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Table of Contents

Editorial

4

Papers:

The Spatial Abundance of Mollusks Species Through the Tidal Profile at Sunken Meadows State Park Beach

Asiedo Freda Owusu

7

Creation of a Novel Genotyping Assay to detect a LDLR Variant Related to Familial Hypercholesterolemia

Bassey A., Singh A., Thomas D., Kusenda M.

11

Native Black Tupelo (*Nyssa sylvatica*) is a Dominant Tree Species in Brentwood & East Islip, NY

Michelle Castillo

22

The Suffolk County Community College Nature Preserve is in Mid Succession between a Coniferous and Deciduous Forest

Tiffany Cuellar

30

Non-Native Plant Species Outnumber Native Plant Species on a Residential Property in Deer Park, Long Island, New York

Matthew Egger

36

Coniferous Trees are Dominant to Deciduous Trees in Huntington Station, New York

Enelda Fuentes, Marjorie Edwards Brown, Miguel Manzanares

41

Analysis of Amoxicillin Resistance in *Escherichia coli* through selective pressure

Jaicel Lopez, Sanawal Farooq, Anusha Fatima, Sean Sarmiento, Amy Linares

48

**Eastern White Oak is the Dominant Tree Species at West Hills Dog Run Parks in Huntington,
New York**

Lorenzo J., Montana G., Shiraishi C., Tyburski F.

53

Deciduous Trees Are Dominant to Coniferous Trees on a Private Property in Southold N.Y.

Jamie McCarthy

58

Editorial

The purpose of the *Science and Technology Undergraduate Research Notes (SATURN) Journal* is to provide a venue for publication of undergraduate research. This research may include any novel findings of note while providing an opportunity for undergraduates to experience dissemination of their findings to the scientific community. Our goal is for the *SATURN Journal* to serve as both an educational and research tool. Each publication in this issue of the *SATURN Journal* has been reviewed by the professor for the course and by an outside scientist. Worthwhile data from embedded research in laboratory course curricula can be disseminated to the world community. By contributing their own novel findings for the greater good, students can be engaged in science through embedded research pedagogy more than through conventional pedagogy, and a source of large-scale cataloging information can be developed by many students contributing novel data.

The *SATURN J. Tree Survey* pedagogy is an ongoing, cost competitive method of including embedded research in a non-majors science course, and has been successfully implemented at SCCC since the Spring Semester of 2012. It easily fits into the curriculum of contemporary Principles of Biology non-major science courses. Also, it has evolved into an instructed, crowd sourcing method for research that can readily be adopted by other institutions. This pedagogy has the capacity to provide valuable and long-term undergraduate research experience nationwide. The *SATURN J.* began its' first issue with students from a Principles of Biology class at Suffolk County Community College (SCCC) in New York contributing their findings from a research project embedded in the laboratory curriculum. Specimens of each tree found on residential properties were brought to class. The species of each tree was identified by using a traditional dichotomous key. Students collaborated in groups to develop hypotheses based on the locations of the properties where the trees were found, the distribution of species, circumferences of trunks and population densities. The students followed the instructions for authors at the web site for the *SATURN Journal* (www.saturnjournal.org), and submitted their manuscripts to their instructor who acted as a peer reviewer. Those students whose manuscripts were accepted upon revision received a grade of "A" and were given extra credit for the revision and publication. This has been a cost-effective exercise that has resulted in enthusiastic student engagement, and is building a catalogue of the distribution of tree species on residential properties in Suffolk County, New York. There was also a publication in this issue by a group of students who were enrolled in a statistics course. They compared the growth rates of different cultivars of the American Elm (*Ulmus americana*) planted on campus at SCCC.

In the second issue of the *SATURN Journal* there was a continuation of student publications pertaining to the embedded research project analyzing tree species distribution. Students found it helpful to compare their findings to the findings of student investigators who have published previously in the *SATURN Journal*, which resulted in citations of previously published students. The second issue also contained publications from a research project embedded in a microbiology course from which students reported their findings from tests of the antimicrobial properties of spices.

In the third issue of *SATURN J.* there was continuation of the tree survey and studies on the antimicrobial properties of spices that produced publications in the previous journals. New publications compared findings to a larger battery of previously identified trees. Students used the web site from the United States Geological Survey (www.usgs.gov) to report the latitude and longitude of properties included in the studies. Additional web-based tools used by students included online dichotomous keys such as vTree at Virginia Tech located in Blacksburg, Virginia (<http://dendro.cnre.vt.edu/dendrology/ident.htm>).

The fourth issue of *SATURN J.* included an article published by students at Molloy College regarding sweeteners and inflammation in macrophages, three additional articles from the microbiology course at SCCC, and a continuation of the *SATURN J.* tree survey. In addition, the abstracts from the MAY 2014 Northeast Regional Sigma Xi Conference held at SUNY Old Westbury were presented.

In the fifth issue of the *SATURN Journal* we presented an additional article from the microbiology course at SCCC that compares soil bacterial communities on Long Island, and multiple articles that continue the *SATURN J.* Tree Survey.

In the sixth issue of the *SATURN Journal* we presented additional articles from the microbiology course at SCCC that compares soil bacterial communities on Long Island. In addition, we presented two articles from students at Molloy College that test the effects of teratogens on *Planeria*. We present an article that is a statistical analysis of a 2016 presidential poll. We also presented multiple articles that compare soil composition, and multiple articles that continue the *SATURN J.* Tree Survey. Both are from a Principles of Biology course at SCCC.

In the seventh issue of the *SATURN Journal* we presented an additional article from a microbiology course at SCCC that compares soil bacterial communities on Long Island, an article that compares soil composition from a Chemistry course, and an article that is a statistical study of variables on opinions regarding voting preferences. We also presented multiple articles that continue the *SATURN J.* Tree Survey from a Principles of Biology course at SCCC.

In the eighth issue of the *SATURN Journal* we presented an article on the effect of carboplatin on tadpole and planarian regeneration, an article on the effects of dopamine and serotonin on bacterial growth, and an article that is a statistical study of variables on opinions of travel bans. We also presented multiple articles that continue the *SATURN J.* Tree Survey from a Principles of Biology course at SCCC.

In the ninth issue of the *SATURN Journal* we presented an article on the identification of a housekeeping gene for use in inflammatory studies, an article pertaining to the water quality of a lake in a developing watershed in Minnesota, and an article that is a statistical study of variables on opinions regarding gun control. We also presented multiple articles that continue the *SATURN J.* Tree Survey from a Principles of Biology course at SCCC.

In the tenth issue of the *SATURN Journal*, we presented two articles authored by students in Ramsey Community College in Minnesota. One of these articles is a study on wildlife restoration, and the other is a water quality study. We also presented multiple articles that continue the *SATURN J.* Tree Survey from a Principles of Biology course at SCCC.

In the eleventh issue of the *SATURN Journal*, we presented a study of the distribution of hard-shelled ticks (*Ixodidae*) in preserves on Long Island, NY. We also present multiple additional articles that continue the *SATURN J.* Tree Survey from a Principles of Biology course at SCCC.

In the twelfth issue of the *SATURN Journal*, we presented a study of variants in the MC4R gene that could potentially contribute to obesity and weight gain from students at Molloy College in N.Y., a second study from students at Molloy College of the MC1R gene and ageing rate and potential skin carcinoma predispositions, and a DNA barcoding study of a dietary profile for the American Cliff Swallow from students at Moreno Valley College, CA. We also presented multiple additional articles that continue the *SATURN J.* Tree Survey from a Principles of Biology course at SCCC. Many of these articles were written by students taking classes during the pandemic, and all of the resources used to

collect and analyze data were available for free online.

In the thirteenth issue of the *SATURN Journal*, we presented a study of the FIGLA gene in humans that affects fertility from students at Molloy College in N.Y., a second study from students at Molloy College of the PPP4C gene and its involvement in autism, and SCCC student's study of a comparison of worm growth and reproduction between a compost pile and natural soil. We also present multiple additional articles that continue the *SATURN J. Tree Survey* from a Principles of Biology course at SCCC.

In this fourteenth issue of the *SATURN Journal*, we present two studies of hypercholesterolemia from students at Molloy University. From students at Suffolk County Community College we present a study of Molluscs on Long Island and a study of amoxicillin resistance. We also again present multiple additional articles that continue the *SATURN J. Tree Survey* from a Principles of Biology course at SCCC.

We encourage instructors to have their students participate in the *SATURN Journal*. The publications in the journal are a source of embedded research project designs that instructors may include in their curricula. The journal serves as a venue for dissemination of student research and a source for students to compare their work to the work of others. Instructors are welcome to design additional projects from which their students can submit manuscripts.

Louis Roccanova, Ph.D.

Editor in Chief *SATURN Journal*

The Spatial Abundance of Mollusks Species Through the Tidal Profile at Sunken Meadows State Park Beach

By Asiedu Freda Owusu

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Keywords: Suffolk County, North Shore Beach, mollusks, invasive species, Oysters, Tides, Bivalves, Gastropods, Common Atlantic Slippersnail, Common Jingle.

Abstract:

Nine different species of Gastropods and Bivalve seashells were surveyed at Sunken Meadows State Park Beach, on the Coastline of the North Shore beach in Suffolk County, New York. A total of 237 shells were surveyed including a total of nine species detected. These mollusks were recorded during the lowest tides in the intertidal zone at Sunken Meadows State Park Beach. The results show that the dominant species were the Common Atlantic Slippersnail (*Crepidula fornicata*) and the Common Jingle (*Anomia simplex*).

Introduction:

The Intertidal zone is an area along the coastline of a beach where the ocean meets the land between high and low tides (NOAA 2023). The species in this zone are best observed when the tide reaches its lowest levels. At that stage, these species are exposed to air.

The Coquina clams range from 0.4 millimeters (about 0.02 in) to 25.4 millimeters (about 1 in) long and migrate to the intertidal zone of beaches by burrowing themselves in the sand during the high tide. They have colorful shells and serve as a food source for several species including birds, some species of crabs and even humans.

Method:

The procedure was a modification of Flanc (2019). Mollusks shells were collected periodically at regular intervals with the decrease in tide of the intertidal zone. The location of this survey at Sunken Meadows State Park Beach has a longitude of 40.910 and a latitude of 73.245 and was obtained by using Google Maps on a smartphone. The high tide of the day was 10:40am (NOAA 2023) and arrival time was 11:00 am. The official starting time of the experiment was 11:40am. An original line with a length of 6 meters was drawn in the sand alongside the highest tideline at 10:40am. Width lines of 4 meters were measured with a tape measure and drawn for the first tide box (box 1) to be surveyed. This box extended downhill towards the location of the tide line at 12:40pm. Every hour, a new box was drawn in which 4 more meters of width were added to the preceding box and extended downhill toward the sea tide line. A total of 4 tide boxes were drawn (Boxes; 1,2,3 and 4). Each box was drawn, observed, and identified at an hour interval with Seek phone application by INaturalist Team (2023). The final box was drawn at 2:40pm and the species of Mollusks were collected from each box drawn at a one-hour interval. The official end time of the survey was 3:00pm.

Results:

Bivalves' species were in greater abundance than Gastropods, however, the number of Gastropod shells outnumbered Bivalve shells. The total Percentage of Gastropods recorded is 85.3% and the total percentage of Bivalves is 14.8%. The Common Atlantic Slippersnail (Gastropod) and the Common Jingle (Bivalve) were the dominant species in the tide boxes. They recorded 81.9% and 8.9%

respectively, of the total species collected. Invasive species such as the Fighting Florida Conch (*Strombus alatus*), Common Jingle (*Anomia simplex*) and Lettered Olive (*Oliva sayana*) were recorded in the tide boxes (as seen in Table 1)

Table 1: Classes of Mollusks and their Quantity

Shell Type	Scientific Name	Quantity	Class	Percentage
Common Atlantic Slippersnail	<i>Crepidula fornicata</i>	194	Gastropod	81.9%
Lettered Olive	<i>Oliva sayana</i>	1	Gastropod	0.4%
Eastern Mudsail	<i>Ilyanassa obsoleta</i>	3	Gastropod	1.3%
Florida Fighting Conch	<i>Strombus alatus</i>	4	Gastropod	1.7%
Common Jingle	<i>Anomia simplex</i>	21	Bivalve	8.9%
Coquina	<i>Donax trunculus</i>	2	Bivalve	0.8%
Atlantic Kitten's Paw	<i>Plicatula gibbosa</i>	5	Bivalve	2.1%
Atlantic Jackknife	<i>Ensis directus</i>	3	Bivalve	1.3%
Eastern Oyster	<i>Crassostrea virginica</i>	4	Bivalve	1.7%

A Chi Square test of independence was then calculated to determine if there was a significant difference in the

number of gastropods and bivalves compared in the two shoreside boxes (Box 1 and 2) to the two Sealine boxes (Box 3 and 4). The result of the Chi Square test of independence is 0.6469. This result was below the critical value of 7.815 in the Chi Square chart. This shows that there is a no significant difference in the number of gastropods and bivalves compared in the two shoreside boxes (Box 1 and 2) to the two Sealine boxes (Box 3 and 4).

Chi Square Calculation for Table 2:

	1/2	3/4
Bivalves	A (31)	B (4)
Gastropods	C (168)	D (34)

$$X^2 = \frac{(AD-BC)^2}{(A+B)(C+D)(A+C)(B+D)}$$

Where A and B represent the total number of Bivalves in tide boxes (1 and 2) and (3 and 4) respectively. C and D represent the total number of Gastropods in tide boxes (1 and 2) and (3 and 4) respectively.

Table 2: Tide Times for observation

Tide Time	Water Lost and Width Measured	Box Drawn	Total number of Gastropods	Total number of Bivalves
10:40am	0 Meters	High Tide	0	0
11:40am	4 Meters	Box 1	117	23
12:40am	4 Meters	Box 2	51	8
1:40am	4 Meters	Box 3	24	3
2:40am	4 Meters	Box 4	10	1

Discussion:

Majority of the Mollusk shells collected were native of Long Island, however, they were in small quantities. Invasive species such as the Fighting Florida Conch (*Strombus alatus*) which is a native of the coast of North Carolina to south Florida (Davis 2005), Common Jingle (*Anomia simplex*) which is a native of Northwest Atlantic from Cape Cod to Brazil were recorded in the tide boxes. The Common Atlantic Slippersnail (*Crepidula fornicata*) which was the most dominant species is also an invasive species to Long Island. The Common Atlantic Slippersnail is a native of the east coast of the United States of America (Burgess 2020). Species such as these can be spread through the unintentional activities of humans, and they grow rapidly in suitable environments. Some ways in which species such as this spread include the ballast water of ships and the propellers of smaller boats. In his paper, Flanc (2019) also discovered Eastern Oyster (*Crassostrea virginica*) in his survey, however, he recorded a larger number of these Mollusks (11 shells) than I recorded in my survey (4 shells).

