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Sommario/riassunto	DNA replication, a central event for cell proliferation, is the basis of biological inheritance. Complete and accurate DNA replication is integral to the maintenance of the genetic integrity of organisms. In all three domains of life, DNA replication begins at replication origins. In bacteria, replication typically initiates from a single replication origin (oriC), which contains several DnaA boxes and the AT-rich DNA unwinding element (DUE). In eukaryotic genomes, replication initiates from significantly more replication origins, activated simultaneously at a specific time. For eukaryotic organisms, replication origins are best characterized in the unicellular eukaryote budding yeast Saccharomyces cerevisiae and the fission yeast Schizosaccharomyces pombe. The budding yeast origins contain an essential sequence element called the ARS (autonomously replicating sequence), while the fission yeast origins consist of AT-rich sequences. Within the archaeal domain, the multiple replication origins have been identified by a predict-and-verify approach in the hyperthermophilic archaeon Sulfolobus. The basic structure of replication origins is conserved among archaea, typically including an AT-rich unwinding region flanked by several short repetitive DNA sequences, known as origin recognition boxes (ORBs). It appears that archaea have a simplified version of the eukaryotic replication apparatus, which has led to considerable interest in the

archaeal machinery as a model of that in eukaryotes. The research on replication origins is important not only in providing insights into the structure and function of the replication origins but also in understanding the regulatory mechanisms of the initiation step in DNA replication. Therefore, intensive studies have been carried out in the last two decades. The pioneer work to identify bacterial oriCs in silico is the GC-skew analysis. Later, a method of cumulative GC skew without sliding windows was proposed to give better resolution. Meanwhile, an oligomer-skew method was also proposed to predict oriC regions in bacterial genomes. As a unique representation of a DNA sequence, the Z-curve method has been proved to be an accurate and effective approach to predict bacterial and archaeal replication origins. Budding yeast origins have been predicted by Oriscan using similarity to the characterized ones, while the fission yeast origins have been identified initially from AT content calculation. In comparison with the in silico analysis, the experimental methods are time-consuming and labor-intensive, but convincing and reliable. To identify microbial replication origins in vivo or in vitro, a number of experimental methods have been used including construction of replicative oriC plasmids, microarray-based or high-throughput sequencing-based marker frequency analysis, two-dimensional gel electrophoresis analysis and replication initiation point mapping (RIP mapping). The recent genome-wide approaches to identify and characterize replication origin locations have boosted the number of mapped yeast replication origins. In addition, the availability of increasing complete microbial genomes and emerging approaches has created challenges and opportunities for identification of their replication origins in silico, as well as in vivo and in vitro.