

综述

m⁶A 甲基化修饰调控肿瘤免疫的研究进展

周海霞, 张 靖

上海交通大学医学院附属第六人民医院消化科, 上海 200233

[摘要] N⁶-甲基腺苷 (N⁶-methyladenosine, m⁶A) 是一种调控真核细胞基因表达最常见的修饰方式, 影响 RNA 的剪接、降解、稳定性以及蛋白翻译等过程。研究表明 m⁶A 甲基化修饰与肿瘤发生发展密切相关, 在肿瘤免疫应答的相关过程中也发挥着重要的调控作用。m⁶A 修饰参与调节免疫细胞的分化、成熟过程以及相关的抗肿瘤免疫反应。在肿瘤微环境中, m⁶A 修饰也可影响免疫细胞的募集、活化和极化等, 从而促进或抑制肿瘤细胞的增殖与转移, 起到重塑肿瘤免疫微环境的重要作用。近年来肿瘤的免疫治疗逐渐应用于临床, 如免疫检查点抑制剂治疗、过继性细胞免疫治疗等, 都取得了较好的临床效果。通过靶向 m⁶A 修饰来干预机体免疫系统, 如通过小分子抑制剂靶向失调的 m⁶A 调控因子、诱导免疫细胞重编程等, 可提高抗肿瘤免疫反应, 加强免疫细胞对肿瘤细胞的识别和杀伤能力。m⁶A 修饰是肿瘤免疫治疗的一个新方向, 具有潜在的临床应用价值。该文围绕 m⁶A 甲基化修饰对免疫细胞及肿瘤免疫应答的调控作用进行综述, 探讨其免疫治疗的新思路。

[关键词] m⁶A 甲基化; 肿瘤免疫; 免疫治疗

[DOI] 10.3969/j.issn.1674-8115.2024.01.016 **[中图分类号]** R730.51 **[文献标志码]** A

Research progress of m⁶A methylation modification in regulating tumor immunity

ZHOU Haixia, ZHANG Jing

Department of Gastroenterology, Shanghai Sixth People's Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai 200233, China.

[Abstract] N⁶-methyladenosine (m⁶A) is the most prevalent modification that regulates gene expression in eukaryotes. It regulates splicing, degradation, stability, and translation of RNA. Numerous studies have demonstrated the close association between m⁶A methylation and tumor development, highlighting its crucial role in regulating tumor immune response. The m⁶A modification actively participates in governing immune cell differentiation and maturation as well as modulating anti-tumor immune responses. Within the tumor microenvironment, m⁶A modification can also impact the recruitment, activation, and polarization of immune cells, thereby either promoting or inhibiting tumor cell proliferation and metastasis. Consequently, it plays a pivotal role in reshaping the tumor immune microenvironment. In recent years, immunotherapy for tumors has been increasingly applied to clinical practice with notable success achieved through approaches such as immune checkpoint inhibitor therapy and adoptive cell immunotherapy. Targeting m⁶A modifications to interfere with the immune system, such as targeting dysregulated m⁶A regulators through small molecule inhibitors and inducing immune cell reprogramming, can improve anti-tumor immune response and strengthen immune cells' ability to recognize and kill tumor cells. The m⁶A modification represents a novel avenue for potential clinical application within tumor immunotherapy. This review provides a comprehensive summary of the regulatory impact of m⁶A methylation modification on immune cells in the context of cancer, while also delving into novel targets for tumor immunotherapy.

[Key words] m⁶A methylation; tumor immunity; immunotherapy

N⁶-甲基腺苷 (N⁶-methyladenosine, m⁶A) 是一种广泛存在于真核细胞 RNA 上的碱基修饰行为。研究^[1]表明, m⁶A 甲基化参与调控多种细胞分子通路, 与肿瘤发生、侵袭以及肿瘤微环境形成密切相关。

m⁶A 修饰在免疫系统的发育和免疫应答的诱导过程中也发挥重要作用^[2]。免疫细胞参与肿瘤微环境的形成, 通过 m⁶A 修饰调控免疫细胞效应功能, 从而发挥抗肿瘤作用, 有望成为肿瘤免疫治疗新靶标。

[基金项目] 上海市自然科学基金 (21ZR1448700); 上海交通大学医学院“双百人”项目 (20191831)。

[作者简介] 周海霞 (2000—), 女, 硕士生; 电子信箱: zhaixia000@163.com。

[通信作者] 张 靖, 电子信箱: jing5522724@163.com。

[Funding Information] Shanghai Natural Science Foundation (21ZR1448700); "Two-hundred Talents" Program of Shanghai Jiao Tong University School of Medicine (20191831).

[Corresponding Author] ZHANG Jing, Email: jing5522724@163.com.

