Multi-scale tracking reveals scale-dependent chromatin dynamics after DNA damage.

Journal: Mol Biol Cell

Publication Year: 2017

Authors: Judith Mine-Hattab, Vincent Recamier, Ignacio Izeddin, Rodney Rothstein, Xavier Darzacq

PubMed link: 28794266

Funding Grants: Single Molecule Biophysics and Biology of Cellular Identity

Public Summary:
The dynamic organization of genes inside the nucleus is an important determinant for their function. Using fast DNA tracking microscopy in S. cerevisiae cells and improved analysis of mean square displacements, we quantified DNA motion at time scales ranging from 10 milliseconds to minute and found that following DNA damage, DNA exhibits distinct sub-diffusive regimes. In response to double-strand breaks, chromatin is more mobile at large time scales but, surprisingly, its mobility is reduced at short time scales. This effect is even more pronounced at the site of damage. Such a pattern of dynamics is consistent with a global increase in chromatin persistence length in response to DNA damage. Scale-dependent nuclear exploration is regulated by the Rad51 repair protein, both at the break and throughout the genome. We propose a model in which stiffening of the damaged ends by the repair complex, combined with global increased stiffness, act like a "needle in a ball of yarn", enhancing the ability of the break to traverse the chromatin meshwork.

Scientific Abstract:
The dynamic organization of genes inside the nucleus is an important determinant for their function. Using fast DNA tracking microscopy in S. cerevisiae cells and improved analysis of mean square displacements, we quantified DNA motion at time scales ranging from 10 milliseconds to minute and found that following DNA damage, DNA exhibits distinct sub-diffusive regimes. In response to double-strand breaks, chromatin is more mobile at large time scales but, surprisingly, its mobility is reduced at short time scales. This effect is even more pronounced at the site of damage. Such a pattern of dynamics is consistent with a global increase in chromatin persistence length in response to DNA damage. Scale-dependent nuclear exploration is regulated by the Rad51 repair protein, both at the break and throughout the genome. We propose a model in which stiffening of the damaged ends by the repair complex, combined with global increased stiffness, act like a "needle in a ball of yarn", enhancing the ability of the break to traverse the chromatin meshwork.