

The Effect of Contamination on the Biodiversity of Arachnids along the Forge River

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Abstract: The Forge River is one of the most highly polluted waterways in New York State. The DNA sample of Spiders from the Forge River, were barcoded to identify their species and analyze the impact of pollution on biodiversity.

Introduction: Spiders were collected from Forge River which was surrounded by duck farms and industrial agriculture causing waste as well as human sewage to leach into the river-water. The increased amount of nitrogen and phosphate in the water is resulting in increased algae growth and reducing the oxygen level. Oxygen depletion also hampers the regulation of metabolic activity of an organism, decreasing biodiversity of the ecosystem (Swanson, Brownawell and Wilson, 2010). Pesticides used in industrial agriculture contain heavy metal, also affect the river. Sediments in the riverbed accumulate heavy metals and release them slowly in the water (Ti, tang, Yi, Yang and Zhang, 2017). Heavy metal in the food web cannot be removed, which can distress the biodiversity.

Spiders are important to the ecosystem because of their consumption of vectors (Vector-borne diseases, 2017). If one organism of the ecosystem is removed, it may cause trophic cascade (Gruner, 2013). The organisms present on lower trophic levels then spiders tend to depend highly on predation. Spiders, aptly, capture their prey; which, acts as an control of continuously growing population of mosquitoes and flies (Lawania et al, 2013). Spiders also aid the decomposition process (Liu, Chen, He, Hu and Yang, 2012). Their disappearance would lead to trophic cascade and affect the rate of decomposition-since other organisms do not occupy the same niche. The fluctuation in the population of the spiders will also affect the population of vectors because spiders are natural control. Since carnivorous spiders prey on vectors, they serve as a way of reducing diseases. The main vectors of Spider's diets are mosquitoes, flies, and ticks. Mosquitoes cause fevers (Chikungunya, Dengue, Yellow, Rift Valley, West Nile), and diseases such as: Zika, Malaria, Lymphatic Filariasis and Japanese Encephalitis (Vector-borne Diseases, 2017). Diseases carried by flies include- Typhoid, Cholera and the ticks spread Lyme Disease and Q Fever (Tick-borne Diseases, 2017).

The research question posed as to whether there is a correlation between spider species and location along the Forge River, will be used in conjunction with a spectral analysis to determine if there are heavy metals in spider chelicerae. Barcoding the spiders will assist us in identifying the species and the niche they occupy along the river. The hypothesis that there are different species found along the Forge River was tested using DNA barcoding.

Methodology: Spiders were collected around the Forge River using natural methods. Spider locations and pictures were recorded. A part of the spider and Lysis solution was mixed in a tube. The samples were grinded and centrifuged. The supernatant, was transferred to a new tube. Silica resin was mixed in the new tube and incubated. The samples were centrifuged to remove the supernatant and wash buffer was added. The samples were centrifuged, supernatants were removed, and distilled water was added. The tubes were incubated for five minutes. Samples were centrifuged and supernatants were transferred to a new tube. The new tube was stored at 4 degrees Celsius. Two microliters of DNA was added to the primer to complete PCR. The COI gene of DNA was amplified in the thermocycler. Two microliters of sybr green were placed in a tube with 5 microliters of DNA, which was loaded into each well of the gel. Pictures of the gel were taken and uploaded onto the sample database. Samples which were successfully amplified were sent to Cold Spring Harbor for analysis. DNA subway was used to compare DNA sequences to other sequences in the NCBI and Bold databases. A cladogram was used to create the phylogenetic tree to see the relation between the species and DNA barcode was used to compare similarities among the species based on one specific gene (COI). A pie chart using Excel, was made to make comparisons among the species and location.

Data Analysis:

Figure 1: The figure compares the unknown species with known species on the basis of Bit Score. The red colored bars indicates the percentage of 95% or above which shows the confidence in the species identity.