1 m⁶A 甲基化修饰成员及其功能

m⁶A 修饰, 即腺苷位于第 6 位的氮原子(nitrogen, N)发生甲基化, 是真核生物 mRNA 最丰富的内部修饰, 主要调节 RNA 的稳定性、剪接、降解、翻译等过程^[3-5]。m⁶A 修饰主要由三类酶参与完成——甲基转移酶(writers)、去甲基化酶(erasers)和甲基化识别酶(readers), 分别调控 m⁶A 的催化、去除和识别。m⁶A 甲基转移酶复合物, 包括核心组分甲基转移酶样 3 (methyltransferase like 3, METTL3)、甲基转移酶样 14 (methyltransferase like 14, METTL14) 和其他调控因子如 Wilms' 肿瘤蛋白 1 相关蛋白(Wilms' tumor 1-associating protein, WTAP)、病毒样 m⁶A 甲基转移酶相关蛋白(vir like m⁶A methyltransferase associated protein, VIRMA/KIAA1429)、RNA 结合基序蛋白 15/15B (RNA binding motif protein 15/15B, RBM15/15B)、Cbl 原癌基因样 1 (Cbl proto-oncogene like 1, HAKAI)、锌指 CCCH 类包含蛋白 13 (zinc finger CCCH-type containing 13, ZC3H13), 此外还有甲基转移酶样 16 (methyltransferase like 16, METTL16) 等单一的甲基转移酶^[6]。去甲基化酶可以逆转 m⁶A 修饰, 主要包括脂肪和肥胖相关蛋白(fat mass and obesity associated protein, FTO)、AlkB 同源蛋白 5 (AlkB homolog 5, ALKBH5)^[6]。甲基化识别酶主要包括 YTH 结构域蛋白家族, 如 YTH 结构域 m⁶A RNA 结合蛋白 1/2/3 (YTH N⁶-methyladenosine RNA binding protein 1/2/3, YTHDF1/2/3)、YTH 结构域包含蛋白 1/2 (YTH domain containing 1/2, YTHDC1/2), 以及胰岛素样生长因子 2 mRNA 结合蛋白 1/2/3 (insulin-like growth factor 2 mRNA-binding protein 1/2/3, IGF2BP1/2/3) 等^[6]。这三类酶共同调控 m⁶A 动态平衡, 对于细胞的生长发育和功能发挥至关重要^[7-8]。

2 m⁶A 修饰与肿瘤固有免疫

固有免疫是机体发育过程中形成的非特异性防御功能, 发挥抗原提呈、吞噬等作用, 是抗肿瘤免疫的第一道防线。固有免疫细胞包括树突状细胞(dendritic cell, DC)、自然杀伤细胞(natural killer cell, NK 细胞)、肿瘤相关巨噬细胞(tumor-associated macrophages, TAM)、单核细胞(monocyte)、中性粒

细胞(neutrophil)、骨髓源性抑制细胞(myeloid-derived suppressor cell, MDSC)、 $\gamma\delta$ T 细胞、肥大细胞(mast cell)等。

2.1 m⁶A 与 DC

DC 是功能最强的抗原提呈细胞(antigen presenting cell, APC), 能有效激活初始 T 细胞, 在免疫应答起始阶段发挥重要作用^[9]。DC 的功能障碍可导致免疫逃逸, 促进肿瘤的发生^[10]。研究^[11]显示, METTL3 介导 m⁶A 修饰增强 CD40、CD80 和 Toll 样受体 4 (Toll-like receptor 4, TLR4) 信号适配器 Toll/白细胞介素-1 β (interleukin-1 β , IL-1 β) 受体结构域衔接蛋白(TIR domain-containing adapter protein, TIRAP)在 DC 的翻译, 以刺激 T 细胞激活, 增强 TLR4/NF- κ B 信号诱导的细胞因子产生。m⁶A 甲基化也可影响 DC 迁移。通过去除 DC 中非编码 RNA lnc-Dpf3 的 m⁶A 修饰, 降低 YTHDF2 介导的 lnc-Dpf3 降解, 可阻碍 DC 迁移, 影响免疫应答启动^[12]。此外 HAN 等^[13]发现, YTHDF1 可以识别 m⁶A 标记的编码溶酶体蛋白酶的转录本, 增加其在 DC 中的翻译, 降解 DC 摄取的抗原。而 YTHDF1 的缺失则可下调溶酶体蛋白酶的表达, 增强 DC 对肿瘤抗原的提呈能力, 从而有效地激活 T 细胞的抗肿瘤反应。

2.2 m⁶A 与 NK 细胞

NK 细胞是固有免疫系统中具有直接杀伤效应的细胞毒性淋巴细胞, 与抗肿瘤、抗病毒感染和免疫调节有关。NK 细胞具有强大的抗肿瘤能力, 被认为是目前除 T 细胞以外, 最有潜力的肿瘤杀伤效应细胞^[14]。研究发现 m⁶A 修饰在维持 NK 细胞稳态和功能效应中起到重要作用。在黑色素瘤中, NK 细胞中 METTL3 的蛋白表达水平与效应分子呈正相关, METTL3 的缺失会改变 NK 细胞的动态平衡, 抑制 NK 细胞在肿瘤微环境中的杀伤功能^[15]。YTHDF2 也在维持 NK 细胞稳态和终末成熟中发挥作用。YTHDF2 在活化的 NK 细胞中表达增加, 通过形成信号转导和转录激活因子 5 (signal transducer and activator of transcription 5, STAT5)-YTHDF2 正反馈环, 促进 NK 细胞的效应功能; 也可通过降低 *Tardb* 基因转录 RNA 的稳定性, 调节 NK 细胞增殖和存活^[16]。

2.3 m⁶A 与 TAM

TAM是浸润在肿瘤组织中的巨噬细胞,在肿瘤微环境的形成等方面发挥重要作用。在肿瘤微环境和刺激因子的作用下,巨噬细胞可以向不同的方向极化,M1型巨噬细胞可以促进免疫反应、抗肿瘤,M2型巨噬细胞则表现为免疫抑制、促进肿瘤进展^[17-19]。METTL3可通过介导*STAT1* mRNA的甲基化修饰,增强其稳定性,从而上调*STAT1*表达,促进M1极化^[20]。YIN等^[21]也证明了METTL3对TAM的调控作用。在黑色素瘤或肺癌的小鼠模型中,METTL3缺陷小鼠TAM在肿瘤中的浸润程度增加,METTL3缺失降低YTHDF1介导SPRED2翻译,通过ERK途径增强NF-κB/STAT3激活,导致肿瘤生长和转移。研究^[22]发现,YTHDF2也可调节TAM抗肿瘤功能,TAM中YTHDF2缺失通过靶向γ干扰素(interferon-γ, IFN-γ)-STAT1信号通路,将TAM重新编程为抗肿瘤表型并增强其抗原交叉提呈能力,进而增强细胞毒性T细胞介导的抗肿瘤免疫。

