

STUDY TRIP REPORT

Name of Applicant:

Dr. Tibor Benedek

Host Institution:

University of Duisburg Essen, Faculty of Chemistry, Institute for Environmental Microbiology and Biotechnology, Group of Aquatic Microbial Ecology

Host Professor:

Prof. Dr. Alexander Probst

Date:

between 14.06.2021-25.06.2021, 2 weeks

Planned topic:

1. Genome resolved metagenomics and whole genome sequence analysis
2. Metagenome binning and metatranscriptomic studies

Short summary of the study trip:

During my stay at the University of Duisburg-Essen I gained basic knowledge in bioinformatics, regarding (i) how to assemble bacterial genomes from metagenome sequence reads (genome resolved metagenomics), and (ii) how to gain insight into metabolic properties of certain cultivated bacteria using the whole genome sequence of a given bacterial isolate or using the assembled genome of a taxonomic unit obtained by metagenome binning.

During my stay I had access to the high computing facility of the university Duisburg-Essen to process my metagenome data originating from pharmaceutical amended selective enrichment cultures. Upon my return, I still have access to the high computing facility of the university through a VPN client.

- (i) To obtain metagenome assembled genomes (MAGs) the following pipeline was applied:

Illumina-artifacts and adapters were removed from raw reads with bbdut. Reads were quality controlled and trimmed with sickle version 1.33. Quality-controlled reads were assembled using the MetaSPAdes pipeline version 3.15.0. Community composition was reconstructed based on the ribosomal protein S3 (rpS3) marker gene. Therefore, Prodigal in meta mode was used to predict genes. Genes were annotated using diamond blast against the UniREF100 database. Coverage of rpS3 carrying scaffolds was calculated by mapping the assembly against quality-controlled raw reads using bowtie2 in sensitive mode and filtered with an in-house script by Alexander J. Probst. For binning (obtaining metagenome assembled genomes) different binning tools were used to create the final set of bins. Abawaca (<https://github.com/CK7/abawaca>) was run twice. First including reads with a minimal length of 3000 base pairs (bps) and sequences split after 5000 bps and secondly with minimal scaffold length of 5000 bps and sequences split after 10000 bps. MaxBin2 was run with both marker sets. All bins created in the four runs were optimized and filtered with DAS Tool and hand curated with uBin.

During metagenome binning the genome of a new to science bacterial species affiliating to the genus *Nocardioides* could be assembled (100% completeness) and functional genes involved in carbamazepine and ibuprofen biodegradation were partly identified in the genome. On the basis of metagenome studies, we know that *Nocardioides* species may play an important role in carbamazepine and ibuprofen biodegradation.

(ii) Annotation of genomes and metabolic profile determination

The annotation of the genomes (isolated cultures and MAGs such as the genome of *Nocardioides*) was performed by the Microbial Genome Annotation & Analysis Platform MicroScope (<https://mage.genoscope.cns.fr/microscope/home/index.php>). Additionally, putative functions of genes associated in the metabolism of xenobiotics were identified and bioinformatically analyzed by using MaGe in conjunction with the UniProt database and BLAST searches.

Beyond science, I could widen my professional network, I was exposed to new research topics and laboratory equipment used in next generation sequencing.

Transfer and dissemination of the acquired knowledge:

1. Giving a lecture in the field of genome resolved metagenomics, whole genome sequencing and metabolic studies for fellow researchers, as well as MSc, PhD students at the University of Agriculture and Life Sciences, Institute of Aquaculture and Environmental Safety, Department of Molecular Ecology (please see the attached list of participants). Date of lecture: 09.07.2021; number of participants 11.
2. Through a poster presentation during the 6th Central European Forum for Microbiology (please see the poster). Date 14.10.2021
3. Sharing experiences gained during the study trip on a workshop in the field of microbial 'omics organized in the frame of the 6th Central European Forum for Microbiology (please see the attached image). Date 14.10.2021

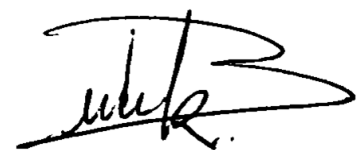
Desired use of financial support from ISME:

During the study trip I travelled by public transportation from my accommodation to the university (Münster – Essen – Münster). Please find enclosed the copies of weekly passes (total price 194.6 euro). I would like to kindly use the support of ISME to cover the price of tickets.

Date. 02.11.2021

Applicant

Dr. Tibor Benedek



Participation on a workshop/ round table discussion at the 6th Central European Forum for Microbiology



