

From current bacterial genomes to the RNA world

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Introduction

In a previous work it was well established that bacterial chromosomes exhibit an inverse bilateral symmetry (IBS), which seems to be a universal type of symmetry in Eubacteria [1]. The IBS observed in whole bacterial chromosomes constitutes an organizing principle that permits a better understanding of the scaling properties of n-tuples [2], and more importantly it allows us to examine hypotheses about the origin of bacterial chromosomes. Herein we test the hypothesis that one half of the chromosome begat the other via an ancient whole genome duplication in order to generate IBS.

[1] Sánchez J. & José M.V. Biochem. Biophys. Res. Comm. 299: 126-134 (2002).

[2] José M.V., et al. Physica A, (2004). 351 : 477-498 (2005).

Methods: Using the 16 codons proposed for the primeval comma-less code (codons of the type RNY) and eliminating the remaining 48 codons from several eubacterial genomes such as *Borrelia burgdorferi*, *Escherichia coli*, *Bacillus subtilis* and *Mycoplasma genitalium*, we generated cumulative position plots of each codon and its complementary in order to test for the presence of IBS. The scaling properties of the distance series of each codon in the whole genomes and in the comma-less genome were analyzed via a renormalization group approach from which the Hurst exponent and hence, the fractal dimension were obtained.

The frequency distributions of codons, triplets and amino acids from the complete genomes as well as the genomes of the RNA world are calculated and discussed.

Results: We have two noteworthy findings: 1. There is IBS in the comma-less genome and 2. The scaling properties of the distance series of codons from the comma-less genome turned out to be identical or very close to those of the whole present genomes.

CONCLUSIONS

1. The RNA comma-less code consists of 16 codons that specify 8 aminoacids (then this code shows a slight degeneracy). Considering that the mechanisms of translation were less than perfect, the three reading frames of the RNA primeval code specify for 17 amino acids.
2. **There is Inverse Bilateral Symmetry (IBS) in the comma-less genome.**
3. When other 16 codons were sampled at random from the complete bacterial chromosomes they did not displayed IBS. Therefore, it seems that the

Primeval Comma-less Code is the only one that retains this type of symmetry.

4. The scaling properties of the distance series of codons from the comma-less genome turned out to be identical or very close to those of the whole present genomes.
5. The distribution of distances for each of the 16 codons showed a power law fractal behavior with no oscillatory behavior as the ones obtained with the original chromosome. All of the amino acids encoded by the RNA comma-less showed a non-oscillatory decaying pattern as function of distance. Then the slight degeneracy of the RNA genome is not the reason of the rhythmical period three oscillations of the distributions of amino acids, triplets or codons observed in the complete present bacterial genomes.
6. We reject the hypothesis that one half of the chromosome gave rise to the other half. Rather IBS existed in the RNA world primeval code and the scaling properties of today chromosomes may be relic dynamic patterns of the primeval bacterial chromosomes.
7. The resulting RNY genomes obtained from different bacteria are of relevance not only for studying the origin of life but also for generating minimal genomes endowed with the properties of life.