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On the computational ability of the RNA polymerase II carboxy terminal domain

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The RNA polymerase II carboxy terminal domain has long been known to play an important role in the control of eukaryotic transcription. This role is mediated at least in part, through complex post-translational modifications that take place on specific residues within the heptad repeats of the domain. In this report, the phenotypic effects of systematic site-directed mutations in the fission yeast RNA pol II carboxy terminal domain (CTD) are investigated. Remarkably, we find that alterations in CTD structure and/or phosphorylation result in distinct phenotypic changes related to morphogenetic control. A hypothesis based upon the concepts of "informational entropy" and "algorithmic transformation" is developed to explicate/rationalize these results. In addition, a formal mathematical conceptualization of CTD modification (in the form of a semi-Thue string rewriting system) is presented. Since the semi-Thue formalism is known to be Turing complete, this raises the possibility that the CTD-in association with the regulatory pathways controlling its post-translational modification functions as a biological incarnation of a universal computing machine. These ideas imply that the controlled manipulation of CTD effectors could be used to "program" the CTD and thus to manipulate biological processes in eukaryotes in a definable manner.

Biography

Jim Karagiannis is an Associate Professor at the University of Western Ontario in London, Ontario, Canada. His research makes use of the model eukaryote *Schizosaccharomyces pombe* and explores the complex post-translational modifications that take place on the carboxy-terminal domain (CTD) of the largest subunit of RNA polymerase II. Through an empirical examination of the informational properties and regulatory potential of the CTD, he hopes to decipher the "programming language" used by eukaryotes to control aspects of gene expression.

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