

SCIENCE AT THE EDGE

2017 SEMINAR SERIES

Quantitative Biology Graduate Program | Gene Expression in Development and Disease

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“Evolution of the RNAP II C-Terminal Domain and Eukaryotic Diversity”

An explosion in genomic resources has impacted views of global eukaryotic evolution in dramatic ways. With increased understanding in some areas, new issues of uncertainty have emerged. For example, comparative genomic investigations have highlighted, for the first time, the enormous impacts of endosymbioses on many eukaryotic genomes, complicating phylogenetic inferences from large, multi-gene studies. This means that currently predominant views of organismal relationships are based upon years of phylogenomic investigations that did not take endosymbiotic gene transfer into account. Nevertheless, interpretations of the evolution of key molecular and developmental systems, such as the C-terminal domain of RNA polymerase II and associated protein-protein interactions, generally are based on presumed relationships from those same phylogenomic investigations. This presentation aims to place the current state of eukaryotic phylogenomics within an historical perspective and highlight novel approaches we have used to try to break out of inherently circular methodologies.

REFERENCES

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- Yang, C., Hager, P.W. and Stiller, J.W. 2014. The identification of putative RNA polymerase II C-terminal domain associated proteins in red and green algae. *Transcription*. DOI:10.4161/21541264.2014.970944.
- Yang, C. and Stiller J.W. 2014. Evolutionary diversity and taxon-specific modifications of the RNA polymerase II C-terminal domain. *Proceedings of the National Academy of Sciences, USA*. 111:5920-5925.

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