



**University of Venda**  
**A Mathematical Modelling Frame-work  
for Immuno-epidemiology of Guinea  
Worm Infection**

by

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## Abstract

Infectious diseases have great impact on our life and socio-economic realm. They account for 43% of global burden and they still remain a leading cause of mortality and morbidity more especially in the developing country. Most of them are linked to environmental health, as they are influenced by pathogens that are capable of adapting and evolving in the environment. In this study we develop two mathematical models (epidemiological and immuno-epidemiological model) of Guinea worm disease for the study of the transmission dynamics of Guinea worm parasites known as *Dracunculus medinsis* within a human population. Guinea worm disease results after drinking water that has been contaminated by infected copepods with mature Guinea worm larvae. We study the mathematical properties of both models and show that all the models are mathematically and epidemiologically well-posed. We determine the basic reproduction number ( $R_0$ ) of both models by using the next generation operator. The ( $R_0$ ) was used to analyse the local and global stability of disease-free equilibrium as well as the local stability of endemic equilibrium. We deduce that if  $R_0 < 1$ , then the disease-free equilibrium point of both models is locally and globally asymptotically stable, however if  $R_0 > 1$  the endemic equilibrium point of both models is locally asymptotically stable. We then analyse the sensitivity of  $R_0$  of both models on the variation of their model parameters and finally we simulate the behaviour of both the models numerically. In both cases, our results show that their reproduction number  $R_0$  is more sensitive to the changes of the death rate of copepods  $\mu_E$ . Therefore reducing the population of copepods in the physical water environment can eventually contribute in eradicating the disease.