Expression des ARNm et des microARN dans les cellules de cumulus humains : impact de l'âge maternel

Abstract:

The oocyte develops into a follicle where it is in close contact with cumulus cells (CCs), of somatic origin. The two cell types undergo a bidirectional communication via gap junctions, which results in the regulation and coordination of the metabolism during oocyte development and maturation. We assume that gene expression and regulation in the CCs play a crucial role in functions that are essential for oocyte growth and competence acquisition. The present study may be subdivided in two parts. In the first part we used deep sequencing to investigate the repertoire of miRNAs in the cumulus cells and the oocyte. MicroRNAs that are noncoding RNA sequences whose length is approximately 19-25 nucleotides have emerged as important regulators in many biological processes including aging. Our data showed that 32 miRNAs were specifically expressed in human cumulus cells while only 3 miRNAs were identified in MII human oocyte. The impact of maternal age on gene expression in cumulus cells was addressed in a second part of my thesis work. While the correlation of oocyte competence decline with advancing maternal age is well established, little is known on its molecular basis. In a first attempt to address this issue, we used microarrays to study gene expression profiles of human cumulus cells according to maternal age. Remarkably, maternal age greatly impacted expression of genes that are critical for oocyte maturation such as genes involved in angiogenesis, TGF-β signaling, and insulin signaling pathways. Also, using bioinformatic tools, we identified miRNAs that potentially target some of the genes involved in the aging-impacted processes and pathways; this could candidate them as new biomarkers to predict premature ovarian aging and oocyte quality and competence.