

Authors: Kat Simone van der Meer¹, Philijoy Li², Rae Lin³, Dr. Michael Friedman⁴

¹High School for Environmental Studies, ²Staten Island Technical High School, ³Stuyvesant High School, ⁴Pratt Institute

Abstract

Salt marshes are vital ecosystems, supporting diverse plant and animal life, buffering storms, and filtering pollutants. **Seasonal changes** influence resident and migratory species' adaptations and behaviors, particularly regarding migration timing. Climate change, including sea-level rise and altered weather patterns, significantly threatens these ecosystems, negatively impacting plant communities, nutrient cycling, and avian habitats. This study analyzes patterns and factors impacting salt marsh avian biodiversity using **E-Bird data** and **DNA barcoding**. Of 50 samples, 20 specimens were identifiable using **BLAST**, revealing a small fraction of the Marine Nature Study Area's biodiversity. While the small sample size limits conclusions about climate change impacts, our observations may reflect potential effects on food supply, nesting sites, and bird displacement due to **habitat loss and climate change**.

Introduction

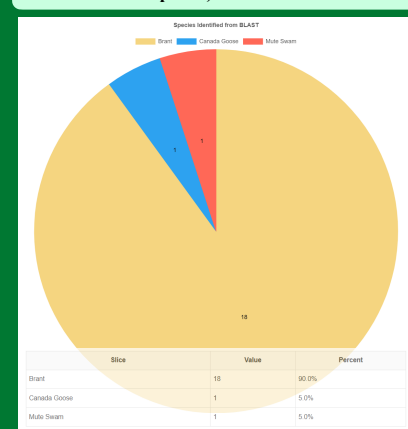
The Marine Nature Study Area, or MNSA, located in Oceanside, Long Island, New York, is a nature preserve comprising 52 acres of salt marsh, sand dune, and wooded areas. Salt marshes are coastal wetlands characterized by moist soils and high salinity. The sub tidal zone is normally underwater, with aquatic plants and fauna. The intertidal zone is subject to regular tidal flooding (Li et al. 2022). Certain halophytic grasses suited to tolerate the high salinity are found in the intertidal zone. Farther up, the upper intertidal zone and super tidal zone have less frequent tidal flooding and higher diversity of halophytic grasses and soil plants with lower salinity tolerance.

It has become increasingly essential to assess the avian biodiversity of this IBA in order to maintain ecosystem stability and resilience against climate change and anthropogenic pollution. This study will focus on the prevalent bird species in the salt marshes of the MNSA on Long Island. Common birds in the area include the brant, Canada goose, mourning dove, salt marsh sparrow, and many more. The MNSA is recognized as part of an Important Bird Area by Audubon NY, and being on the path of the Atlantic Flyway, it is crucial for avian biodiversity conservation (Audubon New York, n.d.).

This study aims to assess the prevalent bird species in the MNSA during the fall migration period and changes in migratory patterns over the past 3 years using data from this year's feather sampling and previous UBRP data as well as eBird. To what extent has the avian population demographics in the MNSA salt marsh on Long Island been altered in the past 3 years, and what factors have influenced the results? From reviewing eBird data, we believe that there will be significant differences in population demographics of common avian species observed this fall compared to previous years due to an earlier sampling date, the rapid acceleration of climate change, and variable environmental conditions affecting the biodiversity of New York. (Cornell Lab of Ornithology, n.d.).

Results

Figure 1. A visualization of the data noted in Table 2 (Slice → Species; Value → # of specimens identified as said species)



Bird #	Accession #	Bit score	Results	Species	Quadrant + Total Zone
Brd 3	GU571279.1	884	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	B. Zone 3
Brd 8	GU571279.1	1247	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 11	GU571279.1	1086	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 15	GU571279.1	887	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 23	GU571279.1	1110	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 26	GU571279.1	1131	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 30	GU571279.1	1132	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 33	GU571279.1	1136	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 36	GU571279.1	1109	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1
Brd 40	GU571279.1	1142	Branta bernicla voucher NHMO-BC104 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Brant	C. Zone 1

Table 1. The figure above lists most specimens that returned BLAST results. A total of 20 specimens were returned, with 3 identified species: Brant (90%), Canada Goose (5%), and Mute Swan

Materials and Methods

- In late November of 2026, our group collected 92 bird feathers from a salt marsh in the Marine Nature Study Area, Oceanside, NY
 - Randomized modified quadrant approach with 5 squares, lettered A-E, dimensions of 5x5 yards.
 - Every feather seen in the 5x5 yard quadrant was collected using sterile gloves. Observations were recorded.
- For the DNA barcoding process, 50 feathers were randomly selected from the 92 feathers collected. One positive control (a Parakeet feather) and one negative control (no sample) were added. These 52 samples went through the incubation and PCR.
 - To lyse the keratin in the feathers, a prolonged incubation and the reagent dithiothreitol (DDT) was used (Lijtmaer et al., 2012)
 - To amplify the COI gene for the Qiagen DNA extraction, the samples were subjected to PCR using the Qiagen DNEasy Blood and Tissue Kit.
 - Two sets of forward and backward nested primers for the COI mitochondrial gene: BirdF1 and COIBirdR2, AvMiR1 and AvMiF1
 - Gel electrophoresis on PCR results was conducted. Gel electrophoresis allows for contamination detection such as primer dimers, degraded DNA, or RNA contamination (Lee et al., 2012). The results showed there was a **contamination issue**.
 - DNA learning center ran the PCR again, with only external primers.
 - Of the 52 gels, 20 showed no contamination.
 - The 20 samples were sent to Genesis for sequences
 - The sequences were identified and BLASTn using DNA Subway 2.
- Errors occurred during the DNA lysis and extraction process.
 - The lysis process did not fully dissolve the feathers. Material got clogged in the collection tubes, which leads to extraction issues.
 - We removed large debris from these tubes, which may have lowered the concentration of DNA to sequence.
 - To prevent in the future: Add more proteinase K, increase time in the shaking incubator, and cut the feathers in smaller pieces.

Discussion

- Our specimens, although not high in the number of unique species, all correspond to the top 25 species noted in the Marine Nature Study Area. The presence of a Mute Swan and Canada Goose feather in zone 2 likely indicates habitat alteration that is generally bad for native ecological health.
 - Because of warmer climates, Canada geese are less inclined to fly south, which results in reduced migration during the year. On the other hand, mute swans generally have non-migratory behavior.
 - The Brant was the most common from our results, which makes sense; zone 1 is their primary wintering habitat, providing access to food before the winter freeze. They also have larger and more robust feathers, which could have led to more reliable sequencing.
 - Although they show high adaptability, sea level rise is destroying coastal wetlands and eroding intertidal zones, causing brants to rely on inland areas such as fertilized golf courses and urban parts for alternate food sources.

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