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Understanding the mechanisms of novel histone modifications *in vivo*

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Post-translational modifications (PTMs) of histones have emerged as key players in the regulation of gene expression. However, little is known to what extent PTMs can directly impact chromatin. It has been suggested that PTMs of core histones (H2A, H2B, H3 and H4) have the potential to govern chromatin function according to the so called "histone code" hypothesis by recruiting specific binding proteins. The goal of my project is to gain insight in the function acetylation within the globular domain of H3 (H3K56/64/115/122) and to compare these modifications with histone tail modifications, *in vivo* by using the mouse ES cells. To study the impact of PTMs *in vivo*, all endogenous wild type (WT) H3 gene copies have to be replaced with mutant copies. Hence, the primary focus of my project is to establish a model system that exclusively express mutated H3 (e.g., mimicking acetylation) in order to study effects of H3 globular domain modifications on gene expression, chromatin architecture as well as to study, cross talks and synergisms between globular domain modifications and compare the effects with tail modifications.

Biography

Nithyha Parameswaran Kalaivani has completed her Master of Science from King's College London, UK and is currently a Doctoral student in IGBMC, France.

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