Public Abstract
First Name:Aaron
Middle Name:James
Last Name:Bonk
Adviser's First Name:Randall
Adviser's Last Name:Prather
Co-Adviser's First Name:
Co-Adviser's Last Name:
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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 a modification to DNA known as methylation. The purpose of this research is to study the differences in DNA methylation in porcine gametes, donor cells and early embryos by using Porcine Differential Methylation Hybridization analysis.
These results show that the DNA 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 DNA methylation profiles of the donor cells were shown to correlate to developmental potential after somatic cell nuclear transfer. Furthermore, 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 incorrect DNA methylation remodeling may be a factor in the low efficiency of reproductive technologies which utilize in vitro techniques.