Life Sciences Seminar

Exploring the interactome of a human genetic parasite: affinity proteomics versus LINE-1 retrotransposons

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LINE-1 (L1) retrotransposons are catalysts of evolution and disease whose sequences constitute a significant proportion of the human genome, propagating via a copy-and-paste mechanism through an RNA intermediate. Despite tremendous influence on genome composition, L1 RNAs only encode two proteins (creatively termed ORF1p and ORF2p). Consequently, in vivo, L1 macromolecules engage a combination of permissive host factors that are essential to their lifecycle as well as repressive factors that constitute host defenses against L1's deleterious activity. In an attempt to better understand the molecular biology of L1, we have characterized host proteins associated with human L1 retrotransposons, as expressed in cell culture, using a combination of techniques including metabolic labeling and affinity proteomics. In this seminar I will primarily discuss our production and use of these data to create a multi-dimensional interactomic characterization of affinity isolated L1s; an interactive discussion with the audience concerning general and technical aspects of affinity proteomic experimental design is encouraged.General background(1) Taylor, M. S. et al. Affinity Proteomics Reveals Human Host Factors Implicated in Discrete Stages of LINE-1 Retrotransposition. Cell 155, 10341048 (2013).(2) LaCava, J. et al. Affinity proteomics to study endogenous protein complexes: Pointers, pitfalls, preferences and perspectives. BioTechniques 58, 103119 (2015).(3) Taylor, M. S. et al. Dissection of affinity captured LINE-1 macromolecular complexes. Elife 7, e30094 (2018).

Wednesday, February 7, 2018 11:00am - 12:00pm
Mondi Seminar Room 3, Central Building

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