2.4 m⁶A 与单核细胞

单核细胞在血液循环中能吞噬、清除受伤或衰老的细胞及其碎片,并可迁移到组织分化为巨噬细胞^[23]。在结直肠癌患者的外周血免疫细胞中,单核细胞中的m⁶A水平与单核细胞免疫反应呈负相关^[24]。另外,ZHANG等^[25]发现METTL3介导的m⁶A修饰和YTHDF2介导的识别可促进*PGC-1α* mRNA降解,诱导单核细胞分化为M1型和M2型巨噬细胞,从而发挥调节肿瘤免疫作用。

2.5 m⁶A 与中性粒细胞

中性粒细胞在肿瘤微环境中发挥双重作用,可以直接杀伤肿瘤细胞或与其他免疫成分相互作用介导抗肿瘤反应,也可通过促血管生成、细胞外基质重塑、免疫抑制等促进肿瘤进展^[26]。OU等人^[27]发现,C5aR1⁺中性粒细胞亚群通过WTAP介导的m⁶A甲基化上调*ENO1*诱导乳腺癌细胞糖酵解,与肿瘤进展和患者不良预后有关。衰老的中性粒细胞分泌的外泌体piRNA-17560可增强乳腺癌细胞中FTO表达。FTO通过减少m⁶A甲基化增强锌指E盒结合蛋白1(zinc finger E-box binding homeobox 1, *ZEB1*)基因稳定性,从而导致肿瘤细胞的化学治疗耐药和上皮间质转化。衰老中性粒细胞可作为乳腺癌潜在治疗靶点^[28]。

2.6 m⁶A 与 MDSC

MDSC是由未成熟的前体单核细胞和中性粒细胞组成的骨髓细胞群,具有较强的免疫抑制活性,它们与许多病理条件下的免疫反应调节和肿瘤不良预后密切相关^[29]。METTL3通过碱性螺旋-环-螺旋转录因子家族成员E41(basic helix-loop-helix family member e41, *BHLHE41*)-C-X-C模体趋化因子配体1(C-X-C motif chemokine ligand 1, *CXCL1*)/C-X-C模体趋化因子受体2(C-X-C motif chemokine receptor 2, *CXCR2*)信号通路促进MDSC迁移,促进结直肠癌进展^[30]。在非酒精性脂肪性肝炎相关的肝癌中,YTHDF1在肿瘤组织过表达,诱导IL-6分泌及MDSC募集和激活,抑制抗肿瘤免疫^[31]。

2.7 m⁶A 与 γδT 细胞

γδT细胞是一种执行固有免疫功能的T细胞,其TCR由γ和δ链组成,分布于肠道、呼吸道以及泌尿生殖道等黏膜和皮下组织。γδT细胞既能杀伤肿瘤细胞,又能识别某些肿瘤抗原,参与抗肿瘤免疫应答^[32]。研究表明,m⁶A去甲基化酶ALKBH5调节γδT细胞发育,胸腺细胞中ALKBH5缺失使*Jagged1/Notch2*信号转导受损,有助于增强γδT细胞前体的增殖和分化^[33]。METTL3介导的m⁶A甲基化则可调节mRNA稳定性和双链RNA(double-stranded RNA, dsRNA)含量,以平衡γδT1和γδT17这两个主要功能不同的亚群细胞^[34]。

2.8 m⁶A 与肥大细胞

肥大细胞通过分泌多种细胞因子,参与免疫调节。肥大细胞在肿瘤组织中浸润,分泌组胺、血管内皮生长因子等,可刺激肿瘤血管新生,促进肿瘤生长及转移,还可调控T细胞等免疫细胞的招募和活性,影响抗肿瘤免疫^[35]。研究^[36-37]发现,在食管鳞状细胞癌和胃癌中,METTL3、WTAP等高表达,并且肥大细胞等免疫细胞在肿瘤中浸润增加,提示肥大细胞的浸润受到m⁶A甲基化影响。m⁶A甲基化修饰与肥大细胞功能也密切相关。m⁶A甲基转移酶复合体参与调节肥大细胞的生长增殖,并可影响细胞因子mRNA的稳定性,抑制肥大细胞介导的炎症反应^[38]。

m⁶A修饰对固有免疫细胞的调控作用见表1。

表1 m⁶A修饰对固有免疫细胞的调控作用

Tab 1 Role of m⁶A modifications in innate immune cells

Immune cell	m ⁶ A regulator	Type	Related factor	Function	Reference
DC	METTL3	Writer	CD40, CD80 and Tirap	Positively correlates with DC maturation and function in promoting T-cell activation	[11]
	YTHDF1	Reader	Lysosomal proteases	Negatively correlates with cross-presentation of engulfed tumour neoantigens	[13]
	YTHDF2	Reader	Inc-Dpf3	Positively correlates with DC migration	[12]
NK	METTL3	Writer	SHP-2	Positively correlates antitumor immunity of NK cells	[15]
	YTHDF2	Reader	Tardb	Positively correlates with NK cell antitumor activity as well as NK cell homeostasis and maturation	[16]
TAM	METTL3	Writer	STAT1, STAT3	Positively correlates with M1 macrophage polarization	[20-21]
	YTHDF2	Reader	STAT1	Negatively correlates with macrophage reprogramming and antitumor immunity	[22]
Monocyte	METTL3	Writer	PGC-1α	Positively correlates with monocyte differentiation into different types of macrophages	[25]
Neutrophil	WTAP	Writer	ENO1	Positively correlates with tumor glycolysis mediated by C5aR1-positive neutrophils	[27]
	FTO	Eraser	ZEB1	Positively correlates with senescent neutrophils-mediated chemoresistance in breast cancer	[28]
MDSC	METTL3	Writer	BHLHE41	Positively correlates with MDSC migration	[30]
	YTHDF1	Reader	EZH2	Positively correlates with MDSC recruitment and activation	[31]
γδ T cell	METTL3	Writer	STAT1	Positively correlates with equilibrate γδ T1 and γδ T17 cells	[34]
	ALKBH5	Eraser	Jagged1/Notch2	Negatively correlates with proliferation and differentiation of γδ T cell precursors	[33]
Mast cell	METTL3	Writer	IL-13	Negatively correlates with inflammatory responses of mast cells	[38]

