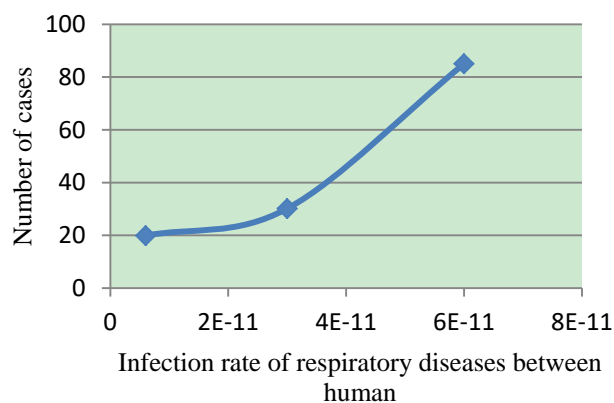

Fig. 2. Number of cases for the different Infection rates of respiratory diseases between human.
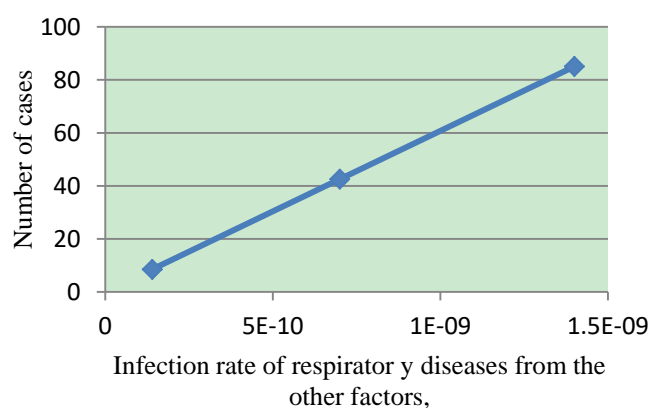

Fig. 3. Number of cases for the different infection rate of respirator y diseases from the other factors.
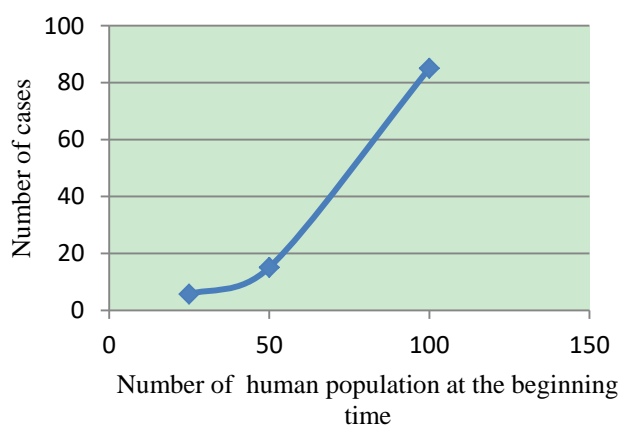

Fig. 4. Number of cases for the different number of human population at the beginning timeไ.
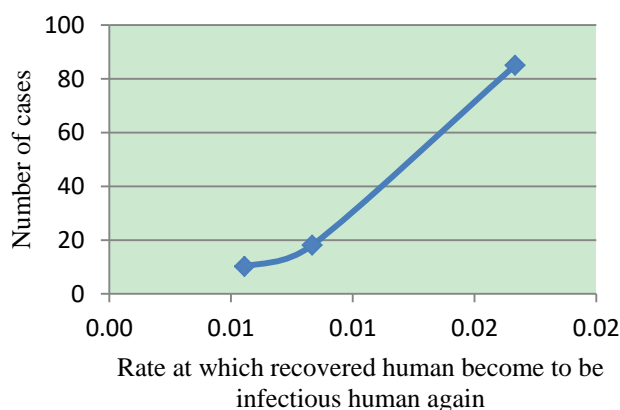
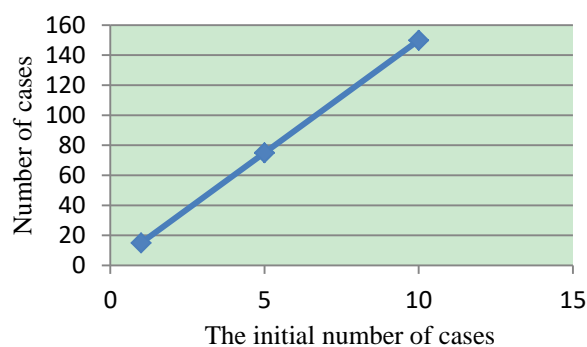Fig. 5. Number of cases for the different rate at which recovered human become to be infectious human again.

Fig. 6. Number of cases for the different initial number of cases.

Table 1. Parameters of Our Model

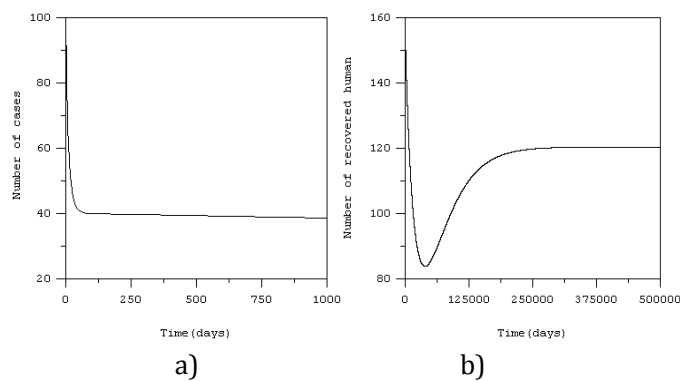| Parameters	Values		
β_h	0.00000000006	0.00000000003	0.000000000006
β_o	0.0000000014	0.0000000007	0.00000000014
B	100	50	25
a	0.02	0.01	0.01
β_h	1	5	10

a)   b)

Fig. 7. Times series solution behaviors of our model. The parameters are B = 100, β_o = 0.0000000014, d = 1/(365*70), β_h = 0.00000000003, α = 1/60; $A_i := 0$; r := 1/15. $R_0 = 1.1.$ a) For respiratory disease cases. b) For the recovered human.

3. Conclusion

In this paper, we study the mathematical models for describing the transmission of respiratory disease. S-I-R-I is used for this study. We analyzed our model by dynamical modeling method. The stability condition is used to be guided for reducing the transmission of this disease. The local stability condition of two steady states is determined by R_0. If $R_0 < 1$, then the first steady will be stable. The second steady state will be stable for $R_0 > 1$. The following figures are the example of numerical results for $R_0 > 1$.

From Fig. 7, we can see that when we use the above parameters, the cases can be reduced and also the recovered human increased until they converge to the second steady state.

We found that the parameters β_h, β_o, B, a and A_i are influenced to the number of cases. From Fig. 2 to Fig. 6, we can see that if the infection rate of respiratory diseases between human, the infection rate of respiratory diseases from the other factors, the number of human population at the beginning time, the rate at which recovered human become to be infectious human again and the initial number of cases are higher, then the number of cases are higher too.

Acknowledgment

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P. Pongsumpun received her bachelor of science in mathematics (second class honors) and the doctor of philosophy in mathematics (international programme) from Mahidol University, Thailand. From 2004 to 2012, she was an as assistant professor of Mathematics. From 2012 till date, she is an associate professor of mathematics, thesis Ph.D. and M.Sc. advisors in King Mongkut's Institute of Technology Ladkrabang, Thailand. Her research interests are mathematical modelling in medical science, differential equations and numerical analysis.