

New insights into the 3-D organization of the human genome

March 25 2010

Insights into the genomics of the human nucleolus have been revealed in a study by researchers from the University of Regensburg and the Ludwig Maximilians University in Germany and the Centro de Investigación Príncipe Felipe in Spain. The research, published March 26 in the open-access journal *PLoS Genetics*, sheds new light on the functional organization of human genetic material.

One major challenge of the post-genomic era is to understand how the [genome](#) is organized inside the cell's nucleus to fulfill the dynamics and regulation of DNA access to regulatory factors. Previous studies on the nuclear architecture of the cell suggest that the three-dimensional structure of genomic information is non-random. However, few discrete genomic loci have been analyzed for their spatial location, prompting the current study.

The researchers, led by Attila Németh and Gernot Längst, examined the DNA network of the nucleolus, the nucleus' largest sub-compartment, using sequencing, microarray analysis, and single-cell analysis. The work resulted in a high-resolution sequence map of this nuclear structure, detailing the position of the several thousand genes and non-coding sequences that form the nucleolus within the three-dimensional space of the nucleus.

"The results help us understand how nuclear information is packaged into functional compartments of the nucleus," say the authors. At the same time, the authors emphasise that this research was confined to just

two cell types, and that further studies are needed to address the conservation of these packaging mechanisms during evolution, and to monitor the developmental dynamics of three-dimensional [genome](#) organization.

More information: Németh A, Conesa A, Santoyo-Lopez J, Medina I, Montaner D, et al. (2010) Initial Genomics of the Human Nucleolus. PLoS Genet 6(3): e1000889. [doi:10.1371/journal.pgen.1000889](https://doi.org/10.1371/journal.pgen.1000889)

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