

Review Article

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Targeting the Immunosuppressive Microenvironment in Colorectal Cancer: Pharmacological and Nanomedicine Strategies

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ABSTRACT

The immunosuppressive stroma in colorectal cancer (CRC) plays a central role in therapeutic resistance. Modulating key targets within this stromal compartment has been proposed as a promising strategy for restoring antitumor immunity and overcoming resistance mechanisms. Several immunomodulatory agents, including next-generation immunotherapies, small-molecule inhibitors targeting specific receptors or signaling pathways, and natural compounds, have shown potential for remodeling the tumor immune microenvironment (TIME). In addition, nanoparticle-based delivery systems may further enhance the therapeutic efficacy of these agents. Evidence from both preclinical and clinical studies suggests that targeting stromal and immunosuppressive cells can effectively remodel the antitumor immune response in CRC. Furthermore, specific inhibitors, natural products, and their nanoformulations may enhance antitumor immunity by suppressing the recruitment and activity of immunosuppressive stromal and immune cells. This review summarizes the current knowledge of emerging pharmacological agents, including immunomodulators, therapeutic drugs, and their nanoformulations, for restoring antitumor immunity in CRC. It first discusses the fundamental immunosuppressive interactions within the TME and subsequently examines how these agents enhance immune responses by reprogramming stromal and immune cells, as well as their secreted mediators within the TIME.

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Introduction

Colorectal cancer (CRC) remains a major challenge in cancer research and clinical practice. It is the third most frequently diagnosed malignancy worldwide and the second leading cause of cancer-related mortality.¹ Standard treatment strategies for CRC include surgery,² radiotherapy (particularly for rectal cancer), cytotoxic chemotherapy (e.g., fluoropyrimidine- and oxaliplatin- or irinotecan-based regimens),³ and targeted therapies such as anti-vascular endothelial growth factor (VEGF) and anti-epidermal growth factor receptor (EGFR) agents in biomarker-selected patients.^{4,5} More recently, novel therapeutic agents, including antibodies targeting pro-survival and pro-angiogenic factors, have also been introduced for the treatment of metastatic CRC.⁶ Despite these advances, several limitations continue to compromise treatment efficacy. Both primary and acquired resistance to chemotherapy and targeted therapies frequently arise through molecular adaptations.^{7,8} Moreover, tumor recurrence remains a major clinical challenge following treatment.⁹ These challenges indicate a need for new approaches.

A critical determinant of treatment response in CRC is the tumor immune microenvironment (TIME), which consists of malignant epithelial cells, stromal components—particularly cancer-associated fibroblasts (CAFs) and the extracellular matrix (ECM)—vascular cells, and diverse immune cell populations.¹⁰ In many tumors, especially mismatch-repair-proficient/microsatellite-stable (pMMR/MSS) CRC, the TIME is characterized by the exclusion of CD8⁺ T cells, accumulation of myeloid-derived suppressor cells (MDSCs), metabolic reprogramming, and the secretion of pro-tumorigenic cytokines and chemokines, including transforming growth factor (TGF)- β , IL-6, and C-X-C motif chemokine ligand 12 (CXCL12). Together, these factors impair the cytotoxic functions of cytotoxic CD8⁺ T lymphocytes (CTLs) and natural killer (NK) cells.¹¹ By contrast, mismatch-repair-deficient/microsatellite instability-high (dMMR/MSI-H) CRC generally exhibits greater immunogenicity and responds more favorably to immune checkpoint blockade.¹² This distinction underscores the importance of understanding the unique cellular and molecular interactions within the TIME when designing immunotherapeutic and other targeted treatment strategies.¹³

This review focuses on druggable immunosuppressive mechanisms in CRC and evaluates pharmacological agents, as well as formulation and delivery strategies, that can reprogram the TIME. Particular emphasis is placed on actionable therapeutic barriers, including stromal (CAF- and ECM-mediated) immune exclusion, immunosuppressive immune cell populations, and metabolic and hypoxia-associated pathways that contribute to the suppression of antitumor immunity. We discuss representative therapeutic approaches, including small-molecule inhibitors, monoclonal antibodies, selected immunomodulatory natural products, vaccine- and immune-priming strategies, and nanomedicine-based delivery systems. The evidence reviewed encompasses *in vitro* studies, animal models, early-phase clinical trials, randomized clinical studies, and approved clinical applications. Finally, we discuss key translational challenges relevant to pharmaceutical development, including pharmacokinetics, toxicity, manufacturability, and regulatory considerations.

