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REVIEW



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HIGHLIGHTS

Nanomaterial-Based Repurposing of Macrophage Metabolism and Its Applications

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- A large-scale metabolic adaptation in M1-polarized macrophages compared with M2 macrophages, along with multiple altered metabolite parameters that can serve as potential targets, have been discussed.
- Nanomaterial-based repurposing of macrophage metabolism and its applications are systematically summarized and illustrated using representative examples.
- Potential challenges, additional information about future research objectives, and priorities of nanomaterial-based macrophage immunotherapy are highlighted.

ABSTRACT Macrophage immunotherapy represents an emerging therapeutic approach aimed at modulating the immune response to alleviate disease symptoms. Nanomaterials (NMs) have been engineered to monitor macrophage metabolism, enabling the evaluation of disease progression and the replication of intricate physiological signal patterns. They achieve this either directly or by delivering regulatory signals, thereby mapping phenotype to effector functions through metabolic repurposing to customize macrophage fate for therapy. However, a comprehensive summary regarding NM-mediated macrophage visualization



and coordinated metabolic rewiring to maintain phenotypic equilibrium is currently lacking. This review aims to address this gap by outlining recent advancements in NM-based metabolic immunotherapy. We initially explore the relationship between metabolism, polarization, and disease, before delving into recent NM innovations that visualize macrophage activity to elucidate disease onset and fine-tune its fate through metabolic remodeling for macrophage-centered immunotherapy. Finally, we discuss the prospects and challenges of NM-mediated metabolic immunotherapy, aiming to accelerate clinical translation. We anticipate that this review will serve as a valuable reference for researchers seeking to leverage novel metabolic intervention-matched immunomodulators in macrophages or other fields of immune engineering.

KEYWORDS Immunomodulatory nanomaterial; Macrophage polarization; Macrophage metabolic reprogramming; Immune engineering

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1 Introduction

Macrophages are vital cellular components of the innate immune system, playing crucial roles in regulating inflammatory responses to maintain tissue homeostasis [1–3]. However, macrophage responses represent a double-edged sword, acting both as a protective "safety guard" and as a potential instigator of disease [4]. They exhibit a full spectrum of polarized phenotypes, encompassing proinflammatory-like (M1) and anti-inflammatory-like (M2) states [5–9] (Table 1). Macrophage polarization (M1/M2) remains dynamic and finely balanced due to their heterogeneity and plasticity, adapting to tailored cues in the physiological microenvironment [9, 10].

Immunometabolism has provided novel insights into the hyperactivation of macrophage metabolism. M1 macrophages rewrite their metabolic program to coordinate the adaptive immune response compared to M2 macrophages, which rely on oxidative phosphorylation (OXPHOS). The metabolic adaption includes an interrupted tricarboxylic acid (TCA) cycle, increased activation of glycolysis and the pentose phosphate pathway (PPP), and alterations in various metabolic parameters such as succinate or itaconate, reactive oxygen and nitrogen species (RONS), and amino acids [11-15]. Several excellent reviews have elaborately described the intricate relationship between macrophage polarization and metabolism [11, 13, 14, 16]. This alteration-coordinated metabolic rewiring profoundly influences macrophage gene expression, leading to unbalanced M1/M2 polarization [16-19], which determines the progression of diseases such as osteoarthritis (OA) [20], acute lung injury (ALI) [21], myocardial infarction (MI) [22], diabetic wounds [23, 24], atherosclerosis [25], and inflammatory bowel disease (IBD) [26]. Conversely, tumor-associated macrophages (TAMs) initially exhibit a higher glycolysis rate to support antitumor M1 activity, but gradually transition toward more efficient OXPHOS and fatty acid oxidation (FAO) to promote protumor M2 functions, thereby facilitating tumor immune escape [18, 27–30]. Given the critical role of altered metabolic profiles as positive or negative regulators of macrophage fate in driving disease evolution, in situ tracking of macrophage metabolism holds significant importance for elucidating disease progression. Moreover, intervening in metabolism to exacerbate metabolic imbalance or restore metabolic homeostasis has been exploited as a fascinating avenue to reshape macrophage phenotypes and elicit the corresponding immune response against diseases.

Nanomaterials (NMs) have been extensively fabricated to display and transmit macrophage regulatory signals in a precise and closely physiological manner, simulating artificial microenvironments and guiding macrophage fate [31]. This is benefited by their intrinsic physicochemical properties and macrophage phagocytosis, in which foreign particles are preferentially internalized [32, 33]. Recently, the metabolic pathways of M1/M2 macrophages have garnered increasing attention from researchers, leading to their adoption in macrophage diagnosis and therapeutic exploitation. This trend has facilitated the blossom of suitable theranostic agents for macrophage-driven diseases. Several researchers have exploited imaging probes, integrating them with advanced technologies such as magnetic resonance imaging (MRI), to track macrophage activity in situ and reveal disease progression [34-38], such as dual-responsive nanoreporters for monitoring macrophage phenotypes [39]. NMs serve as emerging immunomodulatory weapons, enabling the remote manipulation of macrophage metabolism [19, 31, 40], thereby directing their

 Table 1
 Potential metabolic targets of macrophages and M1/M2-like biomarkers

Metabolic targets	M1 biomarkers	M2 biomarkers (1) Activated inducer: IL-4, IL-13	
(1) RONS	(1) Activated inducer: LPS, IFN-γ		
Itaconate	(2) Surface marker: CD80, CD86, CD68, TLR-2/4	(2) Surface marker: CD163, CD206	
Iron	(3) Secreted cytokines: TNF-α, IL-1β, IL-6/12/23/17A, IFN-β	(3) Secreted cytokines: IL-10, TGF-β, VEGFα, bFGF	
IL-4	(4) Secreted chemokines: CCL-2/9/11, CXCL-2, CCR7	(4) Secreted chemokines: CCL-1/17/	
IL-10	(5) Marker gene: NOS2, Nfkbiz, IFN-α, S100a9a, IFN-α/β, Edn-, Irf-5	(5) Marker gene: Arg-1, Fizz-1, Ym-1, KLF-4, Smad3	
Calcium	(6) Signaling molecule: iNOS, Socs-3, STAT-1	(6) Signaling molecule: STAT6, Arg-1	
Amino acid		(7) Receptor: MerTK, TLR1/8	
Lactate			

polarization toward desired phenotypes for disease therapy [41], such as nanozymes combating inflammatory diseases by ROS scavenging-primed M2-like [42, 43]. However, there remains a lack of in-depth summary and discussion regarding current strategies for tracing metabolic signatures to elucidate diseases and subsequently reorienting macrophage fate for immunotherapy targeting macrophage-centered diseases.

Here, we review recent advances in NM-mediated macrophage immunotherapy from a metabolic perspective (Fig. 1 and Table 2). We first provide a comprehensive overview of differentiated metabolism in polarized macrophages, followed by the relationship between metabolism and disease. Next, we systematically summarize the visualization of macrophage behavior in situ using NMs to reveal disease progression, as well as NM-mediated metabolic rewiring to re-educate macrophage fate for disease therapy. This review could serve as a versatile toolbox for researchers in various fields. Finally, we discuss the challenges and future research directions in exploiting NMs to reprogram macrophage metabolism. We anticipate that this review will contribute to advancing the understanding of research progress in regenerative medicine materials mounted on macrophage immune responses by modulating metabolism, guiding the reasonable design of immunomodulatory biomaterials to re-educate macrophage responses, and driving the application of macrophage immunotherapy in the field of immune engineering.

2 Macrophage Metabolism: An Underlying Target for Tailoring Macrophage-Centered Diseases

The metabolic reprogramming of macrophages is strongly associated with their polarization [44–46] (Fig. 2). Macrophages coordinate their own response to oxygen gradient [8]. Contrary to M2, which have an intact TCA cycle that maintains a sustained supply of ATP (~30 per glucose) through OXPHOS and FAO to improve tissue repair, M1 macrophages substantially undergo enhanced glycolytic metabolism and impaired OXPHOS to adapt to hypoxia. Glycolysis produces less ATP (~2 per glucose) at a faster rate than OXPHOS and provides metabolic intermediates required for the biosynthesis of nucleotides, amino acids, and fatty acids [47]. LPS(+IFN- γ)-activated M1 macrophages upregulate glucose transporter-1 (Glut1) to enhance glucose uptake [48] and upregulate glycolytically rate-limiting enzymes such as pyruvate kinase M2 (PKM2) to activate the glycolytic pathway. This pathway generates pyruvate to fuel the TCA cycle and produces lactate by lactate dehydrogenase (LDH)-catabolized pyruvate [49]. PKM2 enhances IL-6 and IL-1 β secretion by phosphorylating signal transducer and activator of transcription (STAT) 3 and induces inflammasome-mediated pro-IL-1 β and IL-1 β secretion through HIF-1 α activity [50, 51]. Moreover, NAPDH derived from upregulated PPP in M1 macrophage overproduced ROS via NADPH oxidase [24, 52].

