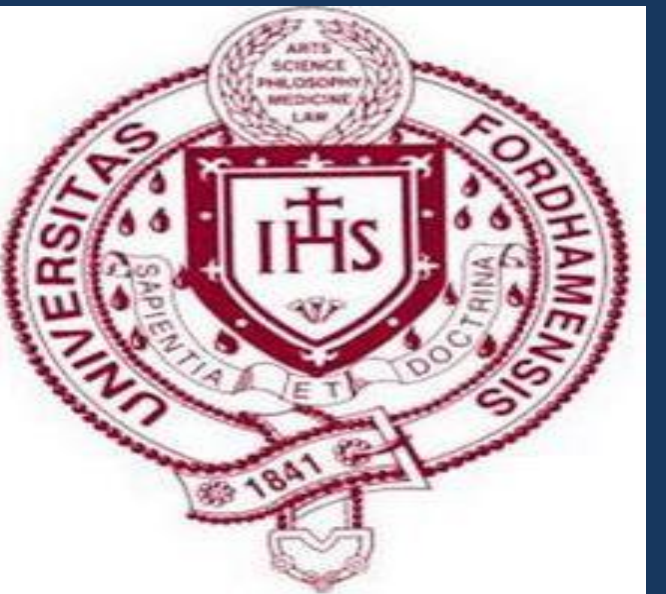




# Molecular ecology of coyotes in the New York metropolitan area

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## Introduction

- The eastern coyote (*Canis latrans*) is a generalist species that is able to adapt to new habitats and food sources easily.
- Originated in West, had a historic range across North America
- Recent expansion into the Northeast resulting from the extirpation of the gray wolf, new habitats due to human development, and its generalist nature
- Found in New York state around 1920 first arriving in North
- Recently moving into major urban areas in New York City (NYC)
- Little in known of the genetic relatedness between sites across the New York metropolitan area



Figure 1. Eastern coyote (*Canis latrans*)

- Identify number of unique individuals in each site
- Determine where these individuals are coming from
- Examine genetic relatedness between coyotes in:
  - Westchester County
  - NYC parks in the Bronx and Queens
  - Between these populations
- Movements of individuals sampled multiple times

