Identification of Target IVF Preimplantation Screening Regions via Developmental Pathway and RNA-Seq Expression Analysis

Phanphongsa, Emily (School: Waipahu High School)

Embryonic development is a universal process that is elucidated amongst healthcare professionals and researchers in the field of obstetrics. During particular stages of development, families of genes are differentially expressed and regulated by developmental transcription factors. It is suggested that genes involved with the production of protein subunits portray significance in the earlier stages of embryonic development. Currently, embryonic cells cultured by in vitro fertilization (IVF) procedures undergo genetic sequencing where potential mosaicism within blastocysts are observed and used to promote successful implantation and growth. With a combination of dataset manipulation methods, the concept of comparison between successful IVF and embryo development genes within their respective developmental pathways was explored. Computational analysis tools including DESeq2 and pathfindR analyzed and compared IVF (n = 6) and standard embryonic development (n = 124) RNA-seq dataset regulation levels in pathway clusters. The output displayed a great correlation between ribosome, spliceosome, and proteasome clusters and highlighted the upregulation of gene groups such as RPS, RPL, SNR, FUS, SF3, etc. The investigated genes were found to be greatly associated with regulated pathways pertaining to cellular regulation and growth. With the identification of key genes that play crucial roles in both processes, particular preimplantation screening regions could be explored for differential gene expression and lead to successful IVF implantation.

Awards Won: