

Impacts of habitat fragmentation on genetic diversity in a tropical forest butterfly on Borneo

Abstract

Many areas of rain forest now exist as habitat fragments, and understanding the impacts of fragmentation is important for determining the viability of populations within forest remnants. We investigated impacts of forest fragmentation on genetic diversity in the butterfly *Mycalesis orseis* (Satyrinae) in Sabah (Malaysian Borneo). We investigated mtDNA diversity in 90 individuals from ten forest sites typical of the sizes of forest remnants that currently exist in the region. Nucleotide diversity declined with increasing isolation of remnants, but there was no effect of remnant size or population size, and haplotype diversity was similar among sites. Thus, approximately 50 y after forest fragmentation, few changes in genetic diversity were apparent and remnants apparently supported genetically viable populations of this butterfly. Many studies have shown that responses of species to habitat fragmentation usually follow a time delay, and so we developed a Monte Carlo simulation model to investigate changes in genetic diversity over time in small remnants. Model output indicated a substantial time delay (> 100 y) between fragmentation and genetic erosion, suggesting that, in the smallest study remnants, an increased risk of extinction from reduced genetic diversity is likely in the longer term. Copyright © 2007 Cambridge University Press.