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Commentary

The Transformation of Bacterial Genome Design

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ABOUT THE STUDY

When bacteria and eukaryotes are subjected to genetic drift, their genome architecture evolves in opposing ways, owing to the fact that bacteria have a mutational bias that deletes redundant sequences, whilst eukaryotes have a mutational bias that favors big insertions. Non-functional sequences, including as repetitive sequences and transposable elements, are added to eukaryotic genomes to expand them, whereas functional accessory genes are acquired and lost to change the size of the bacterial genome. Because of these features, eukaryotes with equal amounts of genes can have radically varied genome sizes, whereas gene counts scale linearly with genome size in bacteria. However, certain bacterial genomes, particularly those of species that have recently been associated with hosts.

Accumulate pseudogenes and mobile elements, giving them a low gene content compared to their genome size. After long-term connection with hosts, these non-functional sequences are gradually eroded and deleted, resulting in obligate symbionts having the shortest genomes of any cellular entity. Complex and diverse mechanisms impact the architecture of bacterial genomes, although for most bacterial species, genome size is driven by a non-adaptive process, namely genetic drift combined with a mutational bias toward deletions. As a consequence, bacteria with minimal effective population numbers have the smallest genomes. Despite having enormous population densities, certain marine bacteria use selection rather than drift to shrink genome size in response to metabolic restrictions in their nutrient-limited habitat.

Microarrays (or microchips) are a recently developed genomic technology and are listed as one of 10 breakthrough technologies, along with genomics. Microarray-based genomic technologies have changed genetic study of biological systems in the same way that microprocessors have revolutionized computation. Microarray technology is a powerful new technique that allows researchers to examine a living cell in various physiological stages from a complete and dynamic molecular standpoint. The widespread, routine use of genomic technologies will shed light on a variety of important research areas, including how cells grow, differentiate, and evolve; medical challenges such as pathogenesis, antibiotic resistance, and cancer; agricultural issues such as seed breeding and pesticide resistance; biotechnological challenges such as drug discovery; and environmental contamination remediation.

Even before golden period of genome sequencing, the overall structure and organization of bacterial genomes were well understood. It was known that bacterial genomes varied in size by at least an order of magnitude, and that genome size within a bacterial species could vary significantly that bacterial genomes typically comprised one circular chromosome but frequently harbored extra chromosomal elements in the form of plasmids or phages and that base composition was relatively uniform along the chromosome but highly variable across species, ranging from 14% to 80% G+C that bacterial genomes mostly consisted of functional protein-coding regions, with little non-coding or intervening sequences that genetic maps (and thus gene order and gene content) remained fairly stable among related species of that genome architecture could be altered by insertions, duplications, inversions, and translocations, which were aided in part by mobile elements.

Since bacteria could acquire Horizontal Gene Transfer (HGT) on a regular basis, the genome contents and architecture of closely related strains within a bacterial species can differ in ways that eukaryotes cannot. The gene repertoires of members of the same eukaryote species seldom differ, and HGT rarely results in the acquisition of functional sequences in eukaryotes. These significant distinctions between bacteria and eukaryotes contribute to the development of genome sizes in opposing directions when subjected to drift, in addition to their separate biases toward insertions and deletions. When subjected to novel selection pressures, bacterial genomes grow in size by aggregating adaptive gene modules, whereas eukaryotic genomes grow in size by amassing enormous quantities of non-functional DNA.

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