GENETICS, BIOINFORMATICS, AND SYSTEMS BIOLOGY COLLOQUIUM

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THURSDAY JANUARY 19
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"A COMMON GENOMIC ARCHITECTURE FOR INTERACTING WITH THE EXTERNAL WORLD"

The radiation of mammals at the extinction of the dinosaurs produced a plethora of new forms—as diverse as bats, dolphins, and elephants—in only 10–20 million years. Behind the scenes, adaptation to new niches is accompanied by extensive innovation in large families of genes that allow animals to contact the environment, including chemosensors, xenobiotic enzymes, and immune and barrier proteins. These large gene families share a common genomic organization and are often characterized by unusual modes of transcriptional regulation: they are clustered in tandem arrays in AT-biased isochores and exhibit tissue-specific and sometimes stochastic expression. Here, we use population genetic data and evolutionary analysis to examine the relationship between gene family diversification and genomic organization in mammals. First, we find that AT bias emerges as gene families expand in cis. Second, AT-biased, clustered gene families experience relatively low rates of de novo point mutation, and we suggest that multi-copy gene families have accrued high AT content due to relaxed selection compared to single-copy genes. Finally, we find that AT-biased, clustered gene families exhibit low rates of recombination and are depleted for binding of the recombination-seeding factor PRDM9. We posit that tolerance of point mutation and intolerance of recombination together result in depressed GC content of multi-copy versus single-copy genes. In turn, differential sequence content of gene blooms exerts a profound effect on their chromatin organization and transcriptional regulation.

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