

## ABSTRACT

The conservation of gene order is a genomic measure that can be used to analyze the relationships between prokaryotes and the evolutionary forces shaping their genomes. Gene organization is significantly conserved in some genomic regions, and further studies are required to explain why this is the case.

## INTRODUCTION

In the last decade, a lot of research has been done to understand the evolutionary origins of gene order conservation (GOC) in prokaryotes. Among the many explanations for GOC, the most prominent is the observation that GOC is conserved throughout the eukaryotic genome and that this conserved GOC is responsible for the evolution of many genes. The GOC hypothesis has been proposed as a potential explanation for the evolution of many genes, including the eukaryotic genome, and the molecular mechanisms involved in the evolution of GOC are still not understood. The most recent work on the evolution of GOC has focused on the evolution of the C-terminal gene and its regulatory role in the regulation of gene expression. However, the GOC hypothesis is also considered to be a candidate for the origin of the prokaryotic genomes that have been fully sequenced can be used to study the relationships between organisms by examining the complete set of genes. Genomic properties are considered a practical solution to avoid the challenges of classical molecular phylogenies, as they can provide valuable information about the function and interactions of these genes in both natural and synthetic environments. Close phylogenetic distances are typically associated with well-preserved gene order, which is easily lost during evolution due to low conservation rates in closely related species. This loss can also lead to the disruption of operons, in some cases wiping them out entirely. Nevertheless, there are some instances of well-preserved gene clusters that exist in divergent species. The best examples are the genes for ribosomal proteins and the *dcw* cluster. Lathe and co-workers recently discovered genomic regions where gene order is highly conserved, with the general trend being to keep the genetic information closer to the original location and ordering of the relevant genes. This suggests that selective selection for gene location or ordering may be present in certain cases. However, the structural and common regulation cannot be easily account for this phenomenon. Conservation of gene order can be achieved through three factors: recent divergence, lack of destruction of ordered order by the species; lateral gene transfer due to a block of genes; and importance of the cluster's integrity to cell fitness. Recommendations for selection in determining gene ordering, such as aiding the interaction of proteins expressed by the cluster's genes, advocating for lateral gene transfer, or co-localizing of mRNAs in the same area of the cell, are suggested. However, these explanations are not mutually exclusive. Studies of how the *dcw* cluster formed within a few weeks suggest that maintaining gene order within the group may be linked to cellular morphology and therefore identifying phenotype. Evolution is increasingly recognizing the significance of gene order: even though some genes are now more conserved than their sequences, much of the conservation remains at relatively small phylogenetic distances—such as between *Escherichia coli* and *Bacillus subtilis*—conservation provides valuable information about how organisms are related, and whether events like lateral gene transfer contribute to the evolution of genomes. My current research on gene order conservation in prokaryotes involves examining the extent and characteristics of its conservation. Is there a uniformity in the conservation of gene sequences across all prokaryotic species, and are the conserved regions located

within the genomes?

## CONCLUSION

Remarkable conclusions When organisms are phylogenetically closely related, gene order is a relatively ambiguous genomic trait. However, the loss of conservation quickly, possibly to tier above other genetic or genomic traits, may indicate that selection pressures have kept them together (especially in environments where lateral gene transfer may not have been as effective as the operon governing assembly), but other reasons may justify reconsidering alternative explanations for how gene ordering might act within certain cases. The existence of units larger than operons seems to support other theories. Gene order conservation is a useful tool for determining relationships between organisms as it is not influenced by parameters that affect other genomic measures, such as the content of unique genes. Genomic properties have been proposed as alternatives to classical molecular phylogenies due to their ability to measure global features. However, there are no options available today that require information from other sources or can be integrated into existing gene expression measures.