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Influence of genetically modified mosquitoes in dengue epidemic network

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There are many examples of complex systems in the world from different domains of life. For example, the social contacts includes, the social networks of friendship, a covert network of terrorists, sexual contact network, and scientific collaboration network are all complex networks. Complex networks play a significant role in the research of epidemic diseases and in their modeling such as HIV/AIDS. The dengue epidemic is a dynamic and complex phenomenon which has gained much attention due to its harmful effects that sometimes becomes a cause of death of a person. According to WHO, it is estimated that approximately 3.6 billion people are living in the dengue affected part of the world. It has become an emerging challenge to health authorities and legislators, as there are presently no authorized antibodies or particular therapeutics for its treatment. The dengue fever is caused by a mosquito of specific specie named as *Aedes aegypti*. It is important to discuss here that only female *Aedes aegypti* is the dengue vector that is also the super spreader of ZIKA virus. The dataset (obtained from MOH Selangor, Malaysia) showed the results that proved the dengue epidemic as a scale-free network (SFN) instead of random network. The scale-free feature is very important in the treatment of epidemic diseases. Here, we observe the influence of Genetically Modified Mosquitoes (GMM) in a complex network of the dengue epidemic. The results showed that GMM technique is much suitable in SFN and can suppress the wild population of *Aedes aegypti*. The results are important for the researchers and policy makers who deal with the arbovirus epidemic diseases like ZIKA virus.

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