Conclusion:

In conducting this survey, I discovered that the closer to the low tide line, the lower the abundance of mollusks. The last box measured (Box 4), recorded the lowest number of Mollusks, 11 out of 237 shells. Even though Bivalve species outnumbered Gastropods, Gastropods recorded a larger percentage of shells, that is, 85.3% of shells recorded. Secondly, I discovered that, the closer to the low tide line I measured, the fewer the diversity of the mollusks. In comparing the diversity between the First and Last Boxes, Boxes (1 and 4) respectively, Box 1 recorded more abundant diversity including; the Fighting Florida Conch (*Strombus alatus*), Coquina (*Donax trunculus*), Common Jingle (*Anomia simplex*), Eastern Mudsail (*Ilyanassa obsoleta*), Lettered Olive (*Oliva sayana*), and the Common Atlantic Slippersnail (*Crepidula fornicata*). Box 4 recorded less diversity including; the Common Atlantic Slippersnail (*Crepidula fornicata*) and the Eastern Oyster (*Crassostrea virginica*).

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Creation of a Novel Genotyping Assay to detect a LDLR Variant Related to Familial Hypercholesterolemia

Authors: Bassey A., Singh A., Thomas D., Kusenda M.

Keywords: Biology, Genetics, Familial Hypercholesterolemia, Genotyping

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Abstract

Familial Hypercholesterolemia (FH) is a genetic condition in which low-density lipoprotein (LDL) cholesterol levels are elevated beyond what is considered normal, resulting in a buildup of plaque in the bloodstream. Left untreated, this disorder increases the risk of cardiovascular disease that can result in myocardial infarction. The prescribed use of statins may lower cholesterol levels if the disease is caught later in life, but preventative treatment such as increased exercise levels with an emphasis on a heart healthy diet is most effective when started before the onset of symptoms. FH can be inherited through a mutation in the low-density lipoprotein receptors (LDLR) gene found on chromosome 19. A missense mutation creating single nucleotide variation (SNV) rs768563000 results in a change of the 11,106,587th base pair from G to A within an exon (E240K). This study proposes a method to identify a significant pathological difference between the DNA of those with and without the identified variant, ultimately contributing to the early detection and prevention of familial hypercholesterolemia. Using bioinformatic techniques, a Polymerase Chain Reaction (PCR) assay with a restriction enzyme protocol was created to amplify and isolate the region of the SNV, which could be run through gel electrophoresis to distinguish the difference between a person with the wild-type allele (G) and a person with the mutated allele (A). This technique could be used to determine from a young age if a person is susceptible to developing FH, so they can begin holistic interventions early and have more positive long-term results.

Introduction

LDL cholesterol is abundant in the liver and, once broken down, can be released for other cells to store, use, or remove. Familial hypercholesterolemia is a genetic disorder characterized by abnormally high levels of LDL cholesterol ($\geq 190\text{mg/dL}$) that the body cannot remove in totality from the bloodstream. Symptoms include fatty deposits in the eyelids, knees, and elbows, chest pain, and fatigue at a young age (14). Individuals with this condition may have up to a 20-fold increase in their lifetime risk of cardiovascular disease (13). FH is inherited in an autosomal dominant pattern, meaning that if one parent is diagnosed with FH and has heterozygous alleles, they will have a 50% chance of passing it on to their children (14). Though there is no known cure, knowing if a person is carrying one of the genetic variations for FH can allow early interventions to begin before any symptoms appear. Establishing healthy lifestyle habits like a well-rounded diet and regular exercise during childhood may prevent cardiovascular disease and other related conditions from forming. Should a higher cholesterol level present over time, administering medications such as statins can decrease the presence of LDL in the bloodstream (2). Early identification and intervention has been shown to drastically reduce the risk of heart disease in individuals with mutations predisposing them to FH (14).

This study aims to create a genotyping assay for a pathogenic variant associated with FH to improve disease screening protocol. To begin, a suspect variation in the LDLR gene was identified as SNV rs768563000 (1). Typically, the allele at this position is found in the form of guanine (G), acting as a major allele. When acting as a minor allele, it is found as adenine (A). This change results in a

missense mutation, causing a different amino acid to be incorporated into the resulting protein during translation. In particular, this SNV substitutes glutamic acid (E) for lysine (K). Glutamic acid is a positively charged amino acid, while Lysine is a negatively charged amino acid. This change may lead to altered protein function due to the disruption of side-chain interactions that contribute to the protein's folding pattern and stability. In order to test this, a PCR assay was designed with a restriction enzyme protocol to prepare DNA samples for analysis using gel electrophoresis. If successfully performed, the DNA would differentiate between strands with the genetic variation (G-A) and those with the wild-type allele (G). The optimal restriction enzyme was found to be EcoRI, which cleaves the LDLR gene after the wild-type nucleotide, but does not cut after the mutated one. This will create a size difference in the DNA fragments that can determine if the mutation is present or not.

Methods

Bioinformatics

- The University of California Santa Cruz Genome Browser was used to explore LDLR on the (GRCh38/hg38) genome in order to sequence the gene and identify its normal function (8).
- The gene was then entered into the National Center for Biotechnology Information (NCBI) dbSNP database to narrow down and select a SNV that was associated with potentially pathogenic phenotypes. SNV rs768563000 was chosen due to its low global allele frequency (0.0051%) and its presence within an exon (position chr19:11106588), both of which are potential signs of pathogenic effects (3).
- 500 base pairs on either side of the SNV were extracted from the sequence, creating a 1,000bp sequence that could be entered into Primer3 and used to identify the most effective left and right primers for PCR testing (9).
- An 11bp section surrounding the SNV was entered into New England Biolabs (NEB) cutter V2.0 twice, once with the wild-type nucleotide (G), and once with the mutated nucleotide (A). The restriction enzyme EcoRI was selected for this experiment PCR protocol, as it was found to cut the wild-type right after the highlighted G, but not after the SNV-affected A (11).
- With the ideal restriction enzyme identified, the hypothetical protocol for a PCR assay followed by gel electrophoresis was designed. The final bioinformatic step was to identify structural changes in the LDLR protein due to the mutation.
- The gene was run through MusiteDeep to predict modifications that may be made post-translation but prior to secondary structure formation (12).
- To predict the secondary structure of the mutated protein, the gene was processed using the Phyre2.2 search engine (5).
- Finally, any changes to the protein structure that occurred during the creation of the tertiary structure were predicted using MutPred2 (4).

Bench Work

The PCR protocol for this assay would follow the *QIAGEN Multiplex PCR Protocol* from Qiagen (6). This protocol requires Qiagen Master Mix, a left and right primer, water for buffering, and a sample of DNA from a person with the SNV-affected A allele. Using a thermocycler, the PCR would be run at 95°C for 5 min to achieve total denaturing, followed by 30 to 40 cycles (95°C for 15 sec, 64°C for 30 sec, and 72°C for 20 sec) for amplification. Lastly, the PCR would run at 72°C for 10 min to create the final product, followed by a 4°C hold to stop the taq polymerase and keep the products stable. The restriction enzyme EcoRI will be added to the PCR at this point, and processed using the *Protocol for*

Digestion of PCR Products Directly after Amplification from Thermo Fisher Scientific (7). This portion of the reaction runs at 37°C for around 8 hours. Once the PCR is completed in full, the samples would be run on 1% agarose gel for 20 minutes using gel electrophoresis, followed by visualization of the gel using an alpha imager.

Results:

SNV rs768563000 was confirmed to be pathogenic by the NCBI ClinVar system (Table 1). This finding would be corroborated by the PCR and gel electrophoresis protocol proposed in the benchwork section.

Upon running LDLR's genetic code through Primer3, it was determined that the best left primer is ACACAGGCTGGTCTTGAAC, while the best right primer is, in reverse, CATATTCCCGGTCACACTGC (9). The primers amplify a sequence that is 249 base pairs long. Using NEB Cutter V2.0, EcoRI was chosen as the ideal restriction enzyme for the proposed benchwork (11). EcoRI cuts the wild-type LDLR after the G at base pair 11,106,587, but will not cut if that position mutates into A (Figure 1a, 1b). After being cut by EcoRI, the PCR fragment would be run through gel electrophoresis and amplified at 189bp and 60bp, as these are the expected fragment sizes for wild-type LDLR. If a subject gives a sample containing the wild-type allele, the gel electrophoresis would show two bands appearing at 189 and 60 when compared to the reference ladder. This finding would be consistent with the subject not having FH. However, if the subject gives a sample containing the SNV-affected allele, the gel electrophoresis would show a single band at 249 when compared to the reference ladder. This finding would be consistent with the subject having FH (Figure 2).

MusiteDeep revealed there are no detrimental post-translational modifications detected before secondary structure formation (12). The secondary structure of the mutated protein was analysed using the Phyre2.2 search engine, but no significant detriments were detected when compared to the wild-type (5). Finally, tertiary protein structure was analysed by MutPred2 (4). The findings suggested a loss of disulfide linkage at C243, with a significant p-value of 9.2e-03 (Table 2)

Table 1:

rs768563000 RefSNP Report - DbSNP - NCBI

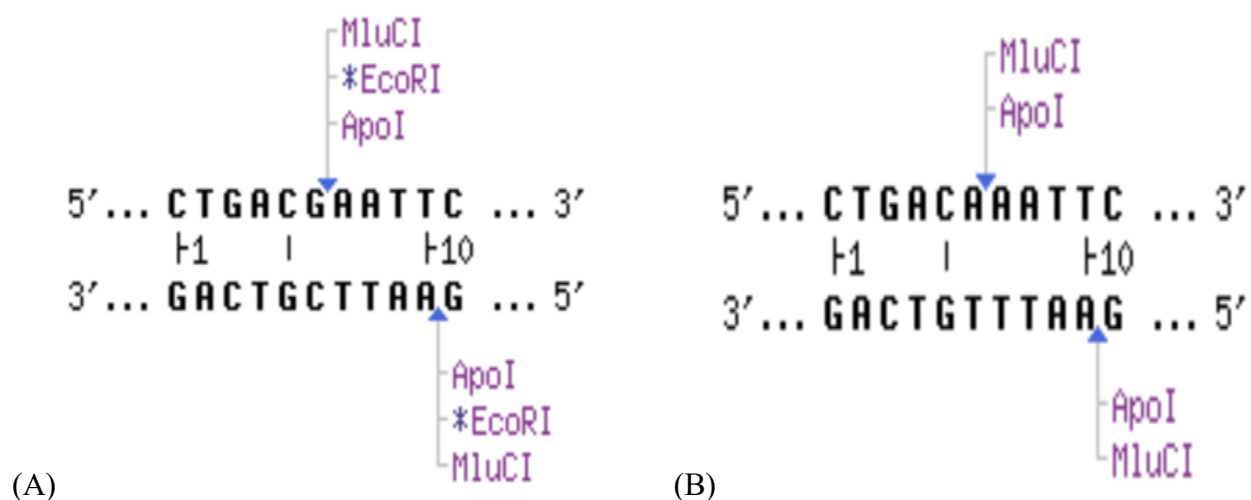
ClinVar Accession	Disease Names	Clinical Significance
RCV000238256.6	Hypercholesterolemia, familial, 1	Pathogenic
RCV002229688.4	Familial hypercholesterolemia	Pathogenic

NOTE: From the U.S. National Library of Medicine (10)

Figure 1:

(A) Reference sequence of wild-type LDLR, indicating EcoRI cleavage location.

(B) Reference sequence of SNV-affected LDLR, missing the EcoRI restriction enzyme.



NOTE: EcoRI cleavage can be affected by CpG Meth, though this is not relevant to SNV rs768563000.

Figure 2:

Expected genotyping assay results when run through gel electrophoresis.

	Wild-type LDLR (G)	SNV- Affected LDLR (A)
1000		
900		
800		
700		
600		
500		
400		
300	189bp	249bp
200		
100	60bp	
0		

Table 2:

MutPred2 results, showing the most significant contributors to the SNV, rs768563000, being pathogenic.

ID	Substitution	MutPred2 score	Remarks	Affected PROSITE & ELM Motifs
Wild-type	E240K	0.544		None
Molecular mechanisms with P-values ≤ 0.05			Probability	P-value
Loss of Disulfide linkage at C243			0.24	9.2e-03
Loss of O-linked glycosylation at T235			0.21	0.02
Gain of ADP-ribosylation at R237			0.19	0.05
Altered Transmembrane protein			0.15	0.02

NOTE: The loss of Disulfide linkage at C243 has a significant p-value of 9.2e-03.

Discussion:

The expected results from the gel electrophoresis would indicate one of two possibilities. The EcoRI restriction enzyme would divide samples with the wild-type allele (G) product into two pieces, 60 base pairs and 189 base pairs long, causing two bands to appear on the gel. On the other hand, a sample with the mutated allele (A) would produce a single product that is 249 base pairs long, as EcoRI would not cleave the PCR product. This would cause a single band to appear on the gel, indicating the subject is positive for the SNV rs768563000 mutation and may be susceptible to developing FH.

This proposed benchwork protocol would allow for the identification of which specific allele a subject has. At this point, a correlation was identified between having the SNV-affected allele and developing FH, but the reason for this pathogenicity was still unknown. Bioinformatic tools were used to identify the result of the mutation.

Both the wild-type and mutated genome sequences were put through Musitedeep to see if there were any identifiable differences in the post-translational modifications of the gene, however none were identified (12). Phyre2 was then used to see if there were any differences in the folding patterns at the secondary level, but yet again, the results showed no differences between the wild-type and variant modifications (5).

Finally, the wild-type and mutated genome sequences were run through Mutpred2 to identify any higher level structural changes that could reasonably produce a pathogenic phenotype (4). The results indicate the loss of a disulfide linkage at C243 with a significant p-value of 9.2e-03 (Table 2). These disulfide bridges are identified by strong, covalent bonds that are made between sulfur molecules on the amino acid cysteine, and are found surrounding the specific base pair in question. If they are broken or unable to form, the protein will lose stability, potentially causing their tertiary and quaternary structures to unfold and damage protein function. The extremely significant p-value of this finding confidently indicates that this loss of disulfide bridges contributes to the SNV being pathogenic.

This assay provides a valid technique to identify individuals at high risk for developing Familial Hypercholesterolemia. Early detection of this variant allows for lifestyle changes such as improved diet and exercise at a young age to reduce the possibility of developing cardiovascular diseases before any symptoms begin. The bioinformatic techniques used in this study affirm the relationship between SNV rs768563000 and FH, and support this assay's ability to enhance personalized medicine in the treatment of FH.

