Current Applied Science and Technology Vol. 18 No. 1 Jan.-Apr. 2018

Mers Model of Thai and South Korean Population

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Received: 28 February 2017, Revised: 18 November 2017, Accepted: 14 March 2018

Abstract

Coronavirus (MERS-Cov) caused the occurrence of Corona. First infected case was reported in 2012 during a poultry outbreak in Saudi Arabia. After that, there were the reports of the sporadic outbreaks in all regions. In this study, we considered the transmission cycle between two population groups: Thai and South Korea. Each population group was divided into susceptible, exposed, infected, quarantine and recovered groups. The behaviors of the solutions were obtained using a standard dynamical modeling method. The stability conditions for the disease free equilibrium state and disease endemic equilibrium states were determined. The basic reproductive number R_0 is obtained. When $R_0<1$, the disease-free state was locally asymptotically stable. If $R_0>1$, the endemic equilibrium state was locally asymptotically stable. The numerical solutions were shown for supporting the theoretical results. We found that when we decreased α_1 (the rate of susceptible Thai human changes to become an exposed Thai human and μ_1 (the rate at which South Korean population moved out the country), the number of coronavirus case was decreased and outburst of coronavirus epidemic was shorter.

Keywords: Basic reproductive number, mathematical models, MERS, stability, standard dynamical modeling theorem

1. Introduction

The Ministry of Public Health, Thailand had declared Middle East Respiratory Syndrome or MERS as a dangerous communicable disease. MERS was caused by coronavirus [1]. First infected case of MERS-Cov was reported in Saudi Arabia during a poultry outbreak in 2012 [2, 3]. After that, there were the reports of the sporadic outbreak in all regions. In 2016, an epidemic was recognized as the first time occurrence in Thailand. The first case is a traveler, a male from Oman. On 12 June 2015, South Korean confirmed 126 infectious cases with coronavirus and 10 deaths [4]. On 24 January 2016, Thailand confirmed Middle East respiratory syndrome coronavirus (MERS-Cov) disease in a traveler, the second case in the country in the last seven months [5]. Globally cases of this disease had been reported in some countries. On 16 May 2016, World Health Organization (WHO) confirmed infectious cases with coronavirus (MERS-Cov) of 1,723

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laboratory, including at least 628 deaths from 27 countries [1, 6, 7]. Coronavirus (MERS-Cov) had been infected to human and outbreak in many countries. The corona virus transmitted from camel to human and human to human. The pandemic corona virus can be transmitted to human by camel. Human can be infected by direct contact with animals. Human can be also infected through biological fluid contact, hospital setting, family cluster and closed contact cluster. In human, the virus incubated for 2 to 14 days before symptoms appear. Typical symptoms of corona virus included fever, shortness of breath and cough. Pneumonia was also a common presentation [1]. There were many tourists who travel between Thai and South Korea, thus there were the high risk of infections between Thai and South Korean with coronavirus. The numbers of South Korean tourists travel to Thailand from 2012 to 2016 were shown in Figure 1. Figure 2 shows the numbers of Thai tourists traveled to South Korea. We can see that there were many South Korean traveled to Thailand. Thus, in this study, we formulated the mathematical model of MERS considered the moving of South Korean to Thailand.

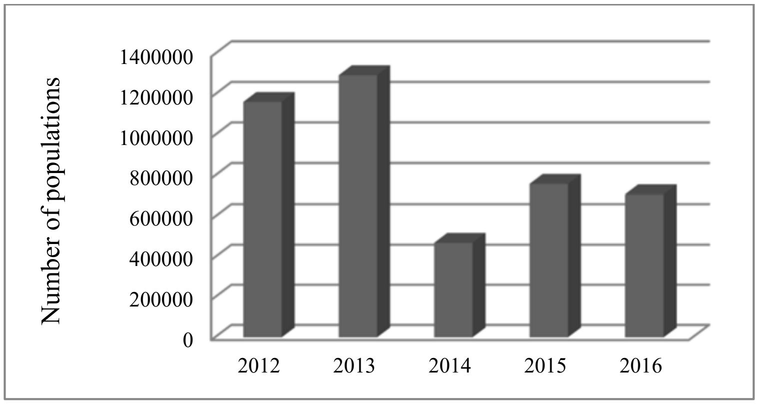
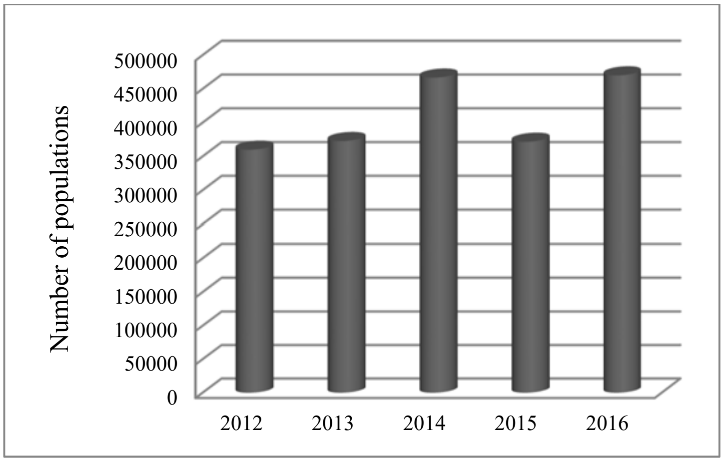


Figure 1. Number of South Korean tourist to Thailand, 2012-2016 [8].



