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Persistence of Rift Valley fever virus in East Africa

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Rift Valley fever virus (RVFv) is a mosquito-borne pathogen of livestock, wildlife and humans that causes severe outbreaks in intervals of several years. One of the open questions is how the virus persists between outbreaks. We developed a spatially-explicit, individual-based simulation model of the RVFv transmission dynamics to investigate this question. The model, is based on livestock and mosquito population dynamics. Spatial aspects are explicitly represented by a set of grid cells that represent mosquito breeding sites. A grid cell measures 500 by 500m and the model considers a grid of 100 by 100 grid cells; the model thus operates on the regional scale of 2500km2. Livestock herds move between grid cells, and provide connectivity between the cells. The model is used to explore the spatio-temporal dynamics of RVFv persistence in absence of a wildlife reservoir in an east African semi-arid context. Specifically, the model assesses the importance of local virus persistence in mosquito breeding sites relative to global virus persistence mitigated by movement of hosts. Local persistence is determined by the length of time the virus remains in a mosquito breeding site once introduced. In the model, this is a function of the number of mosquitoes that emerge infected and their lifespan. Global persistence is determined by the level of connectivity between isolated grid cells. Our work gives insights into the ecological and epidemiological conditions under which RVFv persists. The implication for disease surveillance and management are discussed.