Review Article
Volume 14:04, 2021

Journal of Computer Science & Systems Biology

ISSN: 2165-7920 Open Access

Mathematical Model for Transmission Dynamics of Hepatitus-A Viral Disease with Optimal Control Strategies

Mamo Shigute Wameko*, Alemu Geleta Wedajo and Purnachandra Rao Koya

Department of Mathematics, Wollega University, Nekemte, Ethiopia

Abstract

An epidemic model with optimal control strategies was investigated for Hepatitus-A Viral disease that can be transmitted through infected individuals. In this study, we used a deterministic compartmental model for assessing the effect of different control strategies to control the spread of Hepatitus-A viral disease in the community. Stability theory of differential equations is used to study the qualitative behavior of the system. The basic reproduction number that represents the epidemic indicator is obtained by using the condition of endemicity. Both the local stability and global stability conditions for disease free equilibrium is established. Uniqueness of endemic equilibrium point and its global stability conditions are proved. Numerical simulation of the model showed that applying all the control strategies can eliminate the disease from the community. However, using all intervention strategies is impractical in most circumstances; therefore, using prevention strategies can be recommended in the present mathematical modeling context.

Keywords: Mathematical model • Hepatitus a virus • Basic reproduction number • Protection • Optimal control

Introduction

Hepatitis, plural hepatitides, is an inflammation of the liver characterized by the presence of inflammatory cells in the tissue of the organ [1,2]. The inflammation of liver causes soreness and swelling. Hepatitis is most commonly caused by one of the 5 hepatitis viruses: hepatitides A, B, C, D and E. Hepatitus A infection is associated with poor sanitation and hygiene and is transmitted by the ingestion of contaminated food or water or by direct contact with an infectious person. Congregate living conditions, both within and outside shelters, increase the risk for disease transmission, which can result in outbreaks [3]. Peoples at increased risk for HAV infection include international travelers to areas with high or intermediate hepatitis A endemicity, men who have sex with men, users of injection and non-injection drugs, persons with chronic liver disease, person with clotting factor disorders, persons who work with HAV-infected primates or with HAV in a research laboratory setting, and persons who anticipate close contact with an international adoptee from a country of high or intermediate endemicity [4].

Hepatitis A is very common, potentially fatal disease. Globally, it was estimated that 119 million people were infected with HAV in 2005, with 31 million symptomatic illnesses and 34000 deaths [5]. This infection is very common in developing countries. Hepatitis A causes only acute hepatitis. HAV is transmitted mostly through exposure to contaminated food or water, or through exposure to infected persons. A safe and effective vaccine is available. According to the report of WHO published in 2015, globally it is estimated that each year, hepatitis A caused approximately 11,000 deaths accounting for 0.8% of the mortality from viral hepatitis [6-8].

A study conducted by Anthony E. Fiore also revealed that Hepatitis A is caused by hepatitis A virus. The disease spreads by the fecal-oral route, either by direct contact with an HAV infected person or by ingestion of HAV contaminated food or water. Food borne or waterborne hepatitis A outbreaks are relatively uncommon in the United States. However, people's who prepares food infected with hepatitis A are frequently identified, and evaluation of the need for immunoprophylaxis and implementation of control measures are a considerable burden on public health resources. Moreover, HAV- contaminated food may be the source of hepatitis A for an unknown proportion of persons whose source of infection is not identified [7].

A systematic review and meta-analysis was used to provide a clear and comprehensive estimation of viral hepatitis epidemiology and the potential clinical burdens in Ethiopia [8]. This review indicated that all types of viral hepatitis origins are endemic in Ethiopia. Incorporating a recommended diagnostic and treatment algorithm of viral hepatitis in the routine healthcare systems and implementing prevention and control policies in the general population needs an urgent attention.

Different mathematical models have been developed to analyze the transmission dynamics of HAV as well as the effectiveness of some intervention strategies against the spread of HAV infections. For example, Marco Ajelli and Stefano Merler developed an individual–based model with dynamic network of contacts, parameterized by employing sociodemographic and epidemiological data and accounting for millions of individuals [9]. Their study showed that very low vaccination coverage is sufficient to control Hepatitus A in Italy while its elimination is not possible since new cases are continuously imported from high endemic areas outside the country.