Fiure 2. Number of Thai tourist to South Korea, 2012-2016 [9].

Small *et al.* [10] formulated the mathematical model for describing the transmission of SARS virus and a stochastic small-world network model. Their model studied the behaviors of solutions by using numerical simulations. In 2013, Chowell *et al.* [3] used dynamical transmission model describing the progression of MERS-Cov cases that incorporated community and hospital compartments, and distinguished transmission by zoonotic cases and secondary cases. In 2016, Yong and Owen [11] studied the transmission of MERS-Cov in two areas and formulated SISI model. They used the next generation matrix method to evaluate the basic reproductive number and analyzed the sensitivity of the model. In this paper, we considered the transmission cycle between two population groups: Thai and South Korea. Each population group was divided into susceptible, exposed, infected, quarantine and recovered classes. The standard dynamical modeling method was used for analyzing our model [12]

2. Formulation of the model

The mathematical model of MERS-Cov was formulated by considering the transmission cycle between two population groups (Thai and South Korean human). Each group was divided into susceptible (S_T), exposed (E_T), infected (I_T), quarantine (Q_T) and recovered (R_T) classes. We assumed that there is no Thai human move out the country.

We denoted the variables of our model as follows:
$S_T(t)$ is the number of susceptible Thai human at time t;
$E_T(t)$ is the number of exposed Thai human at time t;
$I_T(t)$ is the number of infected Thai human at time t;
$Q_T(t)$ is the number of quarantine Thai human at time t;
$R_T(t)$ is the number of recovered Thai human at time t;
$S_K(t)$ is the number of susceptible South Korean human at time t;
$E_K(t)$ is the number of exposed South Korean human at time t;
$I_K(t)$ is the number of infected South Korean human at time t;
$Q_K(t)$ is the number of quarantine South Korean human at time t;
$R_K(t)$ is the number of recovered South Korean human at time t;
The diagram for the transmission of this disease can be described as shown in Figure 3:

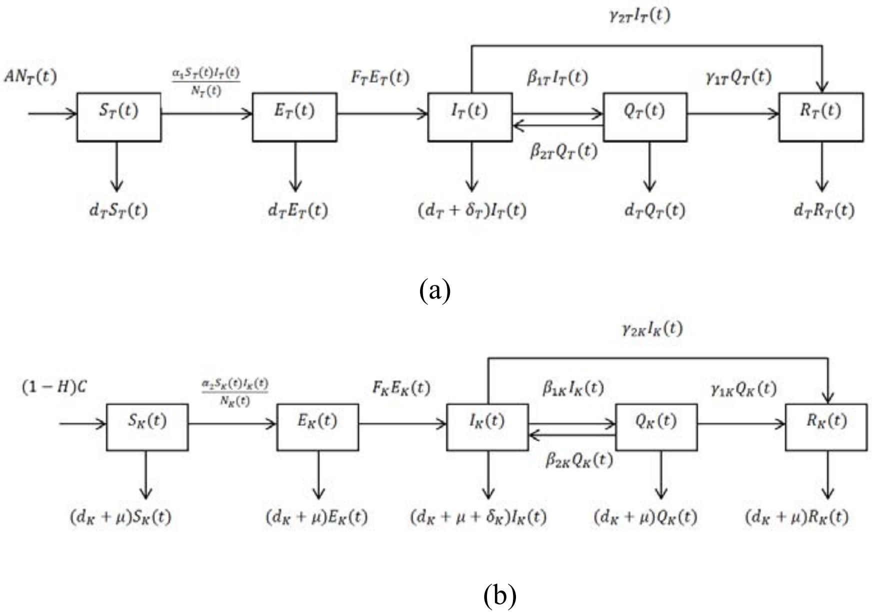


Figure 3. Flow chart of the model (a) for Thai human population (b) for South Korean human population

Rate of change for the number in each class was equivalent to the number entering minus the number leaving. The dynamical equations were as follows:
The number of susceptible Thai human population was increased by new recruitment, but it was reduced through natural death and infection.

$$\frac{dS_T(t)}{dt} = AN_T(t) - \frac{\alpha_1 S_T(t) I_T(t)}{N_T(t)} - d_T S_T(t) \tag{1}$$

The exposed Thai human population was increased by the infection of susceptible humans whereas their reductions were caused by infection and natural death.

$$\frac{dE_T(t)}{dt} = \frac{\alpha_1 S_T(t) I_T(t)}{N_T(t)} - (F_T + d_T) E_T(t) \tag{2}$$

The infected Thai human population was increased by the infection of exposed and quarantine human. Their reductions though quarantine, recovery from the disease, natural death and death due to MERS-Cov. The dynamical equation of infected Thai human population was

$$\frac{dI_T(t)}{dt} = F_T E_T(t) + \beta_{2T} Q_T(t) - (\beta_{1T} + \gamma_{2T} + d_T + \delta_T) I_T(t) \tag{3}$$

The quarantine Thai human population was increased by the infection of infected human but they diminished by infection, recovery from the disease and natural death. The dynamical equation of quarantine Thai human population was

$$\frac{dQ_T(t)}{dt} = \beta_{1T} I_T(t) - (\beta_{2T} + \gamma_{1T} + d_T) Q_T(t) \tag{4}$$

The recovered Thai human population was increased by the recovering of infected human and quarantine, but their reduction through natural death. The dynamical equation of recovered human population was

$$\frac{dR_T(t)}{dt} = \gamma_{1T} Q_T(t) + \gamma_{2T} I_T(t) - d_T R_T(t) \tag{5}$$

