

Kati Korhonen: SABRE Placement Report for visit to Bonn University

My four week visit to Bonn University was funded by a SABRE integrating award. I worked at the Institute of Animal Sciences lead by Professor Karl Schellander, and more precisely in the group of Animal Breeding and Husbandry lead by Dr. Dawit Tesfaye.

The aim of the visit was to analyze the embryo biopsy samples (SABRE WP6), and at the same time learn the qPCR-procedure for small (low RNA/DNA content) samples.

Embryo biopsy samples were collected earlier as follows: Embryos were flushed on day 7, and prior to transfer to a recipient the biopsies were cut. After the pregnancy result was recorded, biopsy samples were labelled either as pregnant (P) or non-pregnant (NP). From these samples cDNA microarray (BlueChip) study was performed to find out the genes differently expressed in these two groups (P and NP). The found, up- or down-regulated (=expressed) genes in P-group were the candidate genes that needed to be confirmed with qPCR.

After my arrival to Bonn the first task was to decide the genes to be validated in qPCR from the microarray candidate gene list. We chose genes that had fold change at least 1.5 and p-value <0.05 between the P and NP groups according to microarray result. From both up- and down regulated genes (in P-group) we selected four genes. During the first three weeks we optimized the qPCR conditions to fit these genes, and made the plasmids of the gene products to be used for the standard curve. In the last week we performed the qPCR runs of these selected genes from the embryo biopsy samples. During my stay I also learned how to analyze qPCR results and had many useful conversation with Dr. Tesfaye and the PhD students in the group concerning qPCR methology, result analyzing and gene selection in these kind of studies.

The results we got from the qPCR runs confirmed the gene trends (if gene was up- or down-regulated in P-group) got from the microarray study. Now these eight, confirmed candidate genes can be used as indicators of *in vivo* embryo's ability to initiate pregnancy.

The aims set to this visit (analyze the samples and learn the qPCR-procedure) were met. The same qPCR-procedure can be now used in MTT in forthcoming projects where gene expression of small embryos samples is needed to be analyzed.

I would like to thank SABRE for giving me the funding for this very useful visit.

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