# Differential Expression of Retrotransposons in Stem Cell Lineages of the Preimplantation Embryo

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Approximately 40% of the human genome is comprised of retrotransposons, which are genetic elements capable of amplifying themselves within the genome. Throughout the course of human life, retrotransposons are expressed in germ cells, the preimplantation embryo, and the placenta but silenced elsewhere. However, the functions of retrotransposons during embryonic development are poorly understood. Trophoblast stem (TS), embryonic stem (ES), and extraembryonic endoderm stem (XEN) cells are cell lineages derived from the preimplantation embryo and known to have different retrotransposon silencing mechanisms. Thus, it is likely distinct retrotransposons are expressed in each lineage and that proteins coded by these retrotransposons have lineage-specific functions. The purpose of this research was to determine which protein-coding retrotransposons are expressed in each of these stem cell lineages and to compare expression levels between lineages. Each lineage's transcriptome was analyzed by quantifying retrotransposon expression in RNA-sequencing data from mouse stem cells using the Kallisto program. Expression data were then used for differential expression analyses performed between the cell types using the Sleuth program in R software. It was found that certain classes of retrotransposons are distinctly expressed in certain lineages, including the intracisternal A-type particle (IAP) family in TS and XEN cells and the long interspersed nuclear element 1 (LINE-1) family in ES cells. These findings suggest silencing of IAPs and expression of LINE-1 may be essential in the differentiation and development of the ES lineage, the understanding of which can lead to improved stem cell therapies and capacity to study human embryonic development.

**Awards Won:**
Second Award of $1,500