GENETICS, BIOINFORMATICS, AND SYSTEMS BIOLOGY COLLOQUIUM

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ORIGINS AND EVOLUTIONARY CONSEQUENCES OF GENOME STRUCTURE VARIATION

Structural variation is the major frontier for understanding the function of genomes. Although abundant theory has persisted for nearly a century, the massive proliferation of genomic technologies in the past decade has brought the proximate and ultimate causes of structural variation into focus. I will describe two ongoing efforts in my group where we address these questions using a blend of scalable computational methods and targeted experimental techniques. First, we performed a eukaryote-wide survey to identify the proximate molecular origins of new introns. Our team discovered that introner-elements, specialized transposons that encode their own splice sites, generate the vast majority of new introns across diverse eukaryotic genomes. Introner elements display remarkable molecular diversity indicating they have evolved convergently hundreds of times and are a general feature of eukaryotic genome evolution. Second, our team used an experimental approach to investigate the impacts of genome structure on gene expression patterns. Specifically, we produced synthetic chromosomal inversions on a tightly controlled genetic background. Although natural inversions are associated with hundreds of gene expression differences, synthetic inversions have virtually no effect. This suggests that linked genetic variation drives depression differences, but not the genome structure in itself.

Organization Committee: J. Gleeson, J. Sebat & BISB PhD Students
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