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— From Innovation to Impact —

Session OR01 - Gynecology I

Add To Itinerary

O-018 - NGS of Oocytes from Endometriosis Patients Reveals a Differential Transcriptomic Pattern.

March 14, 2019, 5:15 PM - 5:30 PM | Room 242AB

Categories
+2.2 - Gynecology: Endometriosis, Adenomyosis

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Abstract

Introduction: One of the recurrent paradigms of endometriosis has been elucidating if ovarian endometriosis could affect the quality of oocytes and future embryos in IVF treatments. Endometriosis patients has a reduced implantation and pregnancy rates, maybe due to the reduced quality of oocytes produced by these affected ovaries. Thus, the aim of this study was to compare the whole transcriptomic profile of oocytes from endometriosis patients and healthy donors using RNAseq.

Methods: Metaphase II Oocytes (n=32) were recruited from healthy donors (n=16) and ovarian endometriosis patients (n= 16). RNA extraction and cDNA synthesis was generated using SMART-Seq V4 Ultra-low Input and libraries were constructed using NexteraXT DNA and sequenced using Illumina NextSeq 500 Instrument. RNAseq quality metrics and further analysis were developed in R (3.5.0) computing environment, using 'ggplot2', 'SingleCellExperiment', 'scater' and 'scde' packages. Finally, Differential Gene Expression (DGE) matrix and Functional Enrichment Clustering analysis were performed using the DigitalExpression tool and DAVID. Validation was performed by Q-PCR

Results: Clustering the 32 oocytes by all gene expression using a principal component analysis (PCA) showed a clear effect of endometriosis on global transcriptome behavior. Differential Expression Genes (DEGs) were more prominent in oocytes from ovarian endometriosis vs. healthy oocytes (520 DEGs) than oocytes from unaffected (71 DEGs) or affected (103 DEGs) ovaries. Interestingly, most of the DEGs in oocytes from ovarian endometriosis were upregulated compared to healthy donors. Among the upregulated genes, we found genes such as APOE, DUSP1, G02, HES6, ID4, MGST1 and WEE1, which are involved in apoptosis, cell cycle, response to oxidative stress and cellular oxidant detoxification. These genes were validated by Q-PCR.

Conclusion: Our results suggest that endometriosis is affecting gene oocyte expression, independently if the endometrioma is present or not in the ovary and thereby, oocytes coming from ovarian endometriosis patients have a complete different trancriptomic profile, associated with diminished quality.