

DNA METHYLATION IN THE EARLY PORCINE EMBRYO

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ABSTRACT

Reproductive technologies such as *in vitro* fertilization, intracytoplasmic sperm injection, parthenogenetic activation, and somatic cell nuclear transfer are powerful procedures in the production of animals for agricultural research, basic research, and biomedical research. Unfortunately, the production of live animals by using these *in vitro* technologies is very inefficient. One component contributing to this inefficiency is that *in vitro* oocyte maturation and *in vitro* culture can have detrimental effects on the epigenetic factor of cytosine methylation in cytosine-guanine dinucleotides. The purpose of this research is to study the dynamics of cytosine-guanine dinucleotide methylation in porcine gametes, donor cells and early embryos by using Porcine Differential Methylation Hybridization analysis.

These results show that the cytosine-guanine dinucleotide methylation remodeling which occurs in the development of the *in vivo*-derived blastocyst does not occur in blastocysts produced by using *in vitro* techniques such as parthenogenesis, somatic cell nuclear transfer, and *in vitro* fertilization. Also, the cytosine-guanine dinucleotide methylation profiles of the donor cells were shown to correlate to developmental potential after somatic cell nuclear transfer. These results show that Porcine Differential Methylation Hybridization analysis is an effective procedure for the identification of donor cells with high developmental potential following somatic cell nuclear transfer. In conclusion, these studies indicate that aberrant epigenetic remodeling may be a factor in the low efficiency of reproductive technologies which utilize *in vitro* techniques.