3 m⁶A修饰与肿瘤适应性免疫

适应性免疫又称特异性免疫，是机体在抗原刺激下产生的免疫应答。肿瘤相关抗原被APC识别摄取后提呈给效应细胞，包括T细胞和B细胞，从而启动抗肿瘤免疫应答。

3.1 m⁶A与T细胞

T淋巴细胞来源于骨髓干细胞，在胸腺中分化成熟后迁移至外周完成免疫功能。T细胞具有多种生物学功能，如直接杀伤靶细胞、调控或辅助其他免疫细胞发挥功能，以及产生细胞因子等，在抗肿瘤免疫中占主导地位^[39-40]。T细胞按照功能和表面标志主要可分成以下亚群。

3.1.1 m⁶A与CD4⁺辅助性T细胞 未激活的初始CD4⁺T细胞在各种抗原和细胞因子的刺激和调控下，分化为不同类型的辅助性T细胞（helper T cell，Th细胞）。其中Th1亚型通过协助细胞毒性CD8⁺T细胞和B细胞发挥抗肿瘤功能，也可产生IFN-γ和TNF-α等直接作用于肿瘤细胞；Th2亚型主要分泌IL-4、IL-13等细胞因子，可抑制细胞毒性T细胞的杀伤作用^[41]。研究^[42]发现m⁶A影响初始CD4⁺T细胞的分化，METTL3缺陷的初始T细胞表现出Th1细胞减少，而Th2细胞增加。初始T细胞中METTL3基因敲

除导致细胞因子信号家族细胞因子信号抑制因子1（suppressor of cytokine signaling1，SOCS1）、SOCS3和CISH蛋白水平抑制，从而抑制IL-7/STAT5信号通路，影响T细胞稳态和分化^[42]。m⁶A甲基化也影响CD4⁺T细胞的功能。去甲基化酶ALKBH5通过降低CXCL2和IFN-γ mRNA中m⁶A水平，增强其mRNA稳定性和翻译，促进Th1细胞功能^[43]。

3.1.2 m⁶A与调节性T细胞 调节性T细胞（regulatory T cell，Treg细胞）是CD4⁺T细胞分化的一个亚群，可介导对免疫细胞功能的负调节。研究表明m⁶A甲基化同样在Treg细胞的分化和效应功能中发挥关键作用。METTL14缺失可导致初始T细胞无法维持向诱导Treg细胞的分化^[44]。METTL3介导m⁶A甲基化是维持Treg抑制功能所必需的，而Treg细胞中METTL3缺失增加Socs mRNA水平，引起IL-2/STAT5信号通路失活，导致Treg细胞功能和稳定性受到破坏^[45]。

3.1.3 m⁶A与CD8⁺T细胞 CD8⁺T细胞为细胞毒性T细胞，其激活后可释放穿孔素、颗粒酶等杀伤肿瘤细胞。多项研究表明，m⁶A甲基化修饰与CD8⁺T细胞肿瘤浸润密切相关。在结肠癌间质细胞中，METTL14表达与m⁶A水平和CD8⁺T细胞浸润程度呈正相关^[46]；在非小细胞肺癌中，YTHDF1和YTHDF2高表达导致肿瘤间质中包括CD8⁺T细胞在

内淋巴细胞亚群浸润程度均显著增加^[47]。同样在非小细胞肺癌中, LIU等^[48]发现METTL3可介导环状RNA circIGF2BP3的m⁶A修饰促进其环化, circIGF2BP3通过miR-328-3p和miR-3173-5p竞争性上调PKP3,使CD8⁺T细胞浸润减少,抑制肿瘤免疫反应。此外,小鼠黑色素瘤细胞可通过FTO介导糖酵解途径,抑制CD8⁺T细胞激活,逃避免疫监视;而FTO基因敲除后,肿瘤细胞糖酵解活性下降,CD8⁺T细胞功能恢复^[49]。

3.2 m⁶A与B细胞

B细胞在抗原刺激下可分化为浆细胞,产生抗体介导体液免疫应答。在肿瘤免疫中,B细胞主要依赖分泌抗肿瘤相关抗原抗体,活化的B细胞还可通过抗

原提呈促进T细胞激活,发挥抗肿瘤作用^[50]。研究^[51]发现m⁶A修饰参与调节早期B细胞发育,如METTL14的缺失会阻断幼稚B细胞从前B期(pro-B cell)向大前B期(large pre-B cell)的转变,影响B细胞成熟。另一项研究^[52]表明METTL14介导的m⁶A修饰促进负免疫调节因子(如Lax1和Tipe2)的mRNA衰变,从而影响生发中心B细胞的阳性选择和增殖。另一方面,B细胞中异常m⁶A修饰调节肿瘤发生发展。多发性骨髓瘤患者浆细胞中FTO上调,m⁶A甲基化水平显著降低,促进多发性骨髓瘤细胞增殖、迁移和侵袭^[53]。

