Ants' Finding: Identification Of Ant Species Using DNA Barcoding

Author: Tangzhui (Emma) Mentor: John Mark Olson Xinyue Wang
VNEN Academy of Innovation and Excellence

Abstract
This project is about whether the anti-like ants are ants and ant-non-like ants are ants. I collected totally 37 samples in VAE and 4 samples in DNALC, and used Silica method to get the DNA from the insects. PCR method the amplified the cut part, sequenced and got the results. At last, I found that not all anti-like ants are belong to ants.

Introduction
In daily life, it is hard for people to make sure the classification of an unknown insect. My question whether the anti-like ants are ants and ant-non-like ants are ants because through research I found not all anti-like ants are such as termites and Plecoptera (stone flies).

Discussion
The first problem is when collecting the sample, because the cold weather, there are fewer ants, so I choose to catch them, not waiting. When analyzing the agarose gel the second time, I found there were no results from the PCR reaction. I repeated this step again and there were still no results. This suggests there are problems with the DNA extraction step., and these also use the DNeasy Kit method. Another reason may be that PCR works not so well on insects. It may be that the primer is not able to bind to the DNA because of sequence difference. Also, some insects have GC rich regions of DNA that are difficult to amplify by PCR.

Materials & Methods
A sample collection, insect order for better to be stored well. In order, I put crushed insect (this has been on the paper on the ground about 5-8 attitude) from dawn to dusk, trying to catch ants, totally I got 15 ants (including Pheidole baikiana, Amaticola baikiana, Pheidole levis, Pheidole satria, 3x Pheidole termiti, 3x Pheidole hamata, 2x Pheidole burbonica, 2x Pheidole fortunei, 2x Pheidole burbounica, 2x Pheidole hamata, 2x Pheidole burbounica, 2x Pheidole hamata) and two termite ants (2x Termites). My sample collection.

DNA Barcoding:
DNA barcoding is a method of identifying organisms based on a short, standardized fragment of genomic DNA.

Results
1. In figure 3, I obtained PCR products for SPT-001, 002, 005-008, and I saw that SPT-003 and SPT-004 have no PCR results.
2. In figure 7, I obtained Quality Sequence for SPT001,002,004-008,018, and I saw that there’s no sequence in SPT-003, and less sequence in SPT-003, and the SPT-018 luckily survive.
3. In figure 5 (tree NJ) and 6 (tree ML), I see that SPT-001, SPT-005 and SPT-006 are belong to Nylanderia burbonica (robust crazy ants), and SPT-007 is belong to Amata fortunei (not ants) and SPT-008 and SPT-002 are belong to Pheidole nodas (ants), and SPT-018(not ants), and SPT-004 is most similar to Eukrohnia hamata (not ants).
4. SPT-001,005,006 are Nylanderia burbonica called robust crazy ants, and they are invasive species around world that damage banana crops.
5. SPT-006 Eukrohnia hamata is found in Japan.
6. SPT-007 Amata fortune is kind of moth from native Japan, and it may have been carried to DNALC by a recent typhoon.
7. SPT-008 and SPT-002 are Pheidole nodas from North-East China and Jiangsu Province.

Acknowledgements
Thank Professor John Mark Olson and all the teachers in DNALC for helping and instructing in teaching and my own project!

References