Role of Epigenetics in Stem Cell

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ABSTRACT

Pluripotency of stem cells is due to three main factors: transcriptional regulation, epigenetic modifications and chromatin structures. Epigenetic modifications of core histone proteins including methylation, phosphorylation and acetylation, helps to maintain the chromatin structure. The level of chromatin compaction controls accessibility to genomic DNA and therefore has a key role in establishing and maintaining distinct gene expression patterns and consequently pluripotent fate of stem cells. The genome undergoes epigenetic modifications during development and differentiation, from an open euchromatin rich ESC to a more compact heterochromatin rich differentiated cell. Transcription factors bind to *cis*-regulatory elements and control gene expression in response to environmental cues. Promoters active in early developmental stages tend to be GC-rich and mainly use H3K27me3 for repression in non-expressing cells. Whereas genes differentially expressed in later stages are largely CG poor and use DNA methylation for silencing. Transcriptionally active chromatin of stem cells is usually hyperacetylated and hypomethylated. The hyperdynamic chromatin of ESCs has loosely bound histone proteins such as H3, H2B, etc. with very short residency times. Differentiation leads to loss of this dynamic nature by restructuring of the genome. A better understanding of epigenetics will facilitate identification of deficiencies in current approaches, leading to more faithful differentiation strategies as well as providing insights into the rewiring of human regulatory programs during cellular transitions.

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