CDB SEMINAR

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13:30~14:30 C1F Auditorium

POST-TRANSCRIPTIONAL REGULATION DURING EARLY *DROSOPHILA* DEVELOPMENT

Summary

mRNAs representing over half of all the protein-coding genes in *Drosophila* are loaded into the oocyte during oogenesis. A third of these transcripts are eliminated by the midblastula transition two-and-a-half hours after fertilization. Transcript destabilization is triggered by the PAN GU kinase, which directs translation of *smaug* mRNA. The SMAUG RNA-binding protein, in turn, destabilizes a large fraction of these unstable maternal mRNAs by recruiting the CCR4/POP2/NOT deadenylase complex, leading to transcript deadenylation and decay. A subset of the unstable mRNAs is protected from degradation in the posterior cytoplasm, from which the germ cells bud. Cis-elements for both degradation and protection have been mapped using a combination of experimental and computational methods. In addition to its role in transcript destabilization, SMAUG represses the translation of a subset of its target mRNAs in the bulk cytoplasm but not in the germ plasm. Certain posterior-protected mRNAs are localized, not just within the germ cells, but also in the apical cytoplasm of the somatic cells that underlie them. These mRNAs colocalize with SMAUG in 'S-bodies'. Several lines of evidence suggest that S-bodies are distinct from P-bodies and that S-bodies serve as subcellular sites of translational regulation to ensure that the posterior cells maintain somatic characteristics despite inheriting a subset of the germ plasm.

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