Female Aging Alters Expression of Human Cumulus Cells Genes that Are Essential for Oocyte Quality

Abstract

Impact of female aging is an important issue in human reproduction. There was a need for an extensive analysis of age impact on transcriptome profile of cumulus cells (CCs) to link oocyte quality and developmental potential with patient's age. CCs from patients of three age groups were analyzed individually using microarrays. RT-qPCR validation was performed on independent CC cohorts. We focused here on pathways affected by aging in CCs that may explain the decline of oocyte quality with age. In CCs collected from patients >37 years, angiogenic genes including ANGPTL4, LEPR, TGFBR3, and FGF2 were significantly overexpressed compared to patients of the two younger groups. In contrast genes implicated in TGF-β signaling pathway such as AMH, TGFB1, inhibin, and activin receptor were underexpressed. CCs from patients whose ages are between 31 and 36 years showed an overexpression of genes related to insulin signaling pathway such as IGFBP3, PIK3R1, and IGFBP5. A bioinformatic analysis was performed to identify the microRNAs that are potential regulators of the differentially expressed genes of the study. It revealed that the pathways impacted by age were potential targets of specific miRNAs previously identified in our CCs small RNAs sequencing.