STSM Scientific Report

The aim of the project was to identify differently expressed genes in eggs of Sea Bass characterized by different quality. Additionally, the expression of the genes, which were found to be differentially expressed during microarray analysis, was analyzed by qPCR. The material for the project was the data of the transcriptomic analysis and mRNA obtained during the practical classes of the Training School entitled 'Molecular basis of fish gamete quality' which was organized within the AQUAGAMETE COST action in Rennes, France, between 23rd – 27th June, 2014.

During the first period of the STSM the data analysis, obtained from the microarray, was performed. The first step was to gather all the data on the evaluation of biological quality of the eggs (which were used for molecular analysis) and identify two groups characterizing "low" and "high" quality. Next, the data analysis was performed with the GeneSpring GX software which allowed to identify 39 differentially expressed genes between the groups. The further step was to designate 8 the most differentially and 7 the most homogenously (which were used to standardize the data) expressed genes and to annotate them with the use of Basic Local Alignment Search Tool (http://blast.ncbi.nlm.nih.gov) in order to design the primers. During the second period of the STSM the RT-PCR of the mRNA samples was done and next the qPCR analysis of all 15 designated genes was performed. The qPCR analysis allowed to confirm that 5 (out of 7) analyzed genes were differentially expressed between the groups representing low and high egg quality.

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

Dr Julien Bobe, Research Director of the Team of Sex Differentiation and Oogenesis of the LPGP of INRA, certifies that Daniel Żarski visited us between 14.01.2015 and 04.02.2015 thanks to a grant awarded by Short Term Scientific Mission, COST Action FA1205.

Julien Bobe   Daniel Żarski