

***Linking Stochastic Fluctuations in Chromatin Structure and Gene Expression***

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2014/05/02

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**Abstract:**

The number of mRNA and protein molecules expressed from a single gene molecule fluctuates over time. These fluctuations have been attributed, in part, to the random transitioning of promoters between transcriptionally active and inactive states, causing transcription to occur in bursts. However, the molecular basis of transcriptional bursting remains poorly understood. By electron microscopy of single *PHO5* gene molecules from yeast, the authors show that the “activated” promoter assumes alternative nucleosome configurations at steady state, including the maximally repressive, fully nucleosomal, and the maximally non-repressive, nucleosome-free, configuration. The authors demonstrate that the observed probabilities of promoter nucleosome configurations are obtained from a simple, intrinsically stochastic process of nucleosome assembly, disassembly, and position-specific sliding; and we show that gene expression and promoter nucleosome configuration can be mechanistically coupled, relating promoter nucleosome dynamics and gene expression fluctuations. Together, their findings suggest a structural basis for transcriptional bursting, and offer new insights into the mechanism of transcriptional regulation and the kinetics of promoter nucleosome transitions.

**References:**

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