A study in [10] used a compartmental dynamic transmission model stratified by age and setting in rural and urban was developed and calibrated with demographic, environmental, and epidemiological data from Thailand. HAV transmission model was used as a function of urbanization and access to clean drinking water. The model was applied to project various epidemiological measures. Their study indicated that modeling the relationship between water, urbanization, and HAV endemicity is a novel approach in the estimation of HAV epidemiological trends and future projections. This approach provides insights about the shifting HAV epidemiology and could be used to evaluate the public health impact of vaccination and other interventions in a diversity of settings [10].

Mariana Alves de Guimaraens and Cláudia Torres Codeço also used an SIR model to study the transmission dynamics of Hepatitus A disease in the community. Their study revealed that heterogeneous access to sanitation services is a characteristic of communities in Brazil. This heterogeneity leads to different patterns of hepatitis A endemicity: areas with low infection rates have higher probability of outbreaks, and areas with higher infection rates have high prevalence and low risk of outbreaks. Under their study they developed a mathematical model to study the effect of variable exposure to infection on the epidemiological dynamics of hepatitis A [11].

***Address for Correspondence:** Mamo Shigute Wameko, Department of Mathematics, Wollega University, Nekemte, Ethiopia, E-mail: bitmamsab@gmail.com*

Received 07 January 2021; **Accepted** 21 March 2021; **Published** 28 March 2021

Different mathematical models have been developed to analyze the transmission dynamics of HAV as well as the effectiveness of some intervention strategies against the spread of HAV infections. All of the above studies reveal an important result for HAV disease transmission dynamics by considering different conditions. In this study, we considered a PSCIR (Protection, Susceptible, Carrier, Infected, and Recovered) model for HAV. Our model is a modified and extended version of the model presented in with optimal control strategies for the control of the disease.

Description and Formulation of Model

The compartments used in this model consist of five classes: is the compartment used for those peoples who are protected against the disease over a period of time. is used to represent the number of individuals that are prone to the disease at time t. I(t) represents the number of individuals who have been infected with the disease and are capable of spreading the disease to those in the susceptible categories. Denotes the number of individuals who are infected with the disease and are capable of spreading the disease without showing any symptoms of the disease. R(t) denote the number of individuals who are recovered from the disease. Protected individuals are recruited into the population at per capita rate. This compartment is consisting of population groups which are immune due to pediatric vaccination. Susceptible individuals are recruited into the population at per capita rate. Susceptible individuals acquire HAV infection at per capita rate. The susceptible class is increased by birth or emigration at a rate of and from protected class by losing protection with rate. is the effective force of infection which is given by where is effective contact rate of individuals with asymptomatic infectious and is effective contact rate of individuals with symptomatic infectious. is the rate at which asymptomatic infectious individuals become asymptomatic infectious. is the natural mortality rate, is the disease induced mortality rate due to asymptomatic infection, is the disease induced mortality rate due to symptomatic infection is the rate recovery of symptomatic infectious people due to natural immunity and joining recovered class, is the rate of recovery of asymptomatic infectious due to natural immunity and joining recovered class (Figure 1).

The asymptomatic infectious subclass is increased from susceptible subclass by screening rate. The symptomatic infectious subclass is increased from susceptible subclass by screening rate. Those individuals in the asymptomatic infectious can recover due to natural immunity and join recovered subclass with a rate of. And those individuals in the symptomatic infectious subclass can recover due to natural immunity and join recovered subclass with a rate of. The recovered subclass also increases from asymptomatic infectious class due natural immunity at a rate of and symptomatic infectious class will recover at due to natural immunity at a rate of. In all the subclasses, is the natural death rate of individuals, but in the asymptomatic infectious class is disease induced death rate and is the disease induced death rate due to asymptomatic infection. The assumption of this model is that there is no re-infection once an individual is recovered.

Sensitivity Analysis

The total human mortality and morbidity attributable to HAV disease can be best reduced by investigating the relative importance of the parameters featuring in the basic reproduction number. To determine how best we can do in order to reduce mortality and morbidity due to HAV disease, it is crucial to know the relative importance of different factors responsible for its transmission and prevalence.

Sensitivity analysis was carried out to determine the model robustness to parameter values. This will help us in identifying and verifying model parameters that most influence the pathogen fitness threshold for the pathogens. Further, values obtained for sensitivity indexes indicate which parameters should be targeted most for intervention purposes.

