Curr Synthetic Sys Biol 2015, 3:3
http://dx.doi.org/10.4172/2332-0737.C1.003

OMICS International
conferenceseries.com

Targeted chromatin capture (T2C):A new method to unravel the local spatial organization of the genome at a single restriction fragment resolution

Petros Kolovos[1], Harmen J GVan Der Werken[1], Nick Kepper[2], Jessica Zuin[1], Rutger WW Brouwer[1], Christel E M Kockx[1], Wilfred F JVan Ijcken[1], Kerstin S Wendt[1], Frank Grosveld[1] and **Tobias A Knoch[1]**
[1]Erasmus MC, Netherlands
[2]German Cancer Research Center, Germany

The last years have been a significant effort to unravel the spatial organization and the chromatin interactions of the genomes. Towards that objective, chromosome conformation capture technology and its derivatives contributed significantly. However, the need of a technique which is affordable for most of the people and at the same time interrogates large selected regions of the genome has become quite apparent. Furthermore, the borders of the topological associated domains (TADs) as well as the interactions within and between TADs can not been identified in an adequate manner with the usual resolution (40kb) of Hi-C. For that reason we have developed a method termed Targeted Chromatin Capture (T2C). It provides a genome wide analysis of a selected region of the genome at high resolution(single restriction fragment resolution from 2 to 6 kbp)at low cost due to the lower sequencing effort (1/5 up to 1/13 of alllumina based sequencing lane). TADs and their respective boundaries can be identified accurately due to the significantly improved resolution. All the interactions within and between TADs can be observed with T2C because every restriction fragment can serve as a 'viewpoint' and all their interactionsboth cis ortrans can be identified. Thus multiple 3C-seq, 4C-seq or 5C experiments do not have to be performed. We have used T2C for different loci and identified the same topological domains and chromatin interactions which have been observed before.Furthermore, with T2C we can answer the perpetual question of the actual structure of the genome and which model is the most prominent. Hence, T2Ccan be used as an affordable, cost-effective, diagnostic tool with single restriction fragment resolution to explore the local spatial organization of the genome, chromatin interactions and unravel the 3D structure without requiring laborious procedures or massive sequencing efforts.

p.kolovos@erasmusmc.nl

Bioengineering in the whole scale: Integrating protein engineering methods into plant omics research

Pavel Mazura
Mendel University, Czech Republic

With the current developmentof novel omics technologies and through large-scale consortia projects, biological systems are being engineered and further investigated at an unprecedented scale. This approach represents significant challenge in the effort to integrate different technologies, methods and research strategies. In our research we have developed technologies for protein engineering with the application on proteins involved in plant hormone regulation and signaling. Targeted changes in a plant hormone system represent promising direction in plant bioengineering. We have applied various omics approaches to investigate plants with induced changes in their hormone system. Obtained data are important in deciphering complex effects responsible for plant growth and development. We propose a combination of protein engineering and plant omics research as a tool for both basic research uncoveringgenom/phenom functional links and also as a source of knowledge needed for further development of crops.

mazura@sci.muni.cz