	C	1	2	3	4	5	6	7	8	9	10	11	12	13	14
C	-	63.42	59.9	6.4	60.48	72.92	7.76	80.56	46	81.83	88.98	88.16	88.31	91.46	91.34
1	63.42	-	80.7	8.6	82.88	48.71	4.11	48.35	44	50.12	51.06	51.06	53.88	55.06	50.6
2	59.69	80.97	-	9.1	95.35	46.01	5.24	50.56	48	48.71	48.90	50.98	49.67	51.33	36
3	68.44	89.96	97.11	-	98.67	51.74	5.44	52.42	20	52.49	55.22	55.22	56.72	58.21	21
4	60.48	82.88	95.35	98.67	-	46.57	50.79	50.11	06	50.17	49.67	52.16	50.57	52.10	40
5	72.92	48.71	46.01	51.74	46.57	-	7.14	73.55	16	63.17	68.11	67.02	68.91	67.47	47
6	79.76	49.11	51.24	53.44	50.79	71.14	-	96.59	37	70.94	74.35	74.35	72.55	73.95	95
7	80.56	48.35	50.56	52.42	50.11	73.55	96.59	-	57	70.74	75.35	75.35	73.35	74.95	95
8	87.46	53.44	50.48	54.20	51.06	66.16	71.37	71.57	-	98.78	84.12	83.07	83.28	85.19	19
9	81.83	50.12	48.71	52.49	50.17	63.17	70.94	70.74	98.78	-	78.40	76.79	78.18	79.70	19
10	88.98	51.06	48.90	55.22	49.67	68.11	74.35	75.35	84.12	78.40	-	100.00	84.53	85.37	78
11	88.16	51.06	50.98	55.22	52.16	67.02	74.35	75.35	83.07	76.79	100.00	-	83.08	84.26	26
12	88.31	53.88	49.67	56.72	50.57	68.91	72.55	73.35	83.28	78.18	84.53	83.08	-	87.71	93
13	91.46	55.06	51.33	58.21	52.10	67.47	73.95	74.95	85.19	79.70	85.37	84.26	87.71	-	100.00
14	91.34	50.6	52.36	58.21	55.40	67.47	73.95	74.95	85.19	79.70	85.37	84.26	87.71	100.00	-

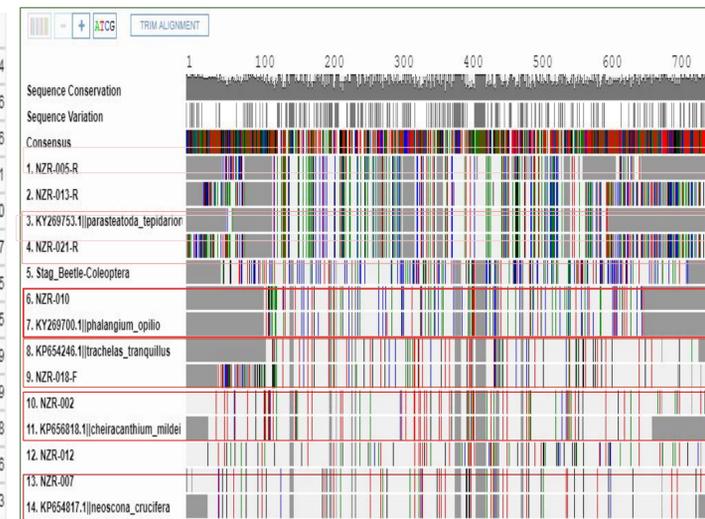


Figure 2: This figure demonstrates the barcode of the DNA using DNA Subway of the analyzed and reference species. Data indicates matching barcodes confirming species identification. The red boxes correspond with Figure 1.

Results:

