

A Short Note on Bacterial Genomes

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Bacterial genomes are generally smaller and fewer variant in size among species in comparison with genomes of eukaryotes. Bacterial genomes can range in size anywhere from about 130 kbp to over 14 Mbp. A study that included, but wasn't limited to, 478 bacterial genomes, concluded that as genome size increases, the amount of genes increases at a disproportionately slower rate in eukaryotes than in non-eukaryotes. Thus, the proportion of non-coding DNA goes up with genome size more quickly in non-bacteria than in bacteria. This is often according to the very fact that the majority eukaryotic nuclear DNA is non-gene coding, while the bulk of prokaryotic, viral, and organellar genes are coding. Immediately, we've genome sequences from 50 different bacterial phyla and 11 different archaeal phyla. Second-generation sequencing has yielded many draft genomes (close to 90% of bacterial genomes in GenBank are currently not complete); third-generation sequencing might eventually yield an entire genome during a few hours. The genome sequences reveal much diversity in bacteria. Analysis of over 2000 *Escherichia coli* genomes reveals an *E. coli* core genome of about 3100 gene families and a complete of about 89,000 different gene families. Genome sequences show that parasitic bacteria have 500–1200 genes, free-living bacteria have 1500–7500 genes, and archaea have 1500–2700 genes. A striking discovery by Cole et al. described massive amounts of gene decay when comparing *Mycobacterium leprae* to ancestral bacteria. Studies have since shown that several bacteria have smaller genome sizes than their ancestors did. Over the years, researchers have proposed several theories to elucidate the overall trend of bacterial genome decay and therefore the relatively small size of bacterial genomes. Compelling evidence indicates that the apparent degradation of bacterial genomes is owed to a deletional bias.

Genomic reduction

Molecular phylogenetics has revealed that each clade of bacteria with genome sizes under 2 Mb was derived from ancestors with much larger genomes, thus refuting the hypothesis that bacteria evolved by the successive doubling of small-genomed ancestors. Recent studies performed by Nilsson et al. examined the rates of bacterial genome reduction of obligate bacteria.

Bacteria were cultured introducing frequent bottlenecks and growing cells in serial passage to scale back gene transfer so on mimic conditions of endosymbiotic bacteria. The info predicted that bacteria exhibiting a one-day generation time lose as many as 1,000 kbp in as few as 50,000 years (a relatively short evolutionary time period). Furthermore, after deleting genes essential to the methyl-directed DNA mismatch repair (MMR) system, it had been shown that bacterial genome size reduction increased in rate by the maximum amount as 50 times. These results indicate that genome size reduction can occur relatively rapidly, and loss of certain genes can speed up the method of bacterial genome compaction.

This is to not suggest that each one bacterial genomes are reducing in size and complexity. While many sorts of bacteria have reduced in genome size from an ancestral state, there are still an enormous number of bacteria that maintained or increased genome size over ancestral states. Free-living bacteria experience huge population sizes, fast generation times and a comparatively high potential for gene transfer. While deletional bias tends to get rid of unnecessary sequences, selection can operate significantly amongst free-living bacteria leading to evolution of latest genes and processes.

Traits introduced through lateral gene transfer

Antimicrobial resistance genes grant an organism the power to grow its niche, since it can now survive within the presence of previously lethal compounds. Because the benefit to a bacterium earned from receiving such genes are time- and space-independent, those sequences that are highly mobile are selected for. Plasmids are quite mobilizable between taxa and are the foremost frequent way by which bacteria acquire antibiotic resistance genes.

Adoption of a pathogenic lifestyle often yields a fundamental shift in an organism's niche. The erratic phylogenetic distribution of pathogenic organisms implies that bacterial virulence may be a consequence of the presence, or obtainment of, genes that are missing in avirulent forms. Evidence of this includes the invention of huge 'virulence' plasmids in pathogenic *Shigella* and *Yersinia*, also because the ability to bestow pathogenic properties onto *E. coli* via experimental exposure to genes from other species.

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