This article explores how the topology of human-mosquito biting networks may affect disease dynamics. It draws on citizen science data to make inferences about the degree distributions of the human and mosquito nodes in the tiger mosquito biting network in Spain, considering geographic variation in mosquito and human population densities, and human mobility patterns. It then uses agent based models to explore the epidemiological consequences of these distributions. It compares the basic reproduction number for simulated outbreaks using the homogeneous mixing assumption and using a range of degree distributions estimated from the data. The results will provide important insights into the extent to which traditional, homogenous mixing models of disease dynamics may be giving misleading risk estimates, and how this may be playing out across geographic space. This will provide a starting point for improving estimates of mosquito-borne disease risk and designing effective interventions.