COST MP1207 – STSM Short Scientific Report

Name of the grantee: Alessandra Procopio

Home Institution: University of Bologna - Department of Pharmacy and Biotechnology

Host Institution: BL09 - MISTRAL CELLS - ALBA Synchrotron

Duration of stay: from   14,   to   3, December
                          November

Purpose of the STSM:

Tomographic image reconstruction of whole Escherichia coli using synchrotron-based cryo-soft X-ray tomography (cryo-SXT).

Description of the work carried out during the STSM:

The goal of this STSM was to reconstruct the tomographic image of a whole Escherichia coli bacteria from data acquired using synchrotron-based cryo-SXT and to segment the volume of the corresponding 3D tomographic reconstruction. The reconstruction was important to investigate the 3D fine structure of the nucleoids, and of the defective FtsZ ring, which most likely, does not properly assemble across the cytoplasm of neighbor cells incapable to divide.
During these weeks, I was trained in using the software IMOD for the alignment of the projections of the acquired tilt series before the tomographic reconstruction and in using the software CHIMERA for the volume segmentation after the tomographic reconstruction. In particular, I learned to manually align the different projections acquired during the tomography measurements with eTomo in the IMOD tomography software suite. For this alignment, I followed during the rotation gold nanobeads to decrease as much as possible the deviations from an ideal rotation that creates artefacts in the reconstructed tomograms.
The tomography reconstruction was performed with the software TOMO3D, using SIRT algorithm (simultaneous iterative reconstructive technique) with 30 iterations.

Description of the main results obtained:

The structural details of the tomograms were displayed and analyzed through different software with image processing tools, for example, the viewer 3dmod IMOD with ZAP, XYZ and Slicer window, or the software ImageJ. In particular, the good quality of the alignment performed using

eTomo was proved. To create a 3D segmentation image, I used the CHIMERA software. This software provided tools for a manual segmentation.

The analysis of the3D volume of the bacteria highlighted the morphological alteration of the mutant bacteria, due to the lack of cell division assumed aberrant chain stitch form.

Future collaboration with the host institution (if applicable):

It was important acquiring the capability to reconstruct and analyze data coming from tomography acquisitions, because I will use this knowledge of post-processing in future beamtimes at Mistral, in which we will investigate using cryo-SXT, the mitochondrial ultrastructure differences mitochondria number, shape and mass in doxorubicin-resistant cells and doxorubicin-sensitive cells.

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

An article will be published once all the topographies on bacteria cells acquired will be analyzed.

Date: 14/12/2016

Bologna

Signature of the grantee

Confirmation by the host institution of the successful execution of the STSM:

Date: 14/12/2016

Signature and stamp of the host institution

Cerdanyola del Volles

ANDREA SORRENTINO