



A narrative review of the role of m6A in oxidative stress and inflammation

Zehao Chen^{1#}, Xin Chen^{2#}, Yanan Ji¹, Lilei Zhang¹, Wei Wang¹, Yuntian Shen¹, Hualin Sun^{1^}

¹Key Laboratory of Neuroregeneration of Jiangsu and Ministry of Education, Jiangsu Clinical Medicine Center of Tissue Engineering and Nerve Injury Repair, Co-Innovation Center of Neuroregeneration, Nantong University, Nantong, China; ²Department of Neurology, Affiliated Hospital of Nantong University, Nantong, China

Contributions: (I) Conception and design: H Sun; (II) Administrative support: H Sun; (III) Provision of study materials or patients: Z Chen, X Chen, W Wang, L Zhang, Y Ji, Y Shen; (IV) Collection and assembly of data: Z Chen, X Chen, W Wang, L Zhang, Y Ji, Y Shen; (V) Data analysis and interpretation: X Chen, Z Chen; (VI) Manuscript writing: All authors; (VII) Final approval of manuscript: All authors.

[#]These two authors contributed equally to this work.

Correspondence to: Dr. Hualin Sun. Key Laboratory of Neuroregeneration of Jiangsu and Ministry of Education, Nantong University, 19 Qixiu Road, Nantong 226001, China. Email: sunhl@ntu.edu.cn.

Objective: To provide a comprehensive overview of the role and possible mechanism of N6-methyladenosine (m6A) in oxidative stress and inflammation.

Background: Oxidative stress and inflammation are involved in many pathophysiological processes. How oxidative stress and inflammation participate in the occurrence and development of diseases, and what factors regulate them have not yet been clarified. In recent years, more and more attention has been paid to the research of m6A. Due to its extensive role in RNA internal modification and maintaining stability, more and more scientists began to study the relationship between m6A modification and diseases. However, the research about m6A on oxidative stress and inflammation is rare.

Methods: We performed a systematic literature search of the MEDLINE literature database through PubMed on m6A, oxidative stress and inflammation. Subsequently, the main findings in the literature were summarized.

Conclusions: Oxidative stress and inflammation are involved in many pathophysiological processes, including tumor, aging, diabetes, cardiovascular disease and so on. Post-transcriptional epigenetic modification of RNA mainly, m6A, is an emerging concept in the scientific community. m6A mediates its effect through the various reader, writer, and eraser proteins, regulating gene expression and involving many biological processes, including oxidative stress and inflammation. This article mainly reviews the role and molecular mechanism of m6A in the occurrence and development of many diseases by regulating oxidative stress and inflammation. There are many problems in the process of oxidative stress and inflammation, which are worthy of further study. m6A plays a key role in the occurrence and development of many diseases by regulating oxidative stress and inflammation.

Keywords: N6-methyladenosine (m6A); oxidative stress; inflammation

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[^] ORCID: 0000-0003-1889-1561.

Introduction

N⁶-methyladenosine (m⁶A) is the most common modification in higher organisms. Studies have shown that m⁶A modification widely exists in mammals, plants, fungi and other organisms (1). The modification of m⁶A mainly occurs on the adenine of DRACH sequence (2,3). After high-throughput sequencing, m⁶A was found mainly distributed in stop codons, mRNA exons, 3'UTRs and protein coding regions (4). The biological function of RNA is based on a variety of modifications, among which methylation accounts for a large proportion (5,6). m⁶A modification plays a fundamental role in the regulation of gene expression (7). At the same time, m⁶A modification is also involved in RNA translation, degradation, splicing, enucleation and folding (5,8,9). The regulation of m⁶A mainly depends on the enzyme system of m⁶A, including "Writer", "Eraser", "Reader". "Writer" is a kind of methyltransferase, and mainly includes METTL3, METTL14 and WTAP. These methyltransferases transfer the methyl group from the methyl donor S-adenosylmethionine (SAM) to the sixth N atom of RNA adenine. "Eraser" is a kind of demethylase, and mainly includes fat mass and obesity-associated protein (FTO) and ALKBH5. FTO is a demethylase first identified in m⁶A modification (9,10). It has been found that FTO is knocked out by siRNA, the content of M⁶A in mRNA increases, and the overexpression of FTO can decrease the intracellular m⁶A level (11). However, some scholars believe that FTO has no obvious effect on m⁶A, especially for small nuclear RNA. In contrast to the view that FTO acts as a demethylation enzyme, some scholars believe that the regulatory sites of FTO and ALKBH5 tend to maintain the stability of the non-methylated state in order to reverse methylation (12). In the case of FTO inhibition or removal, abnormal m⁶A interferes with the output mechanism and may lead to abnormal pre-splicing of mRNA (13). Combined with the above views, the role of FTO and other proteins in the m⁶A enzyme system needs to be more balanced and fully studied. In order to realize its biological functions, methylated modification needs to be combined with corresponding recognition proteins, which are "Reader", including the YT521-B homology domain family (YTHDF) proteins (14). Current studies focus more on YTHDF1/2/3. Although these three are considered to have different roles, due to the similarity of their sequences and convergence of binding targets, they are likely to have superimposed or synergistic effects (15). According to the present results, Readers include proteins such as YTHDF and IGF2BP3,

