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Dynamics of chromatin signatures associated with the differentiation of human embryonic stem cell into neuroectoderm cell

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Abstract

Nucleosome positioning and histone modifications constitute chromatin signatures that involve in many physiological processes. However, the mechanisms under which dynamic chromatin signatures determine cell lineage specification are elusive. In this study, we explored the dynamics of chromatin signatures during the differentiation of human embryonic stem cell (ESC) into neuroectoderm cell. In general, a canonical uniform arrangement of +1, +2, +3 etc. nucleosome starting at the transcription start site (TSS) in gene body is positively linked to the gene activity. Extensive nucleosome occupancy changes occur across the genome, including nucleosome eviction, de novo occupation, and shift. Particularly, a set of genes enriched on neuron development function obtain an open promoter region by loss of the nucleosome adjacently upstream of TSS. Moreover, nucleosome repositioning change regulates the accessibility of transcription factor binding sites (TFBS). The binding sites of pluripotency factors such Oct4, Nanog, c-Myc become protected by nucleosome occupation in neuroectoderm cell. In contrast, the binding sites of other transcription factors such as Egr1, Taf1, Tbp become exposed by loss of nucleosome. Intriguingly, more than 80% of the bivalent nucleosomes, namely the ones simultaneously containing both H3K4me3 and H3K27me3, that lose H3K4me3, gain H3K9ac in the differentiation process. Surprisingly, distinct histone modification signatures control the expression of ESC-, trophoectoderm-, endoderm-, mesoderm-, and neuroectoderm-specific marker genes, respectively. Taken together, nucleosome dynamics, histone modifications, and interaction with other factors from a complex regulatory network to fine tune gene expression during ESC fate decisions.

Biography

Cizhong Jiang obtained his Ph.D. in 2004 from Iowa State University, started his postdoctoral training at Cold Spring Harbor Laboratory and finished it at the Pennsylvania State University. Currently, Dr. Jiang is a professor in the School of Life Sciences and Technology, Tongji University, Shanghai, China. He has worked in the fields of genomics, gene regulation, and epigenetics for more than 10 years, and published more than 25 papers in reputed journals.