

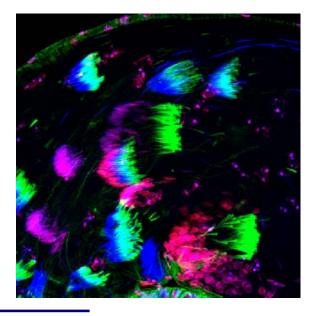


The Red Queen and the Lost Boys: intragenomic conflict and endogenous RNAi in the male germline

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Selfish meiotic drive systems (SMDs) can distort progeny sex-ratio (SR) and/or induce sterility. Although widespread in nature, the molecular mechanisms of SMDs, and they are silenced to restore Mendelian segregation, mysterious. Importantly, their rapid evolution means that classic model organisms may not be suited to reveal their fundamental features, breadth and impact. Using the nonmodel fruitfly D. simulans (Dsim), we uncovered critical roles for hpRNA-class RNAi substrates to suppress incipient sex chromosome conflicts. These arose in the simulansclade ancestor, and are not found in their close relative D. melanogaster. Strikingly, knockouts of Dsim hpRNA-siRNA loci (Nmy and Tmy) exhibit profound defects in the male germline, leading to loss of male progeny or outright sterility. These phenotypes are due to de-repression of recently-evolved members of the "Dox" family, which derived in part from protamine. Protamines mediate condensation of sperm chromatin, raising the possibility that these programs of meiotic drive interfere with packaging the paternal genome. Further analysis of core RNAi mutants in Dsim reveals additional de novo X-linked genes that are suppressed by recently-evolved hpRNAs. Thus, there is broad, unanticipated complexity in rapidly-evolving sex chromosome conflicts. Altogether, these data reveal one of the most overt biological usages of RNAi, and suggests a role for RNA silencing in speciation.



Host: Dr. Howard Lipshitz

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Time: 3:00 PM

Place: Room 254 (MC) Mechanical Engineering Bldg.