

## Research Trip Summary Report

### Task 2. Foreign mobility of WUST doctoral students

#### I. Data of the doctoral student

1. Full name: **Natalia Tyszkiewicz**
2. Year of studies: **3**
3. Educational discipline: **Chemical Sciences**

#### II. Foreign research trip (research visit)

1. Research institute in which the foreign research was implemented: **University of Tartu, Estonia**
2. Name and surname of the host person (mentor): **prof. Jaak Truu**
3. Dates of the research trip: **30.01.2023 r. – 01.03.2023 r.**
4. Title and date of a seminar delivered during the research trip: **Metagenomic analysis of microbial fuel cells' communities, 27.02.2023 r.**

#### 5. Description of work carried out during the research trip:

High-throughput sequencing data from shotgun analysis for ten samples obtained from microbial fuel cells have been subjected to quality control analysis using FastQC program. Data was trimmed using Cutadapt to produce more accurate results. After that quality control for trimmed sequences was also checked. Based on prepared data, taxonomic classification of organisms in each sample was performed using Kaiju program and NCBI-nr database. Classification was made at phylum, class, genus and species level for both bacteria and archaea. Then, after producing appropriately constructed tables, the data was used in Rstudio to produce graphs (bar plots, heatmaps). Afterwards, sequencing data was used for assembly contigs using MegaHit tool. In order to search functional genes, database has been made with models created by the prof. Jaak's team and also models found in the literature. Genes searching procedure and analysis of the data are still in progress. For quantity control of samples qPCR analysis was carried out for both Bacteria and Archaea Kingdoms.

#### 6. Description of the main results obtained:

Analysis of the quality of the raw sequence reads obtained by the shotgun method revealed their good quality. However, quality was improved by trimming sequences. Taxonomy classification allow for identification and quantification of phyla, classes, genera and species. Based on the most abundant groups, barplots and heatmaps were created. Taxonomy analysis showed similarities and differences between the microbial communities of the samples from bioelectrochemical systems. The most abundant phyla in samples were: Proteobacteria, Bacteroidetes, Firmicutes and Acidobacteria. At the genus level microbial consortia were much more diverse and it was possible to identify characteristic types of bacteria, both anaerobic and aerobic. The proportion of the kingdom archaea in the samples varied and for the most abundant samples was around 1.5%. Among them Euryarchaeota, Thaumarchaeota and Crenarchaeota were identified. qPCR analysis allow to quantify the amount of bacterial and archaeal DNA in the samples.

#### 7. Future collaborations (if applicable):

We are planning to prepare a manuscript based on metagenomic results obtained during the internship.



8. Title and date of a seminar presenting the results of the trip delivered at Wrocław University of Science and Technology after returning from the research trip: Metagenomic analysis of microbial consortia derived from microbial fuel cells, 24.03.2023 r.

**III. Doctoral student's signature**

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(Date)

.....  
(doctoral student's signature)

**IV. Confirmation and information from the host**

1. Confirmation of compliance of the information contained in the report: I CONFIRM / DO NOT CONFIRM. *(In justified cases, the confirmation of the host may be sent by e-mail to the Dean's Office of the Doctoral School email: [interdocschool@pwr.edu.pl](mailto:interdocschool@pwr.edu.pl))*

2. Additional information and comments

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(Date)

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(signature(s) of Host)