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Perspective

Modifications in Protein Properties by Methylation

Hicham Labazi*

Department of Molecular and Medical Genetics, University of Toronto, Ontario, Canada

DESCRIPTION

Post-Translational Modifications (PTMs) are covalent processing events that change the properties of a protein by proteolytic cleavage and adding a modifying group, like acetyl, phosphoryl, glycosyl and methyl to any amino acids. Methylation is one of the most widely recognized compound catalyzed modifications. Protein methylation is a mostly used Post-Translational Modification (PTM) process, in which exceptionally specific enzymes called methyltransferases are responsible for the addition of methyl groups to a targeted molecule and S-Adenosyl Methionine (SAM) serve as the essential donor of methyl group. Protein methylation ordinarily happens on arginine, lysine, histidine, proline, and carboxyl groups. Protein methylation assumes a significant part in balancing cell and organic cycles, including transcriptional regulation, RNA processing and metabolism and signal transduction. Most of the methyl-based modifications are conserved from microorganisms to warm blooded animals and plants, their primary functions and metabolic adjustment as well as useful roles in regulating protein translation. Apparently methylation adjusts intra-or intermolecular modulates intra- or intermolecular interactions of the target proteins or affects their affinity for RNA, and, in this way, it influences different cell processes, including transcriptional regulation, RNA processing, ribosome assembly, translation accuracy, protein nuclear trafficking and metabolism. It can occur on the nitrogen-containing side-chains of arginine and lysine, but also at the amino-and carboxy ends of various proteins. In science, methyltransferases catalyze the methylation cycle, activated primarily by S-adenosylmethionine. Protein methylation has been most studied in histones, where the exchange of methyl groups from S-adenosyl methionine is catalyzed by histone methyltransferases. Histones that are protein lysine methylated is a basic and dynamic post-translational change that can regulate protein solidness and capability. This post-translational adjustment is managed by lysine methyltransferases and lysine demethylases. When particular cytosine residues in the promoters of inactive genes are methylated, the resulting methylcytosine helps to stabilize nucleosomes and prevents transcription factors from binding. Methylation on specific residues can act epigenetically to repress or activate gene expression. Multiple sites of proteins can be methylated. For certain sorts of methylation, like N-terminal methylation and prenylcysteine methylation, extra handling is required, while different kinds of methylation, for example, arginine methylation and lysine methylation not require any kind of pre-handling.

A common theme with methylated proteins, as with phosphorylated proteins, is the role these modification plays in the regulation of protein–protein interactions. The arginine methylation of proteins can either inhibit or promote protein interactions relying upon the sort of methylation. The uneven dimethylation of arginine deposits in nearness to proline-rich themes can hinder the limiting to SH3 domains. A well-characterized described example of a methylation dependent protein interaction is the specific methylation of lysine , by SUV39H1 on the N-terminal tail of the histone H3.Di-and tri-methylation of this lysine facilitates the binding of Heterochromatin Protein 1 (HP1). Since HP1 and Suv39h1 interact, it is thought that the binding of HP1 to histone H3 is kept up with and, permitted that to spread along the chromatin. The HP1 protein harbors a chromodomain which is responsible for the methyl-subordinate cooperation among it and lysine 9 of histone H3. Extra chromodomain-containing proteins will bind the same site as HP1, and to other lysine methylated positions on histones H3 and histone H4. C-terminal protein methylation manages the gathering of protein phosphatase. Methylation of the protein phosphatase 2A reactant subunit improves the limiting of the administrative B subunit and works with holoenzyme gathering. Protein methylation, including histone methylation and non-histone protein methylation, is the main sort of posttranscriptional and epigenetic modification. Recent studies have shown that protein methylation is related with consequences for autophagosome arrangement, autophagy-related protein expression, and signaling pathway activation. Over the most recent couple of years, the discovery of lysine and arginine methylation in histones and different proteins and the compounds that carry out these posttranslational modifications has added another aspect to the signal transduction field. Methylation of nucleosomal histones at specific lysine or arginine residues affects chromatin adaptations and either facilitates or inhibits transcription from neighboring genes. Apparently the dependable methyltransferases can be targeted in

Correspondence to: Hicham Labazi, Department of Molecular and Medical Genetics, University of Toronto, Ontario, Canada, E-mail: labazih@sickkids.on.ca

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some cases to specific genes and in other cases to broader regions of euchromatin or heterochromatin. Methylation of histones is mechanistically connected to different sorts of histone alterations, like acetylation, phosphorylation, and mono-ubiquitylation; mixes of these adjustments coordinate to manage chromatin construction and record by stimulating or inhibiting binding of specific proteins. Protein lysine methylation is a basic and dynamic post-translational change that can regulate protein solidness and capability. Protein methylation of lysine and arginine, like many other post-translational changes, is controlled by a variety of different signaling mechanisms. This post-translational adjustment is managed by lysine methyltransferases and lysine demethylases. Protein methylation plays diverse roles in regulating cellular functions in an epigenetic manner.