

Christina Cobbold (University of Glasgow)

Effects of spatial structure on a cyclic herbivore populations

Abstract

Understanding how cycles of forest-defoliating insects (herbivores) are affected by forest structure is of major importance for forest management. Achieving such an understanding with data alone is difficult. We therefore constructed mathematical models to investigate the effects of forest structure on herbivore cycles, focusing on herbivore cycles driven by parasitoids. Typically when we think of spatially structured habitat we think of a habitat fragmentation and a mosaic of suitable and unsuitable habitat. However, suitable habitat can be uniformly distributed, but still show spatial structure via spatial variation in the plant genotype. It has been shown the plant genotype can strongly affect not only individual herbivore performance, but also community composition and ecosystem function. In this talk I will examine the impact of two these types of spatial heterogeneity (fragmentation and genotype variation) on the population cycles of forest-defoliating insects.

Our integrodifference equation model shows that forest destruction can increase herbivore density when parasitoids disperse much farther than the herbivores because the benefits of reduced herbivore mortality due to increased parasitoid dispersal mortality exceed the costs of increased herbivore dispersal mortality. This novel result can explain observations of increased outbreak duration with increasing forest fragmentation in forest tent caterpillar populations.

I will also show how plant genotype, the relative size of genotypic patches, and the rate of herbivore dispersal between them, affect the frequency, amplitude, and duration of herbivore outbreaks. We found that coupling two different genotypes does not necessarily result in an averaging of herbivore dynamics. Instead, depending on the ratio of patch sizes, when dispersal rates are moderate, outbreaks in the two-genotype case may be more or less severe than in forests of either genotype alone.