m⁶A修饰对适应性免疫细胞的调控及在肿瘤免疫中的作用见表2和图1。

表2 m⁶A修饰对适应性免疫细胞的调控作用

Tab 2 Role of m⁶A modifications in adaptive immune cells

Immune cell	m ⁶ A regulator	Type	Related factor	Function	Reference
CD4 ⁺ T cell	METTL3	Writer	SOCS	Positively correlates with proliferation and differentiation of T cells	[42]
	ALKBH5	Eraser	IFN-γ, CXCL2	Positively correlates with Th1 cell activation	[43]
Treg cell	METTL3	Writer	SOCS	Positively correlates with sustaining Treg suppressive functions	[45]
	METTL14	Writer	RORγt	Positively correlates with Tregs differentiation	[44]
CD8 ⁺ T cell	METTL3	Writer	circIGF2BP3	Negatively correlates with CD8 ⁺ T cell responses and facilitates tumor immune	[48]
	METTL14	Writer	Ebi3	Negatively correlates with dysfunctional CD8 ⁺ T cell levels in patients with colorectal cancer	[46]
	YTHDF1/2	Reader	unknown	Positively correlates with tumor-infiltrating lymphocytes, including CD8 ⁺ T cells	[47]
	FTO	Eraser	c-Jun, JunB, and C/EBPβ	Positively correlates with glycolytic metabolism of tumor cells; negatively correlates with CD8 ⁺ T cell responses	[49]
B cell	METTL14	Writer	Lax1, Tipe2	Positively correlates with B cell maturation	[52]
	FTO	Eraser	HSF1	Positively correlates with tumor-promoting and pro-metastatic in multiple myeloma	[53]

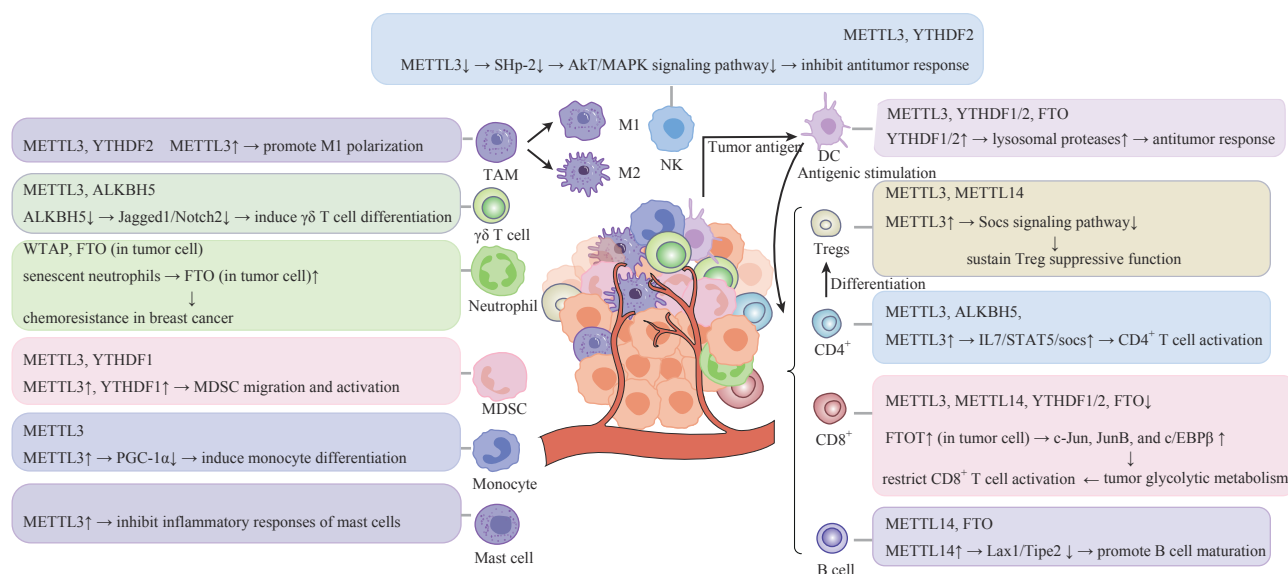
4 m⁶A甲基化修饰在肿瘤免疫治疗中的应用

肿瘤免疫治疗旨在外源干预机体免疫系统,恢复、提高机体的抗肿瘤免疫反应,加强对肿瘤细胞的识别和杀伤能力。目前临床上已应用的肿瘤免疫治疗方法主要包括免疫检查点抑制剂治疗、过继性细胞免疫治疗等;而将m⁶A作为靶点来调控机体免疫系统的抗肿瘤应答,可能是免疫治疗新的方向。

4.1 靶向m⁶A修饰辅助免疫检查点治疗

免疫检查点在调节免疫激活程度、维持免疫稳态

方面发挥着关键作用。肿瘤细胞可表达某些物质来激活免疫检查点,逃避免疫监视,抑制抗肿瘤免疫反应。以程序性死亡受体1(programmed cell death-1, PD-1)抗体为代表的免疫检查点抑制剂类药物可解除这种抑制作用,重新激活免疫细胞。目前m⁶A修饰对免疫检查点的影响也得到了广泛研究。结直肠癌中,敲除METTL3或METTL14可通过YTHDF2稳定Stat1和Irf1 mRNA,促进IFN-γ-Stat1-Irf1信号通路,进而增强结直肠癌抗PD-1治疗中的免疫应答^[54]。研究^[55]发现,YTHDF1通过m⁶A-p65-CXCL1/CXCR2轴抑制抗肿瘤免疫以促进结直肠癌进展,也可作为免疫检查点阻断疗法的治疗靶点。

图1 m⁶A修饰对免疫细胞及肿瘤免疫应答的调控作用Fig 1 Modification of m⁶A in immune cells and antitumor immune response

4.2 靶向m⁶A调节因子增强免疫应答

m⁶A甲基化在肿瘤的发生发展以及抗肿瘤免疫中起到重要作用, 靶向调控失调的m⁶A修饰成为免疫治疗的新策略。目前已经开发出一系列m⁶A调节因子的抑制剂, 并且研究验证了m⁶A抑制剂可增强抗肿瘤反应。如FTO抑制剂Dac51可恢复肿瘤组织中CD8⁺T细胞免疫监视功能, 抑制肿瘤生长^[49]。FB23和FB23-2也可直接与FTO结合, 抑制其去甲基化酶活性, 在控制急性髓系白血病 (acute myeloid leukemia, AML) 进展中发挥作用^[56]。研究也报道了METTL3抑制剂STM2457在抗AML中具有较好疗效^[57]。通过小分子抑制剂靶向失调的m⁶A调控因子具有临床应用潜力, 但仍需深入研究其作用机制并验证其安全性。

