Modelling the effects of tick-host interaction on pathogen dynamics: TBE as a case study

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Tick-borne encephalitis (TBE) is an emerging vector-borne zoonotic disease reported in several European and Asiatic countries with complex transmission routes that involve a number of key vertebrate host species other than a major tick vector. Understanding and quantifying the interaction between ticks and main hosts involved in the TBE virus (TBEv) cycle is crucial in estimating the threshold conditions for TBEv emergence and spread. Some hosts, such as rodents, act both as feeding hosts for ticks and reservoirs of the infection. Other species, such as deer, provide important sources of blood for feeding ticks but they do not support TBE virus transmission, acting instead as dead-end (i.e., incompetent) hosts. We used eco-epidemiological models to explore the dynamics of tick populations and TBEv infection in relation to the density of two key hosts, deer and rodents. Both host may act as tick amplifiers, but at high densities may also dilute pathogen transmission. Model outputs were validated with empirical data regarding the effect of host densities on tick population dynamics and TBE virus infection from selected European foci in Italy and Slovakia. In addition, we investigated the effect of using various models to describe tick aggregation on TBEv dynamics in a long-term study site in Trentino (Northern Italy). Specifically, we modelled the number of ticks per rodent host by using Negative Binomial, Poisson-LogNormal and Power Law (PL) distributions. PL model seems to better describe the strong heterogeneity observed in our data. Using a stochastic model, we observed that TBEv infection is highly dependent on the capability of the implemented model to describe tick burden on rodents. Specifically, we found that the epidemic threshold and the prevalence equilibria obtained in epidemiological simulations with PL distribution are a good approximation of those observed in simulations feed with empirical distribution.