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# Chromosome structure as a component of gene definition

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## Abstract

Session : "What is a gene? the gene concept faced to recent advances in genetics, molecular and developmental biology." (Heams, Deutsch -organizer-, They, Galperin) Alongside gene regulation mechanisms at the sequence level, several sources of variations in chromatin and chromosome structure impact gene expression, and show some cell-to-cell heritability. Therefore these are termed " epigenetic " mechanisms. Among them, the tridimensional folding of chromatin in eukaryotic cells during interphase, organised in semi-stable 'chromosome territories' seems to fit both requirements.

First, the spatial relative positions of such territories can undergo selective pressures, being partially but significantly inherited from mother- to daughter-cells, and between generations in multicellular organisms : these relative positions, yet probabilistic, even show a species-specific component.

Second, the nuclear location of a gene modulates its expression level : caeteris paribus, genes on central or peripheral chromosome territories will have differential probabilities of expression, and so for genes at the center v/s the periphery of a given territory. This advocates for the fact that natural selection operates not only at the sequence 'text' level, but also on the global architectures of genomes (the 'syntax'), e.g. in differentiating gene-poor from gene-dense regions in relation with their location, and in taking advantage of the probabilistic distance between sequences in a 3D space. Furthermore, this reminds that DNA is not only information but first of all matter, also selected for its own trade-off between its physical properties and constraints. This could pave the way for a renewed consideration of biophysical sciences in evolutionary studies. A modern definition of a gene as a functional and heritable unit should take these structural dimensions into account.

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