From: webteam@langara.ca <webteam@langara.ca>
Sent: Tuesday, January 4, 2022 1:34 PM
To: Scholarly Activity <scholarlyactivity@langara.ca>
Subject: New submission from ARC Award Final Report

Name of Researcher

Ji Yong Yang

Department/Faculty

Biology

Position in Department/Faculty

Faculty

Project Title

Ultra DNA Barcoding of Cannabis Varieties

Term of Project

Fall 2019 to Spring 2020

Please introduce yourself – include pertinent background information relating to the topic of your research project.

I have over 20 years of research experience in plants. Specifically, I have focused on the identification of plants using DNA markers. I have developed DNA markers for a number of plant species including cacao, lotus and hops. I have over 14 publications and received several NSERC grants.

Please discuss your educational background and your work experience that led you to taking on this research project. If possible, include a quote that helps define your interest in this project.

I have a PhD in Plant Biology from University of California and MSc in Botany from University of British Columbia (UBC). I was also a Postdoctoral fellow at the Biodiversity Center at UBC. During my educational experience, I specialized in developing DNA markers for plant species and varietal identifications. I wanted to develop useful markers to identify different cannabis varietals.

Please explain the concept for your project in terms that others not in your field would understand, like an executive summary.

Cannabis is set to become one of the most important cash crops in BC due to its recent legalization in Canada. There are hundreds of different varieties of cannabis and correctly identifying them has a great significance for both medical and social purposes but distinguishing them based on morphological traits alone can be challenging. An efficient DNA barcoding method is needed and thus the goal of the project is to develop efficient and reliable DNA markers for the identification of Cannabis varieties.

Identify goals and objectives for the project, and how the results may be used, perhaps to solve a problem, or to inform further research in that field.

Hundreds of different varieties exist and determination of these varieties has important medical and social implications. It is often difficult to identify the cannabis varieties based on morphological characters alone. An efficient and reliable DNA marker-based genotyping method is needed and because we are dealing with variations within the species level, we propose to sequence the whole chloroplast genome as well as the entire ribosomal DNA in order to identify the different varieties of cannabis. We will be using bioinformatics tools to assemble the sequencing reads and to annotate the chloroplast genome.

Briefly explain the steps taken to conduct the project research, and the results found.

I obtained over 75 cannabis samples from the BC cannabis store. The samples consisted of many different cannabis strains grown by different cannabis producers. We tested for the consistency in terms of the identify of the different strains produced by different producers and at different times. We extracted their DNA and used bioinformatics tools to construct a phylogeny tree. We amplified their DNA using 21 SNP (single nucleotide polymorphism) markers. We determined that there were some inconsistencies in identity of some cannabis strains produced by different growers.

Who else was involved in this project? How did their involvement help? Ie: other faculty, students, community partners

I hired four WOC/SWAP students to assist me in this project. In addition, I hired a former Langara student as a research assistant to do the molecular biology work and bioinformatics analysis. I collaborated with Philippe Henry from Egret Bioscience.

What were/are you hoping to get from conducting this research?

I was hoping to develop a rapid, reliable DNA fingerprinting method to distinguish the different cannabis varieties. I was also trying to determine the accuracy in the identify of the cannabis varieties produced by different cannabis producers.

Can you share any personal stories that made this research experience memorable/valuable?

Using 18 SNPs we were able to identify each cannabis variety. Preliminary report suggests that there are some inconsistencies in the identify of cannabis varieties produced by different cannabis growers.

Do you have any tips/suggestions/ideas for applying this research in your field? Or for others in their fields? Or for conducting future research of this kind?

I think it is important to hire as many Langara students to assist in research projects.

Any final comments? What are the “next steps” for this project? And for you?

I am one of the principal investigators of the successfully funded Cannabis NSERC IE Build grant. I used the preliminary results from this grant to write two proposals for the IE Build grant.

Please upload any images that will help to showcase your project.

CANNABISlegal-storephylogeny_circular_ME.pdf