

OOS 21-2 Landscape genetics of white-footed mice (*Peromyscus leucopus*) in New York City: preliminary results from a model system for investigating the evolutionary implications of urbanization

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Background/Question/Methods Urban areas were once thought of as harsh, biologically sparse environments with little ecological value, but urban habitat fragments can support substantial wildlife populations. The degree to which wildlife can move between these fragments (often city parks) is strongly influenced by the intervening urban environment. This study examines native white-footed mice and two other species in New York City (NYC) as models for the impacts of urbanization on population connectivity and genetic structure. We are using molecular genetic tools (18 microsatellite loci) in combination with geographic data sets to determine I) how many evolutionarily-unique small mammal populations exist in NYC, II) how long they have been isolated (or exchanging migrants), and III) what types of urban land use facilitate or hinder the movement of small mammals and their genes between urban habitat fragments.

Results/Conclusions

Preliminary results indicate that white-footed mice (sub)populations in NYC have become isolated over very small geographic scales in a short period of time. In the Bronx, parkways dating from the Robert Moses era are now functioning as effective barriers to migration within the city's largest parks. However, routes for migration and genetic transmission do persist in one of the world's most urbanized landscape. This project has been designed to maximize the participation and training of undergraduates that previously had few opportunities to conduct ecological research, as well as accommodate participation from "citizen science" efforts.