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## Using single cell functional genomics approach to study gene expression network in human early embryos

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Measuring gene expression in individual cells is crucial for understanding the gene regulatory network controlling human embryonic development. We applied single-cell RNA -Seq analysis to human preimplantation embryos, primordial germ cells (PGCs), and human embryonic stem cells (hESCs). We also systematically profiled the DNA methylome of human early embryos from the zygotic stage through to post-implantation. We showed that the major wave of genome-wide demethylation is complete at the 2-cell stage, contrary to previous observations in mice. Moreover, the demethylation of the paternal genome was much faster than that of the maternal genome, and by the end of the zygotic stage the genome-wide methylation level in male pronuclei was already lower than that in female pronuclei. Then we also showed that long interspersed nuclear elements (LINEs) or short interspersed nuclear elements (SINEs) that were evolutionarily young are demethylated to a milder extent compared to older elements in the same family and had higher abundance of transcripts, indicating that early embryos tend to retain higher residual methylation at the evolutionarily younger and more active transposable elements. Furthermore, we analyzed the DNA methylome of human PGCs and found global demethylation of their genomes. Approximately 10 to 11 weeks after gestation, the PGCs were nearly devoid of any DNA methylation, whereas the repeat elements still kept high level of residual methylation. Our work provides insights of critical features of the transcriptome and DNA methylome landscapes of human early embryos and primordial germ cells, as well as the functional significance of DNA methylome to regulation of gene expression and repression of transposable elements.

### Biography

Dr. Fuchou Tang He joined BIOPIC of Peking University as a group leader in 2010. His lab focuses on studying gene regulation network in human early embryos. His lab analyzed the dynamics of gene expression network in human pre-implantation embryos at single-cell and single-base resolution (Nature Structural & Molecular Biology, 2013). His lab also developed single cell DNA methylome analysis technique (Genome Research, 2013) and analyzed the dynamics of DNA methylome in human pre-implantation embryos as well as primordial germ cells, which provides new insights into the critical features of the methylome of human early embryos and primordial germ cells, as well as its functional relation to the regulation of gene expression and the repression of transposable elements (Nature, 2014; Cell, 2015).

**Notes:**