

Accepted Manuscript

Article

Using single-molecule approach to visualize the nucleosome assembly in yeast nucleoplasmic extracts

Xiuqiang Chen, Ershuang Zhao, Yu V. Fu

PII: S2095-9273(17)30102-0

DOI: <http://dx.doi.org/10.1016/j.scib.2017.02.011>

Reference: SCIB 74

To appear in: *Science Bulletin*



Please cite this article as: X. Chen, E. Zhao, Y.V. Fu, Using single-molecule approach to visualize the nucleosome assembly in yeast nucleoplasmic extracts, *Science Bulletin* (2017), doi: <http://dx.doi.org/10.1016/j.scib.2017.02.011>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

Using single-molecule approach to visualize the nucleosome assembly in yeast nucleoplasmic extracts

Xiuqiang Chen, Ershuang Zhao, Yu V. Fu

¹ State Key Laboratory of Microbial Resources, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China

² Savaid Medical School, University of Chinese Academy of Sciences, Beijing, China

³ These authors contributed equally to this work

* Correspondence should be addressed to Y. V. F. (fuyu@im.ac.cn)

Abstract

In eukaryotic cells, the smallest subunit of chromatin is the nucleosome, which consists of a segment of DNA wound on histone protein cores. Despite many years of effort, the process of nucleosome assembly and disassembly is still not very clear. Here, we present a convenient method to investigate the process of nucleosome assembly at the single molecule level. We invented a novel system derived from the yeast nucleoplasmic extracts (YNPE), and demonstrated that the YNPE supports the nucleosome assembly under physiological condition. By combining the total internal reflection fluorescence microscopy with microfluidic flow-cell technique, the dynamic process of nucleosome assembly in YNPE was visualized at single-molecule level. Our system provides a novel *in vitro* single-molecule tool to investigate the dynamics of nucleosome assembly under physiological conditions.

Keywords: Nucleosome assembly, Single-molecule, Yeast nucleoplasmic extracts, Total internal reflection fluorescence microscopy, Microfluidic flow-cell

1. Introduction

The Eukaryotic genome is packaged into chromatin for fitting in the nucleus. The fundamental unit of chromatin is nucleosome which consists of an octamer of four core histones (H2A, H2B, H3 and H4) wrapped by 146 base pairs of DNA[1]. The repeating nucleosomes are further compacted into higher-order structures by the linker histone H1[2]. It is well known that the dynamic regulation of nucleosome assembly is a key to controlling multiple biological processes that require access to nuclear DNA, such as transcription, DNA replication, and DNA damage repair [3, 4].

Download English Version:

<https://daneshyari.com/en/article/5788808>

Download Persian Version:

<https://daneshyari.com/article/5788808>

[Daneshyari.com](https://daneshyari.com)