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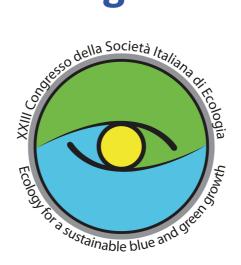
Ecology for a sustainable blue and green growth

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Università Politecnica delle Marche

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Abstract

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S2.5   Understanding the environmental drivers of West Nile Virus (WNV) emergence in Europe

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WNV is a mosquito-borne pathogen with continuous geographic expansion in Eurasia. Its ecology in Europe is still poorly understood due to the high viral diversity and the complexity of its cycle. Several vertebrate and mosquito species are involved in WNV dynamic, although a limited set are playing a major role. Moreover, the interplay among the many biotic and abiotic factors driving WNV amplification is complex. To shed light on the dense relationships among WNV emergence and environmental drivers is therefore essential. The aim of this study was to analyze the relationships among WNV human cases in Europe (2010-2012; ECDC) and a series of climatic and environmental parameters characterizing the areas with WNV cases. The modeling procedure has been carried out using GLMs, WNV incidence as response variable and a complete set of climatic and environmental predictors. Best models were identified using AIC model selection. Preliminary results showed that WNV incidence is positively influenced by summer temperature anomalies while spring precipitation anomalies have negative effects. Besides, the most important environmental predictors include the presence of populated forest, irrigated croplands and mosaic grasslands. Several other parameters are currently under examination. In conclusion, results showed how using a multi-set of predictors within a robust modeling framework could provide a better perception on the parameters creating the favorable condition for WNV spill over.

S2.6   Preventing diseases outbreaks in a network of cattle farms: the case of bovine tuberculosis in Emilia Romagna

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The ecological approach to the analysis of disease dynamics has become relevant in the last three decades since the seminal work by Anderson and May in 1979. Thanks to the ability of parasites to move through the ecological continuum formed by wildlife, livestock and humans, the protection of any of these compartments from disease outbreaks has significant implications also for the health and well-being of the other two. In this work we investigated pathogen dynamics in a network of cattle farms following the introduction of an infected animal in a disease-free region. As a reference example we focused on bovine tuberculosis (bTB) in Emilia Romagna, Italy. This region is currently bTB-free and the surveillance is based on three strategies: on-farm systematic testing, testing of moved cattle and inspection at the slaughterhouse. The goal of this study was to assess the effectiveness of current and alternative surveillance systems in detecting the infection in livestock. To do so, we built a simulation model describing both within-farm and between-farm bTB dynamics. The former was described by a Susceptible-Exposed-Infected model, while the latter by a network model where nodes represent farms and links cattle trade between farms. Preliminary results suggest that there are pros and cons for each surveillance strategy. Tests on traded cattle and slaughterhouse inspection perform better than routine testing in detecting major outbreaks while the latter is better than the former for minor ones.