Two metabolic breakpoints occur in the truncated TCA cycle of M1-polarized macrophages [14, 15, 53]. The first breakpoint occurs at the downregulated isocitrate dehydrogenase (IDH) 1, which converts isocitrate into α -ketoglutarate $(\alpha$ -KG) in M2, resulting in citrate accumulation, facilitating the biosynthesis of fatty acids and prostaglandins in M1 macrophages [12]. Glutamine enters the cytosol via the ASCT2/SN2 transporter and is metabolized to glutamate via glutaminase, followed by forming α -KG to fuel the TCA cycle occurred at interrupted α -KG production caused by IDH1 silence, and is termed glutamine anaplerosis [54]. The accumulated citrate is metabolized by citrate lyase into oxaloacetic acid and acetyl-CoA (precursors for ROS and NO, respectively) after transport to the cytosol via citric acid transporter [14, 15]. Intriguingly, immune-responsive gene 1 (IRG1) redirects citrate to itaconate, which synergizes with NO to block succinate dehydrogenase (SDH), forming the second breakpoint, which accumulates inflammatory succinate [14]. The succinate receptor, G protein-coupled receptor-9 (GPR91), recognizes extracellular succinate from M1 macrophages to form a feedforward loop to induce macrophage activation [55, 56].

The broken TCA cycle is co-opted to form an aspartate–argininosuccinate shunt (AASS) that feeds the TCA cycle at fumarate and replenishes the cycle after the breakpoint at SDH. AASS links the TCA cycle to the urea cycle, a metabolic pathway closely involved in NO production [13, 15, 16]. Intriguingly, blocking the rate-limiting enzyme of AASS, aspartate arginine succinate shunt enzyme, inhibits NO/IL-6 production and inducible nitric oxide synthase (iNOS) expression, both of which are biomarkers for M1 [5].

Amino acids feed the TCA cycle and compensate the level of intermediates in this pathway [13, 16]. Arginine is catabolized via the iNOS/Arg-1 axis. In M1 macrophages,



Fig. 1 A systematic illustration of NM-based repurposing of macrophage metabolism and its applications

upregulated iNOS metabolizes arginine to citrulline and NO [45, 57]. Recycled citrulline synergizes with aspartate to synthesize arginine for NOS reuse in turn by upregulating argininosuccinate synthase and argininosuccinate lyase in M1 macrophages through the citrulline–NO cycle [58]. The initial NO burst in M1 derives from extracellular arginine [59]. Multiple pathways-produced NO nitrosylates iron-sulfur-containing proteins to inhibit the electron transport chain (complexes I, II, and IV), thereby impairing OXPHOS action (e.g., electron transport, ATP production) against bacteria and tumor or causing other diseases [60, 61]. Repurposing mitochondria to produce mitochondrial ROS (mtROS) is an outcome of impaired OXPHOS [62]. Conversely, elevated Arg-1 in M2 competes with the iNOS-arginine pathway and hydrolyzes arginine to polyamines, supporting tissue remodeling [58, 63]. Polyamine production initiates M2 polarization [64].

Macrophages regulate iron metabolism. Physiological iron uptake primarily relies on heme oxygenase (HO)-mediated iron recycling, predominantly stores in labile iron pool (LIP) by binding ferritin (Ft), and releases iron through transferrin receptor 1 [65]. Ferroportin (FPN)-excreted free iron avoids oxidative damage caused by iron-induced Fenton reaction [66, 67]. Iron metabolism defines macrophage subsets, with M1 macrophages increasing iron retention to exhibit an ironsequestering phenotype by upregulating ferritin and hepcidin and downregulating TfR1, FPN, and HO-1 expression, compared to M2 macrophages, which exhibit reduced iron levels (termed the iron-releasing phenotype) [68–70]. Iron deprivation in human macrophages directly blocks the transcription of respiratory chain enzymes, such as Fe-S clusters, and increases glucose-derived citrate pools related to lipid accumulation, impairing OXPHOS and increasing glycolytic flux to activate the M1 phenotype. Iron overload promotes ROS production and deviates glycolysis to activate the M1 response. Acute iron chelation in LPS-activated macrophages increases the itaconate/succinate ratio to decrease IL-1ß and TNF- α secretion, thus blocking M1 polarization [71].

Calcium homeostasis determines macrophage phenotypes. Excess Ca^{2+} stimulates the M1 response. Cytosolic Ca^{2+} concentration ([Ca^{2+}]c) is maintained 1000 times lower than the extracellular level through several Ca^{2+} outflow-mediated

Disease types	Polarized direction	Targets and strate- gies	Potentially polarized mechanism	Application	References
M1-related	M1-to-M2	RONS, Scavenging RONS	HA@RH-CeO _X scavenges ROS and inhibits TLR4 signaling pathway	RA	[159]
			MFC-MSNs produce O_2 and scavenge ROS	RA	[155]
			HTON produces H ₂ to mediate ROS scaveng- ing	RA	[163]
			PNSG scavenges NO and evokes H ₂ S with ROS scavenging ability	RA	[171]
			NAHA-CaP/siRNA releases NO scavenger to eliminate NO and CA9siRNA to silence CA9 expression	OA	[172]
			CAT&SMT@ZIF-8 inhibits NOS activity and catalyzes O ₂ production	OA	[173]
			NOArg-PEA reduces NO by re-equilibrating NOS metabolic pathways	Diabetic wound	[174]
			DEX@PPNP scavenges excess ROS/NO and releases DEX to block inflammatory signals	OA	[175]
			DS/TPP-MMSP releases MnO ₂ to eliminate ROS and SMT to inhibit NOS for NO produc- tion	OA	[20]
		Succinate, Inhibit- ing SDH	Disodium malonate inhibits SDH activity to block mtROS production	Reperfusion injury	[176]
		Itaconate, Supply- ing itaconate or derivatives	ITA-OD/HD/DD releases ITA to exert anti- inflammatory abilities	Inflammatory diseases	[177]
			PCL/DMI also releases DMI to suppress IL-23/17 axis and promote Nrf-2	MI	[178]
		Iron, Depleting iron	P1-3 with DFO and catechol units chelate iron and scavenge iron-induced ROS	ICH	[179]
			P(MMD-co-LA)/DFO captures iron to inhibit ROS formation	Nerve regeneration	[180]
		IL-4, Supplying IL-4	MGC/IL-4 pDNA scavenges ROS and delivers IL-4 pDNA	MI	[181]
			PM-MG-CPIL4 releases IL-4 to initiate IL-4 signaling pathway	Ischemic stroke	[182]
		IL-10, Supplying IL-10	PF-IL-10 releases IL-10	Skin regeneration	[183]
			IL-10 ⁺ EVs release IL-10 to inhibit mTOR signaling	AKI	[184]
		Calcium, Depleting Ca ²⁺	UCNP@mSiO ₂ releases Ca^{2+} regulators to supply or deplete [Ca^{2+}]i	Immune diseases	[185]
			PPTB NPs release BAPTA-AM to glut excess [Ca ²⁺]m to reduce mtROS production	Periodontitis	[75]
			METP NPs release EGTA to block Ca^{2+} influx and inhibit HIF-1 α /ROS production	OA therapy	[186]
			BCP/MVS triggers [Ca ²⁺]i outflow and inhib- its ERK1/2 pathway	Bone regeneration	[187]

Table 2 NMs repurpose cell metabolism to reorient macrophage fate and their applications

Disease types	Polarized direction	Targets and strate- gies	Potentially polarized mechanism	Application	References
			FA – PEG – R – NPs@siERN1 deliver siERN1 to interfere with IP3R1/3 pathway to reduce [Ca ²⁺]i	RA/IBD therapy	[188]
		Amino acid	Au@ZIF-8 enhances GS activity to elevate glutamine and alter other metabolic pathways	Metabolic diseases	[189]
			PEKK-L reemerges MET signaling to modu- late Arg and energy metabolism	Bone regeneration	[190]
M1-related	M2-to-M1	RONS, Inducing RONS production	tTDCR NPs burst ROS	Cancer	[164]
			DMON-SNO mediates NO production	Cancer	[166]
		Iron, Delivering iron	SPF releases iron to induce oxidative stress	Cancer	[191]
			PEG-Fns release iron to induce ROS produc- tion	Cancer	[192]
			HION@Macs degrade into iron to activate the NF-κB pathway	Cancer	[193]
		Amino acid	DON blocks glutamine metabolism to upregu- late M1 TAMs	Cancer	[194]
		Lactate, Metaboliz- ing lactate	DL@NP-M-M2pep delivers DL to block PI3K/Akt and activate the NF-κB pathway	Cancer	[195]
			Lox-loaded Gd/CeO2@ZIF-8 depletes lactate	Cancer	[196]
			<i>E. hallii</i> -loaded E@Fe-DOX metabolizes lactate to butyrate	Cancer	[197]

Table 2 (continued)

pathways in resting cells [72, 73]. Transient Ca²⁺ influx facilitates OXPHOS and ATP production, whereas prolonged influx disturbs several dehydrogenases of the TCA cycle and ATP synthase and triggers increased opening of mitochondrial permeability transition pores (mPTPs), which damages OXPHOS to burst ROS and form a positive feedback loop between Ca²⁺ and ROS, where ROS enhances Ca²⁺ influx and vice versa, initiating glycolysis to activate the M1 phenotype [74, 75].