whose functions are closer to influencing the stability of mRNA or interacting with associated binding sites (16,17). The specific role of these proteins in the m⁶A system needs to be further studied. We present the following article in accordance with the Narrative Review reporting checklist (available at <https://biotarget.amegroups.com/article/view/10.21037/biotarget-21-1/rc>).

Methods

We performed a literature search using the online database (Medline) of articles through PubMed. We included the following search terms/phrases "m⁶A", "inflammation" and "oxidative stress" between January, 2001 to July, 2021, that only English language articles were reviewed.

m⁶A and inflammation related diseases

Inflammation, a defensive response of living tissue with vascular system to foreign body stimulation or injury factors, is mediated by various inflammatory mediators, and participates in and accompanies most diseases, which are characterized by redness, swelling, heat, pain and dysfunction (18). Usually, inflammation is beneficial and an automatic defense response of the human body, but sometimes inflammation is harmful. For example, inflammation attacks the body's own tissues or inflammation occurs in transparent tissues. Although inflammation is a common reaction in the human body, it generally does not lead to serious diseases. However, some inflammations can develop into life-threatening and fatal diseases. Long term inflammation is one of the important causes of many major diseases, including atherosclerosis, cancer, stroke and diabetes (19-23).

In recent years, with the development of medical theory, progress in molecular biology, immunology and various technologies, we have a better understanding of the nature of inflammation. On the whole, inflammation can be roughly divided into infectious inflammation and aseptic inflammation. When the human body is infected by pathogenic microorganisms, bacteria, viruses and protozoa, it causes exudation, necrosis and proliferation of the human body, which is collectively referred to as infectious inflammation. If inflammation is caused by physical and chemical factors, it is called aseptic inflammation. As an intracellular signal platform, inflammation can not only respond to pathogenic components, but also to various endogenous signals, inorganic environmental

components or vaccine adjuvants that may occur under sterile conditions (24-27). The tissue system in the body has many commonalities in participating in various inflammatory responses. That is, in different inflammation, there is the same organ, tissue system involved. The local or overall manifestations of inflammation can be summarized as: arterial congestion, edema, decreased membrane permeability, tissue cell proliferation, abnormal expression of cytokines, etc. Although there are few studies on the relationship between various types of inflammation and m6A, we can analyze the possible role of m6A from the perspective of basic changes and mechanisms of inflammation. We can reasonably speculate that m6A may be widely involved in the process of inflammation at the cellular level. This conjecture has been confirmed in many research experiments in recent years.

