Chromatin compaction and heterogeneity at the single cell level

Vincent Récamier, Ignacio Izeddin, Lana Bosanac and Xavier Darzacq
Institut de Biologie de l'Ecole Normale Supérieure (IBENS) UMR 8197
46 rue d'Ulm 75005 Paris FRANCE
E-MAIL: recamier@biologie.ens.fr
izeddin@biologie.ens.fr
darzacq@biologie.ens.fr

Abstract:

Gene transcription and its regulation occur in a densely packed environment, the nucleus. How nuclear organization impacts nuclear functions is still not clear and, during the last decade, several model of nuclear heterogeneity have been proposed and among them, fractals. Fractal structures are mathematical objects that have the following properties: they are irregular, have a certain form of self-similarity, and they occupy sparsely the space, giving rise to a non-integer fractal dimension. Here, we performed a direct measure of the fractal dimension of chromatin. We used histone H2B, one of the 4 core proteins forming the nucleosome, as a chromatin density marker. Using photoactivated localization microscopy (PALM) and adaptive optics, we measured the three-dimensional distribution of H2B fused to the photoconvertible fluorescent protein Dendra2 with nanometric resolution. We computed the 3D distance distribution between every two points of the chromatin structure, named the Palm K distribution after the teletraffic engineer Conny Palm. The Palm distribution of H2B followed a power law, leading a precise measurement of the 2.7 correlation fractal dimension of chromatin that is part of a larger multi-fractal spectrum. This result is in the line with the fact that chromatin has a particular non-equilibrium folding that could be seen at many different scales.