## Collection Sites

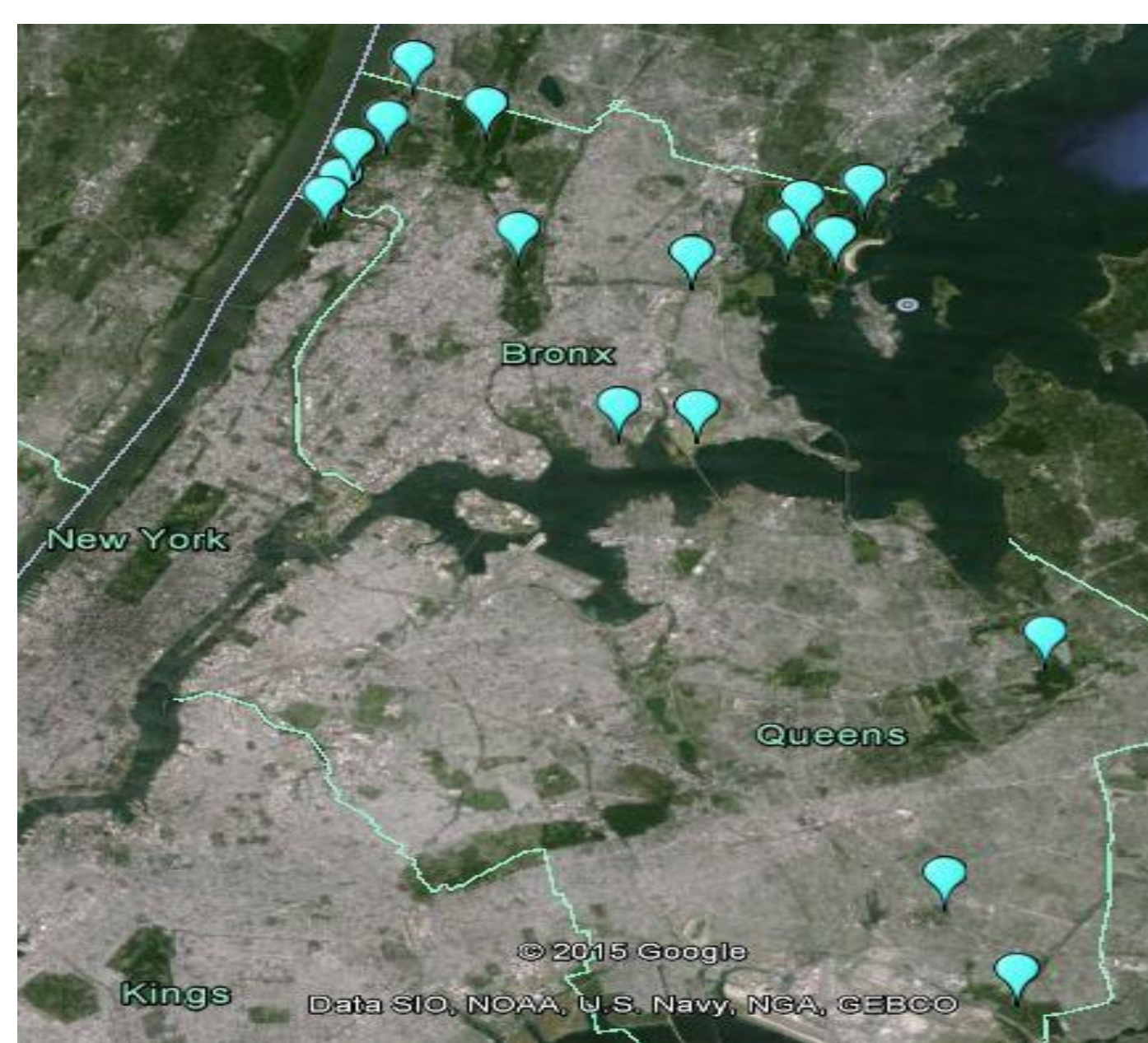


Figure 2. New York City sites (from left to right): Inwood Park, Henry Hudson Parkway, Riverdale South, Riverdale, Riverdale North, Van Cortlandt, New York Botanical Gardens, Ferry Point Park, Hutchinson River Parkway, Pugsley Creek, Pelham Bay Park, Split Rock, Turtle Cove, Bartow Pell, Railroad Park, Jamaica Bay (near JFK), Alley Pond Park