Literature Identification

A targeted narrative literature search was conducted using PubMed/MEDLINE, Scopus, and Web of Science to identify studies investigating pharmacological and formulation-based approaches for modulating the CRC TIME. The primary search period covered January 2015 through December 2025. Earlier landmark publications were

also included when necessary to provide background on established biological mechanisms or first-in-class therapeutic interventions. The search strategy combined disease-specific terms with keywords related to the TIME and therapeutic interventions, including colorectal cancer, colon cancer, rectal cancer, tumor microenvironment, immune microenvironment, CAF, cancer-associated fibroblast, macrophage, TAM, MDSC, Treg, immune checkpoint, PD-1, PD-L1, CTLA-4, STING, TLR, TGF- β , chemokine, adenosine, hypoxia, HIF, lactate, metabolism, drug, inhibitor, antibody, small molecule, vaccine, natural product, polyphenol, nanoparticle, and nanomedicine. In addition, the reference lists of relevant review articles and eligible primary studies were manually screened to identify additional pertinent publications. Only peer-reviewed English-language original research articles (including both in vitro and in vivo studies), clinical trials, and translational studies focusing on CRC were included in this review. For critical evaluation, priority was given to clinical trial reports that provided molecular stratification (e.g., dMMR/MSI-H vs. pMMR/MSS, tumor mutational burden, and POLE/POLD1 mutation status), trial phase, clinical endpoints, and safety outcomes. Evidence from non-CRC malignancies was considered only when CRC-specific data were unavailable and was used primarily to explain conserved mechanisms and interactions within the TIME.

TIME in CRC

TIME in CRC consists of a diverse population of stromal and immune cells that interact through complex signaling networks and soluble mediators. Among these, Cancer-associated fibroblasts (CAFs) are major stromal cells in CRC, which may arise from several cellular sources, including resident fibroblasts, mesenchymal stem cells (MSCs), pericytes, and, in some cases, cells undergoing epithelial-to-mesenchymal transition (EMT).¹⁴ These cells are commonly identified by the expression of markers such as α -smooth muscle actin (α -SMA), fibroblast activation protein (FAP), platelet-derived growth factor receptors (PDGFR α/β), and S100A4. Importantly, CAFs constitute a highly heterogeneous cell population within the tumor microenvironment.¹⁵ They secrete a broad spectrum of cytokines and chemokines, promote glycolytic metabolism and lactate production,¹⁶ and produce major extracellular matrix (ECM) components, including collagen types I, III, and IV, fibronectin, laminins, and several additional matrix proteins.¹⁷

Tumor-associated macrophages (TAMs) represent another major population of immunosuppressive cells within the CRC microenvironment. These cells originate from both infiltrating monocytes and tissue-resident macrophages. Rather than existing as discrete subsets, TAMs occupy a spectrum of transcriptional and functional states that are shaped by their spatial localization and local microenvironmental cues.¹⁸ M1-like TAMs predominantly produce IL-12, tumor necrosis factor (TNF)- α , and reactive oxygen species (ROS). They also participate in antigen presentation and can carry tumor antigens and stimulate cytotoxic responses by CTLs. In contrast, alternatively activated (M2-like) TAMs secrete IL-10, TGF- β , and arginase-1, thereby suppressing CTL activity and promoting tumor growth.¹⁹ M2-like macrophage programs are frequently enriched within immunosuppressive regions of CRC. Although the terms M1-like and M2-like are commonly used to describe predominantly inflammatory and immunosuppressive macrophage phenotypes, macrophages in the CRC microenvironment often display intermediate or mixed activation states that dynamically shift in response to local factors, including cytokines, hypoxia, and metabolites.¹⁹ Cytokines and mediators such as colony-stimulating factor-1 (CSF-1), IL-34, IL-4, IL-13, lactic acid, and prostaglandins are among the major factors that promote macrophage polarization toward an M2 phenotype.²⁰

