

## Expression of Selected miRNAs in Placenta of the Intrauterine Restricted Growth Fetuses in Cattle

**Authors :** Karolina Rutkowska, Hubert Pausch, Jolanta Oprzadek, Krzysztof Flisikowski

**Abstract :** The placenta is one of the most important organs that plays a crucial role in the fetal growth and development. Placenta dysfunction is one of the primary cause of the intrauterine growth restriction (IUGR). Cattle have the cotyledonary placenta which consists of two anatomical parts: fetal and maternal. In the case of cattle during the first months of pregnancy, it is very easy to separate maternal caruncle from fetal cotyledon tissue, easier in fact than removing an ordinary glove from one's hand. Which in fact make easier to conduct tissue-specific molecular studies. Typically, animal models for the study of IUGR are created using surgical methods and malnutrition of the pregnant mother or in the case of mice by genetic modifications. However, proposed cattle model with MIMT1Del/WT deletion is unique because it was created without any surgical methods what significantly distinguish it from the other animal models. The primary objective of the study was to identify differential expression of selected miRNAs in the placenta from normal and intrauterine growth restricted fetuses. There was examined the expression of miRNA in the fetal and maternal part of the placenta from 24 fetuses (12 samples from the fetal part of the placenta and 12 samples from maternal part of the placenta). In the study, there was done miRNAs sequencing in the placenta of MIMT1Del/WT fetuses and MIMT1WT/WT fetuses. Then, there were selected miRNAs that are involved in fetal growth and development. Analysis of miRNAs expression was conducted on ABI7500 machine. miRNAs expression was analyzed by reverse-transcription polymerase chain reaction (RT-PCR). As the reference gene was used SNORD47. The results were expressed as  $2\Delta\Delta Ct$ :  $\Delta\Delta Ct = (Ct_{ij} - Ct_{SNORD47j}) - (Ct_{i1} - Ct_{SNORD471})$ . Where  $Ct_{ij}$  and  $Ct_{SNORD47j}$  are the Ct values for gene i and for SNORD47 in a sample (named j);  $Ct_{i1}$  and  $Ct_{SNORD471}$  are the Ct values in sample 1. Differences between groups were evaluated with analysis of variance by using One-Way ANOVA. Bonferroni's tests were used for interpretation of the data. All normalised miRNA expression values are expressed on a value of natural logarithm. The data were expressed as least squares mean with standard errors. Significance was declared when  $P < 0.05$ . The study shows that miRNAs expression depends on the part of the placenta where they origin (fetal or maternal) and on the genotype of the animal. miRNAs offer a particularly new approach to study IUGR. Corresponding tissue samples were collected according to the standard veterinary protocols according to the European Union Normative for Care and Use of Experimental Animals. All animal experiments were approved by the Animal Ethics Committee of the State Provincial Office of Southern Finland (ESAVI-2010-08583/YM-23).

**Keywords :** placenta, intrauterine growth restriction, miRNA, cattle

**Conference Title :** ICASVM 2017 : International Conference on Animal Science and Veterinary Medicine

**Conference Location :** Paris, France

**Conference Dates :** February 23-24, 2017