m6A and cancer

Inflammation is a recognized feature of cancer. Inflammation is closely related to the development and progression of cancer. Recent studies also show that cancer is closely related to chronic inflammation (28-32). In the enzyme system of m6A, the writer and eraser have been studied more and more. A large number of studies have shown that METTL3 and FTO has a synergistic effect on the occurrence and development of cancer (33-36). A large number of studies have shown that METTL3 and FTO are involved in the abnormal regulation of cells. Han et al found that METTL3 may interact with DGCR8 and positively modulate the pri-miR221/222 process in bladder cancer (37). METTL3 mediated m6A modified AFF4/NF- κ B/MYC signaling network involved in the progress of bladder cancer (38). Chen *et al.* found that METTL3 is often up-regulated in human hepatocellular carcinoma (HCC) and participates in the progression of HCC. METTL3 inhibits SOCS2 expression in HCC via a m6A-YTHDF2 dependent mechanism (39). METTL3 knockout significantly inhibited the abundance of SOCS2 mRNA m6A. FTO showed higher expression in human melanoma, and knockdown of FTO increased m6A methylation in PD-1 mRNA, CXCR4 mRNA, and SOX10 mRNA, leading to increased RNA decay through YTHDF2 in melanoma. Thus, the sensitivity of melanoma to anti-PD-1 therapy is increased (40). ALKBH5 showed higher expression in ovarian cancer tissue and promotes ovarian carcinogenesis in through activating NF- κ B pathway (41). In the study of various types of cancer, we found that m6A has a wide range of regulatory effects on

AHR/SOCS2, TLR4/NF- κ B, TNF- α -NF- κ B inflammatory signaling pathways (37,39). This further suggests that m6A may be involved in tumorigenesis and development by regulating inflammatory signaling pathway.

m6A and atherosclerosis

There are few studies on the cell structure and properties of m6A. However, in the inflammatory response, the change of vascular properties is more significant. Some studies have found that the expression of METTL14 increases in calcified arteries and human aortic smooth muscle cells (HSMCs) induced by indole sulfate, which increases the level of m6A in RNA and reduces the vascular repair function (42). In the characteristics of the disease, atherosclerosis includes the proliferation of cells and tissues, fatty necrotic lesions, and vascular sclerosis. These are typical inflammatory responses. The level of m6A modification and METTL14 methyltransferase were over expressed in atherosclerotic vascular endothelial cells. The results show that METTL14 improves the level of m6A modification of pri-miR-19a, promotes the processing of mature miR-19a, and promotes the proliferation and invasion of atherosclerotic vascular endothelial cells (43). miR-19a/19b has a certain protective effect on cardiac function, which has been confirmed in the mouse model of myocardial infarction (44). These data showed that there is a high correlation between m6A and cardiovascular disease.

m6A and diabetes

m6A plays an important role in the process of metabolic diseases such as obesity, type 2 diabetes (45). Deficiency of m6A modification can lead to a variety of diseases, including type 2 diabetes mellitus (T2DM) (46). T2DM is becoming more common worldwide. T2DM is characterized by lack of insulin, insulin resistance and high-glucose. Inflammation associated with diabetes incidence rate and mortality rate increase. Although the relationship between T2DM and inflammation is still unclear, it is undeniable that inflammation is the key to the occurrence and process of diabetes. Shen et al showed that the m6A contents were significantly low, and the FTO mRNA level was significantly high in T2DM patients, which might further increase the risk of complications of T2DM (47). Yang *et al.* found that m6A contents were decreased, while METTL3, METTL14, and WTAP were increased. This phenomenon

seems to be contradictory to the low level of m6A. The author speculates that the lower m6A content might be responsible for the upregulation of methyltransferases (48). In T2DM patients, highly expressed METTL3 inhibits hepatic insulin sensitivity via m6A modification of Fasn mRNA in liver tissues (49). Li *et al.* found that METTL3 was down-regulated during inflammation and oxidative stress, and islet β -cell-specific deletion of METTL3 induces β -cell failure and hyperglycemia, which is likely due to decreased insulin secretion-related genes (50). These results suggest that m6A plays an important role in the development of diabetes, and provide a new strategy for the targeted treatment of diabetes.