Consistent with their opposing immune responses, M1-polarized macrophages undergo a large-scale metabolic rewriting, accompanied by various metabolite changes compared with M2 macrophages [76, 77], which can be summarized in the following categories: (1) Interrupted TCA cycle, upregulated PPP, and other alterations damage OXPHOS, triggering ROS production; (2) The second metabolic breakpoint induces succinate accumulation and then burst of ROS via SDH-mediated succinate oxidation; (3) Enhanced IRG1 redirects citrate to itaconate, thus inhibiting SDH-mediated succinate oxidation to decrease ROS production; (4) Compensatory AASS and urea cycle are responsible for NO production; (5) Increased iNOS competes with Arg-1, metabolizing arginine into NO; (6) Glutamine anaplerosis forms α -KG to fuel the first breakpoint at IDH1; (7) Persistent Ca^{2+} influx-induced $[Ca^{2+}]i$ overload impairs mitochondrial function to produce mtROS; (8) Iron overload triggered by unbalanced iron transport leads to oxidative stress via iron-induced Fenton reaction; (9) IL-4 links antiinflammatory function with upregulated FAO to support the M2 response; (10) IL-10 blocks the mTORC1 pathway and lowers the iNOS/Arg ratio to inhibit glycolysis; and (11) Lactate depletion orients toward the M2 phenotype despite contradictory conclusions.

Leveraging these metabolic parameters as underlying targets could guide the design of biomaterials for treating macrophage-driven diseases.

3 NM-Mediated Macrophage Activity Visualization and Fate Tailoring Based on Metabolic Parameters

According to the distinguishable metabolism in M1/M2 macrophages (Fig. 3), the subsequent sections in this article will systematically elaborate NM-traced macrophage behaviors relying on multiple imaging techniques and reorient the macrophage phenotype to tailor its fate for immunotherapy.



Fig. 2 Metabolic adaptation in M1 and M2 macrophages in response to environmental cues: an underlying target for macrophage theranostics

3.1 RONS

3.1.1 NMs Visualize RONS to Evaluate Macrophage Activity

ROS are considered a series of chemically active substances generated from intracellular oxygen through electron transfer, primarily including hydrogen peroxide (H_2O_2), hydroxyl radical (OH·), hypochlorous acid (HOCl), and superoxide anion (O_2 ·⁻) [78]. Under stimuli, resting macrophages are polarized to the M1 phenotype with glycolysis, a mode of increased ROS production [11], whereas the M2 phenotype favors OXPHOS to maintain the physiological activity of cells with less ROS production [79]. ROS act as a double-edged sword in modulating macrophage polarization [80, 81]. At low levels, ROS are beneficial for initiating macrophages with M2, whereas at high levels, ROS drive macrophage M1 polarization [82, 83].

With the help of interdisciplinary strategies, a welldesigned fluorescent "off–on" framework is opening the door for real-time imaging of living cells [84–87]. The traditional ROS imaging strategy involves applying fullyor semi-synthetic dyes, which emit fluorescence when oxidized by ROS [88]. H_2O_2 is the most stable and abundant endogenous ROS and acts as the precursor for producing other ROS at concentration $\geq 1 \text{ mM}$ [89, 90], such as HClO [91]. Mao et al. [92] designed a ratiometric two-photon quinolone skeleton-based probe via covalent cross-linking, containing oxathiolane as the HClO identification part, which rapidly responded to HClO by oxidizing oxathiolane in macrophages, accompanied by a shift in absorption peak from 492 to 563 nm, thus monitoring overgeneration of HClO in macrophages. This probe has unparalleled advantages, such as less light drift and background signal and higher spatiotemporal resolution than single fluorescence-based probes. Semi-synthetic dyes seem to be more attractive due to their simple synthesis from commercially available dyes, which are used for ROS imaging in macrophages, such as IR-780 iodide [93], 1,8-naphthalimide [94], and fluorescein [95].

Photoacoustic (PA) imaging with high spatial resolution and deep tissue penetration has been applied to track macrophage activity [96, 97]. Xing et al. [98] embedded ROS-responsive hydrocyanine substrate (HCv5) and RNSresponsive cyanine substrate (Cy7) onto lanthanide-doped nanocrystal surface via hydrophobic interactions to construct core-shell upconversion nanoprobes (size ~ 100 nm). These combined with multispectral photoacoustic tomography could ratiometrically trace RONS in RAW 264.7 cells due to the structural rearrangement or degradation of HCv5/Cv7, accompanied with altered absorbance at 640 or 800 nm, respectively, thus revealing the pathophysiological process in LPS- or acetaminophen (APAP)-induced inflammatory mice (Fig. 4a). The strategy monitors endogenous ROS/RNS distribution and alterations, mapping out the pathological process to advance high-throughput drug screening. Limited by the poor penetrability and stability of probes in vivo [86, 99], MRI has received more attention in cell imaging due to its high spatial resolution, almost zero background signal, and unrestricted signal penetration depth [100]. Our group [84] synthesized Mn-doped mesoporous silica nanoparticles (NPs) (diameter 110 nm) by an in situ hydrothermal method, which rapidly released Mn²⁺ once exposed to ROS to enhanced MRI signal. Thus, ROS imaging could be performed in macrophages derived from acute liver failure and acute pancreatitis mice. The strategy indicates that macrophage-centered diseases can be monitored using MRI-mediated ROS imaging. Sensor technology has broad prospects in macrophage imaging due to its high sensitivity, simplicity, speed, and cost-effectiveness [101]. Kumar et al. developed WaveFlex-structure sensors to monitor various biomarkers [102–107], such as alanine aminotransferase [108], providing valuable reference for tracking metabolic parameters through well-designed sensors.

Macrophages defend themselves against NO damage by forming a storage or transport system, but this protective mechanism may fail in an inflammatory state [14]. LPS(+ IFN- γ)-activated M1 macrophages are characterized by significantly elevated NO, which is 30-fold higher [20, 109] than that in M2 macrophages [8, 45, 61], where NO induces nitrative stress [110]. Recently, exploiting probes to timely image NO for tracking macrophage behavior has attracted great attention, such as the *o*-diaminobenzene unit [111–113], *N*-nitrosation of secondary amines [114–117], and reductive deamination [118, 119]. Nagano et al. did pioneering work in NO imaging probes by introducing *o*-diaminobenzene [111, 120]. The unit has flourished among several researchers.

Yuan et al. [121] first synthesized an NO-responsive NIR-II probe with an *o*-diamine unit (NRP) by multiple cross-coupling reactions and loaded it into amphiphilic block copolymer to self-assemble nanoprobes (NRP@ MPHCO) with a diameter of 34.8 nm. The secreted NO in LPS + IFN- γ -induced RAW264.7 cells oxidized the NRP unit from a weak electron acceptor into a stronger acceptor along with increased absorbance at 600-1000 nm, enabling NRP@M-PHCQ to visualize the migration and polarization of M2 macrophages for tracking early 4T1 cell-bearing tumor metastasis (Fig. 4b). This approach specifically targets M2 macrophages and tracks their polarization with noninvasiveness and deep penetration and provides insights for detecting and inhibiting early tumor metastasis. To overcome the limitations of o-diamine units, N-nitrosifying secondary amines were introduced in the following research [122, 123]. NO further interacts with O_2 . to produce a more cytotoxic peroxynitrite (ONOO⁻), with an aberrant formation rate $(6.7 \times 10^9 \text{ M}^{-1} \text{ S}^{-1})$ in the inflammatory microenvironment [78, 122, 124]. Researchers have developed a series of nanoprobes for imaging intracellular ONOO⁻ to unveil macrophages behaviors [125, 126].

To sum up, these imaging techniques have huge potential in noninvasively visualizing RONS in macrophages to reveal diseases progression. Cost-effective fluorescent technologies cannot avoid background interference, deviating from true results and hindering translation to the clinic. Clinic-utilized technologies, such as MRI, enable analysis of these metabolites with deep penetration and highly programmed accuracy to supply reliable pathologic information, but is limited by high-cost and time-consuming tests. The following questions are often posed in imaging analysis in vivo: (1) Do probes only accumulate in specific macrophages subtypes? (2) How to orthogonally image the dynamic changes of different RONS and tailor their relationship during pathophysiologic processes in real time? (3) Is the current single imaging modality for a single target susceptible to environmental interference? Multimodal probes simultaneously complete at least two imaging processes, which might break through the limitations of single imaging mode in vivo and integrate the advantages of various imaging techniques to achieve satisfactory imaging effects [127–129], perhaps serving as a banner to guide future research. Theoretically, intelligent



Fig. 3 Schematic of distinguishable metabolic signatures of macrophage phenotypes

probes must identify differences between macrophages and other cells, as well as differences in diverse macrophage subtypes, to visualize macrophage behaviors [130].

