Proposal of conceptual model for the mechanism underpinning evolution of operon as pathway gene organizer in bacterial genome

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Abstract

Genes of the same metabolic or signaling pathway are typically organized as concatenated genes on an operon in prokaryotic system. However, the same is not true for genes belonging to a pathway in eukaryotic cells. Specifically, genes of the same pathway in eukaryotic cells could be separated by significant distance along the genome, and may even be on different chromosomes. Thus, what accounts for the observed differences in gene organization, and more importantly, what is the biological basis that underpin the organization of genes of the same pathway into operon in prokaryotic cells? The questions are tough to answer from the bioinformatic perspective as evidence for the definition of operon might have been erased by evolution through the eons. This is because stretches of nucleotides encoding less important information are more vulnerable to mutations and are less well conserved. Thus, one plausible approach is to observe how a bacterium such as *Escherichia coli* evolve the ability to degrade or metabolize a xenobiotic through a pathway comprising multiple genes. Such evolved pathways of multiple concatenated genes might be encoded on plasmids that enter the cell rather than on the chromosome since multiple copies of plasmids provide more opportunities for diversification of gene function and capabilities compared to single gene copy in the chromosome. Hence, different plasmids might be distributed to different *E. coli* cells; thereby, rendering different levels of fitness for survival under xenobiotic challenge in the environment, where the fittest strain would dominate the population. Following selection of specific gene variant with highest efficacy, genetic information on the plasmid could be co-opted and integrated into the genome of phages that infect the cell. The genetic information subsequently becomes integrated into the chromosome through lysogeny of phage. This process would theoretically leave behind lysogeny markers in the genome, which might still be available for bioinformatic interrogation despite possibility of erasure of sequence through evolution. Integration of plasmid into the phage genome would also enable broader spread of the evolved gene amongst bacterial species in the same environment. Collectively, understanding the provenance of concatenation of pathway genes into a single operon under the control of a common promoter remains a difficult challenge in fundamental microbiology due to the lack of clues at the sequence level for bioinformatic analysis. However, one possibility for guiding the evolution of operon could be the evolution of genes on co-opted environmental plasmids for tackling a xenobiotic challenge, followed by integration of plasmid gene into phage genome and their subsequent integration into the bacterial chromosome through lysogeny. Hence, lysogeny markers near operons in the bacterial genome that have not been erased through evolution would offer first clues to the plausibility of the above model.

Keywords: operon, prokaryotic cell, eukaryotic cell, bacteriophage, concatenated genes, plasmid, lysogeny, lysogeny markers, genome integration, gene organization,

Subject areas: molecular biology, bioinformatics, genomics, microbiology, genetics,

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Conflicts of interest

The author declares no conflicts of interest.

Funding

No funding was used in this work.

PeerJ Preprints | https://doi.org/10.7287/peerj.preprints.27767v1 | CC BY 4.0 Open Access | rec: 30 May 2019, publ: 30 May 2019