4.3 调节免疫细胞重编程

通过干扰免疫细胞中发挥特定功能所必需的m⁶A位点, 可诱导免疫细胞重编程从而发挥抗肿瘤作用。鉴于T细胞在肿瘤免疫中的主导地位, 大多数肿瘤免疫疗法和对抗免疫逃逸集中在T细胞重编程。例如, 肿瘤微环境中Treg抑制CD8⁺T细胞的肿瘤杀伤功能, 通过干扰m⁶A修饰选择性去除肿瘤浸润性Treg可能具有一定疗效^[45]。此外, 在TAM中, TLR9激动剂结合小干扰RNA靶向YTHDF2, 可使TAM重新编程为抗肿瘤表型, 提高抗肿瘤作用^[22]。

4.4 预测临床预后

m⁶A修饰也可以作为某些肿瘤早期诊断、预后预测和风险分层的生物标志物。ZHANG等^[58]建立了一套评分系统 (m⁶Ascore) 来量化胃癌中m⁶A修饰模式, 并与肿瘤微环境中免疫细胞浸润特征相联系; 他们发现m⁶A甲基化修饰模式与肿瘤免疫表型和抗PD-1/程序性死亡因子配体1 (programmed cell death ligand 1, PD-L1) 免疫治疗应答显著相关; 结果表明m⁶Ascore有助于预测抗PD-1/L1免疫治疗应答, 是一种可靠的免疫治疗预后和临床评估的生物标志物。

5 总结与展望

m⁶A甲基化修饰参与调控多种免疫细胞的发生、稳态和功能, 在重塑肿瘤免疫微环境过程中发挥重要作用。其表达可能影响免疫细胞在某些肿瘤中的浸润程度, 也可能成为肿瘤进展过程中的促进或抑制因素。因此, 在肿瘤免疫治疗领域, m⁶A修饰是一个重要的潜在靶标。但结合现有研究, 还有较多问题有待进一步深入, 如m⁶A对肿瘤免疫的调节可以促进或抑制, 需要探索更精准的调控方式; 是否存在肿瘤特异性m⁶A靶点或调控因子; 靶向m⁶A调节机体免疫系统的安全性还需进一步验证等。m⁶A甲基化修饰与肿瘤免疫应用于临床尚有许多问题亟待解决, 但其对肿瘤免疫治疗提供了新思路, 具有重要的应用意义和前景。

利益冲突声明/Conflict of Interests

所有作者声明不存在利益冲突。

All authors disclose no relevant conflict of interests.

作者贡献/Authors' Contributions

周海霞与张靖共同构思文章框架,周海霞负责文献整理、撰写初稿并完成修改,张靖提出写作思路并修改、审阅全文。两位作者均阅读并同意了最终稿件的提交。

ZHOU Haixia and ZHANG Jing jointly conceived the framework of the manuscript. ZHOU Haixia was in charge of literature review, wrote the first draft and finished the revision. ZHANG Jing proposed the writing ideas, and revised and reviewed the full text. Both authors have read the last version of paper and consented for submission.

