

Speaker: Ahna R. Skop

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Title: "Using proteomics and functional genomics to understand cytokinesis"

Date: Tuesday, October 25

Time: 13:30~14:30

Place: 7F Conference room of Building A

Summary:

Cytokinesis is an essential process that partitions chromosomes, cytoplasm and organelles into newly formed daughter cells. Errors in cytokinesis cause aneuploidy, which leads to genetic instability and abnormal cell behavior as seen in breast cancer and a variety of birth defects, for example. Not only are the molecular factors required for cleavage furrow establishment unknown, but also how these signals modify the cleavage furrow membrane remains a mystery. To rapidly identify and characterize essential cytokinesis proteins, we employed a functional proteomic and comparative genomic Midbodies were isolated from mammals, proteins were identified by multidimensional protein identification technology (MudPIT), and protein function was assessed in C. elegans. To validate our biochemical screen, we identified 57 known cytokinesis proteins (36%) and 45 known midbody proteins (28%). In addition, ten out of ten identified proteins tested localized at the midbody in HeLa cells. Of 172 homologs and paralogs disrupted by RNAi in C. elegans, 58% displayed defects in cleavage furrow formation, furrow completion or germline cytokinesis. Functional dissection of the midbody, a transient and previously mysterious organelle, highlights the importance of lipid rafts and vesicle trafficking pathways in cytokinesis and illuminates the role of over 100 proteins previously uncharacterized with respect to this process. The utilization of common components in diverse dynamic membrane events in the cytokinetic furrow, the germline, and neurons, indicates ancient mechanisms mediating cell division and complex morphogenetic cellular processes critical in human development and disease. Finally, we have begun to characterize the role of Dynamin/DYN-1, a candidate midbody protein, which is required for cleavage furrow invagination.

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