
Designing replicons: rules from the maintenance functions

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Abstract

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Beside unique main chromosomes, bacterial genomes contain a plethora of secondary replicons differing in copy number, composition and size. They carry various functions involved in their maintenance: some are mandatory, such as replication origins and a mean of resolving dimeric forms, while others are accessory, such as addiction modules or active partitioning systems. Using enterobacteria as models and a combination of bioinformatic and experimental approaches, we are attempting to define the rules and reasons for the distribution of maintenance function, allowing to design *a la carte* replicons. I will summarize the recent advances and focus on the role of replicon size in determining partitioning and dimer resolution functions.

Keywords: replicons, maintenance, segregation

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