The susceptible South Korean human population was increased by new recruitment. Their reductions through natural death, they moved out the country and they were infected. The dynamical equation of susceptible South Korean human population was

$$\frac{dS_K(t)}{dt} = (1-H)C - \frac{\alpha_2 S_K(t) I_K(t)}{N_K(t)} - (d_K + \mu) S_K(t) \tag{6}$$

The exposed South Korean human population was increased by the infection of susceptible humans whereas reduction is caused by natural death, South Korea move out the country and infection. The dynamical equation of exposed South Korean human population was

$$\frac{dE_K(t)}{dt} = \frac{\alpha_2 S_K(t) I_K(t)}{N_K(t)} - (F_K + d_K + \mu) E_K(t) \tag{7}$$

The infected South Korean human population was increased by the infection of exposed and quarantine human and their reduction though quarantine, recovering from the disease, natural death South Korea, move out the country and death due to MERS-Cov. The dynamical equation of infected South Korean human population was shown as

$$\frac{dI_K(t)}{dt} = F_K E_K(t) + \beta_{2K} Q_K(t) - (\gamma_{2K} + \beta_{1K} + d_K + \mu + \delta_K) I_K(t) \tag{8}$$

The quarantine South Korean human population was increased by the infected human who become quarantine but diminished by infection, recovery from the disease, move out the country and natural death. The dynamical equation of quarantine South Korean human was

$$\frac{dQ_K(t)}{dt} = \beta_{1K} I_K(t) - (\gamma_{1K} + \beta_{2K} + d_K + \mu) Q_K(t) \tag{9}$$

The recovered human was increased by the recovery of infected and quarantine human, but their reduction through natural death and South Korean move out the country. The dynamical equation of recovered South Korean human was shown as

$$\frac{dR_K(t)}{dt} = \gamma_{2K} I_K(t) + \gamma_{1K} Q_K(t) - (d_K + \mu) R_K(t) \tag{10}$$

The total number of Thai human populations was the sum of equations (1)-(5)

$$N_T(t) = S_T(t) + E_T(t) + I_T(t) + Q_T(t) + R_T(t) \tag{11}$$

The number of South Korean human population was the sum of equations (6)-(10)

$$N_K(t) = S_K(t) + E_K(t) + I_K(t) + Q_K(t) + R_K(t) \tag{12}$$

Definition of our parameters in our dynamical equations:

Parameters	**Definition**
A	Birth rate of Thai human population
α_1	Rate at which susceptible Thai human changed to become an exposed Thai human
F_T	Rate at which exposed Thai human changed to become an infected Thai human
β_{1T}	Rate at which infected Thai human changed to become quarantine Thai human
β_{2T}	Rate at which quarantine Thai human changed to become infected Thai human
γ_{1T}	Rate at which quarantine Thai human changed to become recovered Thai human
γ_{2T}	Rate at which infected Thai human changed to become recovered Thai human
d_T	Natural death rate of Thai human
δ_T	Death rate due to MERS-Cov of Thai human
$N_T(t)$	Total Thai human population
H	Percentage of South Korea human who were infectious when they enter into Thailand
C	Recruitment rate of South Korean human
α_2	Rate at which susceptible South Korean human changed to become an exposed Korean human
F_K	Rate at which exposed South Korean human changed to become an infected Korean human
β_{1K}	Rate at which infected South Korean human changed to become quarantine Korean human
β_{2K}	Rate at which quarantine South Korean human changed to become an infected Korean human
γ_{1K}	Rate at which quarantine South Korean human changed to become recovered Korean human
γ_{2K}	Rate at which infected South Korean human changed to become recovered Korean human
d_K	Natural death rate of South Korean human
δ_K	Death rate due to MERS-COV of South Korea
μ	Rate at which South Korea move out the country
$N_K(t)$	Total South Korean human population

We can have the following equations:

$$\frac{dN_T(t)}{dt} = BN_T(t) - \left(S_T(t) + E_T(t) + I_T(t) + Q_T(t) + R_T(t)\right)d_T - \delta_T I_T(t)$$

$$\frac{dN_T(t)}{dt} = BN_T(t) - d_T N_T(t) - \delta_T I_T(t) \tag{13}$$

with the assumption $B = d_T$, then we had

$$\frac{dN_T(t)}{dt} = -\delta_T I_T(t) \tag{14}$$

We normalized Thai population class of our dynamical equations (1)-(5) by letting

$$s_T(t) = \frac{S_T(t)}{N_T(t)}, e_T(t) = \frac{E_T(t)}{N_T(t)}, i_T(t) = \frac{I_T(t)}{N_T(t)}, q_T(t) = \frac{Q_T(t)}{N_T(t)}, r_T(t) = \frac{R_T(t)}{N_T(t)}.$$

