

“Non-vertical inheritance in the evolution of bacteria”

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Abstract

Genetic variation is the fuel of evolution. Without variation no evolutionary change can occur. Traditionally, the generation of variation has been equated to mutation and this is indeed the ultimate source of changes in nucleotide sequences. However, most microorganisms acquire variation from other sources. Horizontal/lateral gene transfer (HGT) and recombination have provided and currently provide many bacteria with new genes and variants that can be used to explore the adaptive landscape. The availability of complete genome sequences of bacterial species has allowed a detailed analysis of the role of HGT and recombination in their evolutionary history but also of their involvement in shaping the genetic variability of others, most notably pathogens. This has important consequences from a practical perspective, because one of the most relevant current evolutionary process in bacteria is the spread of resistance to antimicrobial drugs. Most genetic determinants of AMR are readily transferred between and within species. Recombination also played a relevant role in the initial stages of adaptation to a new host, the human species, resulting in the emergence of new pathogens, such as *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae* or *Treponema pallidum*. My research group applies population genomics and molecular evolution tools to analyze the genomes of these and other bacterial pathogens. I will review some of our major findings and how we used the technological and analytical advances to bridge the gap between basic and applied scientific knowledge.