Low Genetic Diversity as a Source of Alkali Bee Population Decline

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Abstract

In efforts to better understand the genetic diversity among alkali bees (*Nomia melanderi*), samples were taken from 11 sites in Southeastern Washington. Historical samples were also collected in order to identify a baseline for our DNA analysis. Alkali bee DNA was extracted and verified by PCR and gel electrophoresis before being analyzed by a microsatellite assay. The assay identified variation in the copy number for each microsatellite which was then used to determine population structure (degree of genetic isolation), rates of inbreeding, and population bottlenecks (loss of genetic diversity) among the bee beds. The information learned was then shared with alfalfa seed growers in hopes of better supporting managed populations of alkali bees.

Introduction

Alfalfa has the third largest production value of any crop in the United States. Pollinators such as alkali bees (*Nomia melanderi*) are essential in the growth and productions of alfalfa crops. In WA, growers in the Touchet-Gardena-Lowden (TGL) area have been managing alkali bees for over 50 years in bee beds adjacent to the seed fields. However, local populations of alkali bees have diminished in recent years, forcing alfalfa growers to search elsewhere for effective pollinators. The cause of this decline is currently unknown, but research has ruled out pesticides, pathogens, and reductions in forage area as major causes. Low genetic diversity among bee beds remains a possible cause which can result in further reduced genetic diversity, inbreeding, and ultimately population loss.

Objectives

The purpose of this research is to gather genetic information for alfalfa seed growers to better manage the alkali bee populations that pollinate their crops. To achieve this, our objectives are to:

1. **Conduct a survey of wild alkali bee populations** in western North America.
2. **Determine population genetic diversity** of wild alkali bee populations.
3. **Identify genetic similarity of wild alkali bee populations** with managed TGL populations.

Methods

- **Sampling:** A historic collection of 95 bees from pre 1990 were collected to establish a baseline of genetic diversity. 422 bees from the 11 sites in WA were also sampled. This was done by immobilizing the bee on ice and removing one of its mid-legs.
- **DNA Extraction:** Using razor blades, the leg was chopped finely to break up the tissue. The Quiagen Blood and Tissue kit was used to isolate the DNA.
- **PCR and Gel Electrophoresis:** PCR was used to amplify the DNA elution at three specific microsatellites. Gel electrophoresis qualitatively verified the success of the DNA extraction and PCR.
- **Analysis:** PCR product was run on a fragment analyzer and scored on the program Geneious to assess variation in the number of microsatellite repeats.

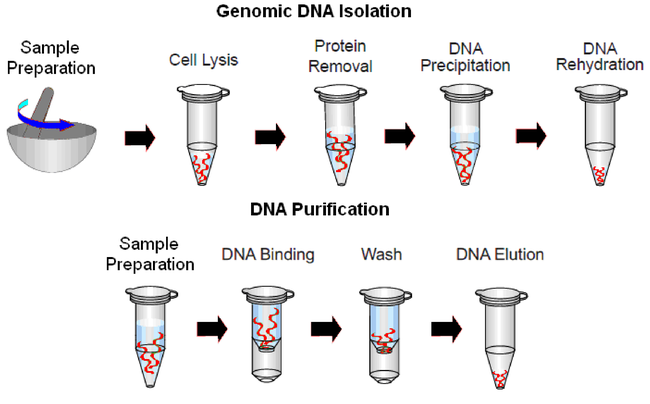

Figure 1: Simplified DNA extraction process similar to the one used for the alkali bees. Image used from https://fairbiotech.com/shopping_show-2a14727aaa.html

Results

Data is still being gathered for this project, but the results will come in both a qualitative and quantitative form.

Qualitative:
After completing the polymerase chain reaction of the extracted DNA, gel electrophoresis will confirm the presence of amplified DNA from the selected microsatellites. Of the few samples that have been amplified and tested the gels show that the DNA extraction and PCR procedures have been successful as seen in figure 2.

Quantitative:
After being verified by gel electrophoresis, the amplified microsatellites will be run through a DNA fragment analyzer. The resulting absorbances in the DNA sequence will then be scored using the bioinformatics software Geneious to determine variations within DNA.

This information will provide insight to the genetic diversity within the alkali bee populations. Determining the genetic diversity of the bees will allow for statistical analyses and models to be run to help assess potential rates of inbreeding, bottleneck events, and assist in providing alfalfa growers with accurate information on how to maintain and breed the populations of alkali bees.

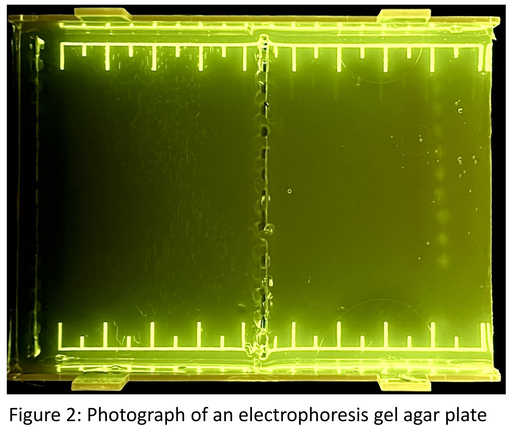

Figure 2: Photograph of an electrophoresis gel agar plate from the alkali bees. All samples tested positively for DNA.

Geneious Bioinformatics Software

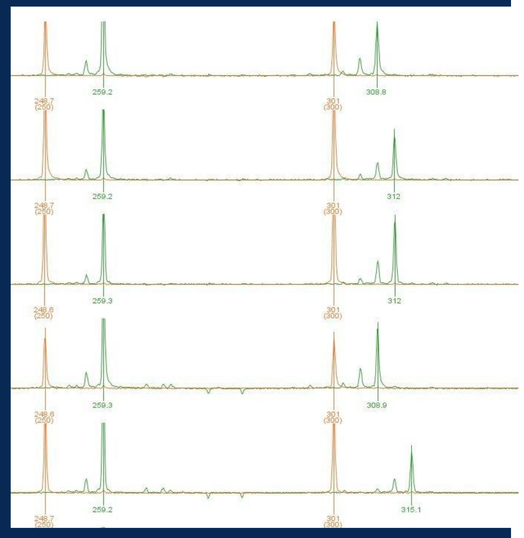

Figure 3: Sample of the microsatellite scoring software that will be used to determine variations in the DNA. Image from https://www.researchgate.net/topic/Microsatellite-Genotyping

Conclusions

This research will provide the necessary information to alfalfa seed growers on how to manage the populations of alkali bees. This research will offer insight into the genetic causes of population decline and allow for alfalfa growers to selectively breed the alkali bees to increase genetic diversity and create a more stable population of pollinators.

Increased genetic diversity among alkali bee populations will result in both increased survival and fecundity. Larger, more stable populations of alkali bees will pollinate a larger area of alfalfa resulting in higher crop yield and maximized use of alfalfa fields.

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