

Toruń, 28.12.15

Sonia Szymańska  
Faculty of Biology and Environmental Protection  
Nicolaus Copernicus University  
87-100 Toruń, Poland

**Scientific report: Short-Term Scientific Mission, COST Action FA1103**

Beneficiary: Ms Sonia Szymanska from Faculty of Biology and Environmental Protection (Nicolaus Copernicus University, Poland)

Host: Dr. Lorenzo Brusetti from Faculty of Science and Technology (Free University of Bozen – Bolzano, Italy)

Period: from 02/11/2015 to 30/11/2015

Place: Bolzano (Italy)

Reference code: COST-STSM-ECOST-STSM-FA1103-021115-063726

**Title: 16S rDNA and *nifH*-based metagenomic analysis of endophytic bacteria associated with halophyte *Salicornia europaea* growing at two saline sites**

Purpose of the STSM:

The main objective of this STSM was to analyse the taxonomic structure of endophytic bacteria associated with the roots of obligatory halophytic plant – *Salicornia europaea* (*herbacea*) L. growing at two saline test sites (located in central part of Poland). The main goal of our study was to assess bacterial biodiversity based on metagenomic analysis using advanced bioinformatics tools.

Description of the work carried out during the STSM

Evaluation of bacterial biodiversity associated with the roots of *S. europaea* was conducted with the use of meta-analysis. We have used Pear and Qiime software to obtain

OTU (operational taxonomic units) table and taxonomy community structure. Received results were analysed using statistics software (e.g. Past and Lefse) to determine the statistical differences in the composition of OTUs and taxonomic structure between two investigated sites.

Description of main results obtained during the STSM:

Obtained results revealed that bacterial endophytes of *S. europaea* growing at both investigated test sites were dominated by representatives of the phylum Cyanobacteria and Proteobacteria. Moreover, we have observed higher biodiversity of endofitic bacteria associated with the roots of *S. europaea* growing at natural saline test site [Ciechocinek, (C) - characterized by higher salinity level (110 dS/m)] compare to anthropogenic saline test site [Inowrocław(I) (55 dS/m)]. Venny diagram revealed higher number of OTUs (5500) in samples from Ciechocinek compare to samples from Inowrocław (4516 OTUs). Additionally we observed 2914 OTUs common for both test sites. Statistical analysis revealed significant differences between test sites on the phylum level: Acidobacteria, Planctomycetes, Fibrobacteres, Bacteroidetes, Verrucomicrobia dominated in samples from Ciechocinek, and Actinobacteria as well as Proteobacteria dominated in samples from Inowrocław (Lefse). Furthermore, the differences at class level were observed: Holophagae and Sva0725 (Acidobacteria) (C>I), Cytophagia and Flavobacteriia (Bacteroidetes) (C>I), Phycisphaerae and Planctomycetia (Planctomycetes) (C>I), Alfabroteobacteria (I>C), Deltaproteobacteria (C>I) and Gammaproteobacteria (C>I) (Proteobacteria), Opitutae (Verrucobicrobia) (C>I) (Lefse).

Future collaboration with host institution (if applicable):

We plan further collaboration between both institutions and preparation of joint project.

Foreseen publications/articles resulting or to result from the STSM (if applicable):

The obtained results will be presented during international conference. Moreover, we plan to prepare joint publication which will be submitted to the selected international journal.

Other comments (if any).

-