

Genome-wide 3C mapping to reconstitute chromosome structure

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Mapping of long-range associations through the fission yeast genome reveals global genome organization linked to transcriptional regulation

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<http://nar.oxfordjournals.org/content/38/22/8164.long>

**Abstract:** We have comprehensively mapped long-range associations between chromosomal regions throughout the fission yeast genome using the latest genomics approach that combines next generation sequencing and chromosome conformation capture (3C). Our relatively simple approach, referred to as enrichment of ligation products (ELP), involves digestion of the 3C sample with a 4bp cutter and self-ligation, achieving a resolution of 20kb. It recaptures previously characterized genome organizations and also identifies new and important interactions. We have modeled the 3D structure of the entire fission yeast genome and have explored the functional relationships between the global genome organization and transcriptional regulation. We find significant associations among highly transcribed genes. Moreover, we demonstrate that genes co-regulated during the cell cycle tend to associate with one another when activated. Remarkably, functionally defined genes derived from particular gene ontology groups tend to associate in a statistically significant manner. Those significantly associating genes frequently contain the same DNA motifs at their promoter regions, suggesting that potential transcription factors binding to these motifs are involved in defining the associations among those genes. Our study suggests the presence of a global genome organization in fission yeast that is functionally similar to the recently proposed mammalian transcription factory.

**References to be mentioned:**

1. Erez Lieberman-Aiden, Nynke L. van Berkum, ..., & Job Dekker   Comprehensive mapping of long-range interactions reveals folding principles of the human genome  
Science **326** 289-293 (2009).
2. Zhijun Duan, Mirela Andronescu, ..., & William S. Noble    A three-dimensional model of the yeast genome    Nature **465** 363-367 (2010).
3. Naoko Tokuda, Tomoki P. Terada, and Masaki Sasai    Dynamical modeling of three-dimensional genome organization in interphase budding yeast  
Biophys. J. **102** 296-304 (2012).