Using Molecular Scatology to Assess the Diet of Barn Cats in Bucks County

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Abstract

The domestic cat (*Felis catus*) is a widely introduced species around the U.S and is known for its negative impact on wildlife and its environment (Loss, et al. 2013). This includes not only feral cats that consume wildlife, but also free-roaming cats. The barn cats on the campus of Delaware Valley University are considered free-roaming, as they are not confined indoors but are fed by agricultural staff. The estimated deaths of wildlife caused by cats, both feral and free-roaming, are estimated at 6.9-20.7 billion per year. (Loss et al. 2013) These cats are impacting ecosystems in negative ways, and this research aims to assess the impact of cared-for barn cats to the surrounding environment.

Introduction

Cats are becoming one of the world's largest conservation issues. In the US, there is not enough research going into the impacts of free-roaming cats on the environment to accurately define the issue and bring about a solution. Now that the feral and outdoor cat issue has become as large as it has, a growth of new research opportunities has grown from this issue.

Feral cats have now been recognized as an ecological issue. However, another group of domestic cat has not been focused upon – the barn cat. These cats are "owned" however they often move across landscapes freely, consuming native wildlife species at high rates.

This research looks specifically at barn cats that are free-roaming and seeks to determine if these free-range cats are actively contributing to the decrease of native wildlife populations in Bucks County. This research seeks to provide more information to the study of domestic cats, and the issues they impose on animals, people and ecosystems.

This study used barn cat fecal samples to assess the presence of wildlife content in barn cat diet. If the cats on campus follow the trends of cats across the US, then the results will yield a high rate of native wildlife species.

Methods

The site of collection was Delaware Valley University's Dairy Science Barn. This site is the primary location of multiple barn cats. These cats are free-roaming but are fed a stable diet of chicken-based cat foods. The cats can go into the barn or out into the fields, and from there can go anywhere they please.

Fecal samples were collected from and around the existing litterbox in the barn that is frequently used by the barn cats. Fecal samples were only collected from in and around the Dairy Barn litterbox. These samples were collected once a week, from August – September 2024 and samples were put into separate tubes marked with the data of collection. Samples were stored at -20^{0}C.

DNA extraction was performed using the QIAamp Fast DNA Stool Mini Kit. Extraction followed kit procedures as modified by Plimpton et al. (2021) to ensure the optimal yield from cat feces. Procedure amendment included incubating samples in inhibitEX buffer at 56^{0}C for 10-12hrs prior to extraction. Post-extraction, a selection of 5 random samples was measured for concentration on a spectrophotometer. These tests showed that the samples had a significant amount of DNA to further the study.

To analyze the components of cat diet, the V5 variable region of the mitochondrial 12S gene was amplified using primers and PCR protocol following Plimpton et al. (2021). The PCR was carried out in a 12.5µl reaction containing 6.25µl HotStart ReadyMix, 2µl of DNA, 0.625µl 12SV5 F primer, 0.625µl 12SV5 R primer, 2.5µl cat blocking buffer, to reduce the prevalence of cat DNA and 0.5µl of PCR grade water. The PCR was run with an initial denaturation of 30s at 98C, 30s at 58C, 10s at 72C and a final elongation for 1 min at 72C. The PCR samples were run through gel electrophoresis in four pooled groups at 120V for 30mins. Products of the optimum length(~200 bp) were purified using the QIAquick PCR & Gel Cleanup Kit.

References and Acknowledgements

Loss et al. 2013
Plimpton et al. 2021

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Results

The process of the PCR and gel electrophoresis was successful in producing DNA in the appropriate size as shown in Figure 1.

Purified samples will be pooled and sent to GENEWIZ for Amplicon-EZ next generation sequencing. Unique sequencing analysis will be performed to identify species present in the cat diet's of free-roaming cats at Delaware Valley University's Dairy Barn.

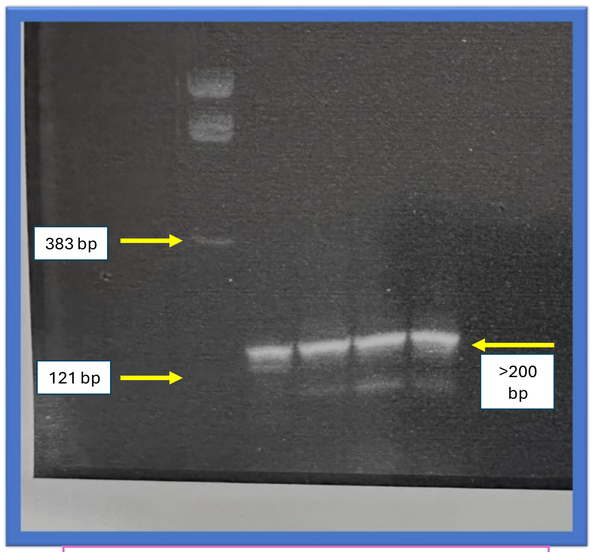

Figure 1:
PCR products on a 2% agarose gel

Impact of Study

The cats at the focus of this study live primarily in the dairy barns and have near constant access to typical cat food, but still these cats may prefer to consume native wildlife species. These barn cats are "cared for" meaning that they have access to adequate shelter and food, at all times so they do not have to hunt for it on their own, and "fend for themselves". However, despite this it is typical for these animals to consume wildlife species, and any cat that lived outdoors is a primary factor in the decline of wildlife species. This research highlights this issue and examines how much this issue is affecting the wildlife near and on Delaware Valley University's campus.