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LDLR Mutation in Familial Hypercholesterolemia: A Genotyping Approach for Early Intervention

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Keywords: Biology, Genomics, Obesity, Genotyping Assay

Abstract:

High cholesterol is a very common medical condition for people in the United States. 10% of adults, 20 years and older, are reported to have cholesterol levels above 240 mg/dL. There are many causes of high cholesterol, which include diet, lack of physical activity, and family history. We predominantly focused on familial hypercholesterolemia (FH), which is an inherited disorder passed down in families through genes and causes low-density lipoprotein (LDL) levels to be drastically elevated. From previous research, it has been shown that inherited mutations of the low-density lipoprotein receptor LDLR gene are one of the leading causes of FH, and this gene will be the focus of our studies. We created a genotyping assay on a pathogenic Single Nucleotide Polymorphism (SNP) found on the LDLR gene to identify individuals susceptible to FH. Our Polymerase Chain Reaction (PCR) assay amplifies a singular band only in individuals with the clinically significant SNP rs144172724 when run on a gel electrophoresis. This allows for the pooling of multiple samples, reducing costs. Our assay, among others, can be applied to universal testing of FH which can identify individuals at a young age when interventions like exercise and diet are most beneficial, resulting in reduced healthcare costs in the long term.

Introduction:

Personalized medicine has been used more recently to get specific medical care based on genetic susceptibility. Personalized medicine uses laboratory procedures such as PCR, sequencing, and microarrays, with bioinformatics to find tailored treatment for the patient. Genomics is classified as the study of a person's genome (the genes) as well as the interactions of those genes with each other and the environment. A type of procedure that is used to point out variations in DNA between people or populations is called a genotyping assay. It allows doctors and researchers to be able to pinpoint genetic differences, which in turn is important for understanding the linkage between genes and traits, diagnosing and treating disease, and reacting to specific drugs. These assays play an important part in personalized medicine, because being able to understand one's genome can allow for such a specific treatment or diagnosis that could be difficult to identify otherwise. Sequencing a patient's genome can allow the identification of mutations or variations in the genome. Mutations or small alterations like the deletion of a nucleotide or the addition of a single base pair may play a role in diseases and abnormal genetic disorders. Single Nucleotide Polymorphisms (SNPs) or mutations are both considered to be changes to the DNA sequence. A SNP is a difference in the DNA sequence among individuals and is found at a rate of 1% or more in the population. A mutation is any heritable change found in DNA in less than 1% of the population¹. Our gene of interest is LDLR, which is a protein-coding gene that contains instructions for making the low-density lipoprotein receptor^{2,3}. This receptor binds to LDL (low-density lipoproteins), which are the primary carriers of cholesterol in the blood. Variants in this gene are commonly found in individuals heterozygous and homozygous for Familial Hypercholesterolemia (FH). FH is a common condition that increases the risk of coronary artery disease, heart attack, and stroke^{3,4}. Many countries have adopted universal screening for variants

contributing to FH to intervene early with diet and exercise, reducing cardiovascular risk⁴. Our assay identifies SNP rs144172724 which is pathogenic according to gnomAD (<https://gnomad.broadinstitute.org/>). Our SNP, in particular, has shown a 2.8×10^{-5} prevalence in the population. We utilized a pooling system to quickly screen many samples simultaneously.

Materials & Methods:

Bioinformatics:

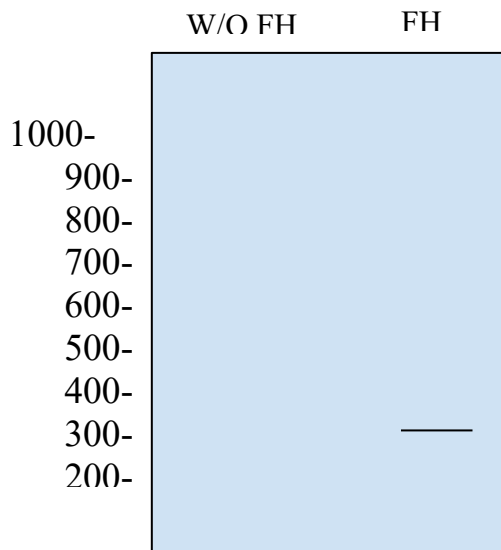
First, to identify the genome sequence, we used the Dec. 2013 (GRCh38/hg38) genome on the University of California Santa Cruz (UCSC) Genome Browser (<https://genome.ucsc.edu/>). Following this, we identified the LDLR SNP that we would be using for our assay. Our SNP was FH Lancashire (Rs #144172724), which we searched the National Center for Biotechnology Information (NCBI) server dbSNP (<https://www.ncbi.nlm.nih.gov/snp/>) in order to identify whether the SNP was deleterious or not. Utilizing our sequence from the genome browser, we identified the introns and exons with a range of above and below 200bp from the SNP. For instance, our original position was 11,102,774 bp, resulting in a range of 11,102,574 - 11,102,974 bp. Once our range and introns/ exons were identified, we used that sequence to find a primer pair. Primer 3 (<https://primer3.ut.ee/>) was used to find the forward primer, however a reverse primer was not found using the program. Utilizing gnomAD, we found that the major allele is G, and the minor allele is A. The SNP substituted a Guanine (G) to an Adenine (A), so we replaced the G of our sequence with A and created a reverse primer using the A as our starting 3'Hydroxyl (-OH) overhang. We made this change in a nucleotide at the 3' overhang because, during the elongation PCR step, nucleotides are added to the 3' end of the growing sequence. If the 3' end of the primer cannot bind to the template there will be no PCR product. In an individual without the SNP in question, the reverse primer will not bind completely because the Thymine (T) cannot bind to a G at the 3' end because T and G are not complementary base pairs. The reverse primer pair will bind to an individual with the SNP because A and T are complementary base pairs.

Bench Work

During the PCR process, there is an initial 5-minute denaturation at 95°C, followed by 30-40 cycles of the following process: 15-second denaturation at 95°C, 30 seconds of annealing primers at 58°C, and 20 seconds of elongation at 72°C. As seen in Figure 1, the band will only appear if the SNP is present in the samples. The primer is only going to bind to the SNP type, meaning that amplification will only occur if you have someone with the FH variant. In the process of amplification, the 3 prime end is unable to anneal due to the overhanging primer, resulting in failed elongation and binding. After PCR amplification, the product will be placed in 1% agarose gel for 10 minutes and visualized by using an alpha imager.

Results:

If the PCR products from our assay of an individual with the SNP and without the SNP were run on a 1% gel electrophoresis, individuals with the SNP would show a band at 264 base pairs (bp) using a 100bp ladder. An individual without the SNP would have no band because no PCR product can be formed based on the primers we designed. This singular band appearing means that the individual has an increased risk for FH. The SNP rs144172724 is a non-synonymous SNP and changes the amino acid sequence from Glutamine (Gln) to Lysine (Lys) mutation. We further analyzed structural changes due to the variant using Pyre 2 and found that there were no secondary structure differences between the wild type and the variant (E240K).



5'... GAGCAAGGCTGTCGTAAG ...3' Wild Type
 3'... TTCGTTCCGACAGCATTC ...5' Primer

5' ... AAGCAAGGCTGTCGTAAG... 3' SNP
 3' ... TTCGTTCCGACAGCATTC ... 5' Primer

Figure 1. The gel electrophoresis model shows a band at 264 bp, while the wild type will not show evidence of a band due to a lack of reverse primer binding. The two sets of sequences display how the wild-type variant is unable to bind to the 3'OH side of the primer because the base pairs do not match. The SNP variant shows how it can bind to the 3'OH side of the primer because the base pairs are complementary.

Discussion:

While a typical genotyping assay of an SNP would include two or more bands, one to identify the wild-type variant and another to identify the SNP, our assay only produced a band when the SNP was present. Only DNA with the variant will exhibit PCR amplification using our primers and DNA without the SNP will not amplify. Since PCR products are made only when an individual is positive for the SNP this enables us to pool thousands of samples at one time, reducing cost and time. This increases the ability to identify FH at a young age, which then gives us the ability to treat individuals with this disease early on, when interventions are most beneficial⁵.

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Native Black Tupelo (*Nyssa sylvatica*) is a Dominant Tree Species in Brentwood & East Islip, NY

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Keywords: Tupelo Brentwood, Islip

Abstract:

In this experiment, a total of 42 trees were surveyed using two dichotomous keys. These tree samples were collected from 8 different sites. Three of them which included residential areas and the rest in Heckscher Park in East Islip. It was found that the dominant tree species was Black Tupelo (*Nyssa sylvatica*) which was 19% of the total trees. Black Tupelo is a member of the Nyssa Genus which is made up of about nine species of trees in the sour gum family (Nyssaceae).

Introduction:

This experiment was conducted in Brentwood and East Islip, two locations in New York with similar environmental conditions. These two areas experience comparable climate patterns with similar seasonal changes. Since these locations have similar climate conditions, they tend to have similar tree species. I hypothesize that there is going to be multiple similar dominant tree species between these areas. The similarities of urban development and green spaces blend in with the consistent backdrop for studying the ecological dynamics (National Weather Service, 2024). Black Tupelo has been found in a wide variety of well-drained, light-textured soil (McGee et al., n.d.). Both areas have a temperate climate, which is a climate in which the climate changes are not extreme, as well as seasonal changes. This tree grows in various environments, including urbanized and forest areas. The selection of these areas is aimed at studying environmental variability, and the end goal is to focus on the characteristics of these tree species in similar settings. This just further justifies that both areas will have similar dominant tree species.

Method:

On July 21, 2024, various ecological surveys were performed to determine and identify the dominant tree species on four sites. In order to identify the trees, I used two dichotomous keys. A dichotomous key is a method to help scientists identify organisms. This method asks you questions that lead you to have two potential answers, which will be repeated later until the organism's species is identified.

Eight ecological surveys included 42 trees. These tree samples were retrieved from residential areas in Brentwood and locations in Heckscher State Park. Each ecological survey involved collecting a tree branch from a defined square area, approximately 10 m 10 m in size. To identify the tree species, I used two dichotomous keys: *Eastern Trees: Peterson Field Guides* (1998) and *Tree Finder: A Manual for the Identification of Trees by Their Leaves* (1998). Subsequently, I used the Compass application (Apple Inc., 2024) to determine the survey sites' coordinates, including latitude and longitude.

Additionally, I utilized Google Maps (Google Corp Inc.) to provide a visual overview of these locations. After gathering the data, I measured the circumference of all the trees using a measuring tape. This data was recorded and compared across different sample locations from other ecological surveys. Finally, I performed the Chi-Square Test of Independence to assess whether Black Tupelo (*Nyssa sylvatica*) is homogeneously distributed across the survey sites.

Results:

This ecological survey concluded that the dominant tree species in Brentwood and East Islip was Black Tupelo tree. Out of all 42 trees, it was analyzed that in comparison to all of them, this species had the most tree dominance. The tables below show the trees identified, the quantity of each tree species, the location where these identified trees were found, and the circumference of all 42 trees.

2 x 2 Contingency Table:

Chi-Square Test of Independence	Black Tupelo	Other Trees
below average circumference	A 2	B 18
above average circumference	C 6	D 16

The Chi-Square Test of Independence Equation is:

$$\begin{aligned}
 \chi^2 &= (ad-bc)^2 / (a+b)(c+d)(b+d)(a+c) \\
 &= (18-24)^2 (42) / (8)(34)(20)(22) \\
 &= 1512/11980 \\
 \chi^2 &= 0.013 \text{ cm}
 \end{aligned}$$

This was used to determine the relationship between the average circumference of all trees. The average circumference size found in this study was 38.3792 cm. The Chi-square test of Independence was used to test whether there was a significant difference between the circumference of Black Tupelo trees compared to the circumference of all the trees. The mean circumference of all trees is 38.3792 cm and the mean circumference for Black Tupelo is 144.4625 cm. No significant difference was found ($\chi^2 = 0.013$).



Figure 1: site A (Reproduced with permission by Google Maps)

Table 1: Trees surveyed in Heckscher Field 3 (Site A)

Quantity of trees	Tree Species	Circumference (cm)	Scientific name	native or nonnative	Latitude	Longitude
3	American Basswood	152.4	<i>Tilia americana</i>	native	40° 42' 33"	-74° 49' 30"
1	Littleleaf Linden	152.4	<i>Tilia cordata</i>	nonnative	40° 42' 33"	-74° 49' 30"
1	Northern Red Oak	104.14	<i>Quercus rubra</i>	nonnative	40° 42' 34"	-74° 49' 29"
2	Red Maple	116.84	<i>Acer rubrum</i>	native	40° 42' 34"	-74° 49' 30"
5	Norway Maple	25.4	<i>Acer platanoides</i>	nonnative	40° 42' 35"	-74° 49' 29"
2	Japanese Snowbell	63.5	<i>Styrax japonicus</i>	nonnative	40° 42' 33"	-74° 49' 29"
3	American Basswood	137.16	<i>Tilia americana</i>	native	40° 42' 33"	-74° 49' 28"
5	Norway Maple	121.92	<i>Acer platanoides</i>	nonnative	40° 42' 34"	-74° 49' 30"
2	Red Maple	81.28	<i>Acer rubrum</i>	native	40° 42' 34"	-74° 49' 29"

3	Sugar Maple	152.4	<i>Acer saccharum</i>	native	40° 42' 35"	-74° 49' 30"
3	Sugar Maple	121.92	<i>Acer saccharum</i>	native	40° 42' 36"	-74° 49' 30"
5	Norway Maple	50.8	<i>Acer platanoides</i>	nonnative	40° 42' 36"	-74° 49' 29"
1	American Sycamore	287.02	<i>Plantanus occidentalis</i>	native	40° 42' 27"	-74° 49' 31"
3	Sugar Maple	162.56	<i>Acer saccharum</i>	native	40° 42' 27"	-74° 49' 32"

