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Top 20 differentially expressed genes across trimesters of normal pregnancy

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Background/Aim. The placenta is essential in pregnancy, facilitating nutrient and gas exchange between mother and fetus. However, the regulatory proteins involved in this process are not fully understood across gestation. This study aimed to identify the top 20 differentially expressed genes (DEGs) in the placenta across different pregnancy stages to elucidate the molecular mechanisms at play. **Methods.** Differential gene expression analysis was performed on the placental samples from the first, second, and third trimesters using microarray data from Gene Expression Omnibus and Array Express. Analysis was conducted in RStudio using the R programming language. DEGs were identified using a significance score (π-value) based on the method developed by Xiao Y *et al.* (2014), which combines fold change and p-value. Volcano plots were created to visualize DEGs, and the top 20 were analyzed for functional enrichment using STRING and EnrichR databases, including Gene Ontology and KEGG pathways. **Results.** In the transition from the first to the second trimester, significant DEGs included genes involved in steroid metabolism such as *HSD11B1*, *HSD3B2*, and *HSD17B2*. These genes are critical in the biosynthesis and metabolism of steroid hormones, essential for sustaining pregnancy and supporting fetal development. Enrichment analysis showed these genes were significantly associated with steroid biosynthesis and steroidogenesis pathways. For the transition from the second to the third trimester, different sets of genes were highlighted, particularly those related to endocrine regulation and pregnancy-specific functions. Key genes included *CRH*, *INHBA*, *REN*, and members of the pregnancy-specific glycoprotein (PSG) family. These genes are involved in hormone regulation, reproductive processes, and maintaining maternal-fetal homeostasis, with significant associations with pathways related to endocrine processes, reproductive health, and vascular function. For example, the involvement of CRH and REN in endocrine regulation suggests their role in modulating maternal and fetal physiology during the later stages of pregnancy. Also, the genes associated with vascular and hemostatic functions were identified, indicating the importance of maintaining proper blood flow and preventing bleeding complications as pregnancy progresses. Notable genes included *SDC1* and *HBE1*, which are crucial for vascular integrity and oxygen transport. Volcano plots illustrated these shifts in gene expression, with the top 20 genes identified by π-value prominently displayed. **Conclusions.** This study provides an analysis of gene expression changes in the placenta throughout pregnancy, identifying key genes and pathways that regulate placental function and impact fetal development. These findings enhance the understanding of placental biology and may highlight potential targets for ensuring optimal fetal development.

Keywords: placental function, gene expression, differential expression analysis, functional enrichment analysis.

REFERENCES

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