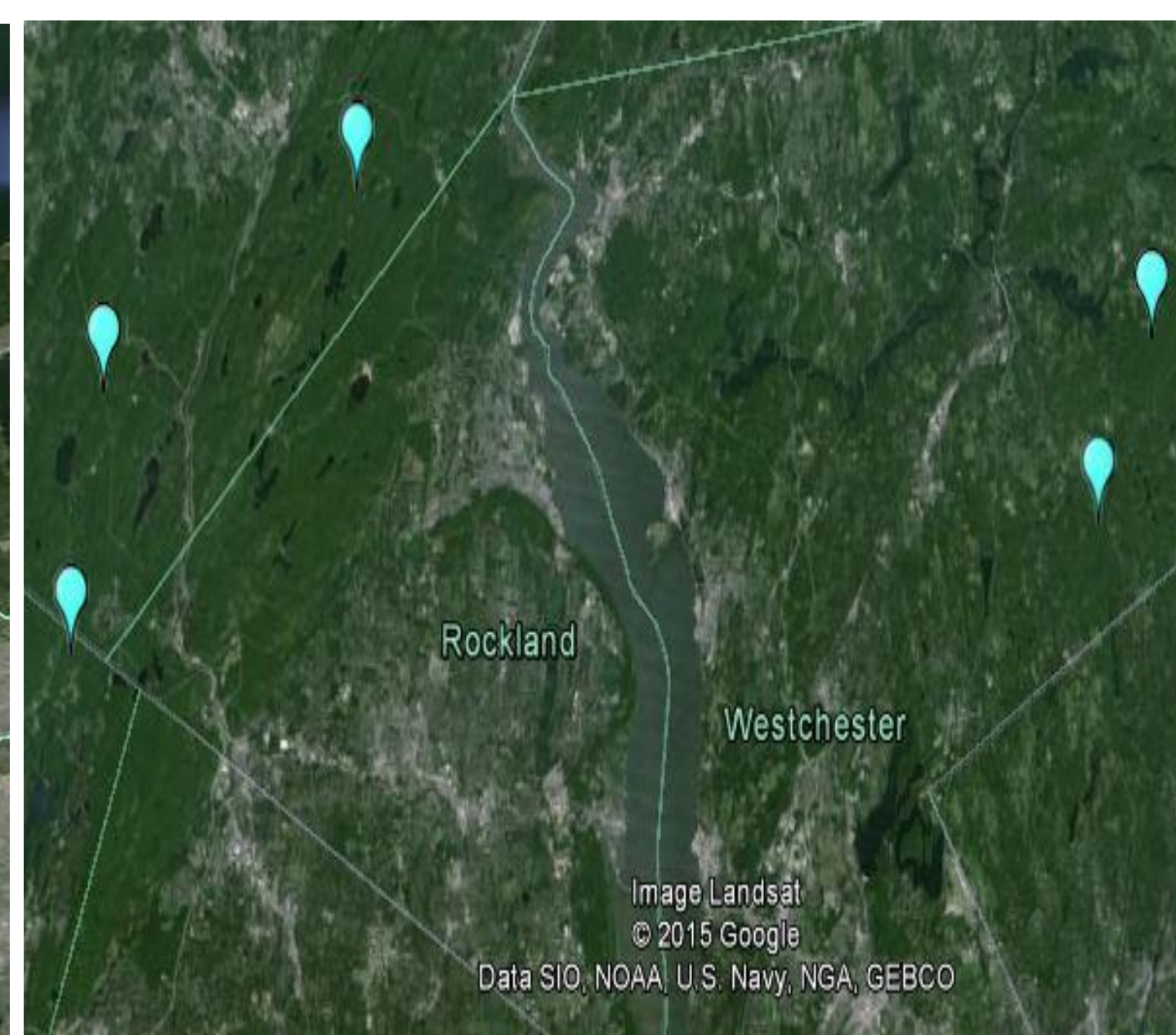


Figure 3. Ringwood Manor, Sterling Forest, Harriman State Park, Mianus River Gorge, Ward Pound Ridge