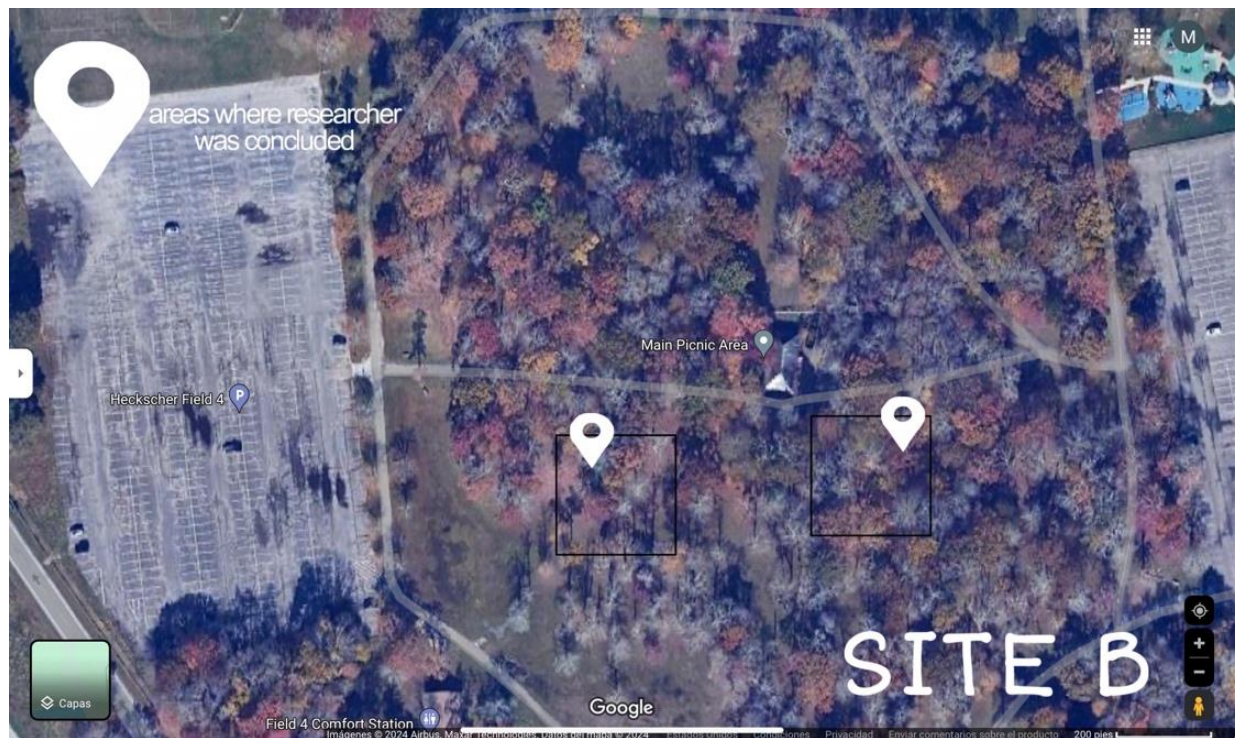


Figure 2: site B (Reproduced with permission by Google Maps)

Table 3: Surveyed trees in Heckscher Field 4 (Site B)

Quantity of trees	Tree Species	Circumference (cm)	Scientific name	native or nonnative	Latitude	Longitude
1	Cherry	187.96	<i>Prunus</i>	nonnative	40° 42' 27"	-74° 49' 45"

	Plum		<i>cerasifera</i>			
2	White Oak	170.18	<i>Quercus alba</i>	native	40° 42' 26"	-74° 49' 45"
8	Black Tupelo	170.18	<i>Nyssa sylvatica</i>	native	40° 42' 26"	-74° 49' 45"
5	Norway Maple	160.02	<i>Acer platanoides</i>	nonnative	40° 42' 26"	-74° 49' 45"
4	Oriental Bittersweet	121.92	<i>Celastrus orbiculatus</i>	nonnative	40° 42' 26"	-74° 49' 45"
2	White Oak	162.56	<i>Quercus alba</i>	native	40° 42' 26"	-74° 49' 46"
1	Crepe Myrtle	132.08	<i>Lagerstroemia indica</i>	nonnative	40° 42' 26"	-74° 49' 46"
8	Black Tupelo	139.7	<i>Nyssa sylvatica</i>	native	40° 42' 26"	-74° 49' 45"
8	Black Tupelo	121.92	<i>Nyssa sylvatica</i>	native	40° 42' 26"	-74° 49' 45"
*4	Oriental Bittersweet	170.18	<i>Celastrus orbiculatus</i>	nonnative	40° 42' 26"	-74° 49' 49"
3	American Basswood	129.54	<i>Tilia americana</i>	native	40° 42' 26"	-74° 49' 49"
8	Black Tupelo	190.5	<i>Nyssa sylvatica</i>	native	40° 42' 25"	-74° 49' 49"
8	Black Tupelo	213.36	<i>Nyssa sylvatica</i>	native	40° 42' 25"	-74° 49' 49"
2	Japanese Snowbell	236.22	<i>Styrax japonicus</i>	nonnative	40° 42' 25"	-74° 49' 50"
4	Oriental Bittersweet	104.14	<i>Celastrus orbiculatus</i>	nonnative	40° 42' 25"	-74° 49' 50"

*=new square box



Figure 3: site C (Reproduced with permission by Google Maps)

Table 4: Residential Homes (Site C)

Quantity of trees	Tree Species	Circumference (cm)	Scientific name	native or nonnative	Latitude	Longitude
8	Black Tupelo	144.78	<i>Nyssa sylvatica</i>	native	40° 46' 39"	-73° 15' 57"
1	Silver Maple	10.16	<i>Acer saccharinum</i>	native	40° 46' 40"	-73° 15' 57"
4	Black Cherry	116.84	<i>Prunus serotina</i>	native	40° 46' 39"	-73° 15' 57"
4	Black Cherry	121.92	<i>Prunus serotina</i>	native	40° 46' 40"	-73° 15' 57"
4	Oriental Bittersweet	105.41	<i>Celastrus orbiculatus</i>	nonnative	40° 46' 40"	-73° 15' 58"
*8	Black	144.78	<i>Nyssa</i>	native	40° 46'	-73° 15'

	Tupelo		<i>sylvatica</i>		38"	57"
1	Common Sassafras	100.33	<i>Sassafras albidum</i>	native	40° 46' 38"	-73° 15' 57"
5	Norway Maple	157.48	<i>Acer platanoides</i>	nonnative	40° 46' 37"	-73° 15' 57"
4	Black Cherry	68.58	<i>Prunus serotina</i>	native	40° 46' 37"	-73° 15' 57"
8	Black Tupelo	30.48	<i>Nyssa sylvatica</i>	native	40° 46' 38"	-73° 15' 57"

*=new square box



Figure 4: site D (Reproduced with permission by Google Maps)

Table 5: Residential Homes (Site D)

Quantity of trees	Tree Species	Circumference (in)	Scientific name	native or nonnative	Latitude	Longitude
1	Virginia Creeper	177.8	<i>Parthenocissus quinquefolia</i>	native	40° 47' 8"	-73° 13' 54"
1	Red Spruce	208.28	<i>Picea rubens</i>	nonnative	40° 47' 7"	-73° 13' 55"
4	Black Cherry	228.6	<i>Prunus serotina</i>	native	40° 47' 7"	-73° 13' 53"

Discussion:

According to my findings, eight Black Tupelo were found in these site areas. This tree species is mainly found in the East Islip and Brentwood areas, as Black Tupelo has been documented over 363 years in Long Island (Karpen et al. 2004).

Conclusion:

The dominant tree species in the recorded sites was Black Tupelo (*Nyssa sylvatica*). This species contributes to biodiversity and highlight their adaptability and importance within these ecological surveys. Although the average circumference of the Black Tupelo tree was larger than the other trees, there was no significant change. Black Tupelo showed dominance in species because out of 18 species recorded in this survey, it was determined that based on my research 19% of the trees found were Black Tupelo.

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The Suffolk County Community College Nature Preserve is in Mid Succession between a Coniferous and Deciduous Forest

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Key Words: Dominant, Deciduous, Coniferous, Trees

Abstract:

Forty trees were surveyed from the nature preserve location in Suffolk County Community College in Brentwood, New York. In order to identify the trees, a dichotomous key was used (Watts, 1998), in addition to a field guide (Petrides, Wehr 1972). From the forty samples, thirty of them were identified as types of deciduous trees, while the other ten were coniferous. The average mean of the circumference of the deciduous trees was 2.5 meters, while the average mean of the circumference of the coniferous trees came out to be 3.6 meters. According to a Chi Square Test of Independence, there was no significance between circumference of Coniferous and Deciduous trees since $\chi^2 = 1.86$. This suggests that the preserve is in mid succession between a Coniferous and Deciduous forest.

Introduction:

A research project was done to find samples of tree leaves from a nature preserve area in Suffolk County Community College, and they were used to figure out if deciduous or coniferous trees were more dominant based on their number and size. Deciduous trees are plants that drop their leaves for a part of every year, usually during periods of dryness or cold weather. Their branches remain free of foliage until conditions improve. For the tree, this means that it can save energy by not working to keep the leaves green and healthy (Beam, 2022). As the climate changes, so do the leaves on deciduous trees. North America's Eastern Deciduous Forest ecosystem stretches over 26 states from Florida up to New England and southern Canada, and extends as far west as Texas and Minnesota. These forests are dominated by broad-leafed trees that shed their leaves annually (deciduous), with evergreen cone-bearing seed plants (conifers) such as pines and hemlocks common in some areas (Eastern Deciduous Forest). On the other side, coniferous trees are trees that bear their seeds in cones (hence the name conifer). The vast majority of conifers have needle-like (e.g. pine or fir) or scale-like leaves (e.g. cypress or juniper). Most conifer species keep their needles all year, so we often refer to these trees as "evergreen" (Communications and Publishing, 2021). In addition to that, another significant difference is how conifers do not lose their green color as temperatures drop, while deciduous trees do.

Method:

Forty trees were identified in a survey conducted in the Suffolk County Community College Nature Preserve. The latitude and longitude, in addition to the elevation of the space, can be found in the results section in Table 1: Property Location Used for Sample Collection. In order to find the

Latitude and Longitude, I used an iPhone application called “Compass” (Apple Inc. 2022). A measuring tape was used to find the circumference of every individual tree and they were all recorded in Table 2 and 3: Identification of Samples found on Property. The dimension of the area used for the survey was 929.03 m². A series of books were provided to help identify the trees being surveyed. The main one used was a dichotomous tree called “Tree Finder: A Manual for the Identification of Trees by their Leaves” by author May Theilgaard Watts. In addition to that, “Eastern Trees” by authors George A. Petrides and Janet Wehr was also an aid in the research and identification process. The Genus species and common name of every tree can also be seen in these tables. The dichotomous key was used to find the scientific name of every tree (Watts, 1998). The Chi Square Test for Independence was used to see if there was a significant difference between the circumference of the Coniferous and Deciduous trees.

Results:

There was a total of thirty deciduous trees that were classified out of the forty samples, and the remaining ten were classified as coniferous. As seen in Table 2, the thirty deciduous trees that were identified are: Flowering Dogwood (*Cornus florida*), Umbrella Magnolia (*Magnolia tripetala*), American Beech (*Fagus grandifolia*), Willow Oak (*Quercus phellus*), Texas Sophora (*Dermatophyllum secundiflorum*), American Mountain Ash (*Sorbus americana*), Red Maple (*Acer rubrum*), Box Elder (*Acer negundo*), White Mulberry (*Morus alba*), Green Ash (*Fraxinus pennsylvanica marsh*), Hardy Capalta (*Capalta speciosa*), Poison Sumac (*Toxicodendron vernix*), Kentucky Coffee Tree (*Gymnocladus dioicus*), Cucumber Magnolia (*Magnolia Acuminata*), Pignut Hickory (*Carya glabra*), English Holly (*Ilex aquifolium*), Washington Hawthorn (*Crataegus phaenopyrum*), Black Locust (*Robinia pseudoacacia*), Honey Locust (*Gleditsia triacanthos*), Swamp Cottonwood (*Populus heterophylla*), Redbud (*Cercis canadensis*), Sugar Maple (*Acer saccharum*), Black Birch (*Betula lenta*), Bitternut (*Carya ovata*), American Hornbeam (*Carpinus caroliniana*), Paper Birch (*Betula papyrifera*), American Basswood (*Tilia americana*), American Sycamore (*Platanus occidentalis*), White Ash (*Fraxinus americana*), and Black Walnut (*Juglans nigra*). The ten coniferous trees can be seen in Table 3, the which are: Yellowwood (*Cladrastus Kentukea*), White Spruce (*Picea glauca*), Grand Fir (*Abies grandis*), Douglas Fir (*Pseudotsuga menziesii*), Live Oak (*Quercus virginiana*), Atlantic White Cedar (*Chamaecyparis thyoides*), Buttonbush (*Cephalanthus occidentalis*), American Holly (*Ilex opaca*), Pinch Pine (*Pinus rigida*), and Sour Gum/ Tupelo (*Nyssa sylvatica*). It was found that deciduous trees were more numerous than coniferous trees. When it came to size and circumference, the average mean circumference for coniferous trees was 3.6 meters, while the average mean circumference for deciduous trees was 2.5 meters. This shows that while deciduous trees are dominant in numbers, when it comes to size, coniferous trees tend to be greater in circumference. To test if there was a significant difference between the deciduous and coniferous trees, the Chi Square Test for Independence was conducted. The final result came out to be $\chi^2=1.86$, meaning that there is no significant difference. However, since the mean of the Coniferous trees is 3.6 meters and the mean of the Deciduous trees is 2.5 meters, then that suggests that there is a mid-succession between a Coniferous and Deciduous forest.

TABLE 1: Property location used for sample collection

Location	Latitude & Longitude	Elevation
Suffolk County Community College, Brentwood, New York	Latitude: 52° 11' 14.0892" Longitude: 58° 14.80''	33.5 meters

-Table 1 shows the location of where the tree samples were found in addition to its Latitude and Longitude and the elevation of the center as well.

