OMICs signatures to cumulus cells to predict oocyte quality in Assisted Reproductive Techniques (ART).

Project Overview

Infertility rates in European couples are on the rise. Oocyte quality is the primary indicator for reproductive success and most human oocytes used for ART do not exhibit developmental competence and only one third of the treatments are successful and only one of six oocytes results in a successful pregnancy. There is a profound lack of knowledge of the complex biological mechanisms underlying oocyte maturation. Since cumulus cells play a major role in the development and competence of the oocyte, they may be used as a surrogate for oocyte function and future embryo competence as well as pregnancy outcome. Cumulus cells are removed without damaging the oocyte during ART and they are currently a waste product without any further use. For the proposed study, we will use CCs for further experimental analyses, aiming at unravelling the mechanisms underlying oocyte maturation and interactions within the cumulus oocyte complex, as well as identifying differences in the transcriptomes and proteomes stratified by pregnancy outcome. We plan to conduct high sensitivity mass spectrometry analyses and RNA sequencing of the human cumulus cells` transcriptomes, metabolomics, lipidomes and proteomes to fulfill this aim.

Aim of the underlying research project is to find human transcriptome and proteome profiles of cumulus cells that correlate with high oocyte competence to build a base for higher success rates of ART in the future through effective oocyte selection. We aim to contribute to a broader understanding of the human oocyte maturation process and thereby open doors to various further projects in this field.