CHANJ Gene Flow Analysis

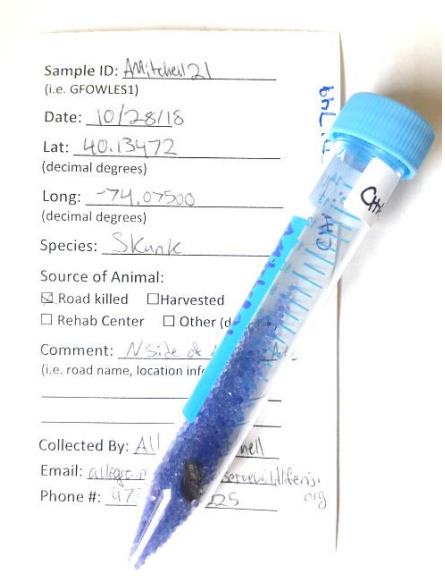
Statewide across New Jersey

Beginning in January 2018, a study is underway by the CHANJ team to assess the functional connectivity of New Jersey's landscape and the impacts that habitat fragmentation and roads may be having on our terrestrial mammal species.

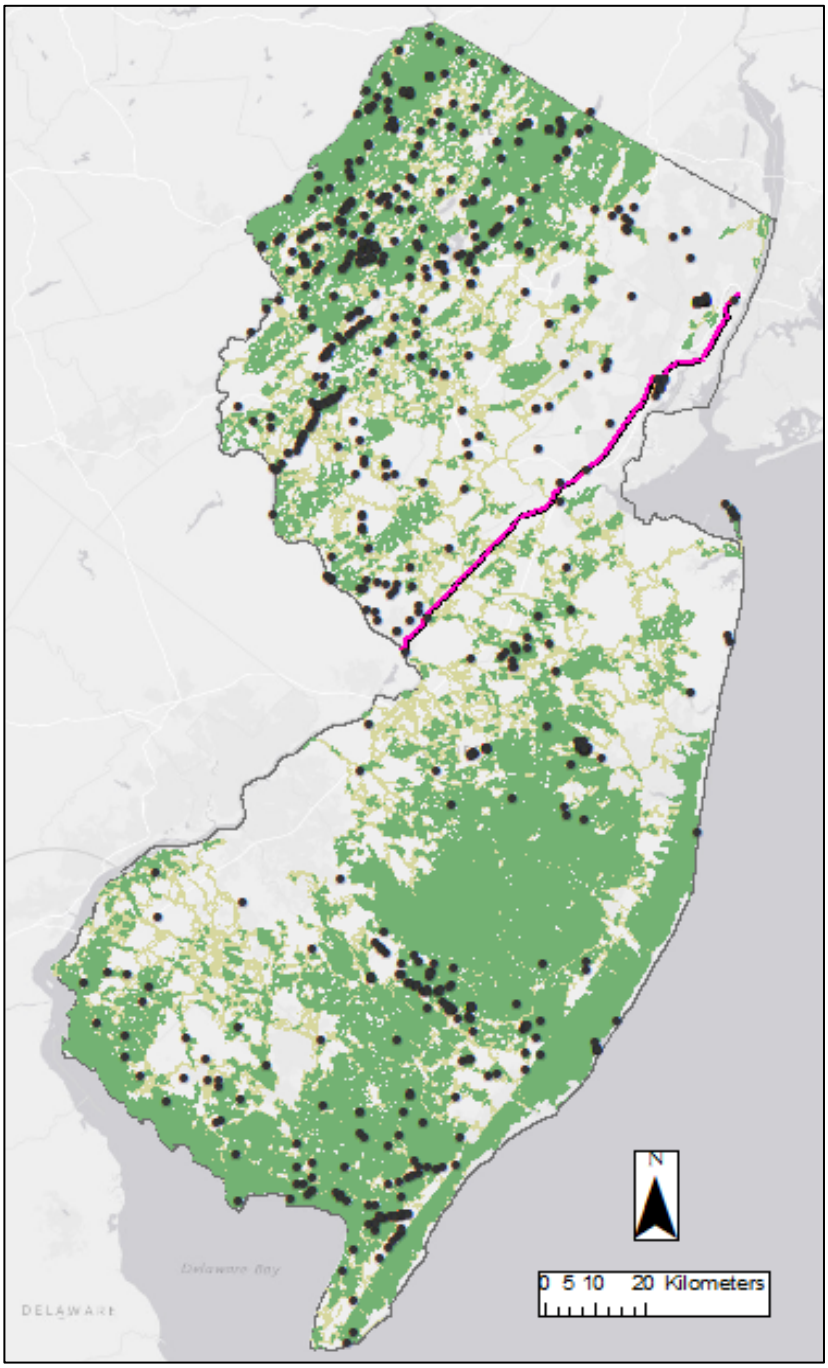
Gretchen Fowles of NJ's Endangered and Nongame Species Program samples a road-killed red squirrel. Photo by MacKenzie Hall

The goal of this project is to collect DNA samples from a variety of native mammal species across New Jersey, from wide-ranging animals like coyotes to small-ranging squirrels, mice and voles, etc. Most samples are simply a ¼" ear-clip taken from road-killed animals encountered during our everyday travels. Additional sources of DNA include wildlife rehabilitation centers, harvest check-stations, and scat specimens from other biological studies. A crew of 62 volunteers from all across NJ are now "equipped to clip" and preserve samples for this project. We aim to collect a minimum of 40 samples per species – 20 from north of the Route 1 corridor and 20 from below Route 1. Are animals (and their genes) making it across this major barrier? Are some mammal species having a harder time staying connected than others? These are questions we're hoping to answer.

The DNA samples will be analyzed by the National Genomics Center for Wildlife and Fish Conservation in Montana. From each tiny sample they will be able to determine the species, sex, relatedness (for example, a sibling or offspring relationship between two individuals), and the genetic distance between them. Our gene flow analysis will begin at the north/south scale and then delve into finer detail if the results suggest that Route 1 is, in fact, keeping some populations apart. With a robust enough sample and statewide coverage, we should be able to pinpoint the most serious barriers to wildlife movement. These insights will help to validate the CHANJ mapping tool (depicting habitat cores, corridors and barriers across New Jersey), to better inform the recommendations provided in our Guidance Document, and to ultimately target actions that will restore connectivity where it's needed most.



By the end of September 2018, a total of 683 samples from 22 different mammal species were collected from across NJ. The National Genomics Center will work on genotyping white-tailed deer, raccoon, and opossum first, given our large sample sizes of each.



At left, a map shows all samples collected as of September 2018 (shown as black dots). The Route 1 corridor is highlighted pink. This major roadway is travelled by more than 10,000 vehicles each day.

Below, the current tally of DNA samples collected to the north and south of Route 1.

Species	North	South
Beaver	9	10
Black Bear	70	0
Eastern Chipmunk	20	1
Coyote	13	5
Eastern Cottontail	15	34
Flying Squirrel	3	0
Gray Fox	1	0
Eastern Gray Squirrel	41	39
Groundhog	22	13
Mink	4	4
Mole	2	0
Muskrat	7	7
Opossum	39	25
Northern River Otter	18	42
Porcupine	3	0
Raccoon	39	35
Red Fox	34	27
Shrew	2	0
Striped Skunk	11	4
Weasel	2	0
White-footed mouse	3	4
White-tailed deer	30	45
Total	388	295

This study will be ongoing for up to 5 years (until 2022), with preliminary results being available in the interim.

See a gap in our map? If you're local and would like to help, please email Gretchen.Fowles@dep.nj.gov and we'll get you a DNA sampling kit.

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