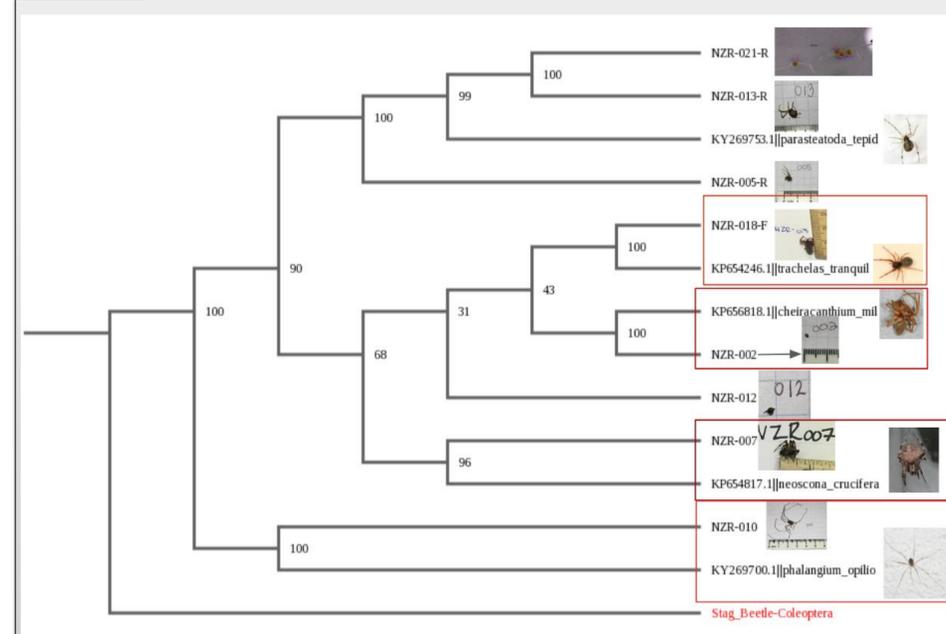


Figure 3: This phylogenetic tree explains the evolutionary relationship between the analyzed and reference species. Analyzed species that are identical to the reference species are boxed in red which correspond with Figures 1 and 2. Figure 3 further confirms the confidence of species identification.

Number of Spiders at Locations around the Forge River



William Floyd High School
Riviera Drive
Alcolade Dr. W
Osprey Park
Mirror Lane

Figure 5: This figure shows the number of spiders at locations around the Forge River. Most of the amplified spiders were found in the Riviera Drive. It indicates that the locations have more favorable habitats for the species of spiders.

Number of Species of Spiders at Locations around the Forge River



William Floyd High School
Riviera Drive
Alcolade Dr. W
Osprey Park
Mirror Lane

Figure 6: This figure illustrates the biodiversity of the Forge River. It also indicates to the diverse and connected ecosystem of along the region of the river.

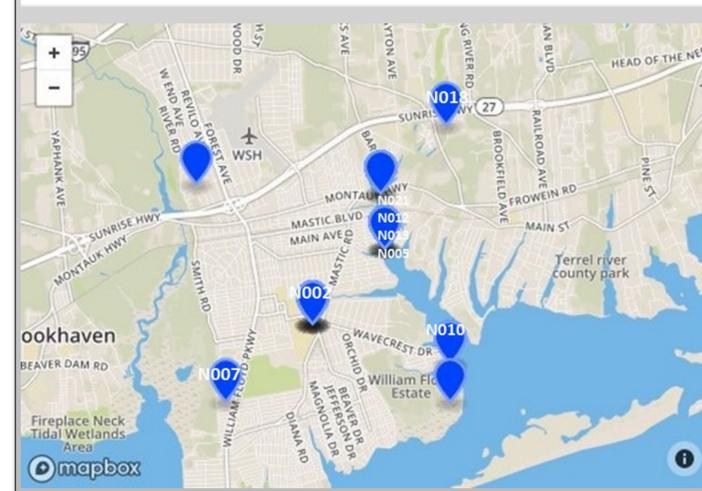


Figure 4: This figure demonstrates the location of each spider. The map indicates possible relationship between the spiders because similar species will occupy similar niches.

Discussion & Conclusion:

The results of this study show a correlation between spider species and location. As hypothesized, different species of spiders were found throughout the Forge River. The outcome of this study demonstrates different species occupy different niches and slightly different ecosystems. Data collected indicates a diverse spider ecosystem which contributes to the biodiversity along the Forge River. The absence of a spider species could cause trophic cascade influencing the homeostasis of the ecosystem. In saltwater marshes, spiders are a natural control of vectors, such as mosquitos. The loss of a spider species will also affect the rate of decomposition along the river. The purpose of the experiment was to analyze the biodiversity along the Forge River. The results of this experiment demonstrate that the biodiversity along the Forge River and also suggests that the species of spider and their location are correlated.

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