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Protein L-Isoaspartate O-Methyltransferase (PCMT1): A Key Player of Spontaneously Arisen Protein Damage Repair



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Abstract

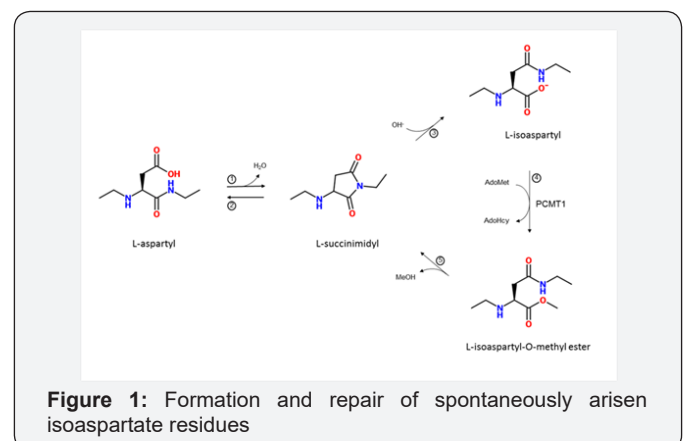
Proteins undergo spontaneous non-enzymatic chemical modifications due to the exposure to e.g. oxidative reagents. The cell copes with the accumulation of such damaged proteins by proteosomal degradation. However, aged or damaged proteins can also be enzymatically repaired. Protein L-isoaspartate O-methyltransferase (PCMT1) catalyzes the methylation of isoAspartate (isoAsp) residues that spontaneously arise as a result of protein aging and facilitates their restoration to the normal state. PCMT1 plays a significant role in maintenance of protein homeostasis as well as in cellular function and integrity by acting on a wide variety of substrates.

Keywords: Spontaneous Protein Damage, Aging, Aspartate Methylation, Isoaspartate, PCMT1, Protein L-Isoaspartate O-Methyltransferase

Introduction

Methylation of aspartic acid residues was first described in the literature in erythrocytes as a possible step of repairing aged membrane proteins [1]. During the process of aging, L-aspartyl residues are spontaneously converted to L-isoaspartyl via the unstable intermediate L-succinimide which undergoes a spontaneous hydrolysis, generating a mixture of normal L-aspartate (15-30%) and abnormal L-isoaspartate (70-85%), pointed out as steps 2 and 3 in Figure 1 respectively [2]. Accumulation of this abnormal form of aspartate is recognized as damage in the cell and therefore needs to be repaired [3].

It has been previously shown that Protein L-isoaspartate O-methyltransferase (PCMT1, or alternatively called PIMT) can rapidly convert L-isoaspartyl sites to -carboxyl-O-methyl esters in vivo (step 4), which at physiological pH and temperature undergo spontaneous demethylation and give rise to the L-succinimide intermediate (step 5) [4]. Although multiple cycles of the repair mechanism is required to prevent L-isoaspartate sites from accumulating, it is the only repair pathway known so far (Figure 1). The methylation of isoAsp residues by PCMT1 is also suggested to act in targeting aged proteins for proteosomal degradation [5].



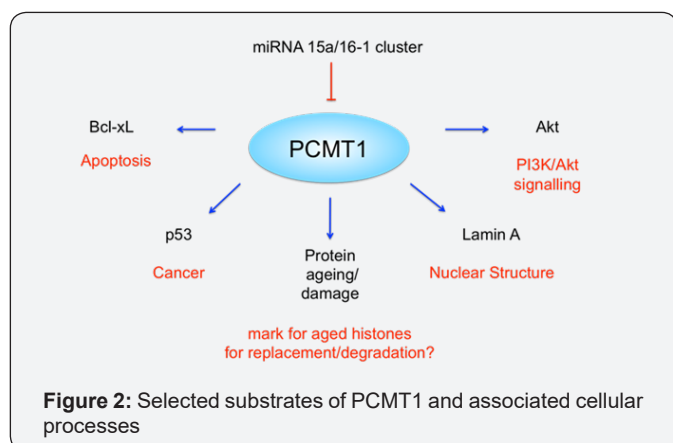
Protein L-isoaspartate O-methyltransferase (PCMT1) is encoded by a single gene located on human chromosome 6q22.3-24 [6]. Alternative splicing of the RNA transcripts gives rise to two isoforms; differing only in their last two or three aminoacids at the C-terminus. The more basic isoform carries a -RWK sequence whereas the more acidic isoforms bears a -RDEL sequence, which is recognized as "endoplasmic reticulum retention signal" and is most likely to be cytoplasmic [7].

