

Editorial on Bacterial Genome Architecture

Volker Kroman*

Department of Veterinary and Animal Sciences, University of Copenhagen, Copenhagen, Denmark

Bacterial genomes are typically smaller and have less variation in size between organisms when compared to eukaryotic genomes. In two essential respects, bacteria's genome architecture differs from that of eukaryotes, firstly, the number of functional genes in a genome is inversely proportional to the size of the genome in bacteria, and those genes are organized into operons. As of now, we have genome sequences from different 50 bacterial phyla and 11 archaeal phyla. Bacterial genome sequences show a great deal of variation. When bacteria and eukaryotes are subjected to genetic drift, their genome architecture evolves in opposite directions, owing to the fact that bacteria have a mutational bias that deletes redundant sequences, whereas eukaryotes have a bias against massive insertions. Non-functional sequences, such as repetitive sequences and transposable elements, are added to eukaryotic genomes to expand them, while functional accessory genes are acquired and lost to change the size of bacterial genomes, because of these characteristics, eukaryotes with identical numbers of genes may have significantly different genome sizes, while gene number scales linearly with genome size in bacteria. The architecture of bacterial genomes is structured by a variety of complex and diverse processes, but genome size is dominated by a non-adaptive mechanism in most bacterial organisms, namely genetic drift combined with a mutational bias toward deletions in most bacterial organisms. Many of these characteristics of bacterial genomes differ from those of eukaryotic genomes in which they are often partitioned into several linear

chromosomes and are usually much larger due to increases in gene number and proliferation of non-coding and repetitive DNA. When it comes to the number of functional genes in eukaryotic organisms, genome size is irrelevant. The strong association between the number of genes and the size of the genome in bacteria, on the other hand, makes the size of bacterial genomes an important subject for study and discussion. Bacteria are commonly regarded as simple organisms due to their unicellularity and uniform genome structure. However, many of their populations' most essential characteristics remain unknown, making it difficult to assess and measure microevolutionary processes. Bacteria began as free-living species, according to the general patterns of bacterial evolution. Some bacteria evolved into pathogens and symbionts as a result of evolutionary paths. Since they have accumulated and accepted more deleterious mutations due to drift, bacterial organisms that are subjected to less successful selection have smaller genomes. This is particularly apparent in pathogen and symbiont genomes, where their host-associated lifestyle both increases the fixation of slightly deleterious mutations and makes several previously useful genes redundant in the nutrient-rich host environment, resulting in a large number of non-essential regions that are then deleted by the prevalent mutational bias against deletions. Natural selection is the primary force preventing gene erosion and elimination, resulting in a high density of usable sequences in both large and small bacterial genomes. Of the three classes, obligate bacterial symbionts or pathogens have the smallest genomes and the fewest pseudogenes. The relationship between bacterial lifestyles and genome size raises concerns about bacterial genome evolution mechanisms. Several hypotheses have been proposed to understand the patterns of genome size evolution in bacteria.

Correspondence to: Volker Kroman, Department of Veterinary and Animal Sciences, University of Copenhagen, Copenhagen, Denmark, E-mail: volerk@ku.dk

Received: May 7, 2021; **Accepted:** April 22, 2021; **Published:** May 29, 2021

Citation: Kroman A. (2021) Editorial on Bacterial Genome Architecture. Clin Microbiol. 10:203

Copyright: © 2021 Kroman A. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.