

## Training on Molecular and Computer-based techniques

Open University, UK

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By Mr. Ermias Balcha from Addis Ababa Science and Technology University, Addis Ababa, Ethiopia.

Under the direction of Prof. Karen Olsson and Dr. Michael Macey from Astrobiology, Open University

The purpose of expert exchange was to gain training in how to produce and analyze metagenomic data sets from extreme, Mars-analogue environments with a view on studying the presence and diversity of novel antimicrobial and their associated production pathways. This work was done to allow us to potentially identify novel antibiotics within these extreme environments, which have never previously been characterized in terms of the potential medical application of their microbial communities and that often host unique metabolic adaptations due to their extreme nature.

Due to the low biomass of extreme environments and the low amount of available sequencing data, which makes this work novel, this work capitalizes on the low biomass capabilities developed by Astrobiology OU and their computer and bio informatics facilities. The work will also fit within the following UN Sustainability goals: SDG3: Good health and well being, as antibiotic are used to ensure healthy lives and SDG17: Global partnerships between the global north and south.

My work during my time at the Open University used a combination of molecular and computer-based techniques to catalogue the diversity of microbes in hyper saline environments in the Afar Depression in Ethiopia and to attempt to maximize the diversity of potential antimicrobial compounds that can be identified within the sequence data.

For the entire 7 days the program was as follows:

Day 1-software program installation and introduction to online database.

Day 2-Working on some calibration of the data on the computer to check for its validity and K base introduction and loading of data

Day 3-data's were set for trimmomatic and assembly. For different assemblers,MEGAHIT, IDBA,metaSPAdes, are used in the process

Day 4-Lab induction and risk assessment for molecular, microbiology and low biomass laboratories.

Day 5-DNA extraction using kits and manual extraction methods. Quality was assessed using nano drop

Day 6-Back to computer, training on binning and metagenome-assembled genomes (MAG)

Day 7-training on antiSMASH, bioinformatic tool used to identify, annotate, and compare gene clusters that encode for the biosynthesis of secondary metabolites in prokaryotes.

In conclusion, the trip was so successful that my data are analyzed to permit the progression of my PhD thesis work and will contribute to two or three data chapters of my thesis. I found the training course very interesting and satisfied too and such event is a good opportunity to reinforce the exchange of experience between scientific communities within the different continent. I really appreciate Europlanet for giving me such opportunity to work with renowned scientists internationally.