Extension into an optimal control

In this section we apply optimal control method for the system (1-5) by using Pontryagin's maximum principle. The optimal control model is an extension of HAV model by incorporating the following three controls mentioned below:

i. Is the prevention effort, that protect susceptible from contracting the disease.

ii. Is the supportive treatment used for asymptomatic infectious individuals.

iii. Is the vaccination used for symptomatic infectious individuals.

After incorporating and in HAV model (1-5), we get the following optimal model of HAV disease.

Numerical Simulations

In the present work, we have used PSCIR epidemic model with control measures. The simulations are carried out in order to explore the impacts of control measures on the HAV disease dynamics. Following parameter values are used in the model for simulation purpose (Figure 2).

And initial values P(0)=1000, S(0)=4000, C(0)=1800, I(0)=1200, R(0)=2000

The optimal control solution is obtained by solving the optimality system (40), which consists of the state system, the adjoint system and transversality condition. To solve the state system we use a forward fourth-order Runge-kutta method and solve the adjoint system using a backward fourth-order Runge-Kutta method. The solution iterative scheme involves making a guess of the controls and solves the state system using forward fourth order Runge-Kutta scheme. Due to the transversality conditions (40), the adjoint equations are then solved by the backward fourth-order Runge-Kutta scheme using the current iterations solutions of the state equations. The controls are then updated using a convex combination of the previous controls and the values obtained using the characterizations. The updated controls are then used to repeat the solution of the state (Figure 3).

The optimal control solution is obtained by solving the optimality system (40), which consists of the state system, the adjoint system and transversality condition. To solve the state system we use a forward fourth-order Runge-kutta method and solve the adjoint system using a backward fourth-order Runge-Kutta method. The solution iterative scheme involves making a guess of the controls and solves the state system using forward fourth order Runge-Kutta scheme. Due to the transversality conditions (40), the adjoint equations are then solved by the backward fourth-order Runge-Kutta scheme using the current iterations solutions of the state equations. The controls are then updated using a convex combination of the previous controls and the values obtained using the characterizations. The updated controls are then used to repeat the solution of the state and adjoint systems. This process is repeated until the values in the current iteration are close enough to the previous iteration values.

In this section we investigate numerically the effect of the following optimal control strategies on the spread of the disease in a population.

i. Using prevention effort, that protect susceptible from contracting the disease.

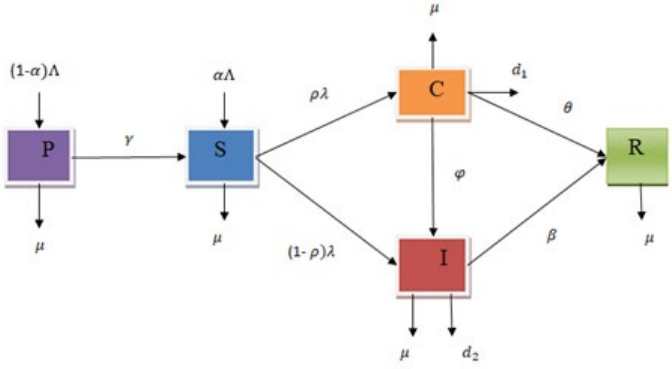

Figure 1. Flow diagram of the model.

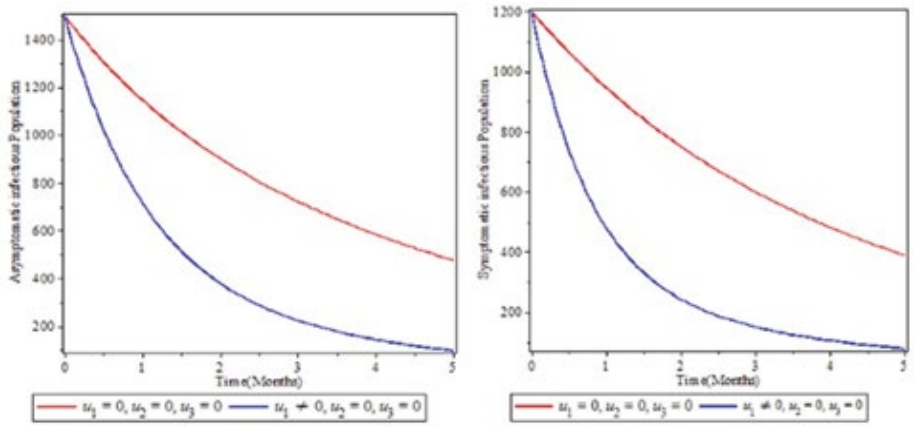

Figure 2. Simulation of optimal control with prevention only.

