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Research Article

Actions and Mechanisms of GCN5L1-Mediated Mitochondrial Acetylation inVital Visceral Diseases

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Abstract

The mitochondrial acetyltransferase GCN5L1 can control the activity of various proteins acetylation in mitochondria, contributing to alterations of metabolic signal transduction. GCN5L1 plays a crucial regulatory role in the development and progression of human diseases such as diabetes, liver diseases (cirrhosis, hepatocellular carcinoma, and non-alcoholic fatty liver disease), heart disease, and kidney diseases (acute kidney injury, chronic kidney disease, and diabetic kidney disease). This review primarily focuses on the current progresses involving the effects of GCN5L1-mediated mitochondrial acetylation on these vital visceral diseases and the underlying mechanism.

Keywords: Fatty Acid Oxidation (FAO); GCN5L1; Gluconeogenesis;Mitochondrial acetylation; Myocardial metabolism; mitochondrial Transcription Factor A (TFAM)

GCN5L1 (GCN5-like 1) is a mitochondrial acetyltransferase protein with a molecular weight of 15-17 kDa, which shares sequence homology with nuclear acetyltransferase GCN5 [1]. The distribution of GCN5L1 varies depending on its molecular weight: the 15 kDa form is predominantly found in mitochondria, while the 17 kDa form is primarily localized in the cytoplasm of tissues such as the liver and kidney [2]. GCN5L1 can inhibit the activity of the mitochondrial deacetylase SIRT3 [3], thereby controlling mitochondrial protein acetylation, regulating metabolic pathways, and coordinating

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retrograde signaling from mitochondria to the nucleus [2]. Increasing literatures highlight that post-translational modifications of proteins, particularly acetylation, play a significant role in human diseases, including neurodegenerative and cardiovascular diseases, diabetes, cancer, and aging [4]. In certain tissues, GCN5L1 has been confirmed to regulate the acetylation of mitochondrial fatty acid oxidation (FAO) proteins, such as short-chain acyl-CoA dehydrogenase (SCAD), long-chain acyl-CoA dehydrogenase (LCAD),mitochondrial trifunctional enzyme subunit alpha (HADHA), glucose oxidation proteins, and electron transport chain proteins [5]. This article provides an overview of the role and molecular mechanisms of GCN5L1-mediated mitochondrial acetylation in related diseases.

The Role of GCN5L1 in Diabetes

GCN5L1 directly binds to key components of mitochondrial glycerol 3-phosphate dehydrogenase 2 (GPD2) and regulates its activity, thereby influencing the cellular redox state and playing a significant role in the regulation of hepatic gluconeogenesis [6]. Generally, the liver is essential for maintaining normal glucose homeostasis [7]. In diabetes, excessive hepatic gluconeogenesis leads to the overproduction of glucose, resulting in fasting hyperglycemia and postprandial hyperglycemia [8]. GPD is a critical enzyme involved in regulating gluconeogenesis, as the conversion of lactate or glycerol to glucose requires cytosolic redox reactions (high levels of NAD⁺), which are controlled by GPD [9]. The previous evidences demonstrated that cells lacking GCN5L1 exhibit reduction of GPD2 activity significantly. GPD2 serves as a target for GCN5L1 action, and GCN5L1 regulates its activity by binding to GPD2, thereby altering the cellular redox state and controlling the conversion of glycerol or lactate into glucose, thus regulating gluconeogenesis [6].

GCN5L1 regulates gluconeogenesis by modulating mitochondrial reactive oxygen species (mROS) and the phosphorylation of extracellular regulated protein kinases (ERK1/2), which in turn affects the stability of forkhead box protein O1 (FoxO1) and its downstream gluconeogenic enzymes, glucose-6-phosphatase (G6Pase), and phosphoenolpyruvate carboxykinase (PEPCK) expression [6]. In hepatocytes of mice with specific GCN5L1 knockout, mitochondrial protein acetylation decreases, PEPCK and G6Pase transcription levels are downregulated, mROS levels increase, ERK1/2 phosphorylation is activated, leading to a decrease in the upstream regulatory factor FoxO1 protein levels [3]. FoxO1 is a transcription factor that plays a role in regulating glucose homeostasis, and its deacetylation can transactivategluconeogenic genes to enhance hepatic gluconeogenesis [10]. Therefore, in the absence of GCN5L1, deacetylation of mitochondrial proteins mediated by ROS-dependent ERK/FoxO1 signaling and transcriptional retrograde regulation contributes to the control of gluconeogenesis [10]. Furthermore, the downregulation of acetylation of peroxisome proliferator-activated receptor γ coactivator 1α (PGC- 1α) leads to increased expression of gluconeogenic genes [10], while the GCN5 acetyltransferase complex can inhibit gluconeogenesis through the acetylation of PGC-1a [11]. In summary, GCN5L1 regulates the activity of GPD2, implicates the intracellular redox state, and modulates hepatic gluconeogenesis by regulating

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mitochondrial ROS, ERK1/2 phosphorylation, and the stability of FoxO1, playing a vital role in glucose homeostasis.

