Using Automated Cell Tracking to Improve Embryo Viability Prediction for In Vitro Fertilization

Nearly one in six couples in the United States experience infertility, many of whom turn to in vitro fertilization (IVF) to have children. However, only 20-25\% of IVF cycles result in a live birth because clinicians can only assess embryo viability based on visual morphology, which has been shown to be only weakly correlated to viability [1]. Because of this low success rate, it is common to transfer several embryos back to the mother at once in hopes that at least one will survive. This causes a high rate of multiple births (~30\%), which are associated with increased health complications for both mothers and children [2]. A more accurate predictor of embryo viability is needed so that clinicians can accurately choose a single embryo to transfer back to the mother, thus decreasing the rate of multiple births while increasing the overall IVF success rate.

One way to more accurately assess an embryo’s viability is simply to let it develop for a longer time in culture (day 5 blastocyst stage instead of day 3), but at the cost of increased embryo stress [3]. Our goal is to observe embryos in culture for 5 days after fertilization, and see if any parameters we observe before day 2 or 3 are predictive of which ones are still surviving by day 5. The parameters we identify could eventually be used clinically to transfer the most viable embryo to a patient by

Previous studies were performed with 2D imaging modalities like dark field microscopy and birefringence, and have shown that the timing and synchronicity of cell divisions can provide a somewhat accurate predictor of blastocyst survival by day 2 or 3 [4, 5].

Using our newly developed 3D Optical Coherence Tomography (OCT) microscopy setup, we hope to extract additional parameters that can improve the accuracy of prediction. We propose exploring cell parameters that are potentially predictive of embryo viability -- cell number, cell shape, cell size, degree of fragmentation, nucleus position, signal intensity, and axis of division - suggested by earlier cytological studies [6-9]. Our algorithm will automate extraction of these key parameters from OCT data using image processing techniques including: adaptive thresholding and noise suppression methods to improve SNR, contrast enhancement to enhance cytological features, morphological and Kalman filtering to track cell position, shape, number, and irregularly shaped regions [10-13]. We will then find the parameters for each cell that are most predictive of whether or not it survived to the blastocyst stage.

References