TABLE 2: Deciduous Trees Found on Property

Common Name	Genus Species	Circumference
American Basswood	<i>Tilia americana</i>	1.8 meters
American Beech	<i>Fagus grandifolia</i>	1.1 meters
American Hornbeam	<i>Caprinus caroliniana</i>	1.7 meters
American Mountain Ash	<i>Sorbus americana</i>	1.8 meters
American Sycamore	<i>Platanus occidentalis</i>	8.4 meters
Bitternut	<i>Carya ovata</i>	1.7 meter
Black Birch	<i>Betula lenta</i>	1.2 meters
Black Locust	<i>Robinia pseudodacacia</i>	1.2 meters
Black Walnut	<i>Juglians nigra</i>	2.3 meters
Box Elder	<i>Acer negundo</i>	1.2 meters
Cucumber Magnolia	<i>Magnolia acuminata</i>	6.7 meters
English Holly	<i>Ilex aquifolium</i>	2.4 meters
Green Ash	<i>Fraxinus pennsylvanica marsh</i>	4.6 meters
Hardy Capalta	<i>Capalta speciosa</i>	7.4 meters
Honey Locust	<i>Gleditsia triacanthos</i>	1.7 meters
Kentucky Coffee Tree	<i>Gymnocladus diolcus</i>	2.3 meters
Paper Birch	<i>Betula papyrfera</i>	5.5 meters
Pignut Hickory	<i>Carya glabra</i>	2.4 meters
Poison Sumac	<i>Toxicodendron vernix</i>	0.7 meters

Redbud	<i>Cersis canadensis</i>	4.6 meters
Red Maple	<i>Acer rubrum</i>	1.0 meters
Sugar Maple	<i>Acer saccharum</i>	1.3 meters
Swamp Cottonwood	<i>Populus heterophylla</i>	2.8 meters
Texas Sophora	<i>Dematophyllum secundiflorum</i>	0.4 meters
Umbrella Magnolia	<i>Magnolia tripetala</i>	1.1 meters
Washington Hawthorn	<i>Crataegus phaenopyrum</i>	0.9 meters
White Ash	<i>Fraxinus americana</i>	3.9 meters
White Mulberry	<i>Morus alba</i>	0.9 meters
Willow oak	<i>Quercus phellos</i>	0.9 meters
Flowering Dogwood	<i>Corrius florida</i>	1.0 meters

Table 3: Coniferous Trees Identified on Property

Common Name	Genus Species	Circumference
American Holly	<i>Ilex opaca</i>	2.1 meters
Atlantic White Cedar	<i>Chamaecyparis thyoides</i>	3.0 meters
Buttonbush	<i>Cephalanthus occidentalis</i>	3.7 meters
Douglas Fir	<i>Pseudotsuga menziesii</i>	1.5 meters
Grand Fir	<i>Abies grandis</i>	9.4 meters
Live Oak	<i>Quercus virginiana</i>	7.0 meters
Pinch Pine	<i>Pinus rigida</i>	1.7 meters
Sour Gum/ Tupelo	<i>Nyssa sylvatica</i>	0.9 meters
White Spruce	<i>Picea glauca</i>	0.5 meters
Yellowwood	<i>Cladrastus kentukea</i>	5.8 meters

TABLE 4: Coniferous vs Deciduous Mean Circumference

OVERALL mean circumference of all trees: 2.7375 meters	< Overall Mean Circumference	> Overall Mean Circumference
Coniferous	(A) 5	(B) 5
Deciduous	(C) 22	(D) 8

EQUATION 1: Chi Square Test of Independence**Formula:**

$$\chi^2 = (AD-BC)^2 / (A+B+C+D) / (A+C) (B+D) (A+B) (C+D)$$

Calculation:

$$\chi^2 = (40-110)^2 (5+22+5+8) / (5+5) (22+8) (5+22) (5+8)$$

$$\chi^2 = 1.86$$

The final result of 1.86 shows that there is no significant difference between the two groups.

Discussion:

It was found that Deciduous trees are dominant in number while Coniferous trees are generally larger in size. Thirty out of the forty samples were deciduous trees and the remaining ten samples were coniferous. Yet, when it came to size, all of the coniferous trees had an average of 3.6 meters, which was greater than the Deciduous trees' 2.5 meters. Conifers are the largest and most diverse group of living gymnosperms comprising more than 600 species of 60-65 genera in seven families, including the Pinaceae, Podocarpaceae, Araucariaceae, Taxaceae, Cephalotaxaceae, Taxodiaceae, and Cupressaceae (Buschow, 2001). Furthermore, Deciduous forests are New York's most widespread habitat, covering about 45 percent of the land, which explains why 75% of the samples all ended up being deciduous (NYSM). Other studies also found that Deciduous trees were more numerous in the surveyed area than Coniferous trees (Navarro et al. 2013; Chiuchiolo et al. 2018)

Conclusion:

In this study, it was found that out of the 40 samples identified in a tree survey conducted in the Suffolk County Community College Nature Preserve Area, 75% of them were deciduous trees and the remaining were identified as coniferous trees. Due to the result of the Chi Square Test of Independence being 1.86, it shows that there is no significant difference between the circumference of the trees. However, since the mean circumference of the Coniferous trees is 3.6 meters, and the mean circumference of the Deciduous trees is 2.5 meters, it suggests that the Suffolk County Community College Nature Preserve is in mid succession between a Coniferous and Deciduous forest.

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Non-Native Plant Species Outnumber Native Plant Species on a Residential Property in Deer Park, Long Island, New York

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Keywords: Dichotomous key, native plants, non-native plants, Deer Park, Long Island

Abstract: In this experiment, 53 plants were surveyed in a residential property in Deer Park, New York. The plants, both bushes and trees, were identified using dichotomous keys and had their circumferences measured. 95% of the plants were found to be non-native from East Asian countries, such as China, Japan, and Korea, or European countries, such as England, Austria, and Balkans. These results show that residents may be more likely to plant non-native species than native species.

Introduction: This study was conducted within a residential property of Deer Park, New York. According to Weather Spark (2023), Deer Park’s climate shifts from “warm and humid” summers to “very cold, snowy, and windy” winters. Accordingly, the average temperature for Deer Park falls between 0 degrees Celsius and 23.8 degrees Celsius (WeatherSpark 2023). Due to Deer Park being located on Long Island, it benefits from the coastal environment: utilizing the Atlantic Ocean’s waters, Deer Park, and other nearby towns, benefit from a more stable climate due to the heat trapped within the ocean’s waves throughout the summer months.

Methods: In this study, 53 plants were surveyed. 53 samples were taken from a residential property within Deer Park and identified using dichotomous keys, including NativePlantTrust.org (2023), “Tree Finder Booklet” (Watts 1991), and the smartphone app “LeafSnap” (Belhumeur et al. 2011). Using “FindLatitudeandLongitude” (Zwiefelhofer 2008), the location of the residential property in this study was recorded. After documenting the different types of plants, the circumference of the plants were taken using a measuring tape and recorded. The data, including the plants common names, scientific names, and measurements, were then organized into tables. The findings were then compared to other surveys that were published in the *SATURN Journal*.

Results: After collecting data and analyzing it using dichotomous keys, it was found that the residential property in Deer Park contained more non-native species of plants than native species. Out of the 19 species of plants that were identified, 18 were found to be non-native species while only 1 was found to be a native species to New York. The tables below show the different species of bushes and trees that were identified and their measurements.

Table 1: Plants identified (40° 44' 49.416" N, 73° 19' 51.42" W)

Name	Scientific Name	Native vs. Non-native	Quantity	Measurement (centimeters)	Origin
Bigleaf Hydrangea	<i>Hydrangea macrophylla</i>	Non-Native	3	5.2 cm; 5.4 cm; 5.7 cm	Japan
Lily of the Valley	<i>Pieris japonica</i>	Non-Native	3	25.0 cm; 21.3 cm; 22.8 cm	Japan
Asian Meadowsweet	<i>Spiraea trilobata</i>	Non-Native	2	2.4 cm; 2.7 cm	East Asia
Azalea	<i>Rhododendronsimsii</i>	Non-Native	13	4 - 2.0 cm; 3 - 2.1 cm; 2 - 2.4 cm; 2 - 2.3 cm; 2.8 cm; 1.9 cm;	China
Spotted Laurel	<i>Aucuba japonica</i>	Non-Native	6	14.3 cm; 13.6 cm; 13.9 cm; 14.1 cm; 14.8 cm; 13.1 cm	Japan
Greenstem Forsythia	<i>Forsythia viridissima</i>	Non-Native	1	3.8 cm	Southern China
Japanese Holly	<i>Ilex crenata</i>	Non-Native	1	7.8 cm	East Asia
Savin	<i>Juniperus sabina</i>	Non-Native	3	7.3 cm; 7.6 cm; 7.1 cm	Southern Europe
Lemon Thyme	<i>Thymus citriodorus</i>	Non-Native	1	2.9 cm	Europe
Cherry Plum	<i>Prunus cerasifera</i>	Non-Native	1	36.5 cm	Western Asia
Korean Privet	<i>Ligustrum ovalifolium</i>	Non-Native	10	3 - 6.6 cm; 2 - 6.9 cm; 2 - 7.3 cm; 7.1cm; 7.6 cm; 7.8 cm	Korea and Japan
Old Fashioned Weigela	<i>Weigada florida</i>	Non-Native	1	3.2 cm	East Asia
Cratoxylum Cochinchinense	<i>Cratoxylum cochinchinense</i>	Non-Native	1	3.0 cm	Southern China
Weeping Yoshino Cherry	<i>Prunus x vedonsis</i>	Non-Native	1	44.3 cm	Japan
Chinese Holly	<i>Ilex comuta</i>	Non-Native	1	7.4 cm	China and Korea
Plymouth Pear	<i>Pyrus cordata</i>	Non-Native	1	24.4 cm	United Kingdom
White Cedar	<i>Thuja occidentalis</i>	Native	1	17.1 cm	North East United States and Canada
Austrian Copper Rose	<i>Rosa foetida</i>	Non-Native	1	12.1 cm	Europe and Persia
Lilac	<i>Syrinag vulgaris</i>	Non-Native	2	13.6 cm; 14.1 cm	Eastern Europe

Of the non-native species, the Azalea (*Rhododendron simsii*) and the Korean Privet (*Ligustrum ovalifolium*) were the most common. The Azalea, with its 13 specimens, made up 25.5% of the non-

native species while the Korean Privet, with its 10 specimens, made up 19.6% of the non-native species present. Of the native species, the White Cedar (*Thuja occidentalis*) made up 100% of the native species present with its one specimen.

When comparing all plants involved in this study, the average circumference was found to be 9.16cm. When looking at the circumferences of the Azalea, the most common of the non-native species present in this study, the average circumference was 2.18cm. Only 5 of the Azaleas, or 38.45%, met or exceeded the average circumference of Azaleas. The Korean Privet, the second most common of the non-native species present in this study, had an average circumference of 7.07cm of which 5, or 50%, met or exceeded the average of Korean Privets. The White Cedar, the only native plant found in this study, had a circumference of 17.1cm. Although the Azalea (*Rhododendron simsii*) and the Korean Privet (*Ligustrum ovalifolium*) were the most numerous, none of these plants reached the average circumference for all plants in this survey. However, the White Cedar (*Thuja occidentalis*) had a circumference that exceeded the average of all plants surveyed.

Discussion: In this study, non-native plants were found to be more dominant than native plants on this residential property in Deer Park. Azaleas were the most common species on this residential property, followed by the Korean Privet. While there are types of Azalea's that are native to North America, *Rhododendron simsii* is native to China and rare to be found in western countries (iNaturalist 2023). The Korean Privet originates from Japan and South Korea, however it has been sold as a hedge shrub to many other countries. According to

InvasivePlantAtlas (2018), the Korean Privet, also called the California Privet in the United States, was listed as an invasive species in 2018 due to the plants tendency to grow dense, thick bushes that outcompete local plants in floodplains and forests.

While the Azalea and Korean Privets were the most common non-native species found in this survey, their average circumferences were less than the average circumferences of all plants in this survey. The White Cedar, the only native species found in this study, however did exceed the average circumference of all plants in this survey. This may suggest that while the Azalea and Korean Privet are more abundant, they are not dominant.

After comparing the results of this study to the results of a study in the past, similarities were found between both. In a survey conducted by Campitiello et al. (2015), a Deer Park residence held six different species of trees where only one of the trees was found to be native. These results were also similar in their findings that the only identified native species was a tree: in the past study, the American Sycamore was identified while this study identified the White Cedar.

Similar results were found again when the results of this study were compared to those found by Longo et al. (2015). The results of their study, which included one of Deer Park's neighboring towns, Brentwood, found that non-native plants, trees specifically, outnumbered the native trees in several towns across Long island. Of their 35 different species of trees, 24 (69%) were found to be non-native and 11 (31%) were found to be native. While these numbers are larger than the results found in this study, the trend of non-native plants outnumbering native plants continues.

The results of a third study by Dooling et al. (2014) were also compared to the findings of

this study. Within their study of 58 tree specimens, they found that 35 specimens (60%) belonged to non-native species while 22 specimens (37%) belonged to native species. They were unable to identify 1 specimen (3%) of their total survey. These specimens were gathered across five residential properties across Long Island, on both the North and South shores. The percentages of Dooling et al. (2014) are larger than those found within this study, however the trend of non-native species outnumbering those that are native continues across Long Island on both of its shores.

Conclusion: Of the 53 plant specimens found on a residential property in Deer Park, 19 species of plants that were identified. 19 species identified: 18 were found to be non-native and 1 was found to be native. The number of non-native species far exceeds that of the native species of Long Island. Native plants, such as the White Oak and the Eastern Red Cedar, that would be thought to be popular due to their locale and ability to succeed in this climate are missing. In their place, non-native species from East Asia and European countries, such as the Asian Meadowsweet and Austrian Copper Rose, have become more abundant.

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Coniferous Trees are Dominant to Deciduous Trees in Huntington Station, New York

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Keywords: Deciduous, Coniferous, Native

Abstract:

Forty-two tree samples were collected from surveys in two local parks in Suffolk County, New York to determine the dominant species. A branch from each tree was collected and the diameter of the tree trunk was measured. The species were identified using three dichotomous keys. It was found that native trees and coniferous trees were dominant in Huntington Station.

Introduction:

Huntington Station is home to a host of coniferous and deciduous trees. This was made possible due to their adaptability to the climate and its environment. Hundreds of trees can be found in Huntington Station alone, and they vary in size and shapes. According to Directree (2020) coniferous trees are cone-bearing trees and shrubs with needle-like or scale-like leaves. Most conifers are evergreen, meaning that they keep their needles throughout the year. Deciduous trees are trees and shrubs that unlike evergreens, they lose their leaves and become dormant during the winter. The American Conifer Society (1983) classifies conifers by growth rate: miniature conifers grow less than 2.54 centimeters per year. Dwarf conifers grow 2.54 to 15.24 centimeters per year. Intermediate conifers grow 15.24 to 30.48 centimeters per year. Large conifers grow more than a foot (30.48 cm) per year. Deciduous trees replace chlorophyll in warmer months. Chlorophyll gives leaves their green color, and it gets used during photosynthesis. This study shows the different types of coniferous and deciduous trees, how they are measured and vary in size, and how they adapt to the different climates.

