TRANSCRIPTIONAL PROFILING BY DEEP SEQUENCING INDENTIFIES DIFFERENCES IN MRNA TRANSCRIPT ABUNDANCE IN *IN VIVO* DERIVED VS. *IN VITRO* CULTURED PORCINE BLASTOCYST STAGE EMBRYOS

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ABSTRACT

In vitro embryo culture systems promote development at rates lower than *in vivo*. The goal of this project was to discover transcripts that may be responsible for a decrease of embryo competency in blastocyst stage embryos cultured *in vitro*. Gilts were artificially inseminated and on Day 2 one oviduct and the tip of a uterine horn were flushed and the recovered embryos were cultured in PZM3 for four days. On Day 6 the gilts were euthanized and the contra-lateral horn was flushed to obtain *in vivo* derived embryos. Total RNA was extracted from 3 pools of 10 blastocysts from each treatment. First and second strand cDNA was synthesized and then sequenced using Illumina sequencing. The reads were aligned to a custom-built database designed to represent the known porcine “transcriptome”. A total of 1,170 database members were different between the two groups ($P<0.05$), and 588 of those were at least 2-fold different. Eleven transcripts were subjected to real-time PCR and each validated the sequencing. There was an overall decrease in both inner cell mass and trophectodermal cell numbers in embryos cultured *in vitro*, however, no difference in ICM:TE ratio was found. Interestingly, the transcript (*SLC7A1*) was higher in the *in vitro* cultured group. This difference disappeared after addition of arginine (0.36 mM) to the 4 day culture. In conclusion, Illumina sequencing and alignment to a custom “transcriptome” successfully identified a large number of genes that yield clues to the derivation of culture media.