3.1.2 NMs-Educated Macrophage Fate Based on RONS

M1 macrophage activation is closely associated with upregulated TNF- α -mediated inflammatory pathways [131–133], such as the downstream mitogen-activated

protein kinase (MAPK) and nuclear factor kappa-B (NF- κ B) pathways [134]. Overall, RONS-scavenging downregulates inflammatory cytokine levels to modulate M2 polarization mainly through the following mechanisms: (1) Significantly reducing the nuclear translocation of p65 NF- κ B by inhibiting I κ B phosphorylation, which inactivates the NF- κ B pathway to silence inflammatory genes, including iNOS [135, 136]; (2) Attenuating the phosphorylation of AMPK (ERK, JNK/SAPK, p 38), thus blocking the MAPK cascade; and (3) Inhibiting STAT-1 phosphorylation to deactivate the JAK/STAT-1 pathway [132, 137–139]. Conversely, RONS supplementation can



Fig. 4 a NIR-responsive UCN visualizing endogenous RONS biomarkers in vivo [98]. Copyright 2019, Springer Nature. **b** Schematic of NRP@M-PHCQ fabrication, NIR-II imaging, and TAM repolarization based on secreted NO [121]. Copyright 2023, American Chemical Society. **c** NIR photocatalytic regulation of arthritic synovial microenvironment with HTON. **d** The effect of HTON photocatalysis on LA/FLS-stimulated macrophages [163]. Copyright 2022, American Association for the Advancement of Science. **e** DMON-SNO releases NO to modulate macrophage polarization. **f** IF staining of F4/80⁺ CD80⁺ and F4/80⁺ CD206⁺ cells in tumor tissues on day 10 after NPs injection [166]. Copyright 2022, American Chemical Society

stimulate these signaling pathway to deteriorate the M1 inflammatory response for tumor therapy [140].

Inspired by the dual role of RONS in macrophage activation, NM-mediated metabolic reprogramming, by regulating RONS levels to activate the required phenotype, has attracted increasing attention in disease therapy [141–146]. The methods that NM-manipulated RONS levels primarily focus on the following categories: (1) Natural antioxidases, such as glutathione peroxidase (GSH-Px) and superoxide dismutase (SOD) [147, 148]. Mao et al. [149] assembled SOD, catalase, and tannic acid (TA) into a spherical nanocomplex (TSC, \approx 50 nm) via multiple noncovalent

interaction between TA and proteins. TSC effectively maintained enzymatic activity and was positively targeted to mitochondria, which scavenged mtROS in H_2O_2 -activated L02 cells and liver tissues (detected by MitoSOX or DHE probes) through the antioxidase cascade, thus restoring mitochondrial function and blocking the inflammatory cascade to exert hepatoprotective efficacy of APAP-induced liver injury and LPS/D-gal-induced acute hepatic failure mice, as measured by Annexin V-FITC/PI, flow cytometry, western blotting (WB), and H&E staining. This strategy develops a TA-based mitochondrial targeted nanoplatform rather than membrane potential-dependent, opening new paradigms in curing mitochondrial-related diseases. (2) Natural enzymemimicking synthetic NMs, such as Cu₅₄O [150, 151], CeO₂ [152-155], and Pt [156-158]. Hu et al. [159] mixed Ce³⁺ with the β -cyclodextrin-engineered hyaluronic acid (HA) framework to form ultrasmall CeO_x (3–5 nm) via the nucleation site of carboxylic groups, finally constructing spherical HA@RH-CeO_x micelles with a diameter of 200 nm, which accurately targeted LPS-induced RAW264.7 cells and released Ce with SOD-like enzymatic activity to scavenge ROS, detected by flow cytometry and confocal laser scanning microscopy (CLSM), thus downregulating inflammatory signals to drive M2 repolarization for incomplete Freund's adjuvant (IFA)/collagen-induced RA mice therapy, measured by RT-qPCR, WB, CLSM, and immunofluorescence staining. The strategy resolves some challenges of CeO_x-based nanozymes in regulating redox homeostasis, such as rapid clearance, and cytotoxicity caused by organic solvent-mediated nanozymes dispersion. (3) Antioxidative substances, including vitamin E/C, gases (e.g., H₂, H₂S), and polyphenols [147, 160, 161]. Hydrogen (H₂) is considered an antioxidant because it selectively scavenges highly cytotoxic radicals (e.g., OH· and ONOO⁻) rather than the physiological ROS involved in cell signaling [162]. Zhao et al. [163] incorporated H₂ into TiO₂ nanorods to prepare monodisperse H_2 -doped TiO₂ (H_x TiO_{2-x}) nanorods (HTON) by a full-solution method, achieving NIR-catalyzed H₂ production due to a narrower bandgap of 1.45 eV, which scavenged ROS in LPS-induced RAW 264.7 cells and facilitated M2 repolarization, as detected by RT-qPCR, IF, and fluorescent staining, thus promoting photocatalytic synovial microenvironment regulation for complete Freund's adjuvant (CFA)/ collagen-induced arthritis (CIA) therapy in mice (Fig. 4c, d). The inexhaustible HTON enabled efficient NIR-photocatalysis on demand and continuously released H₂ for long-term and reproducible therapy while avoiding toxic side effects. Conversely, excessive RONS reprogrammed TAMs from the M2 to M1 phenotype to ameliorate the immune tumor microenvironment (iTME) against tumor [140, 164, 165]. Yu et al. [166] modified tetrasulfide-bridged organosilica NPs with thiol and then generated S-nitrosothiol (SNO) by NaNO₂-mediated thiol nitrosation, to synthesize porously dendritic nanostructured organosilica NO donors (DMON-SNO) with a size of ~230 nm, which increased NO delivery in IL-4-induced bone marrow-derived macrophages (BMDMs)/RAW264.7 cells, detected by Griess reagent and DAF-FM probe. The released NO could interfere with mitochondrial function in macrophages, thus activating M1 macrophages to hinder tumor growth in 4T1 cell-bearing mice. The macrophage phenotype was detected and quantified by flow cytometry, ELISA, WB, and RT-qPCR (Fig. 4e, f).

Each antioxidant method has its advantages and disadvantages, and its specific scenario should be considered when using it. Naturally occurring antioxidases are susceptible to the disease microenvironment, leading to inferior RONSscavenging efficiency [167]. Antioxidative substances exhibit low ROS scavenging efficiency and poor bioavailability due to rapid metabolism and dissipative oxidation resistance [168]. Strategies for regulating RONS are mostly focused on synthetic metal-containing nanozymes with excellent antioxidative properties, which may potentially cause cytotoxicity due to undegradable metal elements and thus require further investigation. Green RONS-scavenging or supply platforms should be exploited to satisfy low toxicity, high biocompatibility, and sustainability issues. For example, the unique photosynthetic properties and easily functionalized surface of microalgae enable them to become an ideal candidate to construct a green RONS-scavenging platform [169] for disease therapy, such as diabetic wounds [170].

3.2 Succinate Metabolism

In 2013, a comprehensive metabolic map profiling derived from Tannahill et al. revealed that sharp succinate accumulation in LPS-stimulated BMDMs directly damaged PHD activity to stabilize HIF-1 α , which drives the expression of IL-1 β and other HIF-1 α -dependent genes, acting as an endogenous inflammatory signal to elucidate innate immunity [198, 199]. SDH, also termed complex II, is a hub that links OXPHOS to electron transport. Intriguingly, LPSinduced mitochondrial hyperpolarization and enhanced SDH-mediated succinate oxidation collectively repurpose mitochondrial metabolism, leading to ROS burst via reversed electron transfer (RET) by forcing electrons back into complex I. This process upregulates the proinflammatory gene profile to drive the M1 response [11, 200]. This phenomenon is reversed by potent SDH inhibitors, malonate derivatives, dimethyl malonate (DMM), which can rapidly hydrolyze to malonate intracellularly, blocking succinate-dependent ROS production and recovering

pro- or anti-inflammatory gene homeostasis (IL-1 β , IL-10, and IL-1RA) to remodel mitochondrial metabolism. This could be a valuable strategy to achieve M1 to M2 polarization. Valls-Lacalle et al. [176] revealed that pretreating reperfusion-injured mice with DMM in a concentrationdependent manner (0.03–30 mmol L⁻¹) decreased the infarct size (24.57±2.32% vs. 39.84±2.78%) by blocking SDH-mediated ROS production and mPTPs. As an attractive target for regulating macrophage metabolism, unlike RONS, which have been extensively studied, researchers need to explore NM-modulated succinate oxidation to address this gap in our understanding of defense against diseases.

3.3 Itaconate Metabolism

3.3.1 NMs Visualize Itaconate to Evaluate Macrophage Activity

Macrophages maintain a physiological pool of itaconate against inflammatory damage. The itaconate level in resting macrophages is as low as the micromolar level compared with > 1 mM in LPS-stimulated macrophages, possibly due to the elevated IRG1-mediated itaconate synthesis [201, 202]. In 2019, Wang et al. [203] introduced the Ac₄ManNAz moiety to develop a thiol-reactive probe, 1-OH-Az, which systematically quantified and profiled itaconate-targeted cysteine sites in proteomes of RAW 264.7 cell lysates, in combination with quantitative chemoproteomic technology. They identified 260 itaconate-modified cysteines and found that itaconate inhibits glycolysis primarily by silencing glycolytic enzymes (e.g., ALDOA) to alleviate the inflammatory response in activated macrophages and revealed the negative feedback between glycolysis and the anti-inflammatory mechanism originating from itaconate. Nonetheless, this profiling method only indirectly monitors itaconate-modified cysteines in cell lysates [203]. Itaconate-alkyne bio-orthogonal probe (ITalk) was developed to directly enter cells [204] and achieve quantitative and sitespecific chemoproteomic profiling of itaconate. They identified 1926 targets of itaconate involved in inflammation-related pathways and provided abundant data for understanding the role of itaconate in macrophages. However, the study was limited by itaconate-monitoring techniques (GC-MS) that failed to monitor the concentration distribution of itaconate in different intracellular regions. An innovative study designed a genetically encoded fluorescent biosensor (BioITA) to timely detect the itaconate dynamics curve at subcellular resolution in macrophages isolated from LPS-bearing mice [205]. The altered fluorescence intensity revealed itaconate fluctuations under inflammatory conditions, making it a powerful tool for imaging itaconate with temporal–spatial resolution in living macrophages.