Regulatory T cells (Tregs) constitute another important immunosuppressive population enriched in CRC. These CD4⁺ T-cell subsets are typically characterized by the expression of CD4, high levels of CD25, and the transcription factor FOXP3. Tregs suppress immune responses through several mechanisms. Cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) expressed by Tregs interacts with CD80/CD86 on antigen-presenting cells (APCs), while the secretion of immunosuppressive cytokines, including IL-10, TGF- β , and IL-35, directly inhibits the activity of both APCs and CTLs. In addition, Tregs suppress the functions of NK cells and CD4⁺ helper T cells. High expression of CD39 and CD73 enables Tregs to convert extracellular ATP into adenosine, a potent inhibitor of CTL-mediated cytotoxicity.²¹

MDSCs are another key immunosuppressive component of the CRC stroma. These cells are recruited into tumors in response to tumor-derived chemokines.²² MDSCs suppress adaptive immune responses through the production of arginase-1, ROS, and inducible nitric oxide synthase (iNOS). Arginase-1 depletes arginine, an amino acid required for optimal CTL function, whereas nitric oxide and ROS impair T-cell receptor (TCR) signaling and may induce apoptosis in CTLs. In addition, MDSCs express programmed death ligand 1 (PD-L1) and secrete immunosuppressive cytokines, including IL-10 and TGF- β , further contributing to immune evasion.²³

CTLs and NK cells are the principal effector cells responsible for antitumor immunity. CTLs are commonly identified by the expression of CD8, TCR, granzyme B, and perforin. Tumor-infiltrating CTLs exhibit considerable phenotypic heterogeneity and may exist in naïve, effector, memory, or exhausted states.²⁴ Exhausted CTLs are characterized by the expression of inhibitory immune checkpoint receptors, including programmed death 1 (PD-1), T-cell immunoglobulin and mucin-domain containing-3 (TIM-3), lymphocyte activation gene 3 protein (LAG-3), T cell immunoreceptor with Ig and ITIM (TIGIT), and CTLA-4, together with diminished cytokine production, and impaired cytotoxic function.^{25,26} Effective CTL-mediated antitumor immunity depends on efficient antigen presentation by dendritic cells (DCs) and M1-like TAMs, as well as supportive cytokines such as IL-2 and IL-12. However, these immune responses are frequently attenuated by multiple immunosuppressive factors limit CTL cytotoxicity.²⁷

NK cells also play a critical role in antitumor immunity. These cells are commonly identified by markers such as natural killer cell protein 46 (NKP46) and natural killer group 2, member D (NKG2D) and eliminate tumor cells through the recognition of stress-induced ligands, including histocompatibility complex class I (MHC-I) chain-related proteins A and B (MICA/B) and ULBPs, as well as the absence of MHC-I expression. Activated NK cells exert their cytotoxic activity through the release of granzymes, perforin, interferon- γ (IFN- γ), and tumor necrosis factor- α (TNF- α).²⁸

Tumor vessels, ECM stiffness, and hypoxia are other distinct features of the tumor stroma that can affect antitumor immunity within the tumor. Tumor angiogenesis is driven by VEGF family ligands, angiopoietins, platelet-derived growth factor (PDGF), and fibroblast growth factor (FGF) released by cancer, endothelial, and stromal cells.²⁹ Abnormal vessel architecture results in heterogeneous perfusion and hypoxia. These vascular changes impair T-cell trafficking and create hypoxic niches that promote polarization toward immunosuppressive immune cell subsets and facilitate adenosine accumulation.³⁰

Hypoxia-inducible factor (HIF)-1 α and HIF-2 α are key mediators activated under hypoxic conditions. These transcription factors reprogram cellular metabolism and angiogenic signaling. HIF signaling upregulates glycolytic enzymes and carbonic anhydrases, while HIF-1 α can induce VEGF expression. Elevated VEGF

promotes the formation of chaotic, leaky blood vessels and contributes to poor tissue perfusion.³¹ Hypoxia also induces the HIF-1 α /PD-L1 axis on in both cancer and myeloid cells.³² In addition, adenosine accumulates through the activity of CD39 and CD73 in the hypoxic microenvironment, suppressing the functions of CTLs and NK cells.³³ Furthermore, hypoxia promotes the recruitment of MDSCs and monocytes and facilitates their differentiation toward M2-like TAMs.³⁴ Lactate accumulation is another characteristic feature of the tumor microenvironment that is further enhanced by hypoxia. The resulting acidification of the tumor stroma inhibits the proliferation and effector functions of CTLs.³⁵ (Figure 1)

