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Jonathan L. Richardson

Sozos Michaelides

Matthew Combs

Mihajla Djan

Lianne Bisch

See next page for additional authors

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Authors

Jonathan L. Richardson, Sozos Michaelides, Matthew Combs, Mihajla Djan, Lianne Bisch, Kerry Barrett, Georgianna Silveira, Justin Butler, Than Thar Aye, Jason Munshi-South, Michael DiMatteo, Charles Brown, and Thomas J. McGreevy Jr.

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

Jonathan L. Richardson¹ | Sozos Michaelides² | Matthew Combs³ |
Mihajla Djan^{2,4} | Lianne Bisch⁵ | Kerry Barrett⁵ | Georgianna Silveira⁶ | Justin Butler¹ |
Than Thar Aye¹ | Jason Munshi-South⁷ | Michael DiMatteo⁸ | Charles Brown⁹ |
Thomas J. McGreevy Jr²

¹Department of Biology, University of Richmond, Richmond, VA, USA

²Department of Natural Resources Science, University of Rhode Island, Kingston, RI, USA

³Ecology, Evolution and Environmental Biology Department, Columbia University, New York, NY, USA

⁴Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Novi Sad, Serbia

⁵Department of Biology, Providence College, Providence, RI, USA

⁶Health and Human Services Department, City of Somerville, Somerville, MA, USA

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*)