Taking the normalized population

$$x_T(t) = \frac{X_T(t)}{N_T(t)},$$

We considered

$$\frac{d}{dt}x_T(t) = \frac{d}{dt}\frac{X_T(t)}{N_T(t)}$$

$$= \frac{1}{N_T(t)}\frac{d}{dt}X_T(t) - x_T(t)\frac{1}{N_T(t)}\frac{d}{dt}N_T(t)$$

$$= \frac{1}{N_T(t)}\frac{d}{dt}X_T(t) - x_T(t)\frac{1}{N_T(t)}(-\delta_T I_T(t))$$

$$= \frac{1}{N_T(t)}\frac{d}{dt}X_T(t) - x_T(t)\frac{1}{N_T(t)}(-\delta_T i_T(t) N_T(t)$$

$$\frac{d}{dt}x_T(t) = \frac{1}{N_T(t)}\frac{d}{dt}X_T(t) + \delta_T x_T(t) i_T(t) \tag{15}$$

with the above equations, the dynamical equation of normalized Thai populations were as follows:

$$\frac{ds_T(t)}{dt} = A - \alpha_1 s_T(t) i_T(t) - d_T s_T(t) + \delta_T s_T(t) i_T(t) \tag{16}$$

$$\frac{de_T(t)}{dt} = \alpha_1 s_T(t) i_T(t) - (F_T + d_T) e_T(t) + \delta_T e_T(t) i_T(t) \tag{17}$$

$$\frac{di_T(t)}{dt} = F_T e_T(t) + \beta_{2T} q_T(t) - (\beta_{1T} + \gamma_{2T} + d_T + \delta_T) i_T(t) + \delta_T i_T(t) i_T(t) \tag{18}$$

$$\frac{dq_T(t)}{dt} = \beta_{1T} i_T(t) - (\beta_{2T} + \gamma_{1T} + d_T) q_T(t) + \delta_T q_T(t) i_T(t) \tag{19}$$

$$\frac{dr_T(t)}{dt} = \gamma_{1T} q_T(t) + \gamma_{2T} i_T(t) - d_T r_T(t) + \delta_T r_T(t) i_T(t). \tag{20}$$

The normalized Korean populations were found by substituting

$s_K(t) = \frac{S_K(t)}{N_K(t)}, e_K(t) = \frac{E_K(t)}{N_K(t)}, i_K(t) = \frac{I_K(t)}{N_K(t)}, q_K(t) = \frac{Q_K(t)}{N_K(t)}, r_K(t) = \frac{R_K(t)}{N_K(t)}$ to our dynamical equations.

We supposed that the total Korean population has constant size. This means that the rates of change for Korean population of equations (6)-(10) equal to zero or $\frac{dN_K}{dt} = 0$.

Then we obtained the relations: $N_K = \frac{C}{d_K + \mu}$ with the condition

$$s_K(t) + e_K(t) + i_K(t) + q_K(t) + r_K(t) = 1.$$

With the above equation, the dynamical equations of the normalized population were given by

$$\frac{ds_K(t)}{dt}=(1-H)(d_K+\mu)-\alpha_2 s_K(t)i_K(t)-(d_K+\mu)s_K(t) \tag{21}$$

$$\frac{de_K(t)}{dt}=\alpha_2 s_K(t)i_K(t)-(F_K+d_K+\mu)e_K(t) \tag{22}$$

$$\frac{di_K(t)}{dt}=F_K e_K(t)+\beta_{2K}q_K(t)-(\gamma_{2K}+\beta_{1K}+d_K+\mu+\delta_k)i_K(t) \tag{23}$$

$$\frac{dq_K(t)}{dt}=\beta_{1K}i_K(t)-(\gamma_{1K}+\beta_{2K}+d_K+\mu)q_K(t) \tag{24}$$

3. Analytical Solutions

3.1 Equilibrium Points:

To find the equilibrium points, we set the right hand side of equations (16)-(24) equal to zero. We got two equilibrium states, the disease free steady state $E_0=(1,0,0,0,0,1,0,0,0)$ and the endemic steady state $E_1=(s_T^*,e_T^*,i_T^*,q_T^*,r_T^*,s_K^*,e_K^*,i_K^*,q_K^*)$

$$s_T^*=\frac{A}{d_T+i_T^*(\alpha_1-\delta_T)} \tag{25}$$

$$e_T^*=\frac{A\alpha_1 i_T^*}{(d_T+F_T-\delta_T i_T^*)(d_T+i_T^*(\alpha_1-\delta_T))} \tag{26}$$

$$q_T^*=\frac{\beta_{1T}i_T^*}{d_T+\beta_{2T}+\gamma_{1T}-\delta_T i_T^*} \tag{27}$$

$$r_T^*=\frac{i_T^*\left(\gamma_{2T}+\dfrac{\beta_{1T}\gamma_{1T}}{d_T+\beta_{2T}+\gamma_{1T}-\delta_T i_T^*}\right)}{d_T-\delta_T i_T^*} \tag{28}$$

where i_T^* is the solution of the following equation:

$$F_T e_T^*+\beta_{2T}q_T^*-(\beta_{1T}+\gamma_{2T}+d_T+\delta_T)i_T^*+\delta_T i_T^*=0 \tag{29}$$

$$s_K^*=-\frac{(-1+H)(d_K+\mu)}{d_K+\alpha_2 i_K^*+\mu} \tag{30}$$

$$e_K^*=-\frac{i_K^*\alpha_2(-1+H)(d_K+\mu)}{(d_K+F_K+\mu)(d_K+\alpha_2 i_K^*+\mu)}$$