Given that its anti-inflammatory efficiency, it is of great significance to develop biological probes to achieve itaconatemonitoring in macrophages to deepen our understanding of the unknown biological functions about itaconate. The current monitoring methods inevitably are dependent on liquid chromatograph mass spectrometer (LC–MS) and rarely directly obtain itaconate dynamic in macrophages, and more in-depth studies are needed to fill this relatively blank field.

3.3.2 NM-Educated Macrophage Fate Based on Itaconate

Itaconate (IA) is highly generated in stimuli-induced macrophages and mediates the cross-talk between immunity and metabolism as an anti-inflammatory metabolite to negatively regulate the inflammatory response and govern M2 polarization in vitro and in vivo via multiple mechanisms [206–208]: (1) It inhibits SDH activity by blocking RET-dependent ROS production at complex I, thereby inhibiting HIF-1α activity and IL-1ß production, and subsequent, inactivating the NLRP3 inflammasome [11, 207]. (2) It alkylates residues of KEAP1 via Michael addition to upregulate the expression of Nrf-2, due to the presence of electrophilic α , β -unsaturated carboxylic acid [209]. (3) It induces electrophilic stress to inhibit IkBC translation that regulates secondary transcription via upregulated ATF3 but not Nrf-2, described as the $I\kappa B\zeta$ -ATF3 inflammatory axis [210]. (4) It dephosphorylates IL-23, failing to bind to the IL-17 gene promoter to inhibit downstream IL-17 transcription [178]. (5) It inhibits the NF- κ B pathway [211].

The properties of itaconate provide a novel direction for exploiting immunometabolism-based disease intervention strategies. Mechanically, the strategy that rewrites itaconate metabolism for achieving additional benefits is primarily dependent on delivering itaconate into macrophages in a locally on-demand manner. Yu et al. [212] fabricated monodisperse hydrogel microspheres by the self-assembly of zinc ions, 2-methylimidazole, and IA (IA-ZIF-8@HMs) (diameter 20.25 ± 0.43 µm) via one-step microfluidic technology under ultraviolet light. These sustainably released itaconate under the acidic environment of lysosomes and exerted excellent antiinflammatory and antioxidative stress damage in vitro and in vivo for mono-iodoacetic acid-induced OA mice therapy (analyzed by ELISA, H&E staining, and O-fast green staining). Nevertheless, limited by the poor cell permeability of itaconate, it is necessary to develop functionally similar itaconate derivatives (dimethyl itaconate [DMI] [177] and 4-octyl itaconate [4OI] [213]) or itaconate-loaded NMs. Nakkala et al. [178] synthesized DMI-encapsulated poly-Ecaprolactone nanofibers by electrospinning technology to downregulate the IL-23/IL-17 inflammatory axis-related genes via the IkBE-ATF3 axis and upregulate the antioxidant Nrf-2 target genes in LPS/IFN-y-stimulated RAW 264.7 cells and BMDMs, thereby rewriting itaconate metabolism to polarize the M1-to-M2 phenotype and relieve inflammation against MI (Fig. 5a, b). The percentage of M1/M2 macrophage in vitro or in vivo were assessed by ELISA, flow cytometry, IF, and PCR. The study unveils the potential metabolic regulatory function of DMI on macrophages in the tissue microenvironment.

However, these derivatives may be insufficient to mimic endogenous itaconate. No conclusive evidence confirms that their therapeutic action is derived from itaconate, and no real consensus exists about how to effectively deliver itaconate intracellularly [206]. The burgeoning field of delivering itaconate via biomimetic carriers to alter intracellular itaconate metabolism may be confronted with great development potential and challenges. Moreover, the role of itaconate in M1 macrophages has been unambiguously investigated, whereas the role of itaconate as an M2 macrophage inhibitor has been scarcely studied [214–216].

3.4 Iron Metabolism

3.4.1 NMs Visualize Iron to Evaluate Macrophage Activity

Iron is an essential trace element that participates in multiple metabolic processes [217, 218]. Macrophages play a core regulatory role in iron homeostasis according to their unique genetic program [219]. Opposite iron metabolism operates in macrophages: iron is sequestered in M1 macrophages against bacterial infection [220], whereas it is released in M2 phenotype to facilitate tissue repair but may promote tumor growth [70, 221]. Tracking iron metabolism to evaluate macrophage activity to understand disease progression is a promising prospect and remains challenging.

Benefiting from noninvasiveness, spatiotemporal optical readout, and low-cost, fluorescent technologies have emerged to track iron homeostasis, such as LIP, which triggers Fenton reaction-induced oxidative stress and oppositely expresses in M1/M2 macrophages [222]. Xing et al. [223] designed a fluorescent probe by covalently coupling coumarin 343 (fluorophore) and 3-nitrophenylazanyl ester to visualize the activation of M1 and M2a macrophages by monitoring LIP levels via a photoinduced photon transfer mechanism induced by Fe(II)-activated N-O bond cleavage. This technology provides insights for imaging iron using fluorescent technologies under pathophysiological conditions. Macrophages containing abundant hemosiderin exhibit high MRI contrast. Limited by susceptibility to interference from background signals of fluorescence, MRI was utilized to investigate iron behaviors in macrophages [224, 225]. However, the slow imaging speed and high-cost limit its application. Secondary ion mass spectrometry (SIMS) was used to for iron analysis, even at low concentrations [226–228]. Lovric et al. developed SIMS imaging to explore the uptake and subcellular localization of iron in alveolar macrophages, providing discernment and therapeutic strategies on iron metabolism at the subcellular level to reduce the cytotoxicity of iron overload [228]. Although SIMS can track iron with high sensitivity and spatial resolution (up to 37 nm), it is a new technology and rarely used due to the need for expensive instrumentations and time-consuming testing, similar to MIR. Moreover, macrophage behaviors are dynamic, whereas current monitoring methods can only be fixed at a certain time and environment. How to dynamically monitor metabolites has not been fully investigated, which motivates researchers to develop methods for dynamically tracking them in biological systems.

3.4.2 NM-Educated Macrophage Fate Based on Iron

Iron overload activates M1 macrophages to fine-tune the innate immune response and iron deprivation may block M1 [71]. Generally, iron levels manipulate REDOX homeostasis intracellularly. Capturing excessive iron can inhibit ROS formation to drive M2 polarization by silencing inflammatory pathways (e.g., NF-κB) [229], whereas



Fig. 5 a Schematic illustration of DMI-loaded PCL nanofibers and modulating M1-to-M2 macrophage polarization. **b** The M2-related gene expression of RAW 264.7 cells (upper) and BMDMs (lower) after treatment with different groups for 24 h [178]. Copyright 2021, Wiley–VCH GmbH. **c** Schematic of SP/SPF formation and SPF reeducates TAMs from M2 to M1 for cancer immunotherapy. **d** IF staining of CD86 to M1 and CD206 to M2 in LPS-induced RAW 264.7 cells after different treatments [191]. Copyright 2021, American Chemical Society

iron replenishment induces oxidative stress to activate pathways, such as NF- κ B, upregulating the inflammatory cascade to initiate the M1 response [221, 230, 231].

Researchers have extensively investigated on shaping the macrophage phenotype by reprogramming iron metabolism, including iron-scavenging and supply, for curing macrophage-driven diseases [232]. Zhu et al. [179] designed dual-functional macromolecular poly(catechol) nanoscavengers loaded with deferoxamine via the selfassembly with a particle size of 36.2 ± 7.6 nm, simultaneously chelating excess iron and relieving iron-induced oxidative stress in RAW 264.7 cells, thus protecting mice with intracerebral hemorrhage (ICH). Iron levels were adopted via CLSM and flow cytometry (Perl's staining). This delivery carrier addresses the dose-limiting toxicity using chelators alone and achieves long-term stable release, providing a clue for iron-depleting therapeutic regimen. Similarly, iron dextran therapy resolved kidney macrophage iron depletion by suppling LIP and downregulating TfR1, which polarizes macrophages toward M1 for chronic kidney disease therapy [233]. Much of the observed therapeutic effects of regulating iron metabolism can be traced to tumor therapy. Contrary to iron-scavenging driving the M2 phenotype against inflammation, repolarizing TAMs from M2 to M1 by replenishing iron is believed to be an attractive strategy against tumors [234, 235]. Sang et al. [191] modified S dots (synthesized by an O₂-assisted top-down method) with TAM-targeted peptides to construct ultrasmall nanotraps (SP) with a size of 3.2 nm, which positively adsorbed and internalized endogenous iron into TAMs, attributed to the plentiful iron-binding sites on SP surface by coordinating with oxygen. SP-derived iron produced ·OH and NO in IL-4-induced BMDMs/RAW264.7 cells, detected by CLSM (·OH, DCFH-DA probe) and Griess kit (NO), which remodeled M2-to-M1 phenotype and formed a positive feedback loop between ROS production and M1 polarization, thus delaying 4T1-bearing breast tumor growth (Fig. 5c, d). The M2-to-M1-polarized behavior was detected through protein and gene levels by IF, flow cytometry, ELISA, WB, and immunohistochemical staining (HC). The nanotrap effectively targeted into TAMs and avoided excessive exogenous iron-caused cytotoxicity, providing opportunities to utilize endogenous substances against various diseases. Similarly, iron oxide NPs can be degraded to iron ions in the lysosomes of macrophages and induce oxidative stress to trigger the M1 response [193, 236, 237].

