Abstract

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Gene expression refers to the sum of processes that enable cells to control their complement of RNA, and the study of gene expression has been spurred by genome-wide techniques such as microarrays and chromatin immunoprecipitation. Placing these data within a cellular context to reveal the underlying mechanisms of gene regulation has been a central challenge in the field of systems biology. In recent years, through parallel advances in microscopy, fluorescent probe development, and computational modeling, it has become possible to describe gene expression in a fundamentally different way: one can now directly observe single molecules of RNA in living and fixed cells using the fluorescence microscope. In this talk, I will describe the use of this single-molecule approach to study transcription kinetics of the GAL10 locus in budding yeast, which is regulated by sugar availability. Transcription is observed to occur in bursts of high activity followed by periods of inactivity, each lasting several minutes. This stochastic, punctate behavior results in 'noise' in gene expression and is not visible in population studies, which instead give the impression of a gradual response to sugar availability. I will describe recent results on the role of non-coding RNA in transcriptional regulation. Genomic data indicates that eukaryotic genomes are ubiquitously transcribed, but the function of these RNAs is largely unknown. Our results indicate that noncoding RNA displays different behavior during repression and activation, suggesting multiple roles, even at the same locus.