(31)

$$q_K^*=\frac{\beta_{1K}i_K^*}{d_K+\beta_{2K}+\gamma_{1K}+\mu} \tag{32}$$

$$i_K^*=\frac{Z_1}{Z_2} \tag{33}$$

where

$$\begin{aligned}Z_1=-((d_K+\mu)(d_K{}^3+d_K{}^2(F_K+\beta_{1K}+\beta_{2K}+\gamma_{1K}+\gamma_{2K}+\delta_K+3\mu)+\mu(\beta_{1K}(\gamma_{1K}+\mu)+(\beta_{2K}+\gamma_{1K}+\mu)\\ (\gamma_{2K}+\delta_K+\mu))+F_K(\beta_{1K}(\gamma_{1K}+\mu)+\alpha_2(-1+H)(\beta_{2K}+\gamma_{1K}+\mu)+(\beta_{2K}+\gamma_{1K}+\mu)(\gamma_{2K}+\delta_K+\mu))\\ +d_K(\beta_{2K}(\gamma_{2K}+\delta_K)+\gamma_{1K}(\beta_{1K}+\gamma_{2K}+\delta_K)+2(\beta_{1K}+\beta_{2K}+\gamma_{1K}+\gamma_{2K}+\delta_K)\mu+3\mu^2+F_K((-1+P)\alpha_2\\ +\beta_{1K}+\beta_{2K}+\gamma_{1K}+\gamma_{2K}+\delta_K+2\mu))))\end{aligned}$$

$$Z_2 = (\alpha_2(d_K + F_K + \mu)(d_K{}^2 + \beta_{1K}(\gamma_{1K} + \mu) + (\beta_{2K} + \gamma_{1K} + \mu)(\gamma_{2K} + \delta_K + \mu) + d_K(\beta_{1K} + \beta_{2K} + \gamma_{1K} + \gamma_{2K} + \delta_K + 2\mu)))$$

3.2 Local asymptotical stability

The local asymptotical stability of each steady state was determined from the Jacobian matrix. The eigenvalues (λ) were solutions of the characteristic equations. If all eigenvalues had negative real parts, then the steady state were local asymptotical stability [13].

$$\left|J_{E_i} - \lambda I_9\right| = 0 \quad ,i = 0,1$$

where I_9 was the identity matrix dimension 9×9 .

J_{E_i} was the Jacobian matrix at the equilibrium point E_i for $i = 0,1$.

3.2.1 The disease free steady state E_0, The Jacobian matrix was given by

$$J_{E_0} = \begin{bmatrix}
-d_T - (\alpha_1 - \delta_T)i_T^* & 0 & -(\alpha_1 - \delta_T)s_T^* & 0 & 0 & 0 & 0 & 0 & 0 \\
\alpha_1 i_T^* & -d_T - F_T + \delta_T i_T^* & \alpha_1 i_T^* + \delta_T e_T^* & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & F_T & -d_T - \beta_{1T} - \gamma_{2T} - \delta_T + 2\delta_T i_T^* & \beta_{2T} & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \beta_{1T} + \delta_T q_T^* & -d_T - \beta_{2T} - \gamma_{1T} + \delta_T i_T^* & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \gamma_{2T} + \delta_T r_T^* & \gamma_{1T} & -d_T + \delta_T i_T^* & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & -d_k - \alpha_2 i_K^* - \mu & 0 & -\alpha_2 s_K^* & 0 \\
0 & 0 & 0 & 0 & 0 & \alpha_2 i_K^* & -d_k - F_K - \mu & \alpha_2 s_K^* & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & F_K & -d_k - \beta_{1K} - \gamma_{2K} - \delta_K - \mu & \beta_{2K} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & \beta_{1K} & -d_k - \beta_{2K} - \gamma_{1K} - \mu
\end{bmatrix}$$

$$(-d_T - \lambda)^2(-\beta_{1K}\beta_{2K}(-W - \lambda)(-\beta_{1T}(-B_1\beta_{2T} - \beta 2T\lambda) + (-V - \lambda)(B_1G - F_T\alpha_1 + B_1\lambda + G\lambda + \lambda^2)) + (-Z - \lambda) (-F_K\alpha_2(-\beta_{1T}(-B_1\beta_{2T} - \beta_{2T}\lambda) + (-V - \lambda)(B_1G - F_T\alpha_1 + B_1\lambda + G\lambda + \lambda^2)) + (-W - \lambda)(-Y - \lambda)(-\beta_{1T}(-B_1\beta_{2T} -\beta_{2T}\lambda) + (-V - \lambda)(B_1G - F_T\alpha_1 + B_1\lambda + G\lambda + \lambda^2))))(-d_K - \lambda - \mu) = 0,$$

where

$B_1 = d_T + F_T$

$G = d_T + \beta_{1T} + \gamma_{2T} + \delta_T$

$V = d_T + \beta_{2T} + \gamma_{1T}$

$W = d_K + F_K + \mu$

$Y = d_K + \beta_{1K} + \gamma_{2K} + \delta_K + \mu$

$Z = d_K + \beta_{2K} + \gamma_{1K} + \mu.$

From evaluating all eigenvalues, the real parts of all eigenvalues had negative signs. We used Routh-Hurwitz criteria when $R_0 < 1$.

$$R_0 = \max\{\frac{D_{T1}}{D_{T2}}, \frac{D_{T3}}{D_{T4}}, \frac{D_{T5}}{D_{T6}}, \frac{D_{T7}}{D_{T8}}, \frac{D_{T9}}{D_{T10}}\},$$

where

$D_{T1} = F_T\alpha_1 + F_K\alpha_2 + \beta_{1K}\beta_{2K} + \beta_{1T}\beta_{2T}$

$D_{T2} = VW + VY + WY + (V + W + Y)Z + G(V + W + Y + Z) + B_1(G + V + W + Y + Z)$

$D_{T3} = F_T\alpha_1(V + W + Y + Z) + F_K\alpha_2(V + Z) + \beta_{1K}\beta_{2K}(V + W) + (B_1 + G)(F_K\alpha_2 + \beta_{1K}\beta_{2K}) + B_1\beta_{1T}\beta_{2T} + (W + Y + Z)\beta_{1T}\beta_{2T}$