- Received: 2023-09-06
- Accepted: 2023-16-18
- Published online: 2024-01-28

参·考·文·献

- [1] YI Y C, CHEN X Y, ZHANG J, et al. Novel insights into the interplay between m⁶A modification and noncoding RNAs in cancer[J]. *Mol Cancer*, 2020, 19(1): 121.
- [2] SHULMAN Z, STERN-GINOSAR N. The RNA modification N⁶-methyladenosine as a novel regulator of the immune system[J]. *Nat Immunol*, 2020, 21(5): 501-512.
- [3] WANG X, LU Z K, GOMEZ A, et al. N⁶-methyladenosine-dependent regulation of messenger RNA stability[J]. *Nature*, 2014, 505(7481): 117-120.
- [4] LI A, CHEN Y S, PING X L, et al. Cytoplasmic m⁶A reader YTHDF3 promotes mRNA translation[J]. *Cell Res*, 2017, 27(3): 444-447.
- [5] ROUNDTREE I A, EVANS M E, PAN T, et al. Dynamic RNA modifications in gene expression regulation[J]. *Cell*, 2017, 169(7): 1187-1200.
- [6] DENG L J, DENG W Q, FAN S R, et al. m⁶A modification: recent advances, anticancer targeted drug discovery and beyond[J]. *Mol Cancer*, 2022, 21(1): 52.
- [7] JIA G F, FU Y, ZHAO X, et al. N⁶-methyladenosine in nuclear RNA is a major substrate of the obesity-associated FTO[J]. *Nat Chem Biol*, 2011, 7(12): 885-887.
- [8] ZHENG G Q, DAHL J A, NIU Y M, et al. ALKBH5 is a mammalian RNA demethylase that impacts RNA metabolism and mouse fertility[J]. *Mol Cell*, 2013, 49(1): 18-29.
- [9] MORANTE-PALACIOS O, FONDELLI F, BALLESTAR E, et al. Tolerogenic dendritic cells in autoimmunity and inflammatory diseases[J]. *Trends Immunol*, 2021, 42(1): 59-75.
- [10] DIAMOND M S, LIN J H, VONDERHEIDE R H. Site-dependent immune escape due to impaired dendritic cell cross-priming[J]. *Cancer Immunol Res*, 2021, 9(8): 877-890.
- [11] WANG H M, HU X, HUANG M Y, et al. Mettl3-mediated mRNA m⁶A methylation promotes dendritic cell activation[J]. *Nat Commun*, 2019, 10(1): 1898.
- [12] LIU J, ZHANG X M, CHEN K, et al. CCR7 chemokine receptor-inducible lnc-Dpf3 restrains dendritic cell migration by inhibiting HIF-1 α -mediated glycolysis[J]. *Immunity*, 2019, 50(3): 600-615. e15.
- [13] HAN D L, LIU J, CHEN C Y, et al. Anti-tumour immunity controlled through mRNA m⁶A methylation and YTHDF1 in dendritic cells[J]. *Nature*, 2019, 566(7743): 270-274.
- [14] WU S Y, FU T, JIANG Y Z, et al. Natural killer cells in cancer biology and therapy[J]. *Mol Cancer*, 2020, 19(1): 120.
- [15] SONG H, SONG J X, CHENG M, et al. METTL3-mediated m⁶A RNA methylation promotes the anti-tumour immunity of natural killer cells[J]. *Nat Commun*, 2021, 12(1): 5522.
- [16] MA S B, YAN J Z, BARR T, et al. The RNA m⁶A reader YTHDF2 controls NK cell antitumor and antiviral immunity[J]. *J Exp Med*, 2021, 218(8): e20210279.
- [17] LEWIS C E, POLLARD J W. Distinct role of macrophages in different tumor microenvironments[J]. *Cancer Res*, 2006, 66(2): 605-612.
- [18] CAUX C, RAMOS R N, PRENDERGAST G C, et al. A milestone review on how macrophages affect tumor growth[J]. *Cancer Res*, 2016, 76(22): 6439-6442.
- [19] PITTET M J, MICHIELIN O, MIGLIORINI D. Clinical relevance of tumour-associated macrophages[J]. *Nat Rev Clin Oncol*, 2022, 19(6): 402-421.
- [20] LIU Y H, LIU Z J, TANG H, et al. The N⁶-methyladenosine (m⁶A)-forming enzyme METTL3 facilitates M1 macrophage polarization through the methylation of *STAT1* mRNA[J]. *Am J Physiol Cell Physiol*, 2019, 317(4): C762-C775.
- [21] YIN H L, ZHANG X, YANG P Y, et al. RNA m⁶A methylation orchestrates cancer growth and metastasis via macrophage reprogramming[J]. *Nat Commun*, 2021, 12(1): 1394.
- [22] MA S B, SUN B F, DUAN S Q, et al. YTHDF2 orchestrates tumor-associated macrophage reprogramming and controls antitumor immunity through CD8⁺ T cells[J]. *Nat Immunol*, 2023, 24(2): 255-266.
- [23] OLINGY C E, DINH H Q, HEDRICK C C. Monocyte heterogeneity and functions in cancer[J]. *J Leukoc Biol*, 2019, 106(2): 309-322.
- [24] XIE J Y, HUANG Z J, JIANG P, et al. Elevated N⁶-methyladenosine RNA levels in peripheral blood immune cells: a novel predictive biomarker and therapeutic target for colorectal cancer[J]. *Front Immunol*, 2021, 12: 760747.
- [25] ZHANG X N, LI X, JIA H T, et al. The m⁶A methyltransferase METTL3 modifies PGC-1 α mRNA promoting mitochondrial dysfunction and oxLDL-induced inflammation in monocytes[J]. *J Biol Chem*, 2021, 297(3): 101058.
- [26] JAILLON S, PONZETTA A, MITRI D D, et al. Neutrophil diversity and plasticity in tumour progression and therapy[J]. *Nat Rev Cancer*, 2020, 20(9): 485-503.
- [27] OU B C, LIU Y, YANG X W, et al. C5aR1-positive neutrophils promote breast cancer glycolysis through WTAP-dependent m⁶A methylation of *ENO1*[J]. *Cell Death Dis*, 2021, 12(8): 737.
- [28] OU B C, LIU Y, GAO Z X, et al. Senescent neutrophils-derived exosomal piRNA-17560 promotes chemoresistance and EMT of breast cancer via FTO-mediated m⁶A demethylation[J]. *Cell Death Dis*, 2022, 13(10): 905.
- [29] VEGLIA F, SANSEVIERO E, GABRILOVICH D I. Myeloid-derived suppressor cells in the era of increasing myeloid cell diversity[J]. *Nat Rev Immunol*, 2021, 21(8): 485-498.
- [30] CHEN H R, PAN Y S, ZHOU Q M, et al. METTL3 inhibits antitumor immunity by targeting m⁶A-BHLHE41-CXCL1/CXCR2 axis to promote colorectal cancer[J]. *Gastroenterology*, 2022, 163(4): 891-907.
- [31] WANG L N, ZHU L F, LIANG C, et al. Targeting N⁶-methyladenosine reader YTHDF1 with siRNA boosts antitumor immunity in NASH-HCC by inhibiting EZH2-IL-6 axis[J]. *J Hepatol*, 2023, 79(5): 1185-1200.
- [32] SILVA-SANTOS B, MENSURADO S, COFFELT S B. $\gamma\delta$ T cells: pleiotropic immune effectors with therapeutic potential in cancer[J].