Iron regulator-loaded nanocarriers release regulators to manipulate oxidative stress intracellularly for disease therapy. However, uncontrollable release in other macrophage phenotypes or cells causes dose-dependent toxicity, which attributes to nonspecifically chelate physiologically essential iron. Modifying these nanocarriers with stimuli-responsive moieties may be a charming avenue to achieve targetable cellular internalization, drawn-out circulation half-time, longterm regional enrichment, and sustainable release [238]. It may be more in line with the on-demand release requirements in specific sites compared with direct physical release [192].

There are contradictory reports concerning its precise effects. Dietary iron overload in mice induces hepatic and peritoneal macrophage M2 polarization and inhibits the M1 phenotype [239]. Iron-incubated macrophages induce the translocation of NF- κ B p65 nuclear and inflammatory cytokine expression, which is consistent with other studies [240, 241]. These contradictory findings illustrate the complexity of the impact of iron metabolism on macrophage polarization.

3.5 Calcium Metabolism

Calcium is a crucial messenger that controls several cellular functions [242]. Prolonged Ca²⁺ influx impairs OXPHOS and phosphorylates certain enzymes (e.g., NOS), thereby facilitating the M1 response by stimulating NF- κ B and MAPK pathways. Conversely, lowering intracellular calcium ([Ca²⁺]i) levels reduces mtROS production and inhibits ERK phosphorylation (MAPK-related), consequently downregulating proinflammatory factors and promoting M2 polarization [243–245]. Macrophage phenotypes link to $[Ca^{2+}]i$ levels, with elevated $[Ca^{2+}]i$ levels responding to M1 stimuli and reduced $[Ca^{2+}]i$ levels responding to M2 stimuli. Increasing attention has been focused on developing NMregulated $[Ca^{2+}]i$ levels to remodel M1-to-M2 phenotype development for macrophage-driven immunotherapy [243, 246–249].

One strategy is to encapsulate Ca^{2+} regulators, such as EGTA [186] and BAPTA-AM [75], glutting excess [Ca²⁺]i, restoring ROS-mediated disordered mitochondrial homeostasis to inhibit M1 activation against Ca2+ overload-driven diseases. Kang et al. [185] loaded Ca²⁺ regulators (supplier DMNP-EDTA-Ca²⁺ or chelator BAPTA-AM) into mesoporous silica-decorated upconversion NPs to prepare UCNP@mSiO₂ with a diameter of 58 ± 6 nm. This was further modified with the Arg-Gly-Asp (RGD) peptide-containing cap and photocleavable linker via cyclodextrin-adamantine host-guest complexation, which temporally enhanced or depleted [Ca²⁺]i (measured by Fura-2 AM probe) under NIR light by on-demand releasing Ca²⁺ regulators, remotely modulating RAW 264.7 cells with the M1 or M2 response to exert immune functions, as detected by IF, qRT-PCR. This system achieves intracellularly targetable uptake and timedependent release. However, the underlying mechanism by which UCNP@mSiO₂-resurged the M2 is unclear.

The other strategy is to block improper Ca^{2+} flow by interfering with related channels or signaling pathways [187]. Feng et al. [188] constructed a macrophage-targetable delivery system using polyethylenimine (PEI) and poly (β-amino amine) (PBAA) as siERN1 carriers (FA - PEG - R (Peptide: RKKRRQRRR) - NPs (ss-PBAA-PEI)@siERN1) with a diameter of ~ 110.0 nm through self-assembly, which released endoplasmic reticulum nucleus signaling 1 gene (siERN1) under pH 5.5/GSH to modulate [Ca²⁺]i levels (detected by flow cytometry and CLSM with fluo-4AM labeling) in LPS-stimulated RAW 264.7 cells by disturbing inositol 1,4,5-trisphosphate receptor 1/3 (IP3R1/3), thereby initiating M1-to-M2 polarization as demonstrated by WB, RT-qPCR to maintain immune homeostasis, demonstrating superior therapeutic efficacy in CIA and dextran sulfate sodium salt-induced IBD (Fig. 6a-c). This study confirms ERN1 as an effective target, providing promising insights into Ca²⁺-regulated siERN1 drugs design and its potential mechanisms.

Cross-talk between macrophage polarization and Ca²⁺ occurs in multiple diseases. Manipulating Ca²⁺ signaling can be regarded as an underlying adjuvant therapy. Akin to iron, Ca²⁺ regulator-loaded nanovehicles modulate intracellular oxidative stress by altering $[Ca^{2+}]i$ to fine-tune macrophage fate. The uncontrolled release within non-specific cells inevitably leads to dose-determined toxicity, as it does interference with ion channels or signaling pathways. Moreover, the accurate mechanisms underlying its functionality remain poorly understood. Strengthening mechanistic understanding of Ca²⁺ signaling provides more opportunities to develop Ca²⁺-based therapeutic approaches. Establishing an intelligent delivery system in terms of specific macrophage subpopulations by modifying targeted or stimuli-responsive moieties, achieving its oriented phagocytic uptake, prolonged regional enrichment, and spatiotemporal release as well as minimizing toxicity to adjacent cells remains a challenge.

3.6 Interleukin-4/10

3.6.1 IL-4

The STAT pathway is associated with macrophage polarization [250, 251]. The IL-4-dependent STAT6 pathway responds to the M2 phenotype [9, 252-254]. In detail, IL-4 binds with its receptor to activate JAK2 downstream, inducing STAT6 phosphorylation and entering the nucleus to bind to promoter elements of IL-4-responsive gene, thus transcribing M2 lineage genes (e.g., Il10, Arg-1) to drive M2 differentiation, which acts as a vital immunoregulator to block inflammatory process [255-257]. Recently, IL-4 links anti-inflammatory potential to mitochondrial oxidative metabolism which was confirmed by Chawla et al. [77], who showed that IL-4-treated macrophages (known as M(IL-4)) strongly activated PGC-1 β expression and upregulated FAO gene profiling (e.g., LPL) to promote M2 polarization, relieving macrophage-driven inflammation. Moreover, IL-4 and CSF-1 cooperatively enhance fatty acid synthesis (FAS)/ FAO via the mTORC-IRF4 axis to support M2 polarization [258, 259]. Thus, M(IL-4) is closely associated with upregulated FAO.

Recognition of the anti-inflammatory potential of IL-4 paves the way for IL-4 supply from reasonable delivery platforms to drive macrophage polarization in some tissue engineering applications. Due to its short half-life of only several minutes and dose-dependent toxicity [260], multiple loading platforms through physical adsorption or encapsulation and chemical coupling have been developed to deliver exogenous IL-4 to cells or tissue for clinical application [182, 261]. Our group [262] developed a multilayered defensive platform (IL-4@PEGRA NAs) with a size of 96.45 ± 7.3 nm via the self-assembly of polycatechol-containing poly(ethylene glycol)-vlated phenolic rosmarinic acid (PEGRA) and IL-4, to preserve bioactivity and prolong circulation time. The platform delivered IL-4 into inflammatory tissues, achieving M1-to-M2 polarization in LPS-stimulated BMDMs and mice colon tissue in dextran sulfate sodium salt-induced acute colitis, thus protecting against IBD. The percentage of M1/M2 was measured by IF, flow cytometry, WB, and ELISA (Fig. 6d, e). The nanoarmor defended IL-4 against rapid biodegradation, prolonging circulation half-life, achieving triggered release, and avoiding immunogenic side effects. In addition to the aforementioned physical methods, Spieler et al. [263] genetically engineered an amino acidincorporated IL-4 variant via genetic code expansion and then directly performed bio-orthogonal PEGylation (PEGfolate, a targeting moiety) by strain-promoted alkyne-azide cycloaddition to overcome the pharmacokinetic challenges of IL-4, which prolonged the half-life to 4 h in healthy mice and polarized primary murine macrophages toward M2 via RT-qPCR detection and accumulated into arthritic joints to cure antigen-induced arthritis mice.

3.6.2 IL-10

IL-10 initiates an anti-inflammatory response mainly dependent on the JAK–STAT3 pathway [264–266]. Briefly, IL-10 binds with IL-10 receptor to activate JAK1, which stimulates STAT3 to translocate into the nucleus, thus combining with specific DNA sequence to initiate DNA transcription and upregulate M2-associated genes (TGF- β 1, Mrc1) for anti-inflammatory cascades. Recently, IL-10 was verified to remodel glycolysis and potentiate OXPHOS by blocking glucose uptake and glycolytic gene expression. IL-10 reprogrammed metabolic processes by inhibiting mTOR complex 1 (mTORC1) signaling via STAT3 signaling and accelerated mitophagy to eliminate impaired mitochondria, thereby controlling inflammation [17, 26, 267, 268]. IL-10 blocked NO production in activated macrophages by silencing iNOS [269, 270] and upregulating arginase [271].



