The Relationship Between Soil and Biodiversity in SIP

Tock Sun,Sam Sun,Hansson Liu
Mentor: Jeffry Petracca
Cold Spring Harbor Asia DNA Learning Center

Introduction

Biodiversity is the variety of species in a specific area. The soil ecosystem is a good indicator for determining the health of an ecosystem. This project focuses on is whether the soil from the Suzhou Industrial Park (SIP) is a good environment for biodiversity. In our estimation, the soil in SIP will have low biodiversity,because of the pollution produced by factories in SIP. To determine this, we will collect soil invertebrates and microorganisms around Park of Life in SIP, a characteristic urban park. We will then use DNA barcoding, which is the technique to use amplified DNA marker sequences as barcodes.The advantages of DNA barcoding are that it identify and classify specimens really fast. More specifically, we will use chelex DNA extraction to extract the DNA of invertebrates and a 16S extraction kit to get the DNA of microbes. DNA Subway will be used to attain COI barcodes for invertebrates, and metabarcoding will be carried out by nanopore technology.DNA metabarcoding is a technique which can analyze a soil or water sample to determine the profile of organisms lived in that sample. For getting the DNA to metabarcoding, we used nanopore sequencing, which is a method to use tiny motor protein combine with a nanopore to get single DNA chain through it. Then, ions will combine with nucleotide to make detector infer the DNA sequence by the voltage change across an artifical membrane. We believe the result can inspire more industrial parks to take care of increasing soil quality to maintain higher biodiversity of soil species.

Methods

1. soil invertebrates samples

We collected soil from different depths in the Park of Life in SIP. After that,we used Berlese traps to get small invertebrates.Chelex DNA Isolation was used as the method to extract DNA sequences from invertebrates using the protocol provided by Cold Spring Harbor Laboratory's DNA Learning Center. Next, PCR(Polymerase Chain Reaction) was used to target amplify the COI gene region. Gel electrophoresis was used to check whether we had successfully amplified the region we wanted. After that, our DNA were sent to the Azenta LifeScience for DNA sequencing.At last of this process, we imported sequence into DNA Subway to identify species to classify and summarize the obtained data.

2. soil samples

We collected soil and grass samples from different depths.We used the 16S Extraction kit from Norgen Biotek Corp. and used a Nanopore 16S Primer kit to conduct PCR. We used Nanopore Sequencing and Epi2me software to sequence and analyze our microorganism samples.

3. comparison

After our analyses, we will compare the biodiversity we get from our samples with the data obtained from Young and Hebert (2022).

Results

Our data from soil is failed because of the ion in soil damage the PCR reaction, we use the grass roots instead. We get a lot of microorganisms, Serratia, Kosakonia, and Nostoc take up the most part. We build the kinship between the species. We have the species Gel electrophoresis as a detection.

Abstract

As we all know, the soil in China's industrial areas is reclaimed soil, and it differs from original soil. We decided to compare the soil in the urban Park of Life in Suzhou to the soil that was researched by Paul .D .N . Hebert in a national park in Canada. The problem we focused on was to explore whether the soil in Suzhou's urban park were suitable for organism's survival. In addition, we wanted to assess the physical composition of the soil. Samples were collected using Berlese traps, and DNA barcoding was used to identify invertebrates and microbes by targeting the COI and 16S gene regions, respectively. Notably, microbe diversity was attained using metabarcoding via the latest Nanopore technology to sequence, which might be the among first times for Chinese students. The results show that soil in industry is much poorer in species than that of Canada's natural park. Obviously, reclaimed soil lacks biodiversity, because it is not an ideal habitat for organisms due to possible soil pollution. We discovered that soil in industry lacks biodiversity and it seems hard for microorganisms to survive.

Keyword: soil, Metabarcoding, DNA barcoding, biodiversity, microorganisms, comparison, ecology environment.

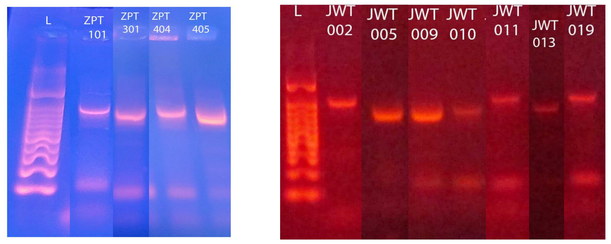

Figure.1&2
The results for gel electrophoresis of soil invertebrates samples after PCR

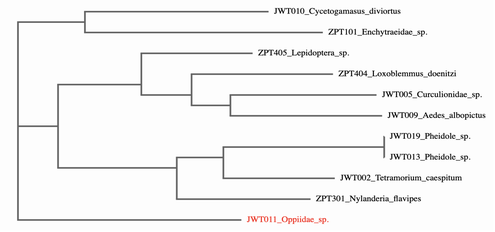

Figure.3
The ML Tree by the DNA sequence getting from soil invertebrates samples(Among them, JWT013 and JWT019 are the same speice)

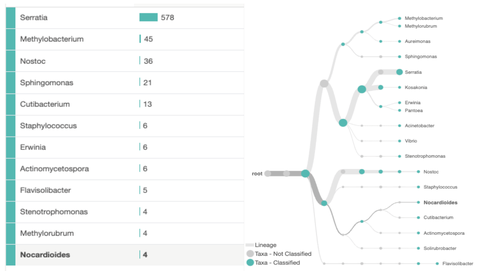

Figure.4
The proportion of different genus of microorganisms from a root of grass in SIP

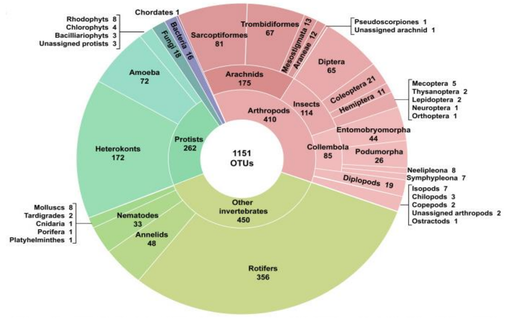

Figure.5
The amount and proportion of different speices in a national park of Canada **(datas getting from the article)**

Discussion

The result that we got from the experiment is inconclusive,because even through the DNA barcoding was success to get a gene tree,the Berlese traps were not as successful because by we were not able to sample all soil types in Suzhou.Furthermore, the metabarcoding for all six soil samples that we collected all failed to get useful results. Limited amounts of sequencing reads were obtained. In addition, soil samples collected by other students at CSHA DNA Learning Center also failed. Sadly, the results still not what we would like to have.We thought the most important problem is that we used the swab as the collection method without the Qiagen Powersoil Kit. Unfortunately we did not have access to this kit at the DNA learning center. Alternatively,we use the metabarcoding results from grass to present for our result.Although we own some error for our experiment, it can still show that the biodiversity in SIP is less abundant than the Eastern Temperate Forests ecoregion(EPA,2015in Ontario,Canada. Compared to the diversity summarized in FIG the, we get less variation with just ten invertebrates representing just 4 orders. However, Young & Hebert found 31 orders with 860 invertebrates in the Eastern Temperate Forests ecoregion(EPA2015)in Ontario,Canada.By contrast, in our metabarcoding study, we found more microbial diversity with four more orders compared to Young & Hebert, which just got 7 orders of protists. Based on these analyses, we got the surprise that the soil in SIP may the suitable habitat for micro organisms. More specifically the soil in SIP may be contain some factors, like chemicals or pollution to attract additional microorganisms to live here. The results suggest that invertebrate diversity is low in the soil of SIPbut a different extraction technique might yield more success with DNA extraction.

References

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