The Role of GCN5L1 in Hepatocellular Carcinoma (HCC) and Other Liver Diseases

Glutamine metabolism is an important metabolic process that exerts a principal regulatory effect on the development of HCC [12]. The isoenzymes of glutaminase, GLS1, and GLS2, are key enzymes involved in glutamine metabolism [13]. It has been reported that the deletion of the GCN5L1 gene in mouse liver tumor cells can alter acetylation to enhance the activity of GLS1 and GLS2 [12,14]. This alteration promotes glutamine metabolism and activates the mammalian target of the rapamycin complex 1 (mTORC1) pathway, thereby facilitating HCC cell proliferation [13]. Disruption of mTOR signaling has been implicated in various diseases, including obesity, diabetes, cancer, fatty liver disease, and neuronal disorders [15]. Non-alcoholic fatty liver disease (NAFLD) encompasses a spectrum of liver diseases, ranging from fatty liver disease (FLD) to non-alcoholic steatohepatitis (NASH), which can progress to liver cirrhosis and hepatocellular carcinoma [16]. Impaired liver regeneration exacerbates liver dysfunction in NAFLD [14], and NASH is characterized by excessive hepatic lipid accumulation and dysregulated lipid metabolism [17]. SIRT3 is a protein that deacetylates and activates various mitochondrial FAO enzymes in the liver [18], while GCN5L1 has the opposite effect, reducing the activity of FAO enzymes [19]. Experimental evidence suggests a correlation between the level of GCN5L1 and the acetylation of HADHA, a FAO protein [19]. Decreased GCN5L1 levels can lead to reduced HADHA acetylation and increased activity of fatty acid acyl-CoA oxidase. Conversely, when GCN5L1 is overexpressed, it reduces the acetylation of FAO enzymes, resulting in dysregulated lipid metabolism and increased risk of FLD and NASH [14]. Briefly, the role of GCN5L1 in the liver is complex, involving not only the promotion of cell proliferation but also the regulation of energy metabolism and redox balance. In summary, GCN5L1 exerts multifaceted modulatory effects on liver diseases by impacting glutamine metabolism, mTOR signaling, and lipid metabolism.Further investigation is necessary to fully understand the intricate mechanisms and potential therapeutic implications of GCN5L1 in liver diseases.

The Role of GCN5L1 in Heart Disease

As a modulator of mitochondrial protein acetylation, GCN5L1 is essential for the regulation of cardiac Fatty Acid Beta-Oxidation (FAO).Studies have shown that a High-Fat Diet (HFD) contributes to increased cardiac mitochondrial protein acetylation and elevated circulating fatty acids, while reduction of GCN5L1 decreases lysine acetylation and impairs FAO in response tonutrient overload [20].Lysine acetylation is an important post-translational modification that can modulate the activity of many enzymes involved in fatty acid and glucose metabolism [21]. Acetyl-CoA serves as a cofactor for lysine acetylation [22] and serves as the main substrate for fatty acid synthesis, which is the primary energy source for the heart [23]. FAO is the primary fuel pathway for mitochondrial ATP production [24]. GCN5L1 enhances cardiac energy output by promoting mitochondrial protein acetylation, and its increased expression in response to HFD promotes an increase in lysine acetylation [23]. As a molecular regulator of mitochondrial protein acetylation, GCN5L1 plays a crucial role in FAO. Reduction of GCN5L1 contributes to the modulation of lysine acetylation and fatty acid metabolism in the context of HFD. Therefore, investigating the influence of GCN5L1 deficiency on in

vivofatty acid metabolism and bioenergetics would provide valuable insights into the significance of lysine acetylation in cardiac metabolism. A study has achieved remarkable results in mice with GCN5L1 gene knockout [20]. In detail, FAO exhibits a significant decrease in response to reduced acetylation activity of SCAD and LCAD. It must be pointed out that SCAD is responsible for oxidizing short-chain fatty acids, while LCAD oxidizes long-chain fatty acids. SCAD function contributes to maintaining cardiac bioenergetic output, whereas increased LCAD activity can enhance cardiac FAO activity [21], and loss of LCAD activity can result in enhanced glucose oxidation dependency. During the treatment of HFD in GCN5L1 KO mice, the acetylation levels of SCAD and LCAD increase, along with an increase in FAO enzyme activity. Similarly, in cultured H9C2 cells derived from the heart, the reduced acetylation activity of the two enzymes causes diminished FAO, leading to a decrease in mitochondrial bioenergetic output [20]. Furthermore, the absence of GCN5L1 in cardiac myocytes leads to functional impairment after myocardial ischemia and increases the development of ex vivomyocardial infarction [25]. GCN5L1 KO mice exhibit elevated levels of ROS in cardiac cells, and scavenging ROS can restore cardiac function and reduce infarct size [26]. Overexpression of acetylated mitochondrial Transcription Factor A (TFAM) has been shown to improve Heart Failure (HF) [27], a condition characterized by metabolic dysregulation and insufficient cardiac energy supply [28]. Experimental evidence suggests that the deficiency of GCN5L1 leads to reduced acetylation of mitochondrial proteins, limiting mitochondrial bioenergetic output, while GCN5L1-mediated acetylation of TFAM helps maintain bioenergetic output to meet the demands of hemodynamic stress [29]. In summary, GCN5L1 is a molecule involved in regulating cardiac FAO or acetylation of TFAM and might be considered as a potential target for treating heart failure.

