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Title:	Three Dimensional Organization of Genome Might Have Guided the Dynamics of Gene Order Evolution in Eukaryotes
Authors:	Bagadia, Meenakshi (/jspui/browse?type=author&value=Bagadia%2C+Meenakshi) Singh, Arashdeep (/jspui/browse?type=author&value=Singh%2C+Arashdeep) Sandhu, K.S. (/jspui/browse?type=author&value=Sandhu%2C+K.S.)
Keywords:	Genome organization, Gene-clusters Genomic rearrangements Chromatin interactions
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Abstract:	In eukaryotes, genes are nonrandomly organized into short gene-dense regions or “gene-clusters” interspersed by long gene-poor regions. How these gene-clusters have evolved is not entirely clear. Gene duplication may not account for all the gene-clusters since the genes in most of the clusters do not exhibit significant sequence similarity. In this study, using genome-wide data sets from budding yeast, fruit-fly, and human, we show that: 1) long-range evolutionary repositioning of genes strongly associate with their spatial proximity in the nucleus; 2) presence of evolutionary DNA break-points at involved loci hints at their susceptibility to undergo long-range genomic rearrangements; and 3) correlated epigenetic and transcriptional states of engaged genes highlight the underlying evolutionary constraints. The significance of observation 1, 2, and 3 are particularly stronger for the instances of inferred evolutionary gain, as compared with loss, of linear gene-clustering. These observations suggest that the long-range genomic rearrangements guided through 3D genome organization might have contributed to the evolution of gene order. We further hypothesize that the evolution of linear gene-clusters in eukaryotic genomes might have been mediated through spatial interactions among distant loci in order to optimize co-ordinated regulation of genes. We model this hypothesis through a heuristic model of gene-order evolution.
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