

Video Article

Mapping of nucleosome positioning by next generation sequencing in *Saccharomyces cerevisiae*

John Aitchison¹
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Correspondence to: John Aitchison at jaitchison@systemsbiology.org

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Abstract

Eukaryotic DNA is packaged into nucleosomes. Each nucleosome consists of 147bp of DNA wrapped around the histone proteins H2A, H2B, H3 and H4 which together form an octameric core. Nucleosome positioning can influence the expression of genes by controlling the accessibility of transcription factor binding sites and genome-wide mapping studies of nucleosomes have revealed complex relationships between chromatin structure and gene expression. The positioning of nucleosomes has also been implicated in the regulation of other DNA related processes including replication, recombination and repair. Thus, understanding the regulation of the numerous functions associated with chromatin will be enabled by analysis of nucleosomes, associated complexes and their influences. Here, we present a protocol for the isolation of mononucleosomal DNA and the preparation of a genomic DNA library for sequencing to generate a high resolution map of nucleosome occupancy in *S. cerevisiae*. We also applied an analytical method to identify nucleosome positions and occupancy from next generation sequencing data.

Disclosures

No conflicts of interest declared.