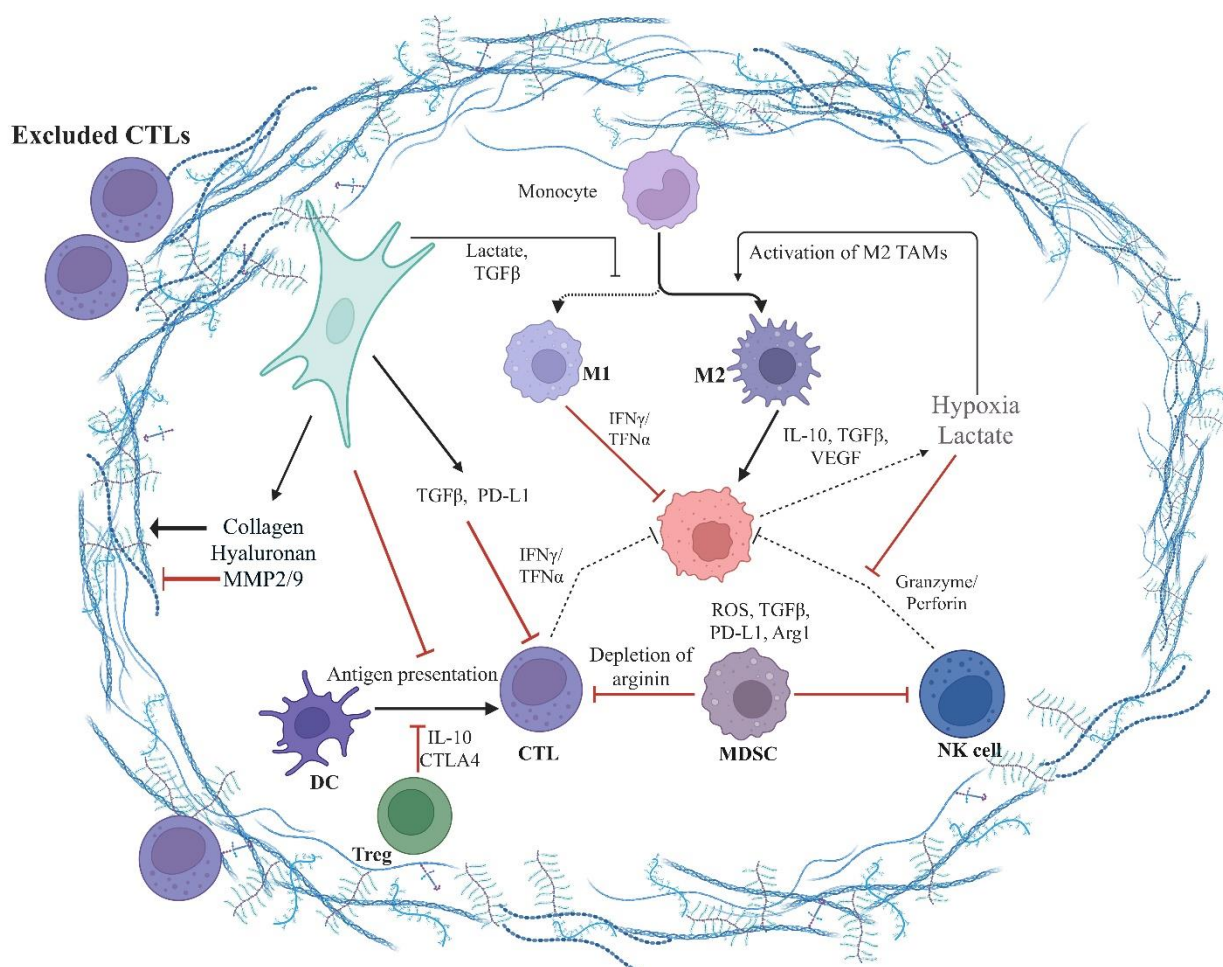


Figure 1. The tumor stroma in CRC and the immunosuppressive secretions and interactions mediated by stromal and immune cells. (This figure is original and was not adapted or reproduced from previously published sources)