The Role of GCN5L1 in Kidney Diseases

GCN5L1 is considered a protein that may serve as a potential intervention target for various kidney diseases. It has been reported that specific deletion of GCN5L1 in renal tubules in mice effectively alleviates mitochondrial injury caused by acute kidney injury (AKI) [30]. Furthermore, increased acetylation of TFAM was observed in the kidneys of AKI mice, while GCN5L1 can acetylate TFAM at the K76 site and inhibit its binding to TOM70, thereby reducing TFAM entry into mitochondria and the subsequent mitochondrial biogenesis [30]. Therefore, the regulation of TFAM acetylation and its intracellular transport by GCN5L1 may be one of the potential targets for intervention in AKI-related mitochondrial diseases. In diabetic kidney disease (DKD), the loss of GCN5L1 has been found to effectively improve kidney damage caused by oxidative stress. Specifically, the loss of GCN5L1 can reduce the acetylation level of manganese superoxide dismutase (MnSOD) at the Lys68 site, thereby activating its activity and scavenging excessive ROS, thereby alleviating kidney inflammation and fibrosis elicited by oxidative stress [31]. In chronic kidney disease (CKD), GCN5L1 has been found to regulate the acetylation levels of Long-Chain 3-Hydroxy Acyl-CoA Dehydrogenase (LCHAD) and hydroxy acyl-CoA dehydrogenase (HADH - hydroxyAcyl-CoA Dehydrogenase Gene, SCHAD), thereby promoting the activity of these enzymes, improving FAO defects and lipid accumulation, and reducing the degree of epithelial-mesenchymal transition and fibrosis [32], thus controlling renal lipotoxicity. In summary, these evidences indicate that GCN5L1 shows promise in intervening in different kidney diseases. Deleting GCN5L1 specifically in renal tubules can alleviate AKI-induced mitochondrial injury

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and the absence of GCN5L1 in diabetic kidney disease can ameliorate kidney damage aroused by oxidative stress. Additionally, modulating GCN5L1 in chronic kidney disease may help enhance lipid metabolism and reduce fibrosis. Consequently, GCN5L1 is expected to emerge as a significant target for further research and development of kidney disease treatments.

Concluding Remarks

GCN5L1, a mitochondrial protein acetyltransferase, was first discovered in 1996 and shares amino acid sequence homology with GCN5, a known transcriptional regulatory protein in yeast [33]. The function of GCN5L1 was first reported in 2012, demonstrating its interaction with SIRT3, a respiratory chain target, and promoting its acetylation, thereby reversing the overall effects of SIRT3 on mitochondrial protein acetylation, respiration, and bioenergetics [34]. An increasing amount of evidence highlights that GCN5L1 plays a significant role in the pathogenesis of diabetes, cardiovascular diseases, liver diseases, and kidney diseases (Figure 1). Under physiological conditions, GCN5L1 regulates mitochondrial FAO, glucose oxidation, and acetylation of electron transport chain proteins in certain tissues. However, in diabetes, GCN5L1 influences the cellular redox state by regulating the activity of mitochondrialGPD2 and FoxO1 pathway, thereby modulating hepatic gluconeogenesis (excessive glucose production) [6]. In liver diseases and hepatocellular carcinoma, GCN5L1 involves in glutamine metabolism, activation of the mTORC1 pathway and HADHA signaling, and enhancement of liver regeneration capacity [14]. In heart diseases, GCN5L1 can regulate FAO to modulate cardiometabolic processes, and can also contribute to pathologenesis of HF through TFAM acetylation [20,27]. In kidney diseases, alteration of GCN5L1 expression contributes to diverse actions: influencing mitochondrial biogenesis via TFAM/TOM70 in AKI [30], impacting ROS clearance by MnSOD in DKD [31], and regulating FAO through LCHAD/SCHAD in CKD [32]. In summary, GCN5L1 plays a crucial role in vital visceral diseases by regulating mitochondrial protein acetylation, influencing metabolic pathways and related signaling transduction, and assuming an indispensable role in pathogenesis of the vital visceral diseases.

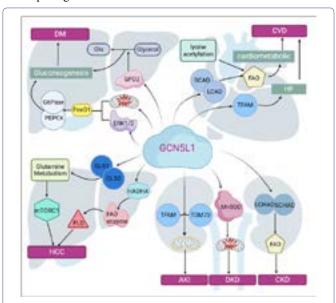


Figure 1: The mechanism of GCN5L1-mediated mitochondrial acetylation in vital visceral diseases.

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However, despite significant progress in the research on GCN5L1, further investigation is needed to gain a deeper understanding of its precise mechanisms of action in vital visceral diseases. This includes studying the interactions between GCN5L1 and other key proteins and pathways, as well as the molecular details of GCN5L1 regulation. Additionally, researchers need to explore the clinical prospects of GCN5L1 as a potential therapeutic target and evaluate the safety and efficacy of intervention strategies targeting GCN5L1.

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