Fig. 6 a Schematic diagram of delivered siERN1 promoting macrophage M2 polarization by interfering with IP3R and modulating $[Ca^{2+}]i$. **b** M2 and **c** M1 marker expression levels detected via RT-qPCR [188]. Copyright 2021, American Chemical Society. **d** Schematic diagram of IL-4@PEGRA nanoarmor modulating M1-to-M2 polarization for IBD therapy. **e** IF staining of CD86⁺, CD206⁺, and CD11b⁺ cells in colon tissue derived from IBD-bearing mice on day 10 after treatment [262]. Copyright 2023, Elsevier

Exogenous IL-10 supply blocks macrophage inflammatory cascade reaction to drive M2 polarization, exhibiting enormous bioregenerative potential [272, 6]. In line with IL-4, researchers are attempting to develop an IL-10-loaded nanoplatform, which releases IL-10 via physical or chemical stimuli-triggered mechanisms, paving the way for targeted delivery [183]. Extracellular vesicles (EVs) have attracted increasing attention as feasible drug delivery systems [273]. Tang et al. [184] designed an IL-10-packaged nanoplatform (IL-10⁺ EVs) with a diameter of 134 nm by engineering dexamethasonestimulated plasmid transfected-RAW 264.7 cells to avoid IL-10 degradation and target to the kidney. IL-10⁺ EVs favored the M2 phenotype of LPS-induced BMDMs by inactivating mTOR1, followed by its downstream targets (e.g., S6K, S6), as detected by flow cytometry, RT-qPCR, and HC, and promoted mitophagy to maintain mitochondrial homeostasis against ischemic acute kidney injury (AKI) (Fig. 7a, b). The versatile delivery strategy enabled IL-10 to evade phagocytosis, prolong circulation time, and decrease immunogenicity.

Overall, IL-4/10 link macrophages metabolism to their anti-inflammatory functionality. The major barriers, such as susceptibility to degradation and short circulation half-life, prevent IL-4/10 from being directly employed for diseases therapy. Physical encapsulation can effectively maintain the biological activity of IL-4/10, but hardly avoids their uncontrolled release. Conversely, chemical stimuli-triggered release may better satisfy the on-demand release needs while reducing off-target effect-induced side effects [274]. Current strategies have resolved pharmacokinetic challenges to some extent. However, bridging them with natural materials to exploit delivery platforms with high load efficiency, which can maintain their effective biological activity, as well as accurately orient exogenous IL-4/10 in targetable sites to achieve long-term continuous release, remains a major challenge that requires more extensive exploration.

3.7 Amino Acid Metabolism

Metabolic adaptation in macrophages facilitates specific immunophenotype transformation [14, 275]. Among them, alterations in the metabolism of some amino acids are the earliest and foremost metabolic features that occur during macrophage polarization and define macrophage subtypes [276].

3.7.1 Arginine

Arginine metabolism remodels macrophage phenotype via the iNOS/Arg-1 axis. M(IL-4)-derived mice upregulate Arg-1 activity, whereas similar results were not observed in human macrophages. Transcription factor Fra-1 reemerges M1 macrophages by silencing Arg-1 to enhance inflammation [277]. Arg-2, another enzyme involved in L-arginine metabolism, modulates mitochondrial dynamics to upregulate OXPHOS, polarizing M1 macrophages to M2 phenotype [278, 279]. Jiang et al. [190] engineered a liver-inspired polyetherketoneketone (PEKK) scaffold with a thickness of 30 µm by femtosecond laser etching technology and sulfonation reaction. They reemerged hepatocyte growth factor receptor (MET) signaling in LPS-induced CVX-BMDMs/ RAW 264.7 cells, followed by activating downstream Ras pathway, which promoted the retrograde transfer of Arg-2 from mitochondria into the cytoplasm and remodeled energy/arginine metabolism by enhancing OXPHOS to mobilize M2 phenotype for improving rat osteoporotic bone defect (demonstrated by flow cytometry, IF, ELISA, and RTqPCR) (Fig. 7c-f). The strategic application of Arg-2 in this study verified its potential as an anti-inflammatory reserve to resurge M2 macrophages. The effect of PEKK on the isoenzyme Arg-1 has not been thoroughly studied, and it may inevitably lead to off-target effects on Arg-1. Nevertheless, there are contradictory viewpoint that Arg-2 stimulates the M1 response through mtROS and is responsible for inflammatory diseases.

3.7.2 Other Amino Acids

The regulatory role and metabolic fate of citrulline remain unclear, although citrulline can be metabolized into argininosuccinate (an inflammatory mediator) by the citrulline–NO cycle. Citrulline rapidly declines in LPS(+ IFN- γ)-primed BMDMs, and ASS1-mediated citrulline depletion is responsible for JAK2–STAT-1 signaling activation and proinflammatory cytokine generation, stimulating the M1 phenotype [280].

Carbon tracing indicates that one-third of the carbon in the TCA cycle metabolites of M2 macrophages derives from glutamine, which fuels the immune system [281], and serves as an anti-inflammatory metabolite to maintain M2 differentiation through the uridine diphosphate N-acetylglucosamine (UDP-GlcNAc) pathway and glutaminolysis-derived α-KG [16, 281, 282]. Glutaminolysis-derived α-KG activates M2 macrophages through Jmjd3-dependent metabolic and epigenetic reprogramming and inactivates the M1 phenotype by silencing the NF-kB pathway via PHD-regulated proline hydroxylation of protein kinase IKKβ [283]. However, glutamine anaplerosis partially replenishes succinate to activate M1 macrophages [198, 282]. Recently, dietary glutamine supply in limb ischemia-bearing diabetic mice reduced the M1/M2 ratio to promote muscle regeneration [284]. Glutaminolysis-induced M2 polarization was identified as an underlying target for obesity and type2 diabetes [282]. Contrarily, blocking glutamine metabolism skewed the macrophage phenotype toward M1 to exert antitumor immunity [194, 285]. Li et al. [189] loaded PVP-coated AuNPs into MOFs to synthesize the metabolic modulator Au@ZIF-8 via a two-step method, which enhanced GS activity (detected by a GS kit) to upregulate glutamine, altered other metabolic pathways (e.g., the TCA cycle), and remarkably decreased TNF- α secretion (analyzed by RT-qPCR) in LPS-induced RAW 264.7 cells, and applied it to glutamine metabolismmediated diseases.

The fate of serine metabolism on macrophage polarization was investigated and a novel mechanism was proposed by which serine deficiency stimulates the M1 phenotype and inhibits STAT6-mediated M2 polarization by activating p38-dependent JAK–STAT-1 axis [286], suggesting that serine metabolism may be an underlying target. A recent study showed that serine supports LPS-dependent IL-1 β



Fig. 7 a, **b** IL-10⁺ EVs promote macrophage M2 polarization [184]. Copyright 2020, American Association for the Advancement of Science. **c** Schematic of liver-inspired PEKK scaffolds that reprogram macrophage metabolism for increasing osteoporotic osseointegration. **d**, **e** IF staining and biomarker (CCR7 and CD206) expression by flow cytometry of RAW 264.7 cells cultured on various scaffolds. **f** A heatmap describing the fold-change in expressed polarization genes after treatment with different groups [190]. Copyright 2023, Wiley–VCH GmbH. **g** Possible mechanisms of DL-modulated TAM repolarization from M2 to M1 (left) and remodeling of the iTME for HCC therapy via DL delivery combined with α -CD47 (right) [195]. Copyright 2023, American Association for the Advancement of Science

production by synthesizing GSH in BMDMs and improving survival in a sepsis model by inhibiting de novo serine synthesis [287].

Considering the newly identified role of amino acid metabolism in macrophage polarization, we are optimistic that exploiting NMs to regulate amino acid metabolism within macrophages to emerge the desired phenotype will be a new research direction, although the blueprint is premature.

3.8 Lactate Metabolism

The metabolic adaptation of M1 macrophages leads to Warburg-type lactate accumulation [49]. Emerging evidence indicates that lactate serves as an immunomodulator [288] and mediates differentially expressed gene production [289], revealing that lactate may be the white swan of reshaping energy metabolism rather than a glycolytic "waste product." Metabolites derived from nonimmune cells have been confirmed to affect the glycolysis–OXPHOS axis of immune cells and then reshape their phenotype [290]. Tumor cell-derived lactate induces TAMs M2-related gene profiling in an HIF-1 α -dependent manner for promoting tumorigenesis [291–293]. This is somewhat confusing, and the accurate mechanism remains unclear, as the conventional view is that glycolysis with lactate accumulation supports M1, whereas OXPHOS responds to M2. A recent study by Zhao may explain the contradictory paradigm, which revealed that accumulated lactate in LPS(+ IFN- γ)-driven BMDMs serves as a precursor to stimulate histone lactylation at lysine residues (known as "Kla"). Increased histone Kla activates M2-like gene transcription via epigenetic modification [294].

