1155-92-379 **Zhilan Feng**, **Katharine Gurski*** (kgurski@howard.edu), **Margaret Grogan**, **Olivia Prosper** and **Miranda Teboh-Ewungkem**. *A vector-borne disease model with non-exponentially distributed infection and treatment stages.*

Most models for vector-borne disease assume exponentially distributed residence times in disease stages in order to simplify the model formulation and analysis. However, tackling drug resistance in malaria causing parasites requires an accurate description of the interaction between drug concentration and parasite load within hosts. For example, how long a human host has been infected is likely to influence their parasite load and their ability to transmit the parasite to a mosquito, especially among the immunologically naive individuals. The onset of clinical symptoms is likely to dictate when treatment begins. How long an individual has been undergoing treatment for an infection will determine their current blood-drug concentration and parasite load, and therefore, their susceptibility to re-infection with drug resistant parasites, along with their ability to transmit. Thus, we formulate a model by considering arbitrarily distributed sojourn for various disease stages. The model formulation is presented using integral equations. When general distributions are replaced by gamma distributions, the system of integral equations can be reduced to a system of ODEs, which has some non-trivial characteristics which are only captured by non-exponential distributions for disease stages. (Received January 19, 2020)