

BiophysTO Lunchtime Talks

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To Cluster or Not to Cluster: New insight into the segregation mechanism of high-copy bacterial plasmids

Plasmids play essential roles in bacterial metabolism, pathogenesis, and evolution, and are commonly engineered for recombinant protein synthesis and industrial fermentation. Deterring the persistence of harmful and enhancing the retention of beneficial plasmids require a better understanding of the fundamental mechanisms behind plasmid maintenance. The maintenance of high-copy number (hcn) plasmids within a colony of bacteria has been commonly thought to result from simple free diffusion and random segregation. Recent microscopy experiments, however, observed hcn plasmids clustering into discrete foci, which seemed to contradict this model, and hinted at an undiscovered active mechanism, as often found in low-copy number plasmids. To address this issue, we investigated the cellular organization of hcn plasmids (ColE1-like) in bacteria using quantitative localization microscopy in combination with DNA single-molecule fluorescence in situ hybridization (smFISH). We observed that, although many hcn plasmids aggregated into large clusters, a majority of the plasmids were randomly distributed throughout the bacteria, minus an excluded volume about the chromosomal DNA. Our results indicate that neither of the previous models are complete, and suggest a "mixed distribution model" of randomly diffusing plasmids and large clustered aggregates. We also found plasmids within the chromosomal volume of the cell, suggesting that the nucleoid may not fully exclude plasmids, and that the nucleoid may be more amorphous than previously thought.

Host: Dr. Josh Milstein

(Refreshments and pizza will be provided)

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Thursday, November 19, 2015 – 12:00 pm, noon
Davenport Room, Chemistry Building
(and via streaming to Davis Building 4001 UTM)