Journal Club Abstract Research Center for Mathematics on Chromatin Live Dynamics (RCMCD)

Capturing Binding Location and Speed of Chromatin Binding Proteins Yasunori Horikoshi

Poorey, K, Viswanathan, R, Carver, MN, Karpova, TS, Cirimotich, SM, McNally, JG, Bekiranov, S, Auble, DT. Measuring chromatin interaction dynamics on the second time scale at single-copy genes. Science 2013;342(6156):369-72.

Abstract: The chromatin immunoprecipitation (ChIP) assay is widely used to capture interactions between chromatin and regulatory proteins, but it is unknown how stable most native interactions are. Although live-cell imaging suggests short-lived interactions at tandem gene arrays, current methods cannot measure rapid binding dynamics at single-copy genes. We show, by using a modified ChIP assay with subsecond temporal resolution, that the time dependence of formaldehyde cross-linking can be used to extract in vivo on and off rates for site-specific chromatin interactions varying over a ~100-fold dynamic range. By using the method, we show that a regulatory process can shift weakly bound TATA-binding protein to stable promoter interactions, thereby facilitating transcription complex formation. This assay provides an approach for systematic, quantitative analyses of chromatin binding dynamics in vivo.

References: (list the papers you are going to cite in the presentation)

1. Rhee, HS, Pugh, BF. Comprehensive genome-wide protein-DNA interactions detected at single-nucleotide resolution. Cell 2011;147(6):1408-19.

2. Suter, DM, Molina, N, Gatfield, D, Schneider, K, Schibler, U, Naef, F. Mammalian genes are transcribed with widely different bursting kinetics. Science 2011;332(6028):472-4.

3. Larson, DR, Zenklusen, D, Wu, B, Chao, JA, Singer, RH. Real-time observation of transcription initiation and elongation on an endogenous yeast gene. Science 2011;332(6028):475-8.