STSM Scientific Report

The purpose of that STSM had as main aims:

- ✓ Become familiar with the process of microarrays-based experimentation, as well as design and production of the chip, sample preparation, hybridization, scanning the chip and image analysis.
- ✓ Learn the software and methodology applied for the analysis of data from microarrays

During my stay in the INRA-Rennes Institution, I was able to introduce me into microarrays assays, carrying out different steps as well as hybridization, washing the samples, scanning the chip and image analysis by "*Agilent one-color platform*".

Hybridization: in the first step the samples are fragmented by fragmentation mix and then, the reaction is stopped by adding hybridization buffer. The main step is the assemble of the samples into the chambers. Then, it place assembled slide chamber in rotisserie in a hybridization oven set to 65°C for 17 hours.

Wash the microarrays slide: the procedure for the Agilent one colour platform must be made in environments where ozone levels are low. Then and immediately, we put the slides in a slide holder to minimize the impact of environmental oxidants on signal intensities

Scan the slides: to obtain a digital image of the each *probe* intensities in a matrix structure to be quantified and can provide a measure of the each gene expression.

Extract data: process by which information from probe features is extracted from microarray scan data, allowing us measure gene expression.

I was able to learn to use the specific software to analysis of the transcriptome in the INRA-Rennes and was able to analysed data from an experiment performed in the University of León. The aim in this experiment was evaluate the effects of fertilization with DNA fragmented sperm on gene expression of trot larvae.

Transcriptome analysis was made by ScripGen software and the ANOVA statistical analysis was performed in order to obtain differential expression in several genes. The first analysis performed showed two expression patterns and with a deeper analysis we obtained an increase in the gene list whose expression patterns were modified.

The most of these genes are include into the key roles into the cellular process such as DNA repair, embryo development and different steps into the cell cycle.

These first steps into of our data analysis encourage continuing working in the same way to obtain the biggest information about genes implicated in the correct functionality of the different cellular processes during embryo development.