**Placental expression of glucose transporters mRNA (GLUT-1, GLUT-3 and GLUT-4) and transcriptome profiling with microarrays in pregnant patients with diabetes.** Rafal Sibiak1,2,3, Pawel Gutaj1, Urszula Mantaj1, Lukasz Adamczak 1, Malgorzata Blatkiewicz2, Marcin Rucinski2, Ewa Wender-Ozegowska1(FirstName Surname1,2,3, FirstName Surname1, etc.) 1Department of Reproduction, Poznan University of Medical Sciences, Poland 2 Department of Histology and Embryology, Poznan University of Medical Sciences, Poland 3 Doctoral School, Poznan University of Medical Sciences, Poland (do not include detailed addresses of your institiutions- just the basic/simplified name and your country as above) **Background and aims** Glucose transport across the human placenta is regulated by the family of glucose transporter proteins (GLUTs), located at both sides of the placental barrier**.** Glucose transport across the human placenta is regulated by the family of glucose transporter proteins (GLUTs), located at both sides of the placental barrier.The primary study objective was to examine the placental expression of GLUTs mRNA (GLUT-1, GLUT-3, and GLUT-4) in patients with type 1 diabetes (T1D), early gestational diabetes (eGDM), and healthy controls. We also aimed to investigate the correlations between the expression of GLUTs and numerous clinical parameters. **Materials and methods** We recruited 59 eligible pregnant women – 23 with T1D, 17 with eGDM diagnosed <20th week of pregnancy, and 19 healthy control individuals. Pregnant patients with diabetes were admitted for at least one control visit in each trimester of gestation to undergo routine clinical follow-up. Patients with T1D were treated with sensor-augmented pumps from the first trimester (Medtronic MiniMed™ 640G, n-15) or with multiple daily injections with flash continuous glucose monitoring (Freestyle Libre 2, n-8). The expression of GLUTs mRNA was assessed in the whole study group using the RT-qPCR technique with specific TaqMan PCR assays. Transcriptomic analyses were performed using the microarray technique - HuGene 2.1 ST Array. The microarray analyses were performed on 12 patients (4 samples per subgroup). **Results** We found significantly decreased (about 2-fold decreased) placental expression of GLUT-3 mRNA in the T1D and GDM group compared to the control group. GLUT-4 mRNA expression was significantly lower (about 6-fold decreased) in the GDM patients compared to the T1D and control group. We identified a significant negative correlation between the GLUT-3 (R=-0.29) and GLUT-4 (R=-0.27) mRNA expression and neonatal birth weight in the whole study group. Moreover, GLUT-4 expression was negatively correlated with the 1st trimester HbA1c values (R=-0.72) and OGTT 120’ results (R=-0.82) in patients with eGDM and 3rd trimester sensor glucose CV% values (R=-0.49) (coefficient of variation) in women with T1D. The microarray analyses revealed significant between-group changes in the transcriptomic profiles. We detected 45 down-expressed and 365 up-expressed sequences in the placental samples of patients with T1D and 21 significant changes in the transcriptomic profiles in women with eGDM. Most significant changes were detected in the sequences associated with protein catabolic processes, regulation of cell activation, extracellular matrix organization, endothelial proliferation, regulation of angiogenesis, and regulation of ERK1, ERK2, and MAPK cascades. **Conclusion** Placental samples obtained from patients with diabetes exhibit multiple transcriptomic changes compared with the healthy control group. Those changes can contribute to the perinatal outcomes.

**The maximum number of characters is 3,200 (excl. spaces) including the title and the author block.** Please use exactly the same format as above- ARIAL font, size 12, **title** and **abstract sections** (**Background and aims, Materials and methods, Results, Conclusion**) **in bold**, no additional/ non-standard spaces between the abstract sections- **single line spacing should be used as above**).