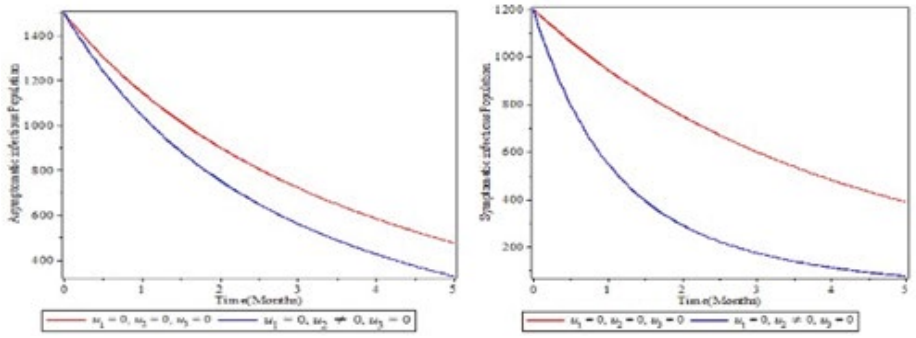

Figure 3. Simulation of optimal control with treatment for asymptomatic infectious only.

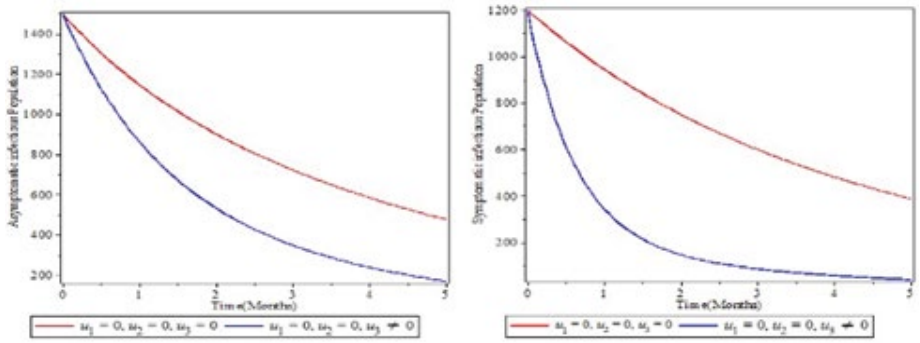

Figure 4. Simulation of optimal control with vaccination for symptomatic infectious only.

ii. Using supportive treatment effort for asymptomatic infectious individuals.

iii. Using vaccination effort for symptomatic infectious individuals.

iv. Using prevention for susceptible and supportive treatment for asymptomatic infectious individuals.

v. Using prevention for susceptible and vaccination for symptomatic infectious individuals.

vi. Using supportive treatment for asymptomatic infectious and vaccination for symptomatic infectious individuals.

vii. Using all the three controls, prevention effort, supportive treatment effort and vaccination effort.

Controls with vaccination only for symptomatic infectious population

The vaccination (control) is used to optimize the objective functional J; the other controls relating to HAV disease are set to zero. From Figure 4 we observe that initially the control has minimal effect on the dynamics of symptomatic infectious population. In the mean-time the proportion of symptomatic infectious population decrease with time leading to faster declining of symptomatic infectious population.

Discussion and Conclusion

In this study a deterministic mathematical model of HAV consisting asymptomatic infectious and symptomatic infectious stages with optimal control strategies has been established. The model assumed the presence of population groups who are protected due to immunization by using pediatric vaccination against Hepatitus A viral disease. Since vaccines are not 100% perfect it was assumed that a certain fraction of those protected groups will be susceptible for Hepatitus A virus. The model also incorporated the assumption that all populations are equally susceptible. Both qualitative and numerical analysis of the model was done. We have shown that there exists a feasible region where the model is well posed and biologically meaningful in which a unique disease free equilibrium point exists. The steady state points were obtained and their local and global stability conditions were investigated. The model has a unique disease free equilibrium if <1 and has endemic equilibrium

if >1. It was also proved that the model has a unique endemic equilibrium. Sensitivity analysis of the parameters of the model was carried out and both recruitment rate and the effective contact rate with infected individuals are responsible in escalating the endemicity of the disease. It also was observed that mortality rate has a higher impact in minimizing the burden of the disease when the parameter increases which is not biologically reasonable to use it as a control mechanism. Moreover, the natural recovery rate also has a higher impact in minimizing the endemicity of the disease.

