

Investigating Invasive Flying Insects in the Local Outdoors of Sayville, NY

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Abstract

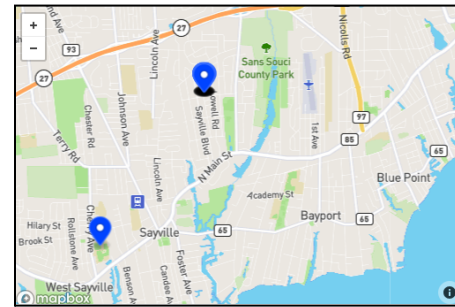
Invasive species pose significant threats to native ecosystems, human health, and economic stability, particularly within the agricultural sector. This research focuses on the prevalence and impact of invasive fly species (order: Diptera) in Sayville, New York. Using mitochondrial DNA sequencing for species identification, this study aims to differentiate between native and invasive fly species. Known invasive species in New York were used to compare DNA with the samples, such as the African fig fly, European crane fly, and spotted wing drosophila. Native species also aided in the comparison like the American hoverfly and bee fly. Out of the twenty samples, ten genetic sequences were identified. The results of the DNA analysis revealed two invasive species out of ten viable samples, indicating a potentially larger problem of invasive flying insect presence in the area. This study highlights the need for more awareness and management to lessen the harmful effects that invasive flies impose on local ecosystems and agriculture.

Introduction

Invasive species pose numerous threats to native ecosystems and human health. These species can destroy habitats, alter the function of ecosystems, infest commercial crops and industrial materials, carry and transmit diseases, and increase competition for resources causing the extinction of native species (Fantle-Lepczyk et al., 2022). Most invasive species are transported through human activity. This invasive interference causes great economic losses, specifically in the agricultural industry. There is a continuous rising cost of invasions and number of invasive species but a large gap in knowledge regarding how much is actually being lost due to known invaders. The methodology involved will include identification through genetic sequencing and comparison of mitochondrial DNA, which will allow for distinguishment between fly species (Asraoui et al., 2008). Further comparison between known species native to New York such and also invasive species will ultimately show whether the collected species are invasive or native to New York (Comeault et al., 2020; Corser, 2018; Lee et al., 2019; LIISMA, 2023; New York Invasive Species Information, 2023; NYNHP, 2017; Peck et al., 2010).

Materials & Methods

Materials used include: Four identical fly traps, tweezers, sample tubes, camera, microcentrifuge and chelex. The fly traps were hung outdoors in four distinct locations. Flies were collected from the traps as needed until twenty different species were collected. The DNA barcoding procedure was followed as specified in the Cold Spring Harbor DNA barcoding manual. Each type of species was identified by comparing its genetic similarities. Then the species was compared with known native and invasive fly species.



Discussion

Identification through genetic sequencing and comparison of mitochondrial DNA will allow for distinguishment between fly species (Asraoui et al., 2008). Further comparison between known species native to New York such as the American hoverfly, bee fly, flesh fly, saproxylic hoverfly, and others and also invasive species such as the African fig fly, European crane fly, spotted wing drosophila, swede midge, European cherry fruit fly, bathroom moth fly, European drone fly, common drone fly, common European green bottle fly, narcissus bulb fly, peg-legged compost fly, thick-legged hoverfly and others will ultimately show whether the collected species are invasive or native to New York (Comeault et al., 2020; Corser, 2018; Lee et al., 2019; LIISMA, 2023; New York Invasive Species Information, 2023; NYNHP, 2017).

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