

Prof. Dr. Omaima M. Kandil

Report of Short term placement from the SABRE Integrated Project (2009)

I am thankful to **SABRE**, for generously offering me a grant to get training for three months (July 24 to October 21, 2009) on the molecular genetics techniques at Institute of Animal Science of the University of Bonn, Germany. I would like to express my sincere gratitude to **Prof. Dr. Karl Schellander** and **Dr. Dawit Tesfaye**, for their valuable advice and guidance during the training. I am particularly grateful to **Institute of Animal Science, Bonn University** for hosting me in the lab of Animal Breeding and Husbandry group during this placement.

The aim of the visit was for training on molecular techniques specially qPCR and for work in microRNA in camel reproductive tissues. During the first month, training on molecular techniques including: DNA isolation from camel tissues, primers optimization, cloning and M13 PCR, Sequencing using CEQ 8000, Plasmid preparation, RNA Isolation and cDNA synthesis from buffalo embryo. In the other two months my work concentrated on analysis of mRNA and miRNA in camel reproductive tissues and RNA isolation and cDNA synthesis from buffalo embryo.

For this work I brought camel tissues from three mothers and their fetus (spleen, liver, lung, CL, ovary endometrium, placenta, fallopian tube and testis) and buffalo embryos.

In the beginning, I isolated total and miRNA from camel tissue samples (using miRNeasy mini Kit and RNase-free DNase kit, no = 40) then miRNA first strand cDNA synthesis from 18 RNA samples of camel reproductive organs (CL, ovary endometrium, placenta, fallopian tube). Semi-quantitative RT-PCR was done in these tissues for 32 miRNAs (let 7a, let 7b, miR125b, miR143, miR 21, 5s, u6, snord47, miR101, 122, 132, 175p, 199a5p, 20a, 212, 92a, 103, 126, 145, 146b, 15a, 15b, 206, 26a, 128, 140, 182, 18a, 211, 22, 222 and 29a). We find that there is significant differences in miRNA expression between camel adult and fetal reproductive tissues and the length of miRNA expression band appear between 50-60 bp. For mRNA work we optimized 12 primers using camel genomic DNA and cDNA. These genes represent those which are involved in miRNA biogenesis (GAPDH, DICER1, EIF2C1, EIF2C4, DGCR8, GEMIN4, XPO4, YBX1, PIWIL1, GEMIN7, EIF2C3, ADAR, RNASEN). Results are being organised to be published in an international journal.

The aim of the visit has been realized (training on molecular techniques especially qPCR and research work in the miRNA in camel). The experience I took from this placement will help me doing research projects with the Egyptian livestock breeds. Furthermore, I am able now to transfer the knowledge and technology I learned in the Institute of Animal Science, the lab of Animal Breeding and Husbandry Group, to research / teaching institutions and universities in Egypt. Moreover, we are looking for future collaboration.

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