MicroRNA profiling of human-induced pluripotent stem cells.

Journal: Stem Cells Dev

Publication Year: 2009

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PubMed link: 19284351

Funding Grants: In Vivo Imaging of Human Embryonic Stem Cell Derivatives and Tumorigenicity

Public Summary:

Scientific Abstract:
MicroRNAs (miRNAs) are a newly discovered endogenous class of small noncoding RNAs that play important posttranscriptional regulatory roles by targeting mRNAs for cleavage or translational repression. Accumulating evidence now supports the importance of miRNAs for human embryonic stem cell (hESC) self-renewal, pluripotency, and differentiation. However, with respect to induced pluripotent stem cells (iPSC), in which embryonic-like cells are reprogrammed from adult cells using defined factors, the role of miRNAs during reprogramming has not been well-characterized. Determining the miRNAs that are associated with reprogramming should yield significant insight into the specific miRNA expression patterns that are required for pluripotency. To address this lack of knowledge, we use miRNA microarrays to compare the "microRNA-omes" of human iPSCs, hESCs, and fetal fibroblasts. We confirm the presence of a signature group of miRNAs that is up-regulated in both iPSCs and hESCs, such as the miR-302 and 17-92 clusters. We also highlight differences between the two pluripotent cell types, as in expression of the miR-371/372/373 cluster. In addition to histone modifications, promoter methylation, transcription factors, and other regulatory control elements, we believe these miRNA signatures of pluripotent cells likely represent another layer of regulatory control over cell fate decisions, and should prove important for the cellular reprogramming field.