REGIONAL CENTRE FOR BIOTECHNOLOGY

Seminar series

"DNA methylation in cancer and other complex-diseases"

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Seminar Room

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Abstract

Methylation of cytosines in DNA is a stable epigenetic mark that is essential for normal mammalian development and regulates diverse biological processes, such as, gene expression, imprinting, X chromosome inactivation as well as silencing of transposable elements and invading viral sequences. DNA methylation patterns are established during embryonic development. In case of imprinting and X chromosome inactivation DNA methylation patterns are parent-of-origin-specific, while in the case of non-imprinted loci, DNA methylation is governed by the underlying genetic component. Importantly, recent research findings have also implicated various environmental and lifestyle exposures in the alteration of this epigenetic mark, particularly in association with almost all malignancies and other complex diseases. However, the contribution of various risk factors/life style/environmental influences and/or genetic-factors, capable of eliciting or modulating such aberrant DNA methylation changes still remain unknown.

In this talk, I will be summarizing my previous work contributions, adding in our understanding of the role of aberrant DNA methylation events in complex disease state, in regulation of allele-specific DNA methylation (in healthy-state human genome) as well as in cellular defence/response against invading viral and bacterial pathogen. Given the importance of aberrant DNA-methylation modifications in various disease states and their implication in human health, as well as in our basic understanding of the cellular processes, I plan to pursue my future research career in the same area. Details of my proposed research plans and their significance will be discussed further.