Catalytic properties of these isozymes appear to be identical [8]. PCMT1 is a ubiquitously expressed enzyme. It was previously shown as a cytoplasmic protein in all mammalian tissues tested [9]; however, a recent study revealed that PCMT1 localizes both

to the nucleus and to the cytoplasm [10]. It is well conserved among species; from human to mouse, chicken, fish, worms, insects and plants, with more than 95 percent similarity in amino acid sequence within mammals (Table 1).

Table 1: PCMT1 (protein L-isoaspartate O-methyltransferase) shows high conservation among species.

Accession	Organism	Length (aa)	Identity (%)
P22061	Homo sapiens (Human)	227	100
G2HIC2	Pan troglodytes (Chimpanzee)	227	99
K9ISG7	Desmodus rotundus (Vampire bat)	281	97
P23506	Mus musculus (Mouse)	227	96
Q5F3N1	Gallus gallus (Chicken)	228	93
Q5U253	Xenopus laevis (Frog)	228	91
Q92047	Danio rerio (Zebra fish)	228	85
Q27869	Drosophila melanogaster (Fruit fly)	226	56
Q27873	Caenorhabditis elegans (Worm)	225	53
Q8GXQ4	Arabidopsis thaliana	227	51



PCMT1 has a wide range of substrates including Bcl-xL, p53, LaminA, Akt, MAP-2, - and -Tubulin, - and -Synuclein, Calmodulin, Calreticulin [3,11,12]. Hence, PCMT1 has been implicated in regulation of many cellular processes and signaling pathways (Figure 2). PCMT1 mediated methylation of p53 has been reported to directly down regulate p53 protein levels and thereby suppress the transcription of p53-target genes [11]. It has also been shown that the methylation of Bcl-XL deamidated at Asp52 and Asp66 is required for maintaining its anti-apoptotic functions and that the over expression of PCMT1 prevents apoptosis in endothelial cells after H₂O₂ induction [13]. In line with this, the miRNA 15a/16-1 cluster mediated silencing of PCMT1 was shown to interfere with the repair of the deamidated Bcl-XL, making cells more susceptible to cisplatin-induced apoptosis [14]. Another important function has been attributed to PCMT1 in PI3K/Akt pathway due to the activation of PI3K/Akt pathway and increased levels of insulin receptor in PCMT1 deficient mice. There are several reports that PCMT1 can also act on histone proteins to repair isoaspartate residues [2,5,15]. Furthermore,

we recently showed that PCMT1 methylates histone H4 at aspartate 24 (H4D24me), implicating a possible role for PCMT1 in marking aged histones for replacement or degradation; which for the first time linked histone modifications with histone aging and histone protein homeostasis.

Conclusion

PCMT1 is a crucial component of the cellular protein repair machinery of the cell, which is evident by its wide variety of substrates that are important regulators of cellular function. In line with this, it has significant physiological and therapeutic implications. For instance, mice lacking PCMT1 exhibit accumulation of soaps in several tissues including brain, which may result in neuronal dysfunction, and they ultimately die of epileptic seizures, suggesting PCMT1 as a potential therapeutic target in certain brain diseases including epilepsy [16]. Therefore, future studies on PCMT1 will not only provide new insights into the cellular protein repair mechanisms, but also possible new targets for therapy.

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