IMEG Seminar Series

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Understanding the Unique Transcriptional Environment of the Mammalian Testis

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Meiotic prophase I is characterized by unique mechanisms of homolog pairing, synapsis, and recombination, which require large-scale changes in chromatin architecture. Events during prophase I are crucial to ensuring accurate homolog segregation at the first meiotic division and, as a result of this added complexity, prophase I is substantially extended compared to its mitotic counterpart. At the same time, during prophase I of meiosis, the germline transcriptome must also prepare for progression to the differentiation step of spermiogenesis after the cell has achieved its haploid status. One of the fascinating conundrums of gamete biology in males, therefore, is how the male germline gene regulatory program is maintained through prophase I while still allowing for the complexities of recombination and synapsis during prophase I. Studies in our lab have been pursuing this question from various angles, from understanding the de novo transcriptional events that occur in a stage specific manner through prophase I during length extension chromatin run-and sequencing (leChRO-seq) to identifying the mechanisms that allow for discrete switches in transcriptional activity at the level of the transcriptional machinery. While exceptions occur, for example at the sex chromosomes, our studies have begun to define the transcription factor profiles that regulate this unique gene regulatory environment. For the sex chromosomes specifically, our ability to monitor de novo transcriptional activity is providing us with novel tools to understand the unique regulation of sex-linked gene regulation during meiosis. In addition, we have recently turned our attention to exploring the role of non-coding RNAs (ncRNA) in driving transcriptional silencing during the pachytene stage of prophase I. Our studies are uncovering unique roles for Argonaute proteins and their ncRNA cargoes in driving meiotic silencing of the sex chromosomes (MSCI). Taken together our ongoing studies suggest that the mammalian spermatocyte features unique transcriptional and post-transcriptions regulatory processes that will allow new insight into gene regulation.

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