The effects of confinement on the structure of the mitochondrial DNA from trypanosomes

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Abstract

Trypanosomatid parasites, trypanosoma and lishmania, are the cause of disease and death in many third world countries. One of the most unusual features of these organisms is the 3 dimensional organization of their mitochondrial DNA into maxi and minicircles. In some of these species minicircles are confined into a small volume and are interlocked forming a gigantic network. How this network was selected during evolution and how it is maintained, replicated and segregated is mostly unknown. Here we investigate the effects of the confinement on the topology of the network. We investigate a simplified model where randomly oriented minicircles are placed on the plane with their centers on the vertices of the simple square lattice. For completeness the formation of networks over a bounded region and over the entire plane was considered. We analytically show that a finite positive critical percolation density exists and that the probability of a saturated network forming (meaning all the minicircles form one unsplittable link) approaches one exponentially as the density increases when the minicircle field is bounded. We carried out numerical studies to obtain numerical estimates of these quantities and also to estimate biologically relevant properties of the network. When these results are considered in the context of the structure of k-DNA then we find that the formation of the network is an expected result provided that strand passage enzymes (such as type II topoisomerases) are present. We also provide estimates for the average and variation of the degree of these networks.

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