$D_{T4} = GVW + GVY + GWY + VWY + (WY + V(W + Y) + G(V + W + Y))Z + B_1(WY + (W + Y)Z + V(W + Y + Z) + G(V + W + Y + Z))$

$D_{T5} = F_T(WY + (W + Y)Z + V(W + Y + Z))\alpha_1 + F_K\alpha_2(GV + GZ + VZ) + \beta_{1K}\beta_{2K}(GV + GW + VW) + (YZ + W(Y + Z))\beta_{1T}\beta_{2T} + B_1(F_K\alpha_2(G + V + Z) + (G + V + W)\beta_{1K}\beta_{2K} + (W + Y + Z)\beta_{1T}\beta_{2T})$

$D_{T6} = VWYZ + G(VWY + WYZ + V(W + Y)Z) + B1(VWY + WYZ + V(W + Y)Z + G(WY + (W + Y)Z + V(W + Y + Z))) + (F_K\alpha_2 + \beta_{1K}\beta_{2K})(F_T\alpha_1 + \beta_{1T}\beta_{2T})$

$D_{T7} = F_T\alpha_1(VWY + WYZ + V(W + Y)Z) + F_K\alpha_2 GVZ + \beta_{1K}\beta_{2K}GVW + \beta_{1T}\beta_{2T}WYZ\beta_{1T}\beta_{2T} + B_1(F_K\alpha_2(GV + (G + V)Z) + (GV + (G + V)W)\beta_{1K}\beta_{2K} + (WY + (W + Y)Z)\beta_{1T}\beta_{2T})$

$$D_{T8} = GVWYZ + F_T\alpha_1(F_K\alpha_2(V+Z)+(V+W)\beta_{1K}\beta_{2K}) + \beta_{1T}\beta_{2T}(F_K\alpha_2 Z + W\beta_{1K}\beta_{2K}) + B_1(VWYZ + G(VWY + WYZ + V(W+Y)Z) + F_K\alpha_2\beta_{1T}\beta_{2T} + \beta_{1K}\beta_{1T}\beta_{2K}\beta_{2T})$$

$$D_{T9} = \alpha_1 F_T VWYZ + B_1(F_K\alpha_2 GVZ + \beta_{1K}\beta_{2K}GVW + \beta_{1T}\beta_{2T}WYZ)$$

$$D_{T10} = \alpha_1 F_T V(F_K\alpha_2 Z + \beta_{1K}\beta_{2K}W) + B_1(GVWYZ + \beta_{1T}\beta_{2T}(F_K\alpha_2 Z + \beta_{1K}\beta_{2K}W)).$$

3.2.2 For the endemic steady state E_1, the characteristic equation was given by

$$(-d_T + \delta_T i_T^* - \lambda)(-\beta_{2T}(\beta_{1T} + \delta_T q_T^*)(d_T + (\alpha_1 - \delta_T)i_T^* + \lambda)(d_T + F_T - \delta_T i_T^* + \lambda) + (-d_T - \beta_{2T} - \gamma_{1T} + \delta_T i_T^* - \lambda)$$
$$(-(d_T + (\alpha_1 - \delta_T)i_T^* + \lambda)(d_T + \beta_{1T} + \gamma_{2T} + \delta_T - 2\delta_T i_T^* + \lambda)(d_T + F_T - \delta_T i_T^* + \lambda) + F_T(d_T(\alpha_1 s_T^* + \delta_T e_T^*) + \alpha_1\lambda s_T^*$$
$$+\delta_T e_T^*(\alpha_1 i_T^* - \delta_T i_T^* + \lambda))))(-\beta_{1K}\beta_{2K}(d_K + F_K + \lambda + \mu)(d_K + \alpha_2 i_K^* + \lambda + \mu) + (-d_K - \beta_{2K} - \gamma_{1K} - \lambda - \mu)$$
$$(F_K\alpha_2 s_K^*(d_K + \lambda + \mu) - (d_K + F_K + \lambda + \mu)(d_K + \alpha_2 i_K^* + \lambda + \mu)(d_K + \beta_{1K} + \gamma_{2K} + \delta_K + \lambda + \mu))) = 0,$$

where $s_T^*, e_T^*, i_T^*, q_T^*, r_T^*, s_K^*, e_K^*, i_K^*$ and q_K^* were defined in (25)-(33). From evaluation, all eigenvalues had negative real parts for $R_0 > 1$, where

$$R_0 = \max\{\frac{D_{T1}}{D_{T2}}, \frac{D_{T3}}{D_{T4}}, \frac{D_{T5}}{D_{T6}}, \frac{D_{T7}}{D_{T8}}, \frac{D_{T9}}{D_{T10}}\}.$$