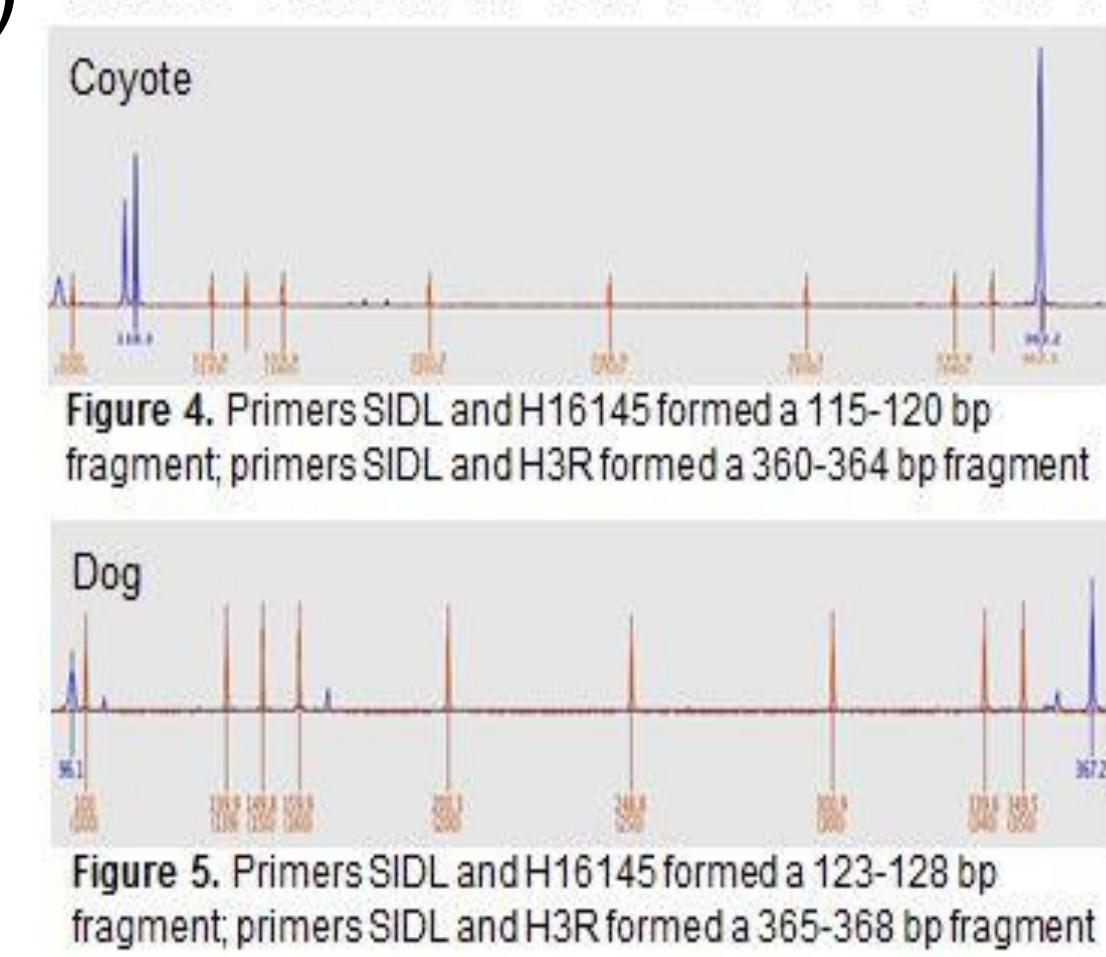
- Sample collections conducted by Gotham Coyote Project and American Museum of Natural History (AMNH)

## Methods

- Extracted fecal samples for mitochondrial DNA PCR (species identification)<sup>2</sup> and microsatellite DNA PCR (identify unique individuals/relatedness)<sup>6</sup>
- Analyzed genotypes through Geneious<sup>5</sup>, ML-Relate<sup>4</sup>, Micro-Checker<sup>1</sup>, and Colony<sup>3</sup> programs

