

ABSTRACT

Charles University

Faculty of Pharmacy in Hradec Králové

Department of Pharmacology & Toxicology

Student: Martina Michalská

Supervisor: doc. PharmDr. Martina Čečková, Ph.D.

Title of diploma thesis: Expression of selected membrane transporters in placentas of pregnant women diagnosed for preterm rupture of membranes

Placenta is a key organ for pregnancy maintenance. One of its main functions is transport of compounds between mother and her fetus. The transplacental penetration is ensured due to membrane transporters that are present in the apical or basal side of trophoblast. Their expression level is affected by many physiological and pathological factors, among others it can be influenced by infection and inflammatory reaction. Inflammation is also one of the risk factors of preterm deliveries and it can be therefore assumed that these pathological states are accompanied by changes in expression of placental transporters.

This study was performed using 51 placentas obtained from Faculty hospital in Hradec Králové from women who underwent preterm delivery and on 15 placentas delivered in term. The study employed quantitative RT-PCR approach. The mRNA expression of membrane transporters ABCB1, ABCG2, OATP1A2, OATP1B3, OATP2A1, OATP2B1, OATP3A1, OATP4A1 was assessed and the results were compared to the expression of the transporters in non-pathological placentas delivered in term.

Evaluation of the data revealed affected expression of OATP2A1 and OATP2B1 in the group of premature ruptures of membranes. The level of transcripts for these transporters was significantly higher than in the term placentas. Contrary, decreased expression of OATP1B3 was observed in the case of preterm deliveries when compared to term placentas. No statistical significance among the placental groups was observed for the other evaluated OATP and ABC transporters. Within the group of premature rupture of membranes, no difference was observed among the placentas from women with/without diagnosed histological chorioamnitis and with/without detected bacterial infection. In order to drive a valid conclusions, it would be necessary to enlarge the cohort of analysed samples and take into consideration also other factors, which might contribute to interindividual variability in the gene expression.