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Dispersal ability predicts spatial genetic structure in native mammals persisting across an urbanization gradient

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Abstract

As the rate of urbanization continues to increase globally, a growing body of research is emerging that investigates how urbanization shapes the movement—and consequent gene flow—of species in cities. Of particular interest are native species that persist in cities, either as small relict populations or as larger populations of synanthropic species that thrive alongside humans in new urban environments. In this study, we used genomic sequence data (SNPs) and spatially explicit individual-based analyses to directly compare the genetic structure and patterns of gene flow in two small mammals with different dispersal abilities that occupy the same urbanized landscape to evaluate how mobility impacts genetic connectivity. We collected 215 white-footed mice (*Peromyscus leucopus*) and 380 big brown bats (*Eptesicus fuscus*)