Currently, the two conflicting methods of supplying D-lactate (DL) and depleting lactate manipulate macrophages toward the M1 phenotype for tumor immunotherapy. DL serves as an endogenous immunoregulator that enhances the phagocytic ability of Kupffer cells (a sign of M1 macrophages) [295]. Guo et al. [195] engineered biomimetic DL-loaded PLGA NPs and decorated them with a M2-binding peptide (M2pep)-modified hepatocellular carcinoma (HCC) membrane to prepare DL@NP-M-M2pep NPs (particle size ~ 120 nm) using an extruder. These NPs accumulated in tumors through HCC membrane-related homing ability and subsequently delivered DL into IL-4-induced BMDMs via the M2 peptide-targeting capacity. This delivery drove M2-to-M1 transition, as measured via RT-qPCR, IF, and flow cytometry, thus remodeling the iTME primarily by blocking PI3K/Akt signaling downstream and activating the NF-kB pathway for carcinogen-induced HCC mice therapy (Fig. 7g). The finding first confirms the regulatory function of DL on TAM polarization and provides a reference for following research in this field.

Depleting lactate through a compatible matrix-laden lactate oxidase (Lox) [296] or bacteria has become an alternative strategy against tumor [197, 297, 298]. Regarding Lox, Liu et al. [196] loaded Lox, syrosingopine, and Gd/CeO₂ into ZIF-8 to develop urchin-like catalysts with a size of 300 nm via a wet-chemical approach, effectively depleting intratumoral lactate by releasing Lox (detected by hippocampal analyzer and lactate kit), achieving glycometabolic reprogramming to activate the M1 response in IL-4-induced BMDMs for achieving HCC-bearing mouse immunotherapy. M1/M2 polarization was identified by RT-qPCR, IF, and ELISA. This metabolic remodeling strategy targeting lactate may open a promising avenue for tumor therapy, which can be expanded to other representative metabolites in the iTME. Conversely, our group [299] incorporated engineered *Lactococcus lactis* (*L. lactis*) into a heparin-poloxamer copolymer to prepare a living hydrogel delivery system (HP@LL_VEGF), which steadily secreted lactate from *L. lactis* as a metabolic signal to remodel LPS + IFN- γ -induced BMDMs toward M2-like, (confirmed by IF, CLSM, flow cytometry, RT-qPCR, and WB, thus ameliorating inflammation in streptozotocin-induced diabetic mice and accelerating wound healing.

Lactate consumption and DL replenishment are believed to support macrophage M2-to-M1 polarization against tumor growth. However, these two mainstream strategies are contradictory, and researchers have not accurately elucidated the regulatory mechanism by which designed NMs influence macrophage polarization by regulating lactate levels. Lactate serves not only as a byproduct of glycolysis but also as a factor driving M2 polarization via Kla-induced Arg-1 expression. Addressing how to selectively deplete or supply lactate to avoid side effects on other physiological cells or tissues may be a major issue for researchers to consider.

4 Conclusion and Perspectives

NM-based repurposing of macrophage metabolism holds considerable potential in various disease scenario. Here, we outline recent advances in the application of NM-based metabolic reprogramming, providing a partial blueprint and insights into macrophage metabolic immunotherapy. We believe that a deeper understanding of the interaction between metabolism, polarization, and NMs can greatly accelerate the exploration of next-generation NMs with optimal performance under the strategic collaboration of multiple disciplines. Nevertheless, thorough research is needed in the future to conquer remaining challenges that have not been addressed and bring engineered NMs into clinical applications. The following section introduces additional information on the key issues that need to be addressed and future research priorities, yielding insights for future research.

 Engineering NMs with macrophage-targeting moieties (e.g., ligand) to enhance phagocytic uptake or bridging stimuli-triggered units may achieve personalized targeting [300, 301]. NMs confront a series of pathophysiologic barriers during transport in vivo. Their complex surface interfaces inevitably interact with proteins and cells in blood and tissues, leading to performance change and inevitable clearance by the immune system [300]. NMs are inevitably internalized by other macrophage subsets or adjacent cells even within the same tissue due to the ubiquitous distribution of cells, resulting in unintended off-target effects and immunogenicity. Establishing a biomimetic Trojan delivery system that accurately targets specific macrophages subsets remains a challenge before entering clinical research. The pathogenesis of metabolic diseases is extremely complex, involving multiple altered parameters. Restricted by suboptimal efficacy of a single target and limited target screening [302], the perspective should gradually shift from the doctrine of "one molecule, one target, one disease" to "all-in-one" NMs based on a multipronged strategy that synergistically modulates multiple metabolic targets in macrophages [175].

- The exploration of theranostic NMs requires more (2)rigorous consideration to devise programmable cargo transport strategies, demonstrating a diagnostic logic to determine cargo release time, followed by a therapeutic logic to program cargo release, to timely adjust the therapeutic schedule. More metabolic parameters, such as fumarate, α -KG, GLUT1, glycolytic enzymes (e.g., PKM2, hexokinase, pyruvate dehydrogenase), FAS-associated enzymes (e.g., fatty acid synthase, acetyl-CoA carboxylase), and other amino acids (e.g., tryptophan, methionine), also undergo significant alteration in the metabolic adaptation of macrophages [24, 303–306] and can serve as theoretical targets for innovative therapies. These are beyond the scope of this review and have not been extensively explored yet. A combination of imaging technologies and metabolic events has enabled us to visualize and quantify macrophage behaviors. To accelerate clinical translation, clinically mature imaging techniques (e.g., MRI, CT) and FDA-approved materials (e.g., PEG) should be prioritized to exploit nanomedicines.
- (3) Most preclinical results originate from cell lines and animal models, and not humans. Metabolic profiles vary between them and humans, as is the behavior of NMs [307, 308]. Undoubtedly, human tissue models will be introduced into metabolic research to eliminate the long-standing dependence on traditional models [309], such as 3D organoids, which better mimic human organs [310]. Due to inappropriate assessment models, inadequate understanding of nano-biointeractions, etc., current macrophage nanomedicines rarely achieve practical clinical translation [311], as evidenced by their limited commercialization. Longterm safe administration in humans is essential. The biodegradability, pharmacokinetics, and long-term

toxicity of NMs must be analyzed in detail. Perhaps we can explore intracellular behavior of internalized NMs utilizing computational toxicology, micro "organ on chip" devices, and high-throughput drug screening to establish pharmacokinetic–pharmacodynamic models for elucidating the toxicological pathway and therapeutic value. The minimum information reporting in bio–nano-experimental literature (MIRIBEL) standard should be followed for accelerating their clinical translation [312].

(4) Precision nanomedicine may be the future research trend, aimed to tailor patient-personalized therapeutic regimens through various cutting-edge technologies based on individual differences, to minimize iatrogenic damage and medical costs and maximize patient benefits [313]. This strategy probably avoids an adverse drug response caused by a "one size fits all" treatment without considering patient heterogeneity [314]. Similar variability probably exists in simple NMs labeled with targeted fragments. Algorithms (e.g., artificial intelligence) may be imperative for implementing precision medicine, which contribute to patient classification and NM design, such as predicting optimal size, pharmacokinetics, and prescreening NMs for better patient compliance [315]. Some questions are raised frequently about precision medicine: Can we provide tailor-designed nanomedicines for each patient? Besides the complex clinical approval process of personalized nanomedicine customization, the limitations of its manufacturing technology and high-cost development are questions for the future.

Overall, although these strategies highlight the impressive preclinical potential of NM-based macrophage immunotherapy, very few have directly entered the clinical arena. This recognition has prompted some experts to raise provocative questions, hoping to transform the discipline from merely potential platforms to those enabling to provide positive clinical outcomes. Encouraged by the prominent progress already made, it could be expected that macrophage immuno-nanomedicines will eventually enter the clinic and market in the near future.

5 Statistical Analysis

Each experiment in the cited literature was independently repeated at least three times, and all quantitative data were expressed as mean \pm standard deviation (X \pm SD). The sample size for all experiments met the requirements for statistical

analysis. Pairwise comparisons of consecutive variables were analyzed using a two-tailed Student's t test to determine statistical significance for normally distributed variables. Nonnormally distributed variables were analyzed using nonparametric tests such as the Mann-Whitney U test (Wilcoxon rank sum test) or the Kruskal-Wallis H test followed by Dunn's multiple-comparison test. The chi-square test was employed to compare and analyze the statistical significance of categorical variables between two groups. For multiple comparisons of variables, one-way ANOVA followed by Tukey's post hoc test was conducted, and two-way ANOVA was used for analyses involving two independent variables. Statistical analyses were performed using GraphPad Prism 9.5 software, with a P value of < 0.05 considered statistically significant. The confidence interval for all statistical tests was set at 95%.

With the help of multiple databases, we identified potential biomarkers of metabolic pathways using Progenesis QI software (Waters Corporation, Milford, USA) for metabolomics analysis. These databases include the Human Metabolome Database (HMDB, http://hmdb.ca/), Genomes (KEGG, http://www.genome.jp/kegg/), mzCloud (https:// www.mzcloud.org/), and MBRole 2.0 (http://csbg.cnb.csic. es/mbrole2/). The metabolites were screened using a combination of multidimensional and one-dimensional analysis methods.

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Declarations

Conflict of interest The authors declare no interest conflict. They have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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