### Extracted samples

#### Mitochondrial DNA PCR



#### Microsatellite DNA PCR

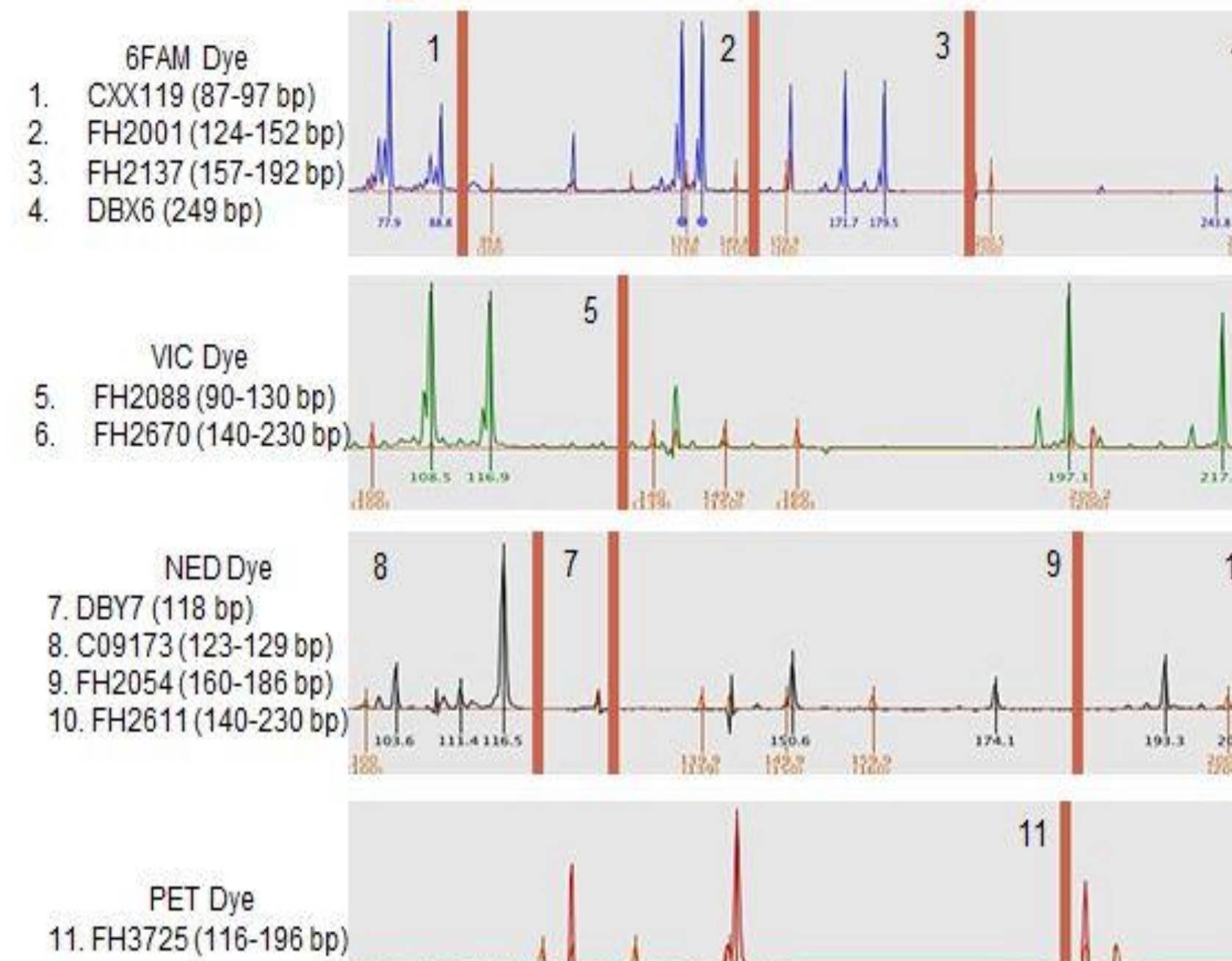
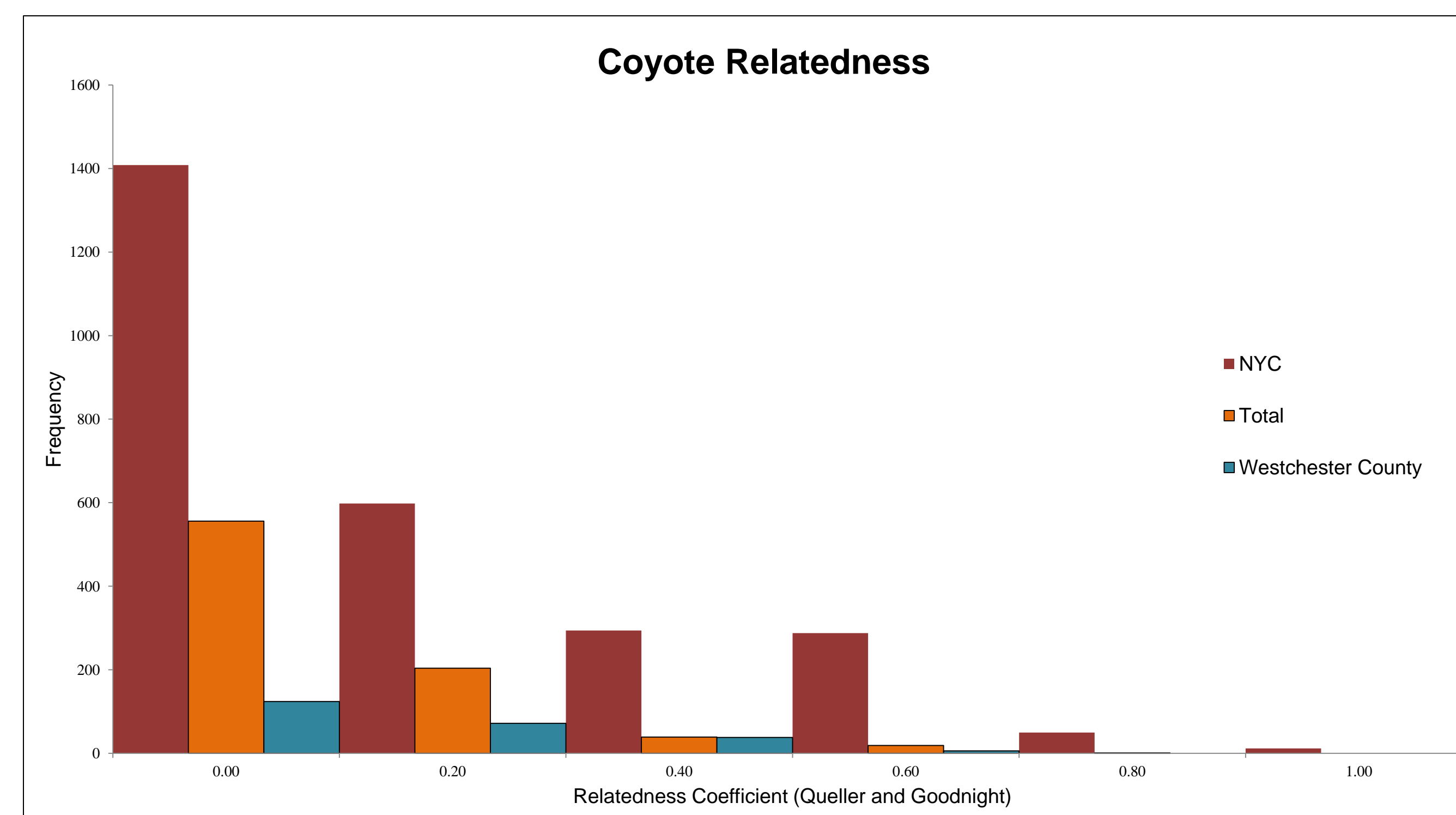