Method:

Two separate 15 x 15-meter areas were selected in Hilaire Woods Park and Fair Meadow Park in Huntington Station, N.Y. in order to survey the species of trees that are dominant in the area. Forty-two tree specimens were collected. For each property, the latitude and longitude were found using a mobile navigation application (40.8683-73.4088, 40.8567- 73.3926) according to Earth Explorer (USGS 2023). The 42 trees were identified using three dichotomous keys (Petrides and Wehr 1998, Watts 1998, Watts and Watts 1970). Then all samples were measured by the circumference of the trunk of each tree using a Stanley tape measure tool. The dichotomous keys were used to identify the species by differences in characteristics such as the leaves and stems in order for the samples to be properly classified. A chi-square test of independence was also used to determine the probability of Coniferous trees being dominant over Deciduous trees.

Chi-square test of independence Formula:

$$\chi^2 = \frac{(AD - BC)^2 (A + B + C + D)}{(A+C)(B+D)(A+B)(C+D)}$$

Results:

For the results 42 trees in total were identified in the Town of Huntington. The tables below demonstrate the data collected in two locations in Huntington Station, NY.

Table 1. Location Surveyed

	Location #1	Location #2
Town	Huntington Station, NY	Huntington Station, NY
Coordinates	Longitude- 40.8683 Latitude-73.4088	Longitude— 40.8567 Latitude— 73.3926
Size m²	15 x 15	15 x 15
Count of Trees	20	22

Table 2: Tree Species Observed in Area 1

Species Name	Scientific Name	Measurements	Native or Non-native	Deciduous or Coniferous
Great Laurel	<i>Rhododendron maximum</i>	330.2 cm	Native	Coniferous
Northern White Cedar	<i>Thuja occidentalis</i>	406.4 cm	Non-Native	Coniferous
White Pine	<i>Pinus strobus</i>	27.94	Native	Coniferous
Mountain Laurel	<i>Kalmia latifolia L.</i>	137.16 cm	Native	Coniferous
Norway Spruce	<i>Picea abies</i>	22.86 cm	Non-Native	Coniferous
Eastern Redbud	<i>Cercis canadensis</i>	27.94 cm	Native	Coniferous
Canada Yew	<i>Taxus canadensis</i>	15.24 cm	Native	Coniferous
Red Pine	<i>Pinus resinosa</i>	40.64 cm	Native	Coniferous
Red Pine	<i>Pinus resinosa</i>	60.96 cm	Native	Coniferous
Oriental Arborvitae	<i>Platycladus orientalis</i>	274.32 cm	Not Native	Coniferous
Spindle Tree	<i>Euonymus europaeus</i>	20.32 cm	Non-Native	Deciduous
Wild Privet	<i>Ligustrum Vulgare</i>	152.4 cm	Non-Native	Deciduous
Rose of Sharon	<i>Hibiscus syriacus</i>	20.32 cm	Non-Native	Deciduous

Balsam Fir	<i>Abies balsamea</i>	60.96 cm	Native	Coniferous
White Pine	<i>Pinus strobus</i>	121.92 cm	Native	Coniferous
Northern Red Oak	<i>Quercus rubra</i>	144.78 cm	Native	Deciduous
Basswood	<i>Tilia americana</i>	76.2 cm	Native	Deciduous
Black Cherry	<i>Prunus serotina</i>	73.66 cm	Native	Deciduous
Northern Catalpa	<i>Catalpa speciosa</i> <i>Warder ex Engelm</i>	27.94 cm	Native	Deciduous
Eastern Black Walnut	<i>Juglans nigra</i>	6.35 cm	Native	Deciduous

A total of twenty trees were identified by their species and circumference in location #1. The Coniferous were more common than the Deciduous trees in this location. 60% of the trees were Coniferous, while 40% were Deciduous. In addition, 70% of the trees that were found were native, while only 30% were non-native.

Table 3: Deciduous Trees in Location #1

Species Name	Scientific Name	Measurements	Deciduous
Wild Prive	<i>Ligustrum vulgare</i>	152.4 cm	Deciduous
Northern Red Oak	<i>Quercus rubra</i>	144.78	Deciduous
Basswood	<i>Tilia americana</i>	76.2 cm	Deciduous
Black Cherry	<i>Prunus serotina</i>	73.66 cm	Deciduous
Northern Catalpa	<i>Catalpa speciosa</i> <i>Warder ex Engelm</i>	27.94 cm	Deciduous
Spindle Tree	<i>Euonymus europaeus</i>	20.32 cm	Deciduous
Rose of Sharon	<i>Hibiscus syriacus</i>	20.32 cm	Deciduous
Eastern Black Walnut	<i>Juglans nigra</i>	6.35 cm	Deciduous

Table 4: Coniferous in Location #1

Species Name	Scientific Name	Measurements	Coniferous
Great Laurel	<i>Rhododendron maximum</i>	330.2 cm	Coniferous

Oriental Arborvitae	<i>Platycladus orientalis</i>	274.32 cm	Coniferous
Mountain Laurel	<i>Kalmia latifolia L.</i>	137.16 cm	Coniferous
White Pine	<i>Pinus strobus</i>	121.92 cm	Coniferous
White Pine	<i>Pinus strobus</i>	27.94 cm	Coniferous
Red Pine	<i>Pinus resinosa</i>	60.96 cm	Coniferous
Balsam Fir	<i>Abies balsamea</i>	63.5	Coniferous
Red Pine	<i>Pinus resinosa</i>	40.64 cm	Coniferous
Eastern Redbud	<i>Cercis canadensis</i>	27.94 cm	Coniferous
Norway Spruce	<i>Picea abies</i>	22.86 cm	Coniferous
Canada Yew	<i>Taxus canadensis</i>	15.24 cm	Coniferous

Table 5: Tree Species Observed in Area #2

Species Name	Scientific Name	Measurements	Native or Non-native	Deciduous or Coniferous
White Pine	<i>Pinus strobus</i>	38.1 cm	Native	Coniferous
Tree of Heaven	<i>Ailanthus altissima</i>	53.34 cm	Non-Native	Deciduous
White Oak	<i>Quercus alba</i>	121.92 cm	Native	Deciduous
Scarlet Oak	<i>Quercus coccinea</i>	243.84 cm	Native	Deciduous
Black Oak	<i>Quercus coccinea</i>	91.44 cm	Native	Deciduous
Northern Catalpa	<i>Catalpa speciosa Warder ex Engelm</i>	167.64 cm	Native	Deciduous
Bur Oak	<i>Quercus macrocarpa</i>	182.88 cm	Native	Deciduous
Black Gum	<i>Nyssa sylvatica</i>	208.28 cm	Native	Deciduous
Silver Maple	<i>Acer saccharinum</i>	162.56 cm	Native	Deciduous
Cherry Blossom	<i>Prunus serrulata</i>	142.24 cm	Non-Native	Coniferous
Cherry Blossom	<i>Prunus serrulata</i>	165.1 cm	Non-Native	Coniferous
Cherry Blossom	<i>Prunus serrulata</i>	106.68 cm	Non-Native	Coniferous
Pitch Pine	<i>Pinus rigida</i>	195.58 cm	Native	Coniferous

Shortleaf Pine	<i>Pinus echinata</i>	149.86 cm	Native	Coniferous
Limber Pine	<i>Pinus flexilis</i>	157.48 cm	Non-Native	Coniferous
Sierra Redwood	<i>Sequoiadendron giganteum</i>	43.18 cm	Native	Coniferous
Scarlet Oak	<i>Quercus coccinea</i>	226.06 cm	Native	Coniferous
Dawn Redwood	<i>Metasequoia glyptostroboides</i>	45.72 cm	Non-Native	Deciduous
Eastern White Pine	<i>Pinus strobus</i>	160.02 cm	Native	Coniferous
Eastern Spruce	<i>Picea rubens</i>	25.4 cm	Native	Coniferous
White Pine	<i>Pinus strobus</i>	25.4 cm	Native	Coniferous
Red Pine	<i>Pinus resinosa</i>	58.42 cm	Native	Coniferous

A total of twenty-two trees were identified by their species and circumference in location #2. Once again, the Coniferous trees were more common than the deciduous trees. 59% of the trees were coniferous, while 41% of the trees were deciduous. In addition, 73% of the trees were native, while only 27% were non-native.

Table 6: Deciduous in Location #2

Species Name	Scientific Name	Measurements	Deciduous
Black Gum	<i>Nyssa sylvatica</i>	208.28 cm	Deciduous
Bur Oak	<i>Quercus macrocarpa</i>	182.88 cm	Deciduous
Northern Catalpa	<i>Catalpa speciosa</i> Warder ex Engelm	167.64 cm	Deciduous
Silver Maple	<i>Acer saccharinum</i>	162.56 cm	Deciduous
White Oak	<i>Quercus alba</i>	121.92 cm	Deciduous
Black Oak	<i>Quercus coccinea</i>	91.44 cm	Deciduous
Red Maple	<i>Acer rubrum</i>	66.04 cm	Deciduous
Tree of Heaven	<i>Ailanthus altissima</i>	53.34 cm	Deciduous
Dawn Redwood	<i>Metasequoia glyptostroboides</i>	45.72 cm	Deciduous

Table 7: Coniferous in Location #2

Species Name	Scientific Name	Measurements	Coniferous
Scarlet Oak	<i>Quercus coccinea</i>	226.06 cm	Coniferous
Pitch Pine	<i>Pinus rigida</i>	195.58 cm	Coniferous
Cherry Blossom	<i>Prunus serrulata</i>	165.1 cm	Coniferous
Limber Pine	<i>Pinus flexilis</i>	157.48	Coniferous
Shortleaf Pine	<i>Pinus echinata</i>	149.86 cm	Coniferous
Cherry Blossom	<i>Prunus serrulata</i>	142.24 cm	Coniferous
Cherry Blossom	<i>Prunus serrulata</i>	106.68 cm	Coniferous
Red Pine	<i>Pinus resinosa</i>	58.42 cm	Coniferous
Sierra Redwood	<i>Sequoiadendron giganteum</i>	43.18 cm	Coniferous
White Pine	<i>Pinus strobus</i>	38.1 cm	Coniferous
Eastern Spruce	<i>Picea rubens</i>	25.4 cm	Coniferous
White Pine	<i>Pinus strobus</i>	25.4 cm	Coniferous

A chi-square test of independence was also used to check if there was a significant difference between the circumferences of the coniferous and deciduous trees that were surveyed. The median circumference was found to be 39 cm. Twelve coniferous trees were above the median and twelve were below the median. For deciduous trees, seven were above the median and ten below the median. After applying the Chi Square formula to these statistics, a Chi-square value of 6.47 was found. This is quite significant at the five percent level of probability ($p < .05$).

Discussion:

This study demonstrated that Coniferous trees were dominant to deciduous trees based on the numerous trees found and their measurements. In a study done by Bermudez (2023), it was found that deciduous trees were the most common type of tree in the town of Islandia with the dominant species being the Northern Red Oak (*Quercus rubra*). According to a study performed by Castro et al. (2018), it was determined that deciduous trees were the most common type of tree in West Babylon and Bayshore. Also, according to Bilbay et al (2019), it was determined that deciduous trees were the most common type of tree in West Babylon and Bayshore.

Conclusion:

According to the identification and measurements of each of the samples taken in surveys from the town of Huntington Station, NY, Coniferous trees are dominant to deciduous trees in Huntington Station based on their circumferences and the number of them, and there were more native trees than

non-native trees.

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Analysis of Amoxicillin Resistance in *Escherichia coli* through selective pressure

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Keywords: Bacteria, Resistance, Amoxicillin, *E. coli*

Abstract:

This experiment investigated the evolutionary adaptations of *E. coli* in response to increasing concentrations of the antibiotic Amoxicillin. In this study, five petri dishes were prepared, each containing varying concentrations of Amoxicillin: 0 mg (positive control), 2.5 mg (A), 5 mg (B), 10 mg (C), and 50 mg (negative control). The bacteria were inoculated using the lawn method, and growth was observed visually over a span of two days. As the bacteria was exposed to higher concentrations, surviving colonies were transferred to plates infused with greater dosages to stimulate selective pressure on the population. This method allowed for a gradual adaptation process under increasing antibiotic stress.

The results showed that *E. coli* developed increasing resistance at the lower concentrations (2.5 mg and 5 mg), while growth was significantly reduced at 10 mg, with no noticeable growth at 50 mg. This trend supports the hypothesis that antibiotic pressure reinforces microevolutionary adaptations in the bacteria. Some of these changes are likely associated with the production of beta-lactamase and alterations in porin proteins, both of which contribute to enhanced resistance. These results serve as a clear reminder of how rapidly bacteria can adapt, emphasizing the importance of maintaining strong antibiotic stewardship to help slow the spread of resistance.

Introduction:

Microevolution refers to small scale genetic changes within a small population of a species over a short period of time. These changes occur due to various factors including selection, genetic drift, gene flow, and a number of others. In this experiment, we are investigating the adaptive resistance capabilities of *E. coli* when exposed to increasing antibiotic concentrations which is a form of microevolution.

E. coli is a gram negative, Rod shaped bacterium commonly found within the intestines of humans and certain mammals. For this study, we are using the K-12 strain, a heavily studied, non-pathogenic strain. This strain is particularly useful for demonstrating antibiotic resistance due to its ability to rapidly acquire genetic changes through horizontal gene transfer, thus making it ideal for bacterial evolution and antibiotic resistance studies.

Hypothesis: We hypothesized that when a population of *E. coli* is exposed to increasing concentrations of amoxicillin in several petri-dishes, the antibiotic will act as a selective pressure, necessitating microevolutionary adaptations. Over time, the population is expected to undergo a series of genetic modifications in order to better adapt to a selective pressure in an environment, and will lead to subsequent bacterial colony growth on said plates. The bacteria's compensatory mechanisms can be inferred due to the specific mechanism of action of amoxicillin, which specifically targets cell wall synthesis.

Methods:

The materials gathered for this experiment included five (5) petri dishes, two (2) 125 mL agar bottles, sterile gloves, five (5) 10 ml normal saline Syringes, one starter colony of K-12 strain *E. coli*,

sterile gloves, and sterile inoculation swabs to ensure a contamination-free environment. Moreover, 500 mg of amoxicillin was used as an antibiotic, and a 50 ml sterile saline solution was used to prepare the stock solution.

To prepare the stock solution, a 500 mg tablet of amoxicillin was crushed and dissolved in 50 mL of sterile saline solution, resulting in a concentration of 10 mg/mL. From this stock, four separate solutions were measured out. Since 1 mL of the stock contained 10 mg of amoxicillin, smaller volumes were taken to get the desired amounts for the experiment. To obtain 2.5 mg, 0.25 mL of the stock solution was drawn using a sterile syringe. For 5 mg, 0.5 mL was taken, and for 10 mg, 1.0 mL was used. Additionally, to obtain 50 mg of amoxicillin, 5mL of the stock solution was measured out. Once measured, the syringes containing the respective volumes were set aside, ensuring they remained sterile and ready to use.

