Rapid Evolution of White-footed Mice in New York City's Urban Forests

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Fig. 1. Sampling sites and vegetation cover in NYC. Not pictured: Black Rock Forest ~70 km north.

Fig. 2. White-footed mouse, *Peromyscus leucopus*. The NYBG harbors one of the densest populations of these mice in NYC.

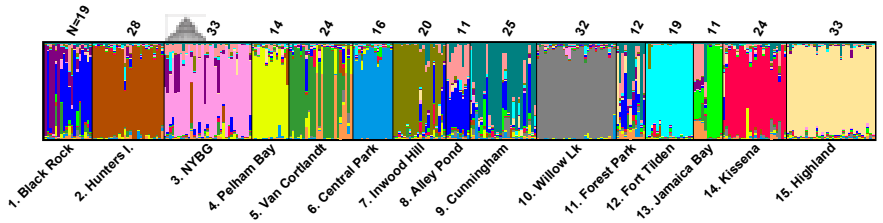

Fig. 3. We trapped 312 mice from 15 NYC locations, snipped the end of the tail to obtain DNA, and genotyped 18 genetic markers distributed throughout the genome. In the analysis above, the program STRUCTURE was used to group individual mice based solely on their genetic information (i.e. the software did not know where the mice came from). **Each colored bar represents one individual's genetic data, and each color represents membership in a unique evolutionary cluster.**

Introduction

Urbanization represents one of the most pervasive forces of human-driven change over the last century. More than 50% of the human population now occupies urban areas, and most ecosystems will experience urbanization in the near future. Severe habitat fragmentation is a frequent outcome of urbanization, and remnant habitat patches are typically managed as patches with discrete, high-contrast edges (e.g. city parks). These urban patches are likely to be small in size, dominated by invasive species, and surrounded by barriers to dispersal, but may support native wildlife with small home range requirements. However, urban patches often contain extremely high population densities of just one or a few urban "adapters". Urban adapters achieve unusually high densities due to artificially high primary productivity, less severe temperature fluctuations due to the "heat island" effect, a more stable and abundant food supply from human supplementation, and release from predators or competition. We are using molecular genetics to examine the evolutionary implications of urban fragmentation for the white-footed mouse, a common urban adapter in NYC's forests.

Objectives

I. Examine overall genetic diversity and differentiation between populations of white-footed mice in NYC.

II. Understand how the composition of the NYC landscape influences the genetic structure of these populations.

III. Identify genes that are evolving through natural selection due to urbanization in NYC.

I. Genetic Diversity and Differentiation

Fig. 4. Mice were trapped at The New York Botanical Garden and other parks using grids of 150 Sherman live traps, and then handled briefly before release.

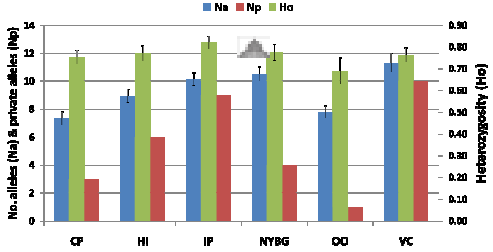

Fig. 5. Genetic variation was similar across urban sites in the Bronx & Manhattan, and remains high despite the population differentiation (Fig. 3). Variation was measured as the mean no. of different forms of each genetic marker (Na, no. of alleles), the no. of alleles found only in that population (Np, private alleles), and heterozygosity (the % individuals that received two different alleles from each of their two parents).

Fig. 6. Our lab is also examining genetic variation in the 2-lined salamander, *Eurycea bislineata*, at NYBG and other NYC sites.

II. Landscape Genetics – canopy cover and migration between Bronx populations

Fig. 6. Model of connectivity b/w Bronx populations based on "least-cost" paths (black lines) through areas with the highest tree canopy cover. Note the important role of The New York Botanical Garden in connecting Van Cortland and southern Pelham Bay parks. This modeling approach was weakly associated with gene flow b/w populations.

Fig. 7. Model of connectivity b/w Bronx populations based on a circuit theory model that includes all low-cost paths through the landscape (darker areas are better paths). This modeling approach was very strongly associated with gene flow b/w populations. These analyses indicated that ***gene flow between populations is much lower once tree canopy cover falls below 70%.***

III. Population Genomics – identification of genes under natural selection in NYC

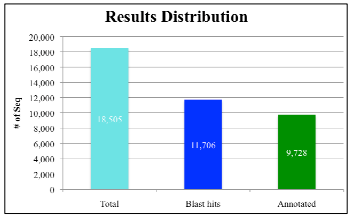

Fig. 8. Isolation and genetic variability create conditions for white-footed mice to adapt to urban environments. We have sequenced 18,000+ genes from mice at The New York Botanical Garden and 4 other sites. Nearly 12,000 were similar to previously-sequenced genes from other mammal species (Blast hits), and 9,728 have known functions discovered in studies on lab mice and rats (Annotated sequences).

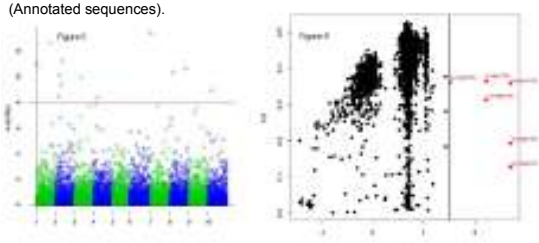

Fig. 9. These results are preliminary, but we are using multiple statistical approaches to identify genes under selection in NYC. In the two figures above, each dot represents one gene. Genes that exceed the horizontal red line (left) or vertical black line (right) significantly vary between urban and rural populations of mice. Some early candidates and their functions appear below. Substantial further work in the native woodlands at NYBG and other sites by our group will examine what these genes do and whether they are associated with the reproduction and survival of mice in urban populations.

Candidate Genes under Selection	Function (Gene ontology)
transferrin / serotransferrin	iron binding; iron transmembrane transporter activity; iron ion homeostasis
metallothionein 2	zinc ion homeostasis; detoxification of copper ion; metal ion binding; circadian rhythm
rRNA promoter binding protein	rRNA transcription; cell proliferation; transcription factor activity
apolipoprotein c-i	metabolic process; many processes involved in lipid metabolism
nadh dehydrogenase	mitochondrial; electron transport; respiratory chain
cytochrome c oxidase	mitochondrial; electron transport; oxidase activity

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