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2018



Arthropod Vector Science
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22nd-26th October 2018

Palermo, Italy



PROGRAM AND ABSTRACT

Estimating mosquito population abundance from standard monitoring devices

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Estimates from standard monitoring devices inform public health authorities about the relative abundance of vector species, a critical parameter to guide control interventions. At present, the estimation of the absolute abundance of a vector species is challenging and relies mostly on laborious methods such as Mark-Release-Recapture. However, estimates of absolute abundance are needed to estimate and quantitatively characterize the risk of pathogen transmission from vectors to hosts. In this study we discuss the potential use of the N-mixture model statistical approach to the estimation of population abundance of vector species, which may not otherwise be estimated by Mark-Release-Recapture methods due to ethical concerns arising from the potential exposure of people to health risks deriving by the field release of disease vectors. Therefore, we applied the N-mixture model to a case study in Rome (Lazio Region, Italy) where monitoring data on the mosquito vector *Aedes albopictus* (Tiger mosquito) are routinely collected. The invasive species *Ae. albopictus* has been the vector for a recent outbreaks of Chikungunya in the Lazio Region in the 2017 and estimates of the species abundance are essential to avoid future outbreaks. Results show that the N-mixture model, when properly informed by prior knowledge on the species biology and trapping methods, could be put in use to estimate vectors population abundance. Therefore, even if ethically questionable methods (when pathogen transmission risk occurs) such as Mark-Release-Recapture still are the golden standard for estimating population abundance, the N-Mixture model approach could be exploited to provide an assessment of vectors population abundance when competing methods are not feasible.