

P004 Transcriptional regulation constrains eukaryotic genome organization

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Genetic material in eukaryotes is tightly packaged in a hierarchical manner into multiple linear chromosomes within the nucleus. Although it is known that eukaryotic transcriptional regulation is complex and requires an intricate coordination of several molecular events both in space and time, whether the complexity of this process constrains genome organization is still unknown. Here, we present evidence for the existence of a higher-order organization of genes across and within chromosomes that is constrained by transcriptional regulation using the transcriptional networks of yeast, *Saccharomyces cerevisiae* and mammalian systems. In particular, we show that (i) the Target Genes (TGs) of a majority of Transcription Factors (TFs) show a strong preference to be encoded on specific chromosomes, (ii) the TGs of a significant number of TFs display a strong preference to be encoded in regions containing particular chromosomal landmarks and (iii) the TGs of most TFs are positionally clustered within a chromosome. Our results demonstrate that specific organization of genes that allowed for efficient control of transcription within the nuclear space has been selected during evolution. Our observations will have implications in genetic engineering experiments, gene therapy, and understanding disease conditions that involve chromosomal aberrations.

References

- 1) Janga SC et.al , *Proc. Natl. Acad. Sci. U S A.* 105(41): 15761-6, 2008
- 2) Babu MM et.al , *Curr Opin Genet Dev.*, 2008