

## Publication

## Genetic effects of anthropogenic habitat fragmentation on remnant animal and plant populations: a meta-analysis

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Habitat loss and fragmentation are among the biggest threats to biodiversity. Anthropogenic habitat fragmentation leads to small and isolated remnant plant and animal populations. The combination of increased random genetic drift, inbreeding, and reduced gene flow may substantially reduce genetic variation of remnant populations. However, the magnitude of these responses may depend on several poorly understood factors including organism group, habitat type of both the fragment and the surrounding matrix, life-history traits, and time since fragmentation. We compiled data for 83 plant and 52 animal species and conducted a meta-analysis following best practices to evaluate how these factors mediate the effects of anthropogenic habitat fragmentation. We calculated 206 effect sizes as correlations between one of four measures of population-level genetic diversity and fragment area. All analyses were repeated using models of increasing complexity (traditional random-effects models, multilevel models accounting for non-independent data, and multilevel models additionally correcting for phylogenetic relatedness). We confirmed that anthropogenic habitat fragmentation has overall negative effects on genetic diversity of organisms. Our meta-analysis shows, however, that plant species responded in general stronger to fragmentation than animal species and that the largest negative impacts of fragmentation occurred in tropical and temperate forest fragments, surrounded by a non-forest matrix. In contrast, we found only weak responses in non-forest fragments. Genetic diversity measured as mean number of alleles (A) showed the strongest response to fragmentation. Expected heterozygosity (He) and percentage of polymorphic loci (PLP) showed similar but weaker responses. In contrast, our meta-analysis indicated that inbreeding (Fis) was not measurably affected by anthropogenic habitat fragmentation. Additionally, our models revealed that effects on genetic diversity became stronger with age of fragments: We found significant negative responses for fragments older than 50 yr but not for those more recently isolated. Our meta-analyses also showed that currently animals are underrepresented in the literature on genetic effects of anthropogenic fragmentation, as are certain geographical regions and habitat types. We expect that future field studies using state-of-the-art approaches will provide further evidence of negative genetic effects, which may reinforce the here reported patterns, even for groups not yet studied.

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