

Christine Große-Brinkhaus: short term placement report

I had the great opportunity to visit the Department of Genetics and Biotechnology, Faculty of Agricultural Sciences, University of Aarhus, Denmark from the 7th of July until 28th of August 2008, together with one PhD-student colleague. The stay was part of WP 6 (Fertility and Reproduction) of the SABRE Project.

The main objective of the research was to investigate the expression profile of genes in the bovine endometrium based on a successful pregnancy after embryo transfer in dairy cattle. The success of pregnancy in cattle after embryo transfer is influenced by many factors, such as oestrus expression, metabolic condition of the recipient or embryo survival ability. For this purpose samples of endometrium cells were taken at two time points: day 7 and day 14 during the pretransfer cycle of the recipients. All day 7 and day 14 endometrium samples were categorized based on the pregnancy success after the transfer. The embryos were transferred to the recipient in the following cycle. Furthermore embryo biopsies (30%) were taken for a molecular analysis. The samples were categorized into pregnant (resulted in calf delivery) or non pregnant (animals return to heat/ without successful pregnancy). The transcriptome analysis of endometrium samples were performed by using Affymetrix GeneChip arrays. The embryo samples were analyzed using cDNA microarray platform. All laboratory work was performed at the Rheinische Friedrich-Wilhelms-University Bonn.

I took the raw data of all gene expression with me to Denmark. The statistical and bioinformatics analysis were performed under the supervision of Dr. Peter Sørensen, who taught me the different steps of the analysis. For this purpose different packages of the analysis R/Bioconductor software were used. Differentially expressed genes were identified using linear modeling and empirical Bayes methods and adjusted for multiple testing to control the false discovery rate. An essential criterion for large scale data analysis is a well organized and complete annotation for biological interpretation and pathway detection. Dr. Sørensen showed us the different possibilities to create research-specific annotation packages using the AnnBuilder and BioMart softwares and to increase the number of annotated bovine genes by adding homologous human information. Afterwards it was possible to characterize different functional groups within the differentially expressed genes using statistical methods such as gene set enrichment analysis.

My stay in Denmark was very advantageous. I was able to acquaint myself by applying different statistical tools to analyze our data. The aim to learn how to analyze and interpret expression data has been totally fulfilled. The collaborations within the SABRE project were a great opportunity for me to learn new techniques to analyze data and to get more knowledge about the R software packages. Finally I would like to express my gratitude to SABRE for the financial support of this short term placement. Furthermore, I would like to thank Prof. Karl Schellander and Dr. Dawit Tesfaye for offering me this training opportunity. Finally I am very much grateful to Dr. Peter Sørensen for the wonderful supervision and hospitality during my stay in Foulum.

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