Sequencing the Epigenome

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Abstract The term 'epigenome' refers to the complete description of chemical changes to DNA and histones as they map onto the genome in a given cell type. A comprehensive genomewide catalog of epigenetic control elements and how these vary across cell states could offer critical insight into the relationships between genotype, phenotype and environment, and serve as a catalyst for future studies of the epigenetic mechanisms that regulate normal physiology and human disease. Our ability to characterize mammalian epigenomes has been markedly enhanced by technological developments in recent years. In particular, the introduction of ultra high-throughput sequencing has improved the precision, comprehensiveness and throughput of techniques for mapping chromatin and DNA methylation. This chapter will largely focus on these new applications and their use for high resolution interrogation of mammalian epigenomes.

Keywords DNA methylation · Histone modifications · Epigenome · Bisulfite sequencing · ChIP-Seq

1 Introduction

1.1 Epigenetics

Epigenetic modifications provide essential regulatory information that does not alter the primary nucleotide sequence (Epi: on top or in addition to). DNA methylation is generally associated with repressive contexts and stably propagated through cell division by DNA methyltransferases. Despite being the most extensively studied epigenetic modification in mammals experimental data for its genome-wide distribution, it's dynamic role during differentiation and its relationship with histone modifications remain limited (Bernstein et al. 2007; Bird, 2002). Post-translational histone modifications are implicated in epigenetic regulatory pathways such as

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