

PERSISTENCE OF INVADING GYPSY MOTH POPULATIONS

Patrick C. Tobin¹ and Stefanie L. Whitmire²

¹USDA Forest Service, Northeastern Research Station, 180 Canfield Street, Morgantown, WV 26505
(304) 285-1514 (Bus.); (304) 285-1505 (Fax), ptobin@fs.fed.us

²West Virginia University, Department of Biology, P.O. Box 6057, Morgantown, WV 26506, whitmir3@msu.edu

Abstract

Exotic invasive species are a mounting threat to native biodiversity, and their direct and indirect effects are gaining increasingly more attention at each detection. Equally important are the dynamics of those exotic invasives that are already well established and for whom eradication is no longer possible. While the literature reports many examples of the ability of a newly arrived exotic invader to persist prior to detection and population growth, we focused on the persistence dynamics of an established invader using the European gypsy moth in North America as a model system. The spread of gypsy moth is largely thought to be the result of the growth and coalescence of isolated colonies ahead of the generally infested area. One important question is thus the ability of these isolated colonies to persist when subject to Allee effects and/or inimical stochastic events. We used U.S. gypsy moth survey data, collected from pheromone-baited traps, to examine persistence of gypsy moth colonies within (1) the transition zone, which extends from Wisconsin to Virginia; and (2) an designated uninfested area along the North Shore, Minnesota.

Within the transition zone of gypsy moth, which is the area between the generally infested and uninfested areas, we used Local Indicator of Spatial Autocorrelation methods. This novel spatial statistical tool was used to objectively identify isolated colonies of gypsy moth from pheromone-baited traps deployed under the Slow-the-Spread project. We then determined region-specific probabilities of colony persistence given the population abundance in the previous year and its relationship to a suite of ecological factors. We observed that colonies in Wisconsin were significantly more likely to persist in the following year than in other geographic regions of the transition zone. Moreover, across all regions, the abundance of preferred host tree species and land use category did not appear to influence persistence. The enhanced rates of persistence in Wisconsin may help explain the more rapid rate of spread in this region, and

motivates important questions regarding the management of established exotics as they invade new areas.

In the North Shore of Minnesota, pheromone-baited traps are used in detection, and space-time data from 2000-2004 were available. Analysis of detection data, particularly for newly arrived exotic invasive species, is complex. In most cases, distributions are not only overwhelming dominated by zeros, but also the majority of counts exceeding 0 are more often than not one. Thus, the distribution is not only highly skewed, but often quite close to binary. One approach to overcoming these issues in invasive species ecology is to consider methods used in the epidemiological community, in which disease incidence can be rare and binary, and many of the underlying objectives are not dissimilar. In an epidemiological context, the focus is to quickly detect space-time clustering of disease prevalence so that potential outbreaks are minimized and epidemics avoided. In invasive species population biology, a similar desire for an early warning system exists so that new invaders can be aggressively addressed prior to population expansion. In our case, the primary goal of an analysis of the North Shore data was to determine if male moths were being trapped at the same place over time, or if they were random in space and time. In other words, do the data suggest the presence of reproducing populations established at low abundance, stochastic introductions from year to year, or some combination of both? We used the Knox test, a common tool in epidemiology, to quantify the space-time signature of the North Shore data, and compared it to a series of simulated data from a (1) random space-time pattern; (2) deterministic space-time clustered pattern; and (3) stochastic model that allowed random introductions and extinctions in each year, as well as stochastic nearest neighbor dispersal of existing colonies. The preliminary results suggest that the North Shore contains a complex mix of established colonies with random introductions and extinctions to some yet unknown degree. The next step in this analysis is to partition and quantify these processes.