- Nat Rev Cancer, 2019, 19(7): 392-404.
- [33] DING C B, XU H, YU Z B, et al. RNA m⁶A demethylase ALKBH5 regulates the development of $\gamma\delta$ T cells[J]. Proc Natl Acad Sci U S A, 2022, 119(33): e2203318119.
- [34] XIAO Z Q, WANG S S, TIAN Y X, et al. METTL3-mediated m⁶A methylation orchestrates mRNA stability and dsRNA contents to equilibrate $\gamma\delta$ T1 and $\gamma\delta$ T17 cells[J]. Cell Rep, 2023, 42(7): 112684.
- [35] LICHTERMAN J N, REDDY S M. Mast cells: a new frontier for cancer immunotherapy[J]. Cells, 2021, 10(6): 1270.
- [36] GUO W, TAN F W, HUAI Q L, et al. Comprehensive analysis of PD-L1 expression, immune infiltrates, and m⁶A RNA methylation regulators in esophageal squamous cell carcinoma[J]. Front Immunol, 2021, 12: 669750.
- [37] XU Z Y, CHEN Q L, SHU L L, et al. Expression profiles of m⁶A RNA methylation regulators, PD-L1 and immune infiltrates in gastric cancer[J]. Front Oncol, 2022, 12: 970367.
- [38] LEONI C, BATACLAN M, ITO-KUREHA T, et al. The mRNA methyltransferase Mettl3 modulates cytokine mRNA stability and limits functional responses in mast cells[J]. Nat Commun, 2023, 14(1): 3862.
- [39] WALSH S R, SIMOVIC B, CHEN L, et al. Endogenous T cells prevent tumor immune escape following adoptive T cell therapy[J]. J Clin Invest, 2019, 129(12): 5400-5410.
- [40] SI J W, SHI X J, SUN S H, et al. Hematopoietic progenitor kinase1 (HPK₁) mediates T cell dysfunction and is a druggable target for T cell-based immunotherapies[J]. Cancer Cell, 2020, 38(4): 551-566. e11.
- [41] BORST J, AHRENDTS T, BAĞBALA N, et al. CD4⁺ T cell help in cancer immunology and immunotherapy[J]. Nat Rev Immunol, 2018, 18(10): 635-647.
- [42] LI H B, TONG J Y, ZHU S, et al. m⁶A mRNA methylation controls T cell homeostasis by targeting the IL-7/STAT5/SOCS pathways[J]. Nature, 2017, 548(7667): 338-342.
- [43] ZHOU J, ZHANG X L, HU J J, et al. m⁶A demethylase ALKBH5 controls CD4⁺ T cell pathogenicity and promotes autoimmunity[J]. Sci Adv, 2021, 7(25): eabg0470.
- [44] LU T X, ZHENG Z, ZHANG L D, et al. A new model of spontaneous colitis in mice induced by deletion of an RNA m⁶A methyltransferase component METTL14 in T cells[J]. Cell Mol Gastroenterol Hepatol, 2020, 10(4): 747-761.
- [45] TONG J Y, CAO G C, ZHANG T, et al. m⁶A mRNA methylation sustains treg suppressive functions[J]. Cell Res, 2018, 28(2): 253-256.
- [46] DONG L H, CHEN C Y, ZHANG Y W, et al. The loss of RNA N⁶-adenosine methyltransferase Mettl14 in tumor-associated macrophages promotes CD8⁺ T cell dysfunction and tumor growth[J]. Cancer Cell, 2021, 39(7): 945-957. e10.
- [47] TSUCHIYA K, YOSHIMURA K, INOUE Y, et al. YTHDF1 and YTHDF2 are associated with better patient survival and an inflamed tumor-immune microenvironment in non-small-cell lung cancer[J]. Oncoimmunology, 2021, 10(1): 1962656.
- [48] LIU Z C, WANG T T, SHE Y L, et al. N⁶-methyladenosine-modified circIGF2BP3 inhibits CD8⁺ T-cell responses to facilitate tumor immune evasion by promoting the deubiquitination of PD-L1 in non-small cell lung cancer[J]. Mol Cancer, 2021, 20(1): 105.
- [49] LIU Y, LIANG G H, XU H J, et al. Tumors exploit FTO-mediated regulation of glycolytic metabolism to evade immune surveillance[J]. Cell Metab, 2021, 33(6): 1221-1233. e11.
- [50] LAUMONT C M, NELSON B H. B cells in the tumor microenvironment: multi-faceted organizers, regulators, and effectors of anti-tumor immunity[J]. Cancer Cell, 2023, 41(3): 466-489.
- [51] ZHENG Z, ZHANG L D, CUI X L, et al. Control of early B cell development by the RNA N⁶-methyladenosine methylation[J]. Cell Rep, 2020, 31(13): 107819.
- [52] HUANG H J, ZHANG G P, RUAN G X, et al. Mettl14-mediated m⁶A modification is essential for germinal center B cell response[J]. J Immunol, 2022, 208(8): 1924-1936.
- [53] XU A S, ZHANG J S, ZUO L P, et al. FTO promotes multiple myeloma progression by posttranscriptional activation of HSF₁ in an m⁶A-YTHDF2-dependent manner[J]. Mol Ther, 2022, 30(3): 1104-1118.
- [54] WANG L L, HUI H, AGRAWAL K, et al. m⁶A RNA methyltransferases METTL3/14 regulate immune responses to anti-PD-1 therapy[J]. EMBO J, 2020, 39(20): e104514.
- [55] BAO Y, ZHAI J N, CHEN H R, et al. Targeting m⁶A reader YTHDF1 augments antitumour immunity and boosts anti-PD-1 efficacy in colorectal cancer[J]. Gut, 2023, 72(8): 1497-1509.
- [56] HUANG Y, SU R, SHENG Y, et al. Small-molecule targeting of oncogenic FTO demethylase in acute myeloid leukemia[J]. Cancer Cell, 2019, 35(4): 677-691. e10.
- [57] YANKOVA E, BLACKABY W, ALBERTELLA M, et al. Small-molecule inhibition of METTL3 as a strategy against myeloid leukaemia[J]. Nature, 2021, 593(7860): 597-601.
- [58] ZHANG B, WU Q, LI B, et al. m⁶A regulator-mediated methylation modification patterns and tumor microenvironment infiltration characterization in gastric cancer[J]. Mol Cancer, 2020, 19(1): 53.

[本文编辑] 张慧俊