

Abstract Submitted  
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**The Fitness of Genomic Order**<sup>1</sup> QIUCEN ZHANG, SAURABH VYAWAHARE, ROBERT AUSTIN, Department of Physics, Princeton University — Most bacteria have a single circular chromosome that can range in size from 160,000 to 12,200,000 base pairs. Considering the typical gene density, i.e. 1 gene per 1,000 base pairs, both the number of genes and the ways to arrange are huge. Intuitively, the arrangement of genes on the circle is not important if all of them can be replicated. However, there is typically one origin of replication, and when bacteria is attacked by genotoxic stress during replication, the whole replication process can not be finished. As a result, which gene is replicated first, which is second, ..., becomes very important. Experimentally, we found a broad increase of DNA copy number near the origin of replication (OriC) of bacteria E.coli (~3200 genes) under genotoxic stress. Since the genes near OriC are mostly efflux pump genes, we propose that there is fitness advantage for those rapid stress response genes got replicated first, because they can facilitate the replication of the rest of genome. Similar to bacterial evolution to present genomic order, in the somatic evolution of cancer, genomic shuffling was also frequently observed, especially under genotoxic chemotherapy. Such rearrangement of genome can be viewed as a journey to optimal point in the rugged fitness landscape of genomic order.

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