For the given model an optimal control problem is formulated by incorporating different control strategies. The optimality condition was established by using Pontryagin's maximum principle. A numerical simulation of the model was conducted and different combinations of control strategies were compared. It was observed that prevention has a significant impact in minimizing the burden of the disease. It was also shown that supportive treatments given for asymptomatic infectious and vaccination given for symptomatic infectious population minimizes the burden of the disease. Finally it was observed that applying all the three control strategies will leads to total eradication of Hepatitus A viral disease from the population. Applying all the control strategies may be impractical in most circumstances. Therefore, using prevention strategies can be recommended in the present mathematical modeling context.

References

1. Wells, Jimmy, and Sanger Larry. "Acute Hep C Virus Infection: Transmission, Diagnosis, Prevention and Treatment." Wikimedia Foundation (2001) Inc.
2. Armstrong, Gregory L, and Beth P Bell. "Hepatitis A Virus Infections in the United States: Model-Based Estimates and Implications for Childhood Immunization." Pediatrics 109 (2002): 839-845.
3. Gambatese, Melissa, Dova Marder, Elizabeth Begier, and Alexander Gutkovich, et al. "Programmatic Impact of 5 years of Mortality Surveillance of New York City Homeless Populations." AM J Public Health 103 (2013): S193-S198.
4. Nelson, Noele P, Ruth Link-Gelles, Megan G Hofmeister, and José R Romero, et al. "Update: Recommendations of the Advisory Committee on Immunization Practices for Use of Hepatitis A Vaccine for Postexposure Prophylaxis and for Preexposure Prophylaxis for International Travel." MMWR Morb Mortal Wkly Rep 67 (2018): 1216-1220.
5. Jacobsen, Kathryn H, and Steven T Wiersma. "Hepatitis A Virus Seroprevalence by Age and World Region, 1990 and 2005." Vaccine 28 (2010): 6653-6657.
6. World Health Organization. "Hepatitis A." (2016).
7. Acheson, David, and Anthony E. Fiore. "Hepatitis A Transmitted by Food." Clin Infect Dis 38 (2004): 705-715.
8. Belyhun, Yeshambel, Melanie Maier, Andargachew Mulu, and Ermias Diro, et al. "Hepatitis Viruses in Ethiopia: A Systematic Review and Meta-Analysis." BMC Infect Dis 16 (2016): 1-14.
9. Ajelli, Marco, and Stefano Merler. "An Individual-Based Model of Hepatitis A Transmission." J Theor Biol 259 (2009): 478-488.
10. Van Effelterre, Thierry, Cinzia Marano, and Kathryn H Jacobsen. "Modeling the Hepatitis A Epidemiological Transition in Thailand." Vaccine 34 (2016): 555-562.
11. Guimaraens, Mariana Alves de, and Cláudia Torres Codeço. "Experiments with Mathematical Models to Simulate Hepatitis A Population Dynamics Under Different Levels of Endemicity." Cad Saude Publica 21 (2005): 1531-1539.
12. Nigussie, Girmaw Ayele, and Purnachandra Rao Koya. "Modeling and Simulation Study of Population Subjected to the Smoking Habit." IOSR Journal of Mathematics 12 (2016): 59-60.
13. Castillo-Chavez, Carlos, and Baojun Song. "Dynamical Models of Tuberculosis and their Applications." Math Biosci Eng 2 (2004): 361-404.
14. Lenhart, Suzanne, and John T Workman." Optimal Control Applied to Biological Models." CRC press (2007).
15. La Salle, Joseph P. "The Stability of Dynamical Systems." Society for Industrial and Applied Mathematics (1976).
16. Fleming, Wendell H, and Raymond W Rishel. "Deterministic and Stochastic Optimal Control." Springer (2012).
17. Lukes, Dahlard L, and Lukes DL. "Differential Equations: Classical to Controlled." (1982).
18. Tilahun, Getachew Teshome, Oluwole Daniel Makinde, and David Malonza. "Modelling and Optimal Control of Typhoid Fever Disease with Cost-Effective Strategies." Comput Math Methods Med (2017).

How to cite this article: Mamo Shigute Wameko, Alemu Geleta Wedajo, and Purnachandra Rao Koya. "Mathematical Model for Transmission Dynamics of Hepatitus-A Viral Disease with Optimal Control Strategies." J Comput Sci Syst Biol 14 (2021): 346.