

Bifurcation and Crossover Processes in the Dynamics of a Marburg Haemorrhagic Fever Model

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Abstract. Just like Ebola disease, the Marburg virus disease (MVD) remains a constant threat to people's life, not only in Africa, but also in the other parts of the globe. Recorded past outbreaks occurred in Europe, America and of course Africa, especially in places where inhabitants come into contact with wild animal products or live alongside wild animals such as apes, monkeys and fruit bats on a daily basis. Therefore, studying the dynamics of the Marburg virus and making some epidemiological assessments remain relevant and important in preventing future outbreaks. In this paper, we analyze a Marburg epidemic model in which the transmission is nonlinear. The well-posedness result is established as well as conditions for boundedness and dissipativity results. Then, we intensively analyze the stability of the Marburg model's equilibria. The bifurcation dynamics indicate the existence of both transcritical (exchange of stability between the endemic equilibrium (EE) point and the disease free equilibrium (DFE)) and backward bifurcation where the classical epidemiological condition for the MVD to die out ($\mathcal{R}_0 < 1$) is not sufficient anymore, but remains necessary. Lastly, some numerical simulations show convergence of the trajectories to both the EE and the DFE. Some adequate preventive measures are provided.

AMS subject classifications: 26A33, 37M05, 65P30, 65P40

Key words: Marburg hemorrhagic fever model, numerical solvability, filovirus, nonlinear incidence, bifurcation, crossover, stability.

1 Introduction

The Marburg virus (MARV) is seen as an extremely pathogenic virus that causes a severe disease leading to mortality rates fluctuating between 20% and 90%. For the genetic side,

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the MARV is characterized by a genome packaged into a unique filamentous virion with length varying between 790 and 970 nm and width of 80 nm [15, 32]. It was first identified in 1967 in the towns of Marburg and Frankfurt (Germany) and Belgrade (Serbia formerly known as Yugoslavia), during a series of outbreaks in which number of laboratory workers were exposed to blood and tissues of infected grivet monkeys, a kind of African green monkeys imported from Uganda. The outbreaks saw the deaths of seven people out of the thirty-one that became infected [33]. Its chronology and early evolution is depicted in Fig. 1. The world experienced many MARV outbreaks and most of them remained sporadic if not occasional. In human population, the disease caused by the MARV is known as the Marburg virus disease. Just like Ebola virus, the Marburg virus also belongs to the family of Filoviridae which regroups number of genera such as Thamnovirus, Cuevavirus and of course Ebolavirus and Marburgvirus. The virus causing the MVD belongs to the filovirus family, which is also part of Marburgvirus genera. Viruses from the filovirus family can provoke hemorrhagic fever and death in both human and non-human populations, such as primates (as depicted in Figs. 2-3). It appears to be deadly with the severity amplified by the lack of adequate infrastructures and amenities able to timely to detect, diagnose, prevent and treat the disease [22, 23, 25, 32]. The MVD usually starts by a severe sore throat, headache and fever followed by maculopapular rash all over the torso down to the limbs and a red exanthem appearing on both the front part and back part of the palate. The patient during the first five days of the symptoms, can suffer from body pain together with nausea, diarrhea and we can see the intensification of hemorrhagic fever's symptoms like mucosal bleeding, bleeding from venipuncture sites and presence of blood in the faeces and vomits. The patient becomes lethargic and he gets dehydrated due to watery diarrhea and vomiting. Internal hemorrhage, organ failure together with the dysregulated immune response to the virus

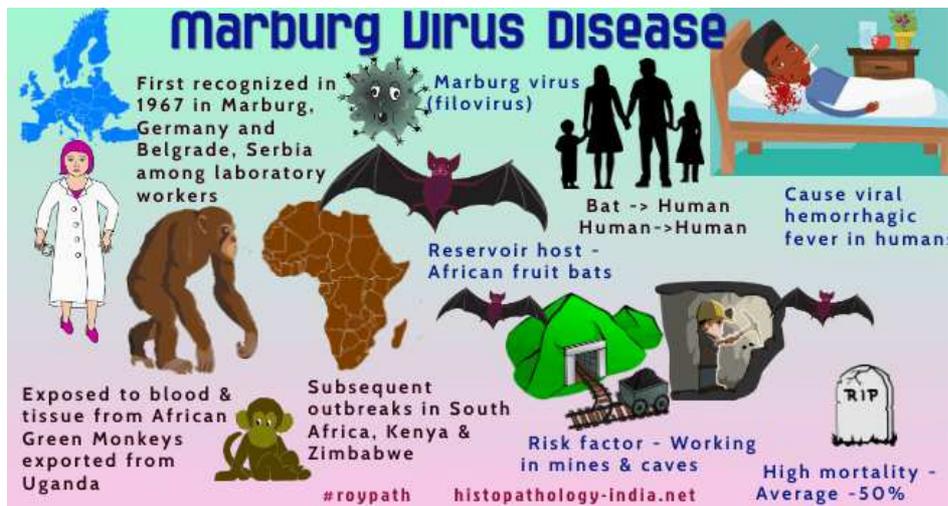


Figure 1: The Marburg virus disease: origin, evolution and parties involved [30].