After preparing the amoxicillin solutions, agar plates were prepared under sterile conditions. Molten agar was poured into five petri dishes. The petri dishes were labeled A, B, C, positive control and negative control. Plate A was treated with 2.5 mg of amoxicillin by using the 0.25 mL solution we prepared earlier, Plate B received 5 mg of amoxicillin with the 0.5 mL solution, and Plate C was treated with 10 mg of amoxicillin using the 1.0 mL solution. The positive control plate was not treated with any antibiotic. On the other hand, the negative control plate was infused with 50 mg of amoxicillin. The plates were then left to cool down and solidify before proceeding to the next step.

After the plates had solidified, the bacteria were inoculated onto the plates using the lawn method to ensure the bacteria was evenly exposed to antibiotics. A sterile inoculation swab with *E. coli* was used in a zig-zag motion to inoculate agar plate A, and was evenly spread onto the surface of the plate. The negative control plate remained untreated. Once bacterial growth was observed after 2 days on plate A, a sample was collected and transferred to plate B, containing 5 mg of amoxicillin. 2 days passed and after the confirmation of bacterial growth on plate B, another sample from plate B was transferred to plate C, which contained 10 mg of amoxicillin. The bacterial growth was examined visually and growth patterns across the different plates were compared to determine the effect of increasing amoxicillin concentrations on bacterial survival.

Results:

The experiment tested the antibiotic resistance of *E. coli* when exposed to different dosages of amoxicillin in three samples (A, B, and C) in comparison to positive and negative controls. The positive control, with no antibiotic dose, indicated a robust bacterial growth shown as (+ + + +) on data table 1.1. This growth can be seen in figure 1.1. Sample A was given a dosage of 2.5 mg and showed the most resistance of all three samples. This sample showed a somewhat strong response as the bacteria started becoming resistant and adapting to the new environment. We marked this sample as (+ + +), to indicate growth and resistance of *E. coli*. The bacterial colonies in sample B were given a greater dosage of amoxicillin (5 mg). Sample B also produced a robust response, marked as (+ + +), as seen in figure 1.2. While sample B was somewhat resistant, sample C (10 mg) demonstrated the least response, earning only two positive points (+ +), as seen in figure 1.3. Only a few colonies adapted but could not reproduce for further growth. These findings suggest that increasing the dosage of amoxicillin decreases the bacterial growth rate, with the lowest dosage (2.5 mg) producing the strongest resistance in *E. coli*.

Figure 1.1: Plate A; 2.5mg Amoxicillin (Before and After)

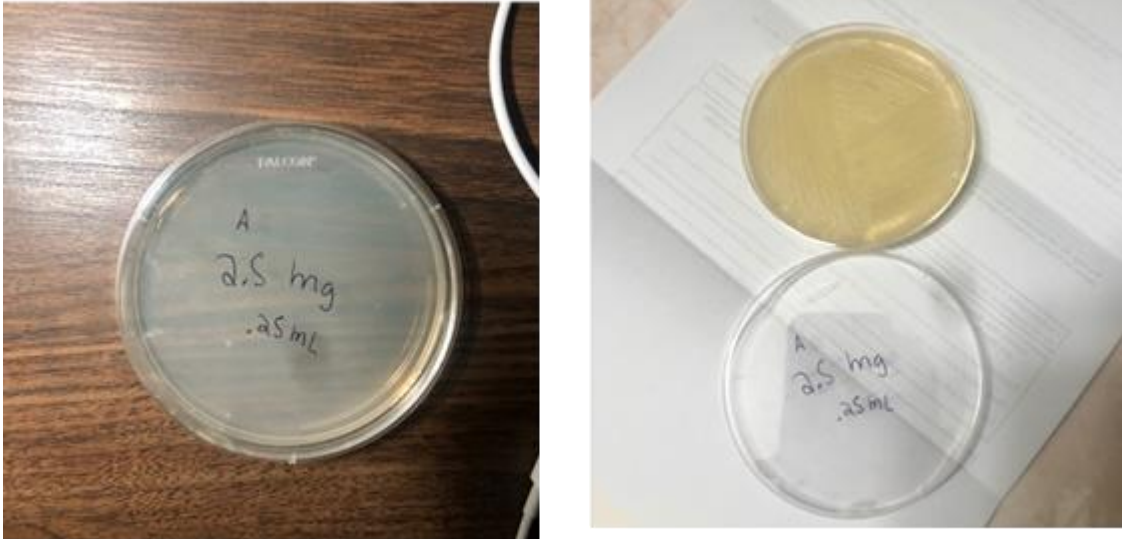


Figure 1.2: Plate B; 5mg Amoxicillin (Before and After)

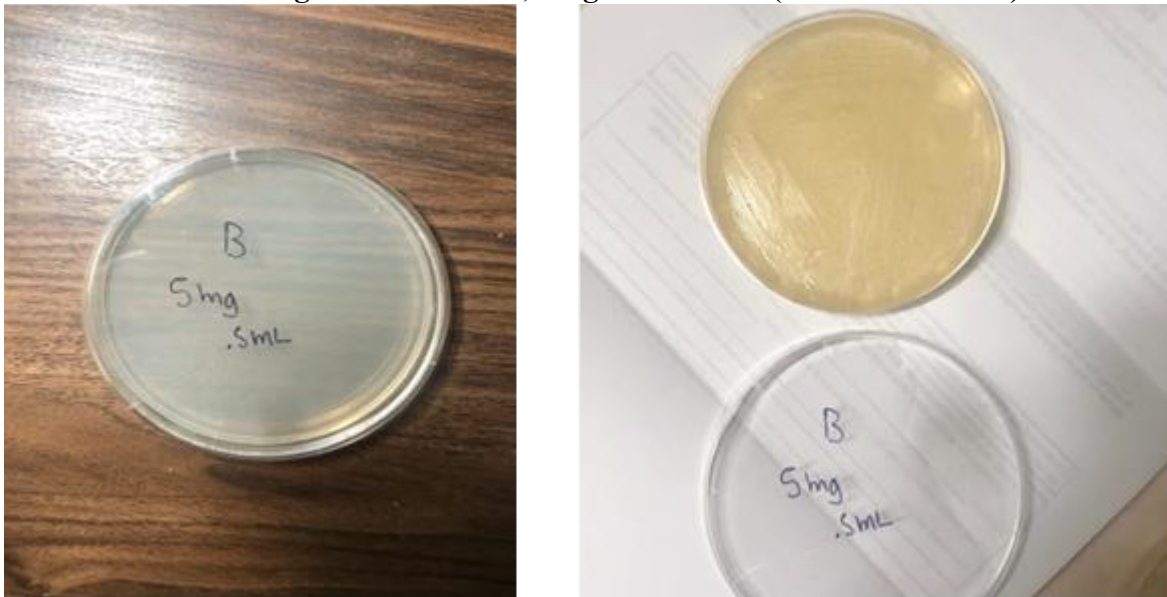
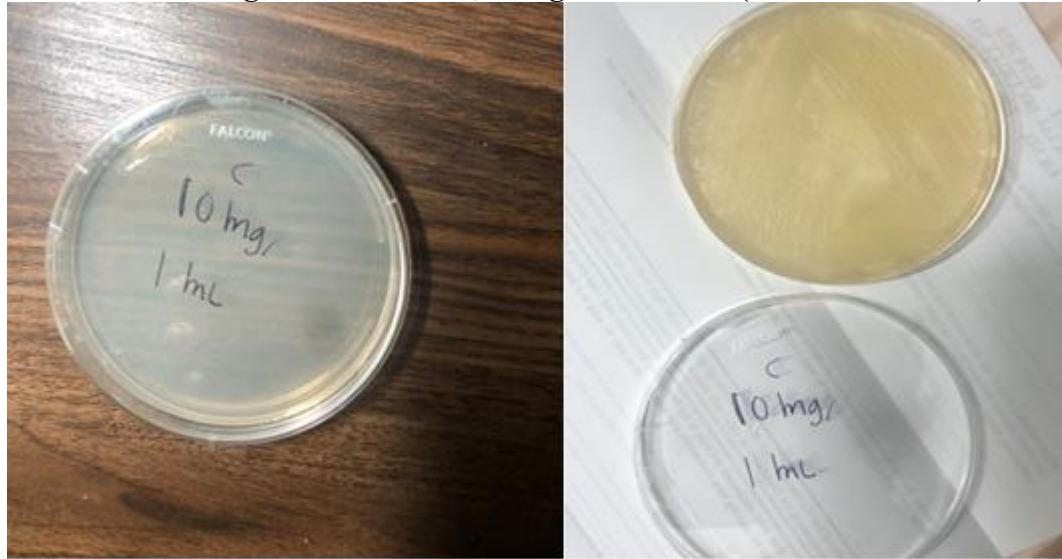


Figure 1.3: Plate C; 10mg Amoxicillin (Before and After)**Table 1.1**

Sample	Dosage	Points (after two days)
Positive control (no dosage)	0 mg	++++
Sample A	2.5 mg	+++
Sample B	5 mg	+++
Sample C	10 mg	++
Negative control (no <i>E.coli</i>)	50 mg	----

Discussion:

The results of the experiment demonstrate that *E. coli* K-12 populations exposed to increasing concentrations of amoxicillin showed clear signs of adaptive resistance in response to a selective pressure; consistent with the hypothesis that antibiotics acting as a selective pressure drives microevolutionary change. Plates A & B both showed robust growth, these findings likely indicated that more resistant variants were selected. The reduced number of colonies in plate C likely reflects a possible evolutionary bottleneck, where fewer individuals were able to survive against the stronger selective pressure. Two key mechanisms likely contributed to the observed resistance, including the production of *beta lactamase*, and *porin alteration* (Khalifa et al., 2021).

The *beta lactamase* enzyme functioned to break the *beta-lactam* ring in the antibiotic molecule, limiting the antibiotic's ability to bind to *penicillin-binding proteins*. Moreover, porin alteration in this population of *E. coli* likely contributed significantly to the enhancement of amoxicillin resistance, as subtle structural changes in the porins could reduce the permeability of the bacterial membrane (Khalifa et al., 2021) and could significantly reduce the intracellular antibiotic concentration, limiting the efficiency of the antibiotic.

Antibiotic resistance in bacteria is a growing global health concern, threatening the efficacy of modern-day treatments. This problem is projected to only grow in the future, and take more human lives. This study serves to increase awareness in the scientific and clinical community about this issue in order to reduce the incidence of antibiotic resistance strains of common bacteria, and encourage clinicians to practice antibiotic stewardship.

Conclusion:

The experiment demonstrated that *E. coli* K-12 can undergo microevolutionary changes when subjected to increasing concentrations of amoxicillin, emphasizing the role of selective pressure as a driving force in antibiotic resistance. Bacterial growth on progressively more concentrated plates indicated that bacteria with more desirable genetic traits were naturally selected for, and their genetic information was more likely to be passed on (see figures 1.1-1.3).

These genetic changes likely involved the production of β -lactamase, as this enzyme likely broke down the antibiotic, and structural changes in the cells' porins (Khalifa et al., 2021). Bacteria that possessed more desirable traits passed down their information, and as the selective pressure increased intensity, less bacteria were able to meet these demands, leading to a lower total colony number in plates with higher antibiotic concentration. This is a classic example of natural selection and a bottleneck effect.

These findings directly support our previously stated hypothesis that antibiotic exposure leads to adaptive evolution in bacteria populations. These findings further emphasize the importance of practicing proper antibiotic stewardship in the clinical setting, as the various complex adaptive mechanisms of everyday bacteria can easily outpace the development of new antibiotics, leading to treatment failures and increased public health risks.

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Eastern White Oak is the Dominant Tree Species at West Hills Dog Run Parks in Huntington, New York

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Key words: Eastern White Oak, West Hills Park, Long Island, Huntington, Melville

Abstract:

Eighty-three trees were surveyed on Long Island, New York; West Hills Dog Run Parks located in the Town of Huntington. We examined two separate sites of land in West Hills Dog Run Park. We used a smartphone application, as well as three dichotomous keys to identify and confirm the tree species. The White Oak (*Quercus alba*) was found to be the dominant tree species in both sites by size and number (23% of all trees in the study). According to the Chi Squared Test of Independence, the circumference of the White Oak was significantly larger than the other trees, at the five percent level of probability ($\chi^2= 6.126$).

Introduction:

The Eastern White Oak (*Quercus alba*) is a common tree species in the Northeast United States. It was commonly used for furniture and was once the tree of choice for shipbuilding during colonial times (Wasowski 2021). This tree grows as tall as 24.4m-30.5m and can have a base circumference of 70-120cm. The Eastern White Oak is a food source in the form of acorns for birds, squirrels, and deer. The trees in our study were found in the West Hills Dog Run Parks in Huntington NY. The trees were surveyed during the mid-Autumn month of October, and late Autumn month of December. The average climate of West Hills, Huntington for October is 19.4 °C, and partly cloudy. The average climate of West Hills, Melville in December is 6.6 °C and overcast (AccuWeather, 2021).

Method:

At West Hills Dog Run on October 16th, 2022, forty trees were surveyed to determine which type of tree is most dominant. The average temperature that day was 19.4 °C and was partly cloudy. Using an application on our smartphones (Compass on iPhone), we found a ten digit grid of the area. Each tree was measured in a 12.2 x 12.2-meter square. Our research was collected surveyed using 40 different tree samples in the West Hills area in Huntington, and measured the base circumference of each species using a tape measure. We used three dichotomous keys to identify each species of our samples (Symonds. 1973, Petrides & Wehr. 1988, Watts. 1939). The latitude and longitude was 40°48'19"N 73°25'7"W at a 76.2m elevation. Again, at West Hills Dog Run on December 2nd, 2022, forty-seven individual trees were surveyed on a different site within the West Hills Dog Run. The average temperature that day was 6.6 °C and was cloudy. On December 2nd, 2022 we surveyed a second ten digit grid adjacent to the one surveyed in October. Each tree was measured in a 12.2 x 12.2 meter square. We surveyed 47 different tree samples in the West Hills area in Melville (an incorporated

hamlet in the Town of Huntington), and measured the base circumference of each species using a tape measure. We used the same three dichotomous keys to identify each species of our samples. The calculated latitude and longitude 40°48'40"N 73°25'4"W at an elevation of 94.4m.

