BIO495 Capstone

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Central Dogma







Coupling

- Cellular processes occur concurrently
 - Ex. Cotranscriptional Splicing
- Coupling is the biological concept that independent cellular processes are linked using similar cellular resources in order to allow for more efficient utilization of energy
 - Enzymes often have multiple roles in different cellular processes
- Analogous to buying a multitool for multiple purposes versus buying seperate tools for each job





An Example of Coupling: Cotranscriptional Splicing



- Though often described sequentially, transcription and RNA splicing occur at the same time
 - Splicing machinery is known to load onto the growing premRNA strand before the termination of transcription
- The Carboxyl Terminal Domain (CTD) of RNA Polymerase II (the main driver of transcription) is known to recruit splicing machinery
- This is a well known phenomenon; however, our lab was interesting in studying how **chromatin modification** (a precursor to transcription) and **3' end processing**could also be coupled to RNA splicing in this way.



Chromatin Modification



- For transcription to occur, DNA must be accessible for RNA Polymerase II to bind and transcribe DNA into mRNA
- 2 classes of proteins that achieve this
 - Chromatin Remodeling Proteins physically removes histones from DNA
 - Chromatin Modifying Proteins chemically modifies amino acid residues to change the bonds of DNA to the histones
 - Subtypes include histone acetlyases (Nua4 Complex), methylases and phosphorylases.



Splicing

- Splicing- the process of removing noncoding introns of pre-mRNA and retaining coding exons
 - Occurs cotranscriptionally
 - Alternative Splicing- mRNAs can be spliced in different ways by selectively retaining or removing introns to create different protein products.
- Accomplished through splicing factors associated in a complex known as the spliceosome:
 - The main drivers the snRNPs (U1, U2, U4/U5/U6
 - Helped by helicases (Prp28, Prp40, NTC)



The Models on the Effects on Splicing

- There are two models that couple how the qualities of transcriptions can affect the effectiveness of splicing
 - a. Kinetic Model the speed of transcription (the speed at which RNA Pol II moves) changes splicing
 - Faster transcription reduces the quality of splicing
 - Slower transcription increases the quality of splicing
 - Recruitment Model proteins involved in transcription actively recruit proteins involved in splicing





Single Mutant Qualitative Growth Assays

YPD 30°C

YPD 33°C





Elongation Restrictions on Single Mutants																		
	Complete 33°C						100 6AU 33°C						200 6AU 33°					
WT			۲	6	1	1.5												
esa1-254																		
hsh155	÷																	
rna14∆																		
eaf3∆	۲		-	26.0	*				-	1	2							
eaf7∆				覅	23													
htz1∆			-	£3		*												

