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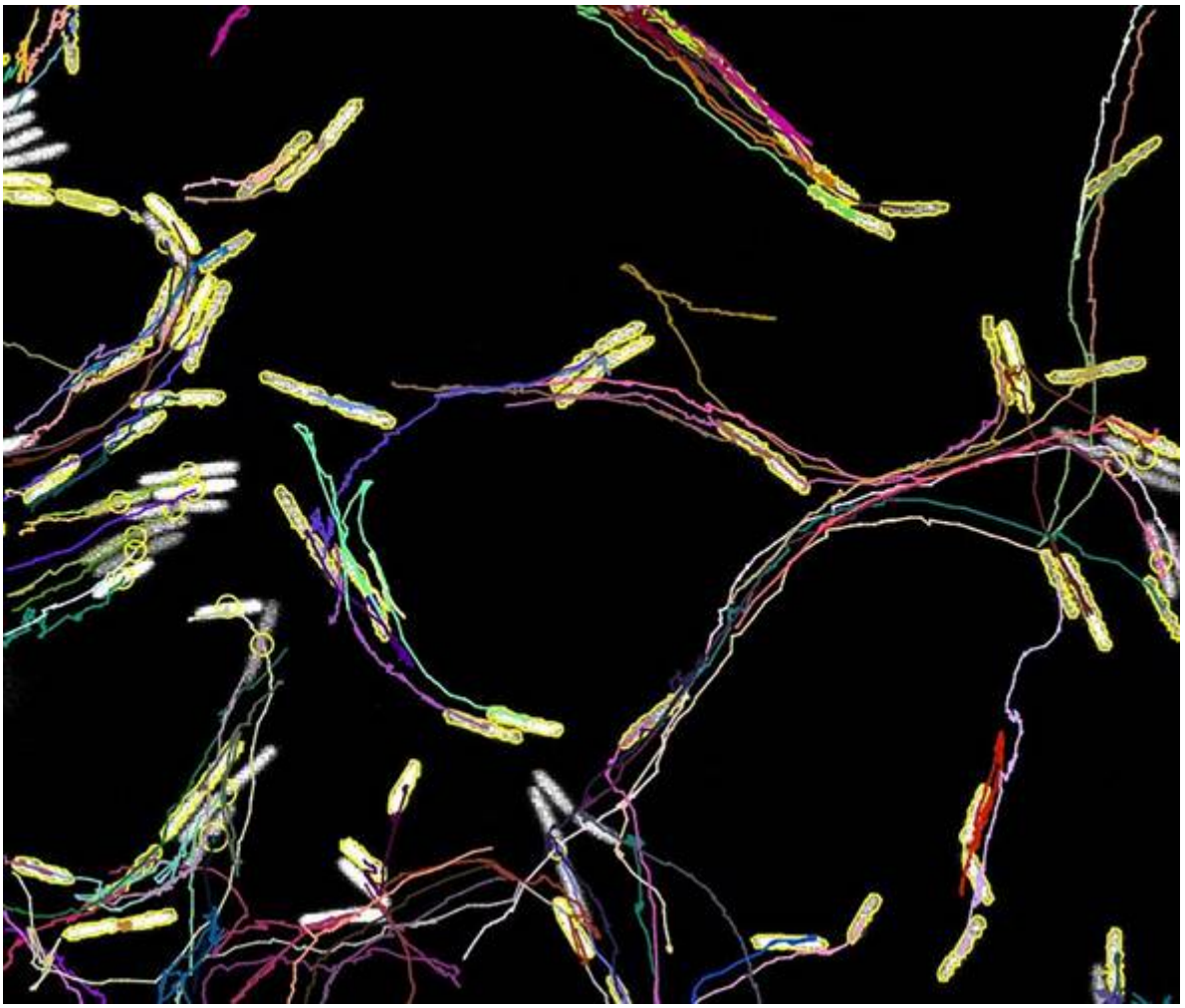

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RELOCALIZATION IMPACT OF GENES INVOLVED IN TRANSLATION AND TRANSCRIPTION ON Vibrio cholerae´s PHYSIOLOGY

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Growth rate is a fundamental parameter in bacterial physiology that varies notably among microorganisms. The genetic factors that determine it are still unknown. Bioinformatic studies show that the chromosomal location of genes encoding for the genetic information flow (i.e. transcription and translation) is biased towards the origin of replication (oriC) in fast-growing bacteria. This may influence their physiology and evolution. Gene order along the chromosomes could play a role: in fast-growing bacteria, the genes encoding ribosomal proteins (RP) and RNA polymerase (RNAP) are located near the origin of replication (oriC). In optimal growth conditions, fast-growing bacteria overlap replication rounds, a process called multi-fork replication (MFR). Hence, genes close to the oriC benefit from a higher dosage during exponential growth compared to those in the terminal region (ter), increasing their global expression. The positional bias of RNAP and RP genes maximize their expression. In parallel, essential genes are mostly located in the replication leading strand to avoid deleterious head-on collisions between transcription and DNA duplication machinery. We studied the role of genome localization of genes involved in translation and transcription processes in Vibrio cholerae. For this purpose, we systematically relocated the S10-spec-? (S10) locus, encoder to half of the ribosomal proteins, and the *rplKAJL-rpoBC* (*rpoBC*) locus, which encodes the catalytic core of RNA polymerase, to different chromosomal positions. Specifically, we analyzed the impact of individually relocating each locus and attempted to simultaneously relocate both loci. We also switched these genes from leading to laggind strand to maximize replication-transcription conflicts. Our results suggest that relocation of each of the loci of interest toward the terminal chromosomal region (ter) affects generation time (GT) due to a decrease in its gene dosage during the exponential growth phase. Simultaneous relocalization of both loci generated an additive effect. However, double S10-rpoBC relocalizations were only viable in genetic contexts involving secondary mutations. For instance, we detected, the complete deletion of the Toxin Corregulated Pilus (tcp) in two out of four clones. Also switching from leadin to lagging strand resulted in reduction of growth rate in the case of *rpoBC* locus but not for S10. We believe that the loci under study are examples of many genes whose chromosomal position affects cellular function. Understanding how the primary structure of the chromosome conditions cellular physiology could help us comprehend bacterial pathogenesis and lead to the development of biotechnological applications.

Palabras clave: V. cholerae - BACTERIAL GENOMICS - CHROMOSOMAL STRUCTURE - PATHOGENESIS