Measuring the time dependent rate of replication origin activation in a single *Saccharomyces cerevisiae* cell by using population dynamics

The complete and faithful transmission of eukaryotic genome to daughter cells involves the timely duplication of mother cell's DNA. DNA replication starts at multiple chromosomal positions called replication origin. From each activated replication origin two replication forks progress in opposite direction and duplicate the mother cell's DNA. While it is widely accepted that in eukaryotic organisms replication origins are activated in a stochastic manner, little is known on the sources of the observed stochasticity. It is often associated to the population variability to enter S phase. We extract from a growing *Saccharomyces cerevisiae* population the average rate of origin activation in a single cell by combining single molecule measurements and a numerical deconvolution technique. We show that the temporal profile of the rate of origin activation in a single cell is similar to the one extracted from a replicating cell population. Taking into account this observation we exclude the population variability as the origin of observed stochasticity in origin activation. We confirm that the rate of origin activation increases in the early stage of S phase and decreases at the latter stage. The population average activation rate extracted from single molecule analysis is in prefect accordance with the activation rate extracted from published micro-array data, confirming therefore the homogeneity and genome scale invariance of dynamic of replication process. All these observations point toward a possible role of replication fork to control the rate of origin activation.

Nucleosome
Initiator factor
Replication origin
Chromatin remodelling factor