

## **Dessie Salilew Wondim: SABRE Placement Report**

I visited Århus university/Faculty of Agricultural Sciences/Department of Genetics and Biotechnology in Foulum, Denmark from 7<sup>th</sup> of July to 14<sup>th</sup> of August, 2008.

### **Purpose of the visit:**

The level and type transcripts orchestrated in the transferrable embryo and the endometrium of recipients during the pre-transfer period of the cow may affect the pregnancy success. Transcriptional profiling of the endometrium at the pre-transfer cycle in relation to the pregnancy outcome may provide unique opportunity to select molecular marker that can give insights to detect and select receptive endometrium before embryo transfer. Hence, a large scale gene profiling approach was applied to analyze and detect differentially expressed genes in the bovine endometrium and embryos based on the pregnancy successes after embryo transfer. For this endometrial biopsies were taken from each recipient animal during the pre-transfer period. Following this the embryo biopsies (70% of the intact embryo) were transferred to the recipient animals. After pregnancy diagnosis, the endometrium biopsies were categorized based on the pregnancy success as those samples derived from heifers resulted in calf delivery were grouped as calf delivery and those biopsies collected from heifers resulted in no pregnancy were classified as non pregnant group. Similarly, the remaining embryo biopsies (30% of the intact embryo) were classified as those resulted in calf delivery (calf delivery group) and those embryo samples resulted for no pregnancy (non pregnant group). The endometrium samples were analyzed using bovine affymetrix arrays consisting of 24128 probe sets and the embryo samples were analyzed using the bovine embryo specific array (Blue-Chip, kindly provided by Prof. Sirard, Department of Animal Sciences, Université Laval, Quebec, Canada). Therefore the aim of my visit to Århus University, Denmark) was mainly focused on processing and interpretation of the microarray data using R and Bio conductor. During my stay at Denmark, I have analyzed 1) differential expressed genes between the pregnant and non pregnant endometrial and embryo samples using linear modeling and empirical Bayes methods and adjusted for multiple testing by controlling the false discovery rate 2) differential expression of functional groups of genes determined using statistical methods such as the gene set enrichment analysis 3) annotation of bovine genes was obtained by gathering information of bovine genes and human homologous genes from several public available databases. 4) classifying each of the differentially regulated genes in different path ways including metabolism, signal, transduction cell, cycle and apoptosis pathways, immune system pathway and endocrine system pathways. In general, my stay at Århus University gave me ample opportunities for analyzing transcriptional differences in relation to animal fertility. On this occasion, it is my great pleasure to express my special thanks to the SABRE Integrated Project for financing my short term placement. My sincere gratitude to Dr. Peter Sørensen (Århus University/ Faculty of Agricultural Sciences/ Department of Genetics and Biotechnology, Denmark) for his enormous guidance and assistance during the data analysis. Special thanks to Prof. Dr. Karl Schellander and Dr. Dawit Tesfaye (Institute of Animal science, Animal Breeding and Husbandry Group, University of Bonn, Germany) for doing all their bests for successful accomplishment my stay in Denmark.

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