



Proteomic analysis of human follicular fluid (hFF) from patients undergoing in vitro fertilization procedure.

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Due to growing infertility rates, more people worldwide decide to take advantage of assisted reproductive technology (ART). One of the most common procedures employed during the in vitro fertilization (IVF) process is the transvaginal oocyte retrieval, during which whole mature follicles, each containing an oocyte, are collected. Human follicular fluid (hFF) constitutes the environment for the oocyte development. It is suspected that investigation of hFF composition could provide a tool for evaluation of oocyte quality. In the future, such diagnostic analysis could lead to generation of less embryos with higher probability of IVF success, therefore limiting the cost of treatment and ethical issues associated with human embryo storage.

In this project, a comprehensive analysis of proteomic composition of human follicular fluid is planned. The method applied in this research is a mass spectrometry technique – SWATH-MS (Sequential Windowed Acquisition of All Theoretical Fragment Ion Mass Spectra). Up until now, the optimization of sample preparation procedure and conditions of mass spectrometry measurements have been established. The initial mass spectral library for proteomic analysis has been constructed and tested in first SWATH-MS experiments, allowing a quantitative measurement of 61 proteins.