3.3 Numerical Solutions

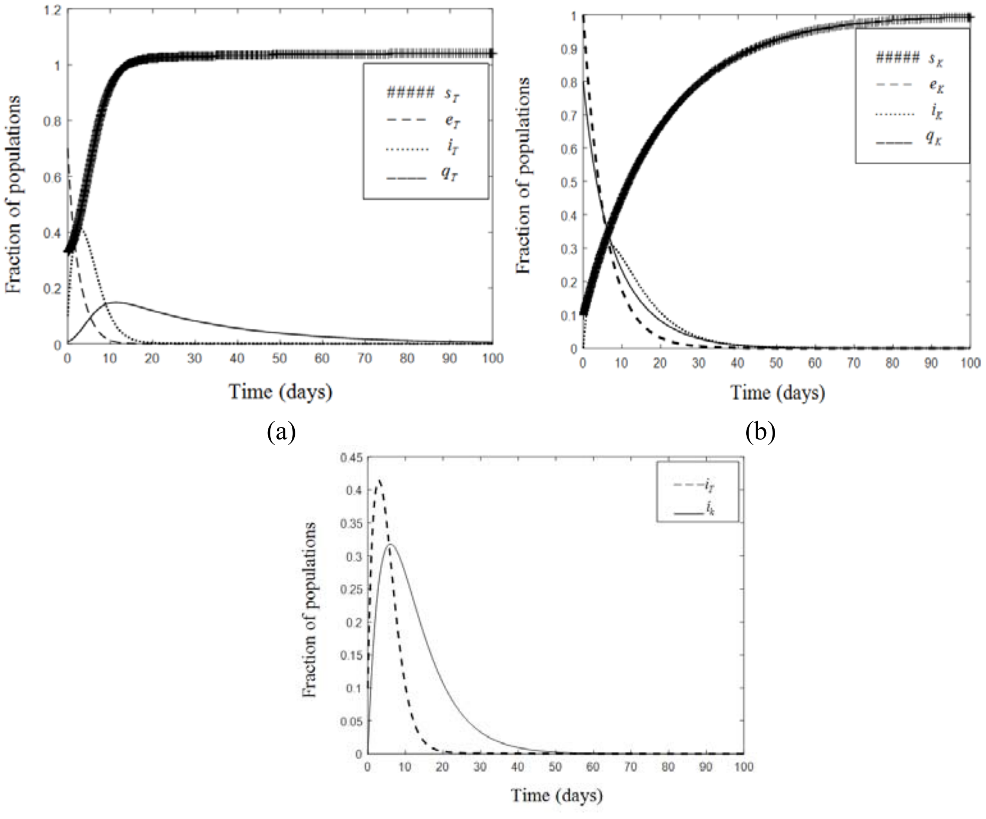
In this paper, we simulated the numerical solutions to show the behaviors of population. The values of the parameters used in this study were $d_T = d_K = 1/(75\times365)$ correspond to the life cycle 75 years of Thai human and South Korean human. $F_T = 1/2$ satisfied to the 2 days of infected human. $\beta_{1T} = \beta_{1K} = 1/30$ corresponded to the 30 days of quarantine for Thai human and South Korean human. $\gamma_{1T} = \gamma_{2T} = \gamma_{1K} = 1/30$ corresponded to the average recovered time of 30 days in infectious quarantine Thai human and quarantine South Korean human. $F_K = 1/8$ satisfied to the average incubation 8 days for South Korea and $\gamma_{2K} = 1/14$ satisfies to the average recovered time of 14 days for infectious person. $\alpha_1 = 1/2.5$ satisfied to the average exposed time of 2.5 days for susceptible person. $\alpha_2 = 1/400$ corresponded to the 400 days of exposed for Thai human. $\delta_T = 1/2.7$ corresponded to the average death rate due to MERS-Cov 2.7 days of Thai human. $\delta_K = 1/20$ corresponded to the average death rate due to MERS-Cov 20 days of South Korean human. $\mu = 1/20$ was the rate at which South Korean move out the country.

4. Discussion

We analyzed the model of MERS-Cov disease between Thai and South Korea when there was the traveling of South Korean population to Thailand. We considered the effective contact rate of Thai and South Korean populations. The moving rate of South Korean to Thailand was considered. The results were found by using standard dynamical modeling analysis. The basic reproductive number was defined in the form of R_0 and it was given by.

$$R_0 = \max\{\frac{D_{T1}}{D_{T2}}, \frac{D_{T3}}{D_{T4}}, \frac{D_{T5}}{D_{T6}}, \frac{D_{T7}}{D_{T8}}, \frac{D_{T9}}{D_{T10}}\}$$

Figure 4 shows the numerical solutions of susceptible Thai population, exposed Thai population, infections Thai population, quarantine Thai population, susceptible South Korean population, exposed South Korean population, infections South Korean population and quarantine South Korean population. We can see that the disease free steady state of the eight populations equal to 1,0,0,0,1,0,0 and 0, respectively. Figure 5 shows the numerical solutions of susceptible Thai population, exposed Thai population, infections Thai population, quarantine Thai population, susceptible South Korean population, exposed South Korean population, infections South Korean population and quarantine South Korean population. We can see that the endemic steady state of the eight populations equal to 0.0769, 0.0216, 0.0092, 0.0243, 0.4855, 0.2198, 0.1273 and 0.0241, respectively. From Figure 6 to Figure 7, we simulated the different values of parameters to see the factors effect to the transmission of this disease. From our solutions, we can see that while a susceptible Thai human changed to become an exposed Thai human (α_1) was increased ($\alpha_1 = 1/2, \alpha_2 = 1/4$) and rate at which South Korean population moved out the country (μ_1) was increased($\mu_1 = 1/20, \mu_1 = 1/30$), then the number of MERS-Cov case was decreased and outburst of MERS-Cov epidemic was shorter as shown in Figures 6 and 7.