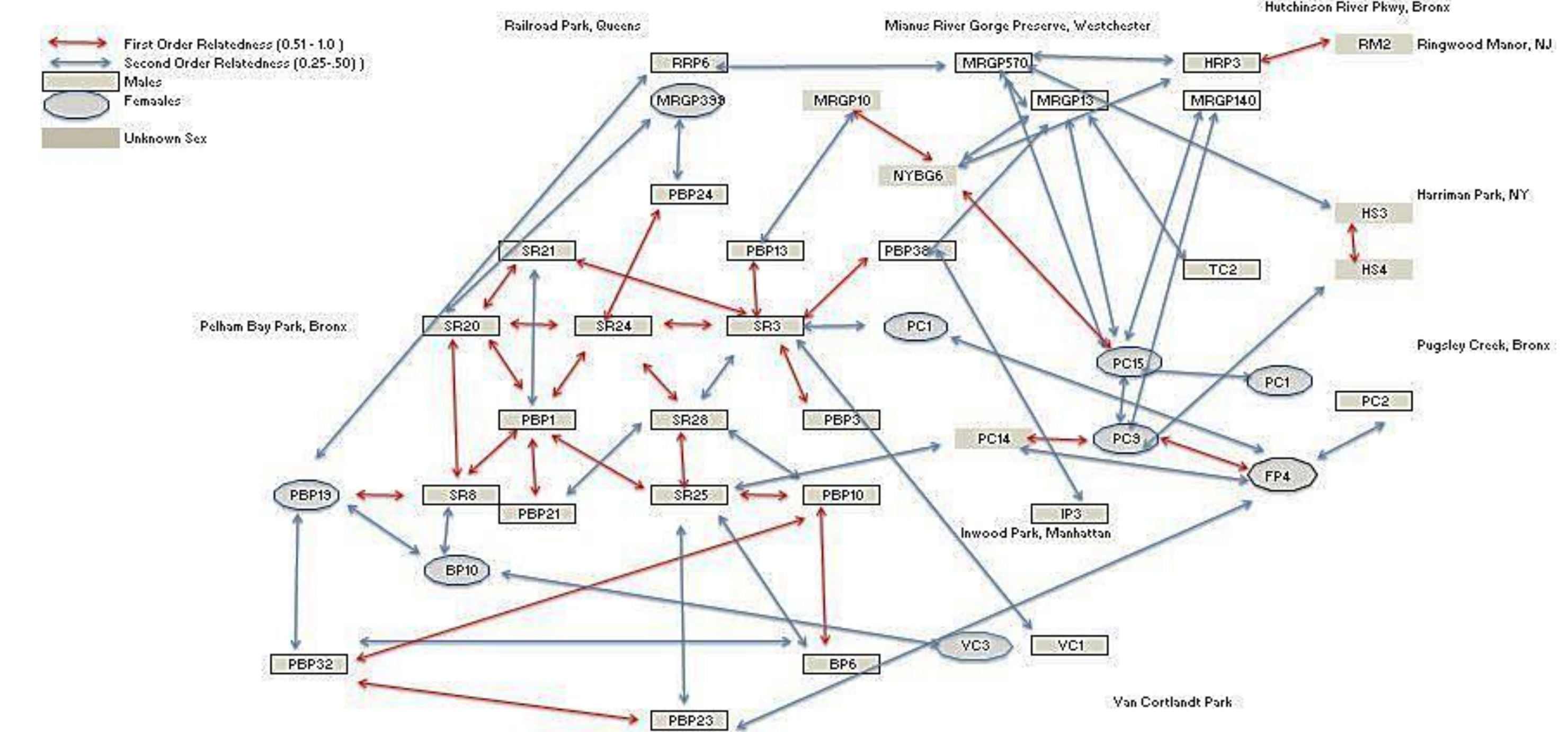
Figure 4. A mitochondrial DNA PCR was used to distinguish between coyote, dog, other carnivores and prey items and microsatellite DNA PCR was used to identify unique individuals and possible relatives

- Of the 144 mitochondrial DNA (mtDNA) PCR reactions, 78 samples were coyote, 6 were dog, and 60 were inconclusive
- Of the 190 microsatellite DNA (msatDNA) PCR reactions, 82 sample genotypes had at least 4 loci amplify
- After comparing the Queller and Goodnight relatedness coefficients<sup>7</sup> of the msatDNA samples, 65 unique individuals were isolated
- Of these unique samples, 38 were male, 15 were female, and 12 were of unknown sex



Graph 1. Coyote relatedness patterns between samples collected in only in New York City, only in Westchester County, and both sites together.

## Results (cont.)



- More male samples found possibly due to males being more mobile and possible territorial reasons
- Individuals in NYC have established family groups and are closely related (mostly 1<sup>st</sup> order relatedness) to each other
- Westchester County individuals are less related to each other than those in NYC
- Individuals that were sampled multiple times in NYC, stayed in the same general area of where the sample was collected
- An NYC individual (HRP3) likely used infrastructure to move between Westchester County and NYC as seen by close relatedness to RM2 and MRGP570

## Future Research

- Replicating the genotypes from this study
- Performing additional extractions and microsatellite PCRs
- Using these replicated results in a landscape genetic framework

## Acknowledgments

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