Approaching the Sequential and Three-Dimensional Organization of Archaea, Bacteria and Eukarya Genomes

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Abstract

The analyses of the sequential organization of genomes and the three-dimensional structure of genomes using genomic DNA sequences allow to gain a better understanding of the functioning of the cell. Such studies can help to understand the origin of life, the evolution of life on Earth and the relationship between the genome and the cell. The three-dimensional structure of the genome is determined by the way the DNA is packaged into chromosomes, the way the chromosomes are organized in the nucleus and the way the chromosome is associated with the nuclear envelope. The three-dimensional structure of the genome is also influenced by the way the DNA is organized in the cell, the way the DNA is modified, and the way the DNA is regulated.

INTRODUCTION

Despite the successful linear sequencing of the genome, the sequential organization of the genome is widely unknown despite its importance for gene regulation and replication. The three-dimensional structure of the genome is determined by the way the DNA is packaged into chromosomes, the way the chromosomes are organized in the nucleus and the way the chromosome is associated with the nuclear envelope. The three-dimensional structure of the genome is also influenced by the way the DNA is organized in the cell, the way the DNA is modified, and the way the DNA is regulated.

Fig. 1: Tree of Eukarya.

CONCLUSION

The analyses of the sequential organization of genomes and the three-dimensional structure of genomes using genomic DNA sequences allow to gain a better understanding of the functioning of the cell. Such studies can help to understand the origin of life, the evolution of life on Earth and the relationship between the genome and the cell. The three-dimensional structure of the genome is determined by the way the DNA is packaged into chromosomes, the way the chromosomes are organized in the nucleus and the way the chromosome is associated with the nuclear envelope. The three-dimensional structure of the genome is also influenced by the way the DNA is organized in the cell, the way the DNA is modified, and the way the DNA is regulated.

Fig. 2: Tree of Bacteria.

ACKNOWLEDGEMENTS

This work was supported by the German Research Foundation (DFG) through the Collaborative Research Centre SFB 680 "Structural and Functional Genomics" at the University of Tübingen.

Fig. 3: Tree of Archaea.

REFERENCES


Fig. 4: Tree of Archaea.

Fig. 5: Tree of Bacteria.

Fig. 6: Tree of Eukarya.

Fig. 7: Tree of Bacteria.

Fig. 8: Tree of Archaea.

Fig. 9: Tree of Eukarya.

Fig. 10: Tree of Bacteria.

Fig. 11: Tree of Archaea.

Fig. 12: Tree of Eukarya.

Fig. 13: Tree of Bacteria.

Fig. 14: Tree of Archaea.

Fig. 15: Tree of Eukarya.

Fig. 16: Tree of Bacteria.

Fig. 17: Tree of Archaea.

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Fig. 76: Tree of Bacteria.

Fig. 77: Tree of Archaea.

Fig. 78: Tree of Eukarya.
Literature


Approaching the Sequential and Three-Dimensional Organization of Archaea, Bacteria and Eukarya Genomes

Knoch, T. A., Göker, M., Lohner, R. & Langowski, J.

TIGR’s 14th International Genome Sequencing & Analysis Conference, Boston, USA, 2nd - 5th September, 2002.

Abstract

The largely unresolved sequential organization, i.e. the relations within DNA sequences, and its connection to the three-dimensional organization of genomes was investigated by correlation analyses of completely sequenced chromosomes from Viroids, Archaea, Bacteria, Arabidopsis thaliana, Saccharomyces cerevisiae, Schizosaccharomyces pombe, Encephalitozoon cuniculi, Drosophila melanogaster, Homo sapiens, chloroplasts and mitochondria. All sequences revealed long-range power-law correlations almost on the entire observable scale. The local correlation coefficient shows close to random correlations on the scale of a few base pairs, a maximum from 40-3400 bp, and often a region of one or more second maxima from 10^5-3x10^5 bp. This multi-scaling behaviour is species specific and can be explained by a block organization of genomes. Within this multi-scaling behaviour an additional fine-structure is present and attributable to the codon usage in all except the human sequences. Here it is connected to nucleosomal binding. Computer generated random sequences assuming a block organization, the codon usage and nucleosomal binding agree with these results. Mutation by simulated sequence reshuffling destroyed all correlations, thus their stability seems evolutionary tightly controlled and connected to the spatial genome organization. On large scales the sequence correlations agree very well with the three-dimensional folding of the 30 nm chromatin fibre into the Multi-Loop-Subcompartment (MLS) model, in which ~100 kbp loops form rosettes, connected by a linker, within chromosomes.

Keywords:

Genome, genomics, genome organization, genome architecture, structural sequencing, architectural sequencing, systems genomics, coevolution, holistic genetics, genome mechanics, genome function, genetics, gene regulation, replication, transcription, repair, homologous recombination, simultaneous co-transfection, cell division, mitosis, metaphase, interphase, cell nucleus, nuclear structure, nuclear organization, chromatin density distribution, nuclear morphology, chromosome territories, subchromosomal domains, chromatin loop aggregates, chromatin rosettes, chromatin loops, chromatin fibre, chromatin density, persistence length, spatial distance measurement, histones, H1.0, H2A, H2B, H3, H4, mH2A1.2, DNA sequence, complete sequenced genomes, molecular transport, obstructed diffusion, anomalous diffusion, percolation, long-range correlations, fractal analysis, scaling analysis, exact yard-stick dimension, box-counting dimension, lacunarity dimension, local nuclear dimension, nuclear diffuseness, parallel super computing, grid computing, volunteer computing, Brownian Dynamics, Monte Carlo, fluorescence in situ hybridization, confocal laser scanning microscopy, fluorescence correlation spectroscopy, super resolution microscopy, spatial precision distance microscopy, auto-fluorescent proteins, CFP, GFP, YFP, DsRed, fusion protein, in vivo labelling.
Literature References