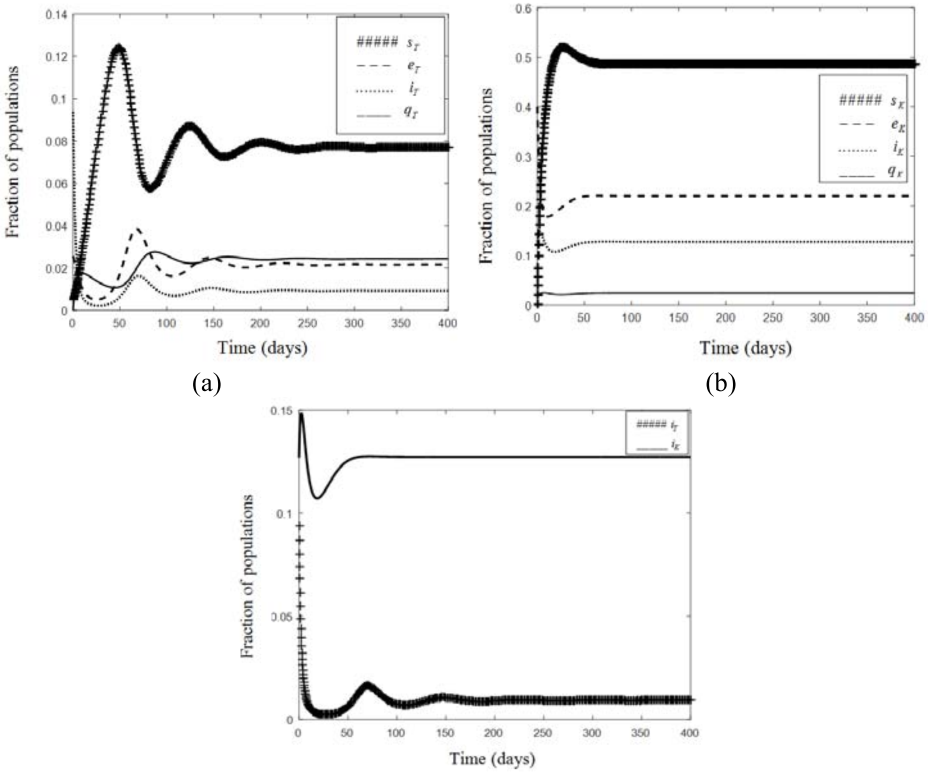


(a)

(b)

(c)

Figure 4. (a) Time series solutions of susceptible Thai population, exposed Thai population, infectious Thai population, quarantine Thai population and recovered Thai population. (b)Time series solutions of susceptible South Korean population, exposed South Korean population, infectious South Korean population, quarantine South Korean population and recovered South Korean population a nd (c) Time series solutions of infectious Thai population and infections South Korean population for $R_0 = 0.055053$.



(a) (b)

(c)

Figure 5. (a) Time series solutions of susceptible Thai population, exposed Thai population, infectious Thai population, quarantine Thai population and recovered Thai population. (b)Time series solutions of susceptible South Korean population, exposed South Korean population, infectious South Korean population, quarantine South Korean population and recovered South Korean population and (c) Time series solutions of infectious Thai population and infections South Korean population for $R_0 = 10.2297$

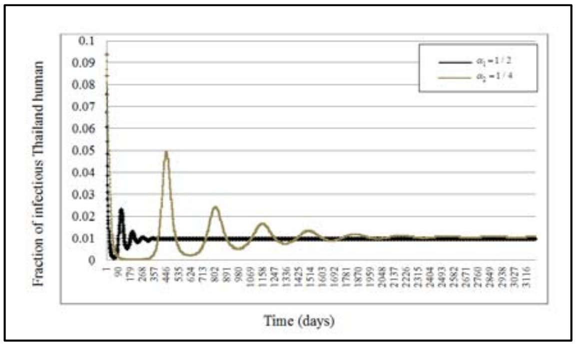


Figure 6. Numerical solution of infected Thai population case when there was the different rate at which susceptible Thai human changes to become an exposed Thai human.

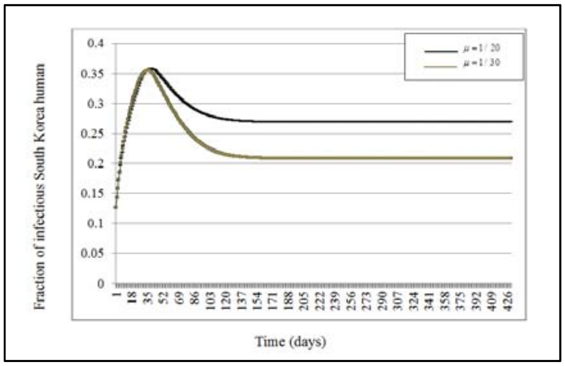


Figure 7. Numerical solution of infected South Korean population case when there was the different rate at which South Korean population moved out the country.

5. Conclusions

We had investigated the effect of repeated introduction of MERS in to Thailand by the entering of South Korea, some of them were infected with MERS. We had two steady state conditions, disease free condition and endemic condition. We can see that the Thai cases can lead to the disease free state in the absence of entering of disease free South Korea. From the numerical simulations, we can see that MERS can become endemic among the Thais when MERS South Korea cases enter in to Thailand.

6. Acknowledgements

This study is supported by Thatphanom College, Nakhon Phanom University, King Mongkut's Institute of Technology Ladkrabang and National Research Council of Thailand. IMT acknowledge the financial support provided by King Mongkut's University of Technology, Thonburi through the KMUTT 55th Anniversary Commemorative Fund.

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