TRANSCRIPTIONAL PROFILING TO IMPROVE PORCINE PREIMPLANTATION EMBRYO DEVELOPMENT IN VITRO

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ABSTRACT

Culture environments can have profound impacts on the developmental program of the preimplantation embryo. Even though significant improvements have been made to embryo culture environments they are still sub-optimal to the in vivo environment. It is our overall goal to understand the metabolism of these embryos so that we can continue to improve our culture system to become more similar to the in vivo environment and thus increasing embryo viability in vitro. Our first aim was to utilize the transcriptional profile of embryos cultured in vitro to mine transcripts involved with metabolism. This will allow us to get a better idea of what these embryos may need in culture. The second aim was to illustrate that by mining a transcriptional profile database of embryos cultured either in vitro or in vivo and assessing the differentially expressed genes we could get an idea of what the in vitro embryos are lacking in culture. The final aim was to continue analyzing the differentially expressed genes in the in vitro or in vivo cultured embryo database and find another way to improve embryo development in vitro. Through these transcriptional profiling efforts, we identify that the transcriptional profile of in vitro embryos seem to be similar to cancer cells in the expression of metabolism related genes. We also found that by adding arginine and glycine to culture, we could improve development to the blastocyst stage in porcine preimplantation embryos.