Results:

Table 1 presents the data for latitude and longitude of the location of where trees were examined. Table 2 shows the location of the samples, the common name and the scientific name, and number of each species found at the location. Table 3 shows the Chi Squared Test of Independence. We found that 22.9% of trees examined in the West Hills area were Eastern White Oak (*Quercus alba*). Using the Chi Squared Test of Independence we were able to determine that the Eastern White Oak was dominant by size as well. The average base circumference of the Eastern White Oak was significantly larger (79.4cm) compared to the base circumference of the other trees (52.3cm). The Eastern White Oak was identified seven times in Huntington and twelve times in Melville. There was a total of nineteen Eastern White Oak trees examined in the area of the West Hills Dog Run Melville/Huntington, which is the largest number in amount.

Table 1: Location of the trees

Town	County	Latitude	Longitude	Square Meters
West Hills/ Huntington	Suffolk	40°48'19"N	73°25'7"W	12.2x12.2 meters
West Hills/ Melville	Suffolk	40°48'40"N	73°25'4"W	12.2x12.2 meters

Table 2A: Identification of Trees in West Hill Dog Run, Huntington

Common Tree	Scientific Name	Total	Percentage	Circumference (cm)
Common Witch Hazel	<i>Hamamelis virginiana</i>	2	5%	4.9, 4.9
Oriental Bittersweet	<i>Celastrus orbiculatus</i>	1	2.5%	69.1
Eastern White Oak	<i>Quercus alba</i>	7	17.5%	45.8, 45.8, 103.1, 41.4, 90.9, 66.5, 3.6
Sourwood Sorrel Tree	<i>Oxydendrum arboreum</i>	6	15%	8.5, 15.2, 8.5, 8.4, 13.3, 31.2
Mountain Laurel	<i>Rhododendron</i>	3	7.5%	11.5, 10.1, 12.3
Red Maple	<i>Acer rubrum</i>	4	10%	45.1, 22.3, 10.2, 83.1
Common Sassafras	<i>Sassafras albidum</i>	4	10%	55.7, 25.3, 16.6, 24.5
American Holly	<i>Ilex opaca</i>	1	2.5%	66.5
Sweet Birch	<i>Betula lenta</i>	1	2.5%	32.2
Bur Oak	<i>Quercus macrocarpa</i>	1	2.5%	105.3
Scarlet Oak	<i>Quercus coccinea</i>	1	2.5%	49.9
Northern Red Oak	<i>Quercus alba</i>	2	5%	46.8, 61.3
Common Buckthorn	<i>Bumelia tenax</i>	1	2.5%	19.3
Laurel	<i>Kalmia latifolia</i>	1	2.5%	12.9
Great Laurel	<i>Azalea</i>	1	2.5%	17.8
Pivet	<i>Ligustrum</i>	1	2.5%	16.7
American Mountain	<i>Sorbus americana</i>	1	2.5%	22.1
Chestnut Oak	<i>Quercus prinus</i>	1	2.5%	8.6
White Mulberry	<i>Morus alba</i>	1	2.5%	42.6

Table 2B: Identification of Trees In West Hill Dog Run, Melville

Common Tree	Scientific Name	Total	Percentage	Circumference (cm)
American Beech	<i>Fagus grandifolia</i>	3	6.3%	110.8, 51, 30.2
Sweet Birch	<i>Betula lenta</i>	5	10.6%	110.1, 130.1, 90.2, 42.5, 92,
Pignut Hickory	<i>Carya glabra</i>	3	6.3%	110.5, 28, 55
Black Gum	<i>Nyssa sylvatica</i>	4	8.5%	20.5, 170, 128, 30.5
White Ash	<i>Fraxinus americana</i>	1	2.1%	80.1
American Hophornbeam	<i>Ostrya virginiana</i>	3	6.3%	40.3, 55.1, 63
Eastern White Pine	<i>Pinus strobus</i>	1	2.1%	50.7
Chestnut Oak	<i>Quercus prinus</i>	9	19.1%	75, 40, 98, 118, 107, 170, 131, 75, 132
Sourwood	<i>Oxydendrum arboreum</i>	1	2.1%	41
Red Oak	<i>Quercus rubra</i>	1	2.1%	46
Common Sassafras	<i>Sassafras albidum</i>	4	8.5%	87,50,43.5,43
Eastern White Oak	<i>Quercus alba</i>	12	25.5%	40, 98, 107, 132, 170, 131, 118, 40, 95, 43, 50, 87

Table 3: Chi Squared Test of Independence

Circumference	Eastern White Oak	Other Trees
	A	B
< 60.18	8	42
	C	D
> 60.18	11	22

Formula: $\chi^2 = (AD-BC)^2 / (A+B+C+D) / (A+C) (B+D) (A+B) (C+D)$

Discussion:

According to a study done by the *Long Island Botanical Society* (2000) The Eastern White Oak (*Quercus alba*) was the most abundant tree in the area of West Hills Park. After conducting our research, we searched online for evidence that the Eastern White Oak was the dominant species in that area. However, we were unable to find any sources that conducted any research in this area other than the study done by the *Long Island Botanical Society*, suggesting that our study may be one of only two studies conducted in this area.

Conclusion:

In our study, we have found that the Eastern White Oak makes up 22.9% of the tree population in the West Hills Dog Run area and is significantly larger compared to the other tree species ($\chi^2 = 6.126$)., therefore this species of tree is the most dominant tree in this area.

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Deciduous Trees Are Dominant to Coniferous Trees on a Private Property in Southold N.Y.

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Abstract:

This study tested if there were more deciduous trees or coniferous trees and which were older on Long Island. On a private property in Southold NY, I surveyed and measured 46 trees to test my hypothesis that deciduous trees were on average older and in higher quantity by measuring the circumference of all the trees. It was found that there was a greater number of coniferous trees than there were deciduous trees, but the deciduous trees had a larger average circumference than the coniferous trees, significant at a 2% level of probability ($\chi^2 = 5.534$) according to the chi-squared test of independence.

Introduction:

New York's landscape is rich with bare-branched deciduous trees and dark, evergreen conifers. Conifer trees have been able to adapt to survive harsh, cold weather (Ruffino 2019). To better deal with the cold, coniferous trees are able move water out of their cells to the spaces in between which allows the cells to remain intact when the tree freezes (Quinlan 2020). Since Long Island is a place where the climate can change and be warm and cold, coniferous trees can survive here in the winter unlike deciduous in the winter when they lose their leaves (Jean 2020). Southolds lowest monthly average temperature is -3.8 C in January and the highest is 26.6 C in July (Jean 2020). The majority of the population of trees on a property in Southold, was Eastern Red Cedar (*Juniperus virginiana*) because the property is on the water. Both the soil and landscape have an impact on the tree and if it will adapt for survival.

Methods:

This study used an area of 23.7 meters (77.7 feet) by 36 meters (118.04 feet) from one corner of the property creating a square. There were 46 trees on half the property that were identified. I started at the first tree and worked my way until I got to the last tree avoiding identifying the same tree more than once. For each tree, a small part of the branch was picked off and identified using a dichotomous key (Petrides and Wehr 1998). After having identifying a tree, I went into the second key, and double-checked it if possible (Watts 1991). After checking to see the species of tree, the tree was measured at chest height with a measuring tape. After finding the circumference of the tree I created a list of all the information in my findings. After repeating this step 45 more times to all my trees, I used all the data from my notebook and transported it into a spreadsheet and recorded more information such as the tree name, scientific name, deciduous trees or coniferous tree, the number of trees, and the average circumference in centimeters (seen in table 1)

- 1) After finding my data I started to split it up even more using another table, I found the average circumference of the deciduous trees, the average circumference of coniferous trees, the number of deciduous trees with a circumference above the mean, the number of deciduous trees with a circumference below the mean, the number of coniferous trees with a circumference above the mean, the number of coniferous trees with a circumference below the mean (can be seen in table 2).

- 2) With the data that I pulled from table 1 and put into table 2 on the trees below and above the mean, I used the chi-square test of independence to find out if my hypothesis, that deciduous trees are older than coniferous trees but the population of coniferous trees is greater in Southold NY is true. I calculated the number of deciduous trees and their circumferences above the mean was greater than the number of coniferous trees (seen in my calculations and in table 3).

Results:

The private property in Southold NY was used in this study by marking off a corner of the property 41°2'51" N 72°25'1" W, 41°2'50" N 72°25'3" W, 41°2'53" N 72°25'2" W, 41°2'52" N 72°25'1" W. The majority of the property was filled with coniferous trees while the minority were deciduous (as seen in Table 2). While there were more coniferous trees (63%) the deciduous trees were found to be older when I measured the circumferences at the 2% significant level of probability ($\chi^2 = 5.534$) according to the chi-square test of independence (seen in Table 3 and in calculations).

Table 1: Total Collection of Tree Data

#	Scientific name	Common Name	Circumference (cm)	Coniferous or Deciduous
1	<i>Juniperus virginiana</i>	Eastern Red Cedar	109.9	Coniferous
2	<i>Juniperus virginiana</i>	Eastern Red Cedar	63.7	Coniferous
3	<i>Juniperus virginiana</i>	Eastern Red Cedar	57.4	Coniferous
4	<i>Juniperus virginiana</i>	Eastern Red Cedar	62.2	Coniferous
5	<i>Juniperus virginiana</i>	Eastern Red Cedar	55.6	Coniferous
6	<i>Juniperus virginiana</i>	Eastern Red Cedar	54.6	Coniferous
7	<i>Juniperus virginiana</i>	Eastern Red Cedar	70.6	Coniferous
8	<i>Juniperus virginiana</i>	Eastern Red Cedar	59.1	Coniferous
9	<i>Juniperus virginiana</i>	Eastern Red Cedar	62.2	Coniferous
10	<i>Juniperus virginiana</i>	Eastern Red Cedar	62.7	Coniferous
11	<i>Juniperus virginiana</i>	Eastern Red Cedar	54.3	Coniferous
12	<i>Juniperus virginiana</i>	Eastern Red Cedar	62.2	Coniferous
13	<i>Juniperus virginiana</i>	Eastern Red Cedar	53.5	Coniferous
14	<i>Juniperus virginiana</i>	Eastern red cedar	44.4	Coniferous
15	<i>Juniperus virginiana</i>	Eastern Red Cedar	56.6	Coniferous
16	<i>Juniperus virginiana</i>	Eastern Red Cedar	57.1	Coniferous
17	<i>Forsythia × intermedia</i>	Border Forsythia	8.89	Deciduous
18	<i>Cornus florida</i>	Flowering Dogwood	26.6	Deciduous
19	<i>Forsythia × intermedia</i>	Border Forsythia	10.6	Deciduous
20	<i>Forsythia × intermedia</i>	Border Forsythia	9.3	Deciduous
21	<i>Forsythia × intermedia</i>	Border Forsythia	9.9	Deciduous
22	<i>Cerasus serrulata</i>	East Asian Cherry	129.0	Deciduous
23	<i>Euonymus alatus</i>	Winged Spindle	13.4	Deciduous
24	<i>Ligustrum ovalifolium</i>	Korean Privet	10.9	Deciduous
25	<i>Rhododendron maximum</i>	Great Laurel	21.5	Coniferous (evergreen shrub)

26	<i>Pieris japonica</i>	Japanese Andromeda	18.0	Coniferous (evergreen shrub)
27	<i>Rhododendron maximum</i>	Great Laurel	20.0	Coniferous (evergreen shrub)
28	<i>Rhododendron maximum</i>	Great Laurel	20.8	Coniferous (evergreen shrub)
29	<i>Prunus cerasifera</i>	Cherry Plum	135.1	Deciduous
30	<i>Quercus palustris</i>	Pin Oak	226.3	Deciduous
31	<i>Quercus stellata</i>	Post Oak	241.5	Deciduous
32	<i>Quercus palustris</i>	Pin Oak	157.4	Deciduous
33	<i>Euonymus alatus</i>	Winged Spindle	26.67	Deciduous shrub
34	<i>Cornus florida</i>	Flowering Dogwood	22.6	Deciduous
35	<i>Vaccinium corymbosum</i>	Highbush Blueberry	23.3	Deciduous shrub
36	<i>Quercus palustris</i>	Pin Oak	128.5	Deciduous
37	<i>Quercus palustris</i>	Pin Oak	168.4	Deciduous
38	<i>Chamaecyparis thyoides</i>	Atlantic White-Cedar	132.5	Coniferous (evergreen)
39	<i>Juniperus virginiana</i>	Eastern Red Cedar	60.19	Coniferous
40	<i>Juniperus virginiana</i>	Eastern Red Cedar	52.0	Coniferous
41	<i>Juniperus virginiana</i>	Eastern Red Cedar	35.8	Coniferous
42	<i>Juniperus virginiana</i>	Eastern Red Cedar	59.1	Coniferous
43	<i>Juniperus virginiana</i>	Eastern Red Cedar	33.5	Coniferous
44	<i>Juniperus virginiana</i>	Eastern Red Cedar	98.8	Coniferous
45	<i>Juniperus virginiana</i>	Eastern Red Cedar	31.49	Coniferous
46	<i>Juniperus virginiana</i>	Eastern Red Cedar	56.8	Coniferous
	Average Circumference		70.97	

Table 2: Averages of the tree circumferences and the number of trees above and below mean

Average circumference of all the total tree	70.97
Average circumference of deciduous trees 17	79.31
Average circumference of coniferous trees 29	44.13
Number of deciduous trees with a circumference above the mean	7
Number of deciduous trees with a circumference below the mean	10
Number of coniferous trees with a circumference above the mean	22
Number of coniferous trees with a circumference below the mean	7

Formula 1. Chi-Square Test of Independence

$$\chi^2 = (ad-bc)^2(a+b+c+d) / (a+b)(c+d)(b+d)(a+c)$$

$$\chi^2 = (7 \times 7 - 10 \times 22)^2(7+10+22+7) / (7+10)(22+7)(10+7)(7+22)$$

$$\chi^2 = (49-220)^2(46) / (17)(29)(17)(29)$$

$$\chi^2 = 1,345,089 / 243,049$$

$$\chi^2 = 5.534: 2\% \text{ level of significance}$$

Discussion:

After surveying the trees in Southold, NY, I compared my results to Milana (2023). Our results were found to be very similar. The majority of their trees were coniferous but the deciduous trees were older as measured by circumference at a significance level of 1%. The majority of my trees were found to be coniferous, but deciduous trees were found to be older as measured by circumference at a significance level of 2%.

Conclusion:

While there was a larger majority of coniferous trees on a Southold private property, deciduous trees were found to be later and a lot older than coniferous trees at a 2% level of significance ($\chi^2 = 5.534$) as seen from the chi-square test of independence. The Eastern Red Cedar (*Juniperus virginiana*) was seen to be the most dominant tree with (52%), and Pin Oak (*Quercus palustris*) with (10%).

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