SUCCESSFUL SIMULTANEOUS GENOMIC AND TRANSCRIPTOMIC ANALYSIS OF HUMAN BLASTOCYST BIOPSIES (4-6 CELLS)

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Abstract Body

Introduction: There is need for improving embryo selection and outcomes in IVF. Genomic assessment of embryos is clinically available (PGS) and has been shown to improve outcomes, to an extent. Analyzing the transcriptomic profile alongside genomic assessment, could potentially improve outcomes even further. Recent advances in technologies have allowed for simultaneous analysis of the genome and transcriptome, and are rapidly being applied in other medical fields. The aim of this study was to examine whether whole genome analysis could be performed simultaneously with whole transcriptome analysis, on a single human embryo biopsy of only 4-6 cells.

Methods: Nine embryos donated for research were used in this proof of concept study. All samples were collected from consenting patients undergoing IVF at the CReATe Fertility Centre, Toronto, Canada. All of these embryos were deemed unsuitable for transfer. To determine if RNAseq is feasible from as little as 4-6 cells, the first 3 embryos underwent 1 TE and 1 ICM biopsy, and the remainder was collected as representative of the full embryo (EMB). Six additional embryos underwent 2 TE biopsies: the first biopsy was used for whole genome analysis only and the second biopsy was split with 1 fraction utilized for whole genome analysis and the other utilized for whole transcriptome analysis Bioinformatic analysis of gDNA and mRNA sequencing, and qPCR validation were performed on all 9 embryos.

Results: We obtained high quality gDNA and mRNA sequencing data from all samples. All TE and ICM biopsies expressed TE and ICM-specific markers, respectively. TE and EMB samples clustered closely on PCA; ICM samples clustered separately from them. Differential expression revealed large transcriptomic differences between TE and ICM. The PGS concordance between split and non-split TE biopsies was 100%.

Conclusions: This is the first study to achieve consistent full genomic and transcriptomic profiles from a single human embryo biopsy of 4-6 cells. The quality of the genomic and the transcriptomic data obtained across all samples was of high quality. This method could have the potential of improving embryo selection and ultimately IVF pregnancy outcomes.