Understanding How Viral Genome Number Drives Cell Fate

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Infection of *E. coli* cells by the virus lambda is a paradigm for cell fate decisions, processes where cells select and transition to stable states. In the case of lambda, the infected cells choose between two fates: rampant viral replication leading to cell death (lysis), or viral dormancy and passive replication with the host cell (lysogeny). Decades of experiments have uncovered the genetic network and multiple external factors that control the decision. Biochemical models of the lambda circuit predict a simple scaling of the probability of lysogeny with viral concentration inside the cell. However, single cell experiments have revealed a more complicated scaling behavior. We have identified multiple processes that previous models have tended to ignore, and which might rectify the discrepancy between theoretical predictions and experimental results. These include the bursty kinetics of gene expression, supercoiling-driven looping of viral DNA, partial dosage compensation as a result of gene network topology, and viral DNA replication. By constructing models incorporating these features, we hope to elucidate the mechanisms by which viral copy number influences the lysis/lysogeny decision and gain broader insights into how gene copy number affects cell fate choices in diverse biological systems.

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