Oxidative stress and inflammation

Oxidative stress is the imbalance between oxidation and antioxidation in organism, which tends to lead to neutrophil infiltration, increase of protease secretion and production of a large number of oxidation intermediates. This process can lead to cell, tissue and organ damage (51,52). The occurrence of oxidative stress is affected by many factors, including hypoxia environment, toxic smoke, ultraviolet radiation, pesticide, etc. Oxidative stress is a major contributor to the pathogenesis of various human diseases, including denervation-induced muscle atrophy (53-57). It was confirmed that the activity of superoxide dismutase (SOD) in the liver of sea bass increased and oxidative stress increased under high temperature and hypoxia (58). Oxidative stress has a great influence on protein synthesis and metabolism (59). In the study of methamphetamine induced dopaminergic neurotoxicity, it was found that methamphetamine induced mitochondrial damage enhanced the susceptibility to oxidative stress, proapoptosis and neuroinflammation in a positive feedback loop. At the same time, the intervention of oxidative stress can inhibit the apoptosis of cells (60). For example, astragalus polysaccharide can reduce the level of oxidative stress in diabetic heart cells, and resveratrol can reduce oxidative stress, alleviate the damage of intestinal epithelial cells caused by oxidative stress (61,62).

Inflammation can cause oxidative stress, and oxidative stress can also cause inflammation (63,64). The proliferation of inflammatory cells can be seen in infectious inflammation. Take neutrophils as an example, when they are activated by pathogens, oxygen consumption increases and a large number of oxygen free radicals are generated, which are used to kill pathogenic

microorganisms. The production of large amount of oxygen free radicals is also the manifestation of oxidative stress, producing a variety of chemotactic substances, such as C3 fragment and leukotriene, to attract and activate neutrophils. A mechanism similar to positive feedback is formed. Even in non-infectious inflammation, many factors, such as degenerative and necrotic tissue cells and their products, ischemia, hypoxia, and immune complexes, can activate inflammatory cells. Oxidative stress can also activate inflammatory cells by causing cell death. Therefore, it can be said that inflammatory response and oxidative stress may not have a fixed sequence, but it must exist at the same time.

m6A and oxidative stress

In a recent experiment, it has been found that there is a regulatory relationship between m6A and oxidative stress. Anders *et al.* found that the number of m6A peaks increased significantly in response to oxidative stress, and described a previously unappreciated function for RNA m6A modification in oxidative-stress response (65). Zhao *et al.* found that induced oxidative stress increased the level of m6A in human keratinocytes, and suggested that this effect may be achieved by increasing the expression levels of WTAP and METTL14. The increase of m6A contents in arsenite-induced oxidative stress might be involved in apoptotic process and platelet activation (66). Highly expressed METTL3 inhibits oxidative stress and apoptosis induced by colistin (67). FB1 induced accumulation of intracellular reactive oxygen species (ROS), accompanied by an increase in METLL3, METLL14, YTHDF1, YTHDF2, YTHDF3 and YTHDC2, and a decrease in ALKBH5 and FTO in human hepatoma cells (68), which indicated that a cross-talk between m6A and redox regulators does occur. Low levels of arsenite up-regulated m6A modification, accompanied with the increase of METTL3, METTL14 and WTAP, in human HaCaT cells, and promoted HaCaT cells survival through inhibiting oxidative stress (69). Cui *et al.* found that the differential m6A modification was mainly enriched in the process associated with oxidative stress during the hepatic fibrosis (70). Mitochondrial activity was restored, and oxidative stress and ROS were induced in Von Hippel-Lindau-deficient cells in which FTO was overexpressed (71). In conclusion, oxidative stress can induce the change of m6A modification, and the change of m6A modification can also change the state of oxidative stress.

Conclusions

Oxidative stress and inflammation are involved in many pathophysiological processes, including tumor, aging, diabetes, cardiovascular disease and so on. As a kind of post transcription modification, m6A is involved in gene expression regulation and involves many biological processes, including oxidative stress and inflammation. This article mainly reviews the role and molecular mechanism of m6A in the occurrence and development of many diseases by regulating oxidative stress and inflammation. There are many problems in the process of oxidative stress and inflammation, which are worthy of further study.

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Footnote

Reporting Checklist: The authors have completed the Narrative Review reporting checklist. Available at <https://biotarget.amegroups.com/article/view/10.21037/biotarget-21-1/rc>

Conflict of Interest: All authors have completed the ICMJE uniform disclosure form (available at <https://biotarget.amegroups.com/article/view/10.21037/biotarget-21-1/coif>). HS serves as an unpaid Executive Editor-in-Chief of *Biotarget*. The other authors have no conflicts of interest to declare.

Ethical Statement: The authors are accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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