Current Treatment Modalities for CRC

A combination of treatment modalities, including surgery, radiotherapy, chemotherapy, targeted molecular therapy, and immunotherapy, can be suggested for patients with CRC. Surgery followed by adjuvant chemotherapy may be recommended for the early stages of CRC. For stage I–III colon cancer and most rectal tumors, complete mesocolic or mesorectal excision can provide long-term disease control. Nevertheless, microscopic residual cancer cells can reduce the efficacy of this approach.³⁶ Locally advanced tumors may receive neoadjuvant chemoradiotherapy or total neoadjuvant therapy. Patients with metastatic CRC require systemic treatment and may also undergo metastasectomy or ablative therapy.³⁷ Adjuvant and neoadjuvant chemotherapy are well-established treatment modalities for CRC, particularly for stage III and high-risk stage II cancers.³⁸ In

rectal cancer, neoadjuvant chemoradiotherapy or chemotherapy alone can be prescribed to downstage tumors and facilitate sphincter preservation.³⁹ Systemic chemotherapy for metastatic CRC can improve survival.⁴⁰

The response of CRC to treatment is strongly influenced by the TME. Conversely, various drugs and radiotherapy can reshape this ecosystem by remodeling immunosuppressive mechanisms, reducing pro-tumor and anti-apoptotic signaling, and restoring the function of CTLs.⁴¹ Chemotherapy drugs may induce immunogenic cell death (ICD). This form of cell death releases tumor antigens and danger-associated signals that activate APCs, such as M1 TAMs and DCs, which in turn prime naïve CD8⁺ T cells and promote CTL expansion.⁴² However, chronic exposure to tumor antigens and the sustained release of inflammatory mediators by CTLs and NK cells can induce the expression of immune checkpoint molecules and increase the infiltration of Tregs, MDSCs, and M2-like TAMs. Under these conditions, treatment with immune checkpoint inhibitors (ICIs) or other immunomodulators that reduce checkpoint molecule expression may improve the therapeutic response.⁴³ Dense stroma and hypovascular regions also limit drug penetration, promoting spatially restricted tumor survival.⁴⁴ In addition, dose-limiting toxicity, neuropathy, and cumulative myelosuppression can reduce treatment efficacy.⁴⁵

Radiotherapy is widely used in rectal cancer and selectively in oligometastatic CRC, particularly for liver and lung lesions.^{46,47} Ionizing radiation (IR) can increase MHC expression and enhance antigen presentation. Type I interferon signaling can also be activated by IR. Together, these changes can convert irradiated tumors into in situ vaccines.⁴⁸ However, the response is context-dependent. High-dose or fractionated regimens may also damage endothelial cells, promote fibrosis, and recruit immunosuppressive MDSCs and macrophages.⁴⁹ In addition, hypoxic tumor regions are relatively radioresistant. Irregular vasculature and poor perfusion further exacerbate this problem.⁵⁰ Combining radiotherapy with immunomodulators may enhance antitumor immune responses while attenuating radiation-induced immunosuppression in CRC.⁴⁹

Targeted molecular therapy is another treatment option for advanced CRC. Bevacizumab and other anti-VEGF antibodies can be used to inhibit tumor neovascularization. This class of drugs improves the efficacy of chemotherapy by normalizing abnormal tumor vasculature. Improved perfusion within the tumor stroma enhances both drug delivery and CTL trafficking. However, tumors may activate alternative pro-angiogenic pathways and develop hypoxia in response to this treatment.⁵¹ Antibodies and drugs that inhibit EGFR and its downstream signaling pathways, such as cetuximab and panitumumab, are other therapeutic options for patients with RAS- and BRAF-wild-type metastatic CRC.⁵² These agents can also modulate the TME. For example, EGFR inhibition can alter cytokine secretion.⁵³

ICIs are effective for CRC with dMMR or MSI-H. Pembrolizumab and nivolumab have demonstrated good efficacy and durable tumor control in patients with dMMR/MSI-H gastrointestinal cancers.⁵⁴ These tumors harbor a high neoantigen burden and abundant infiltrating CTLs. As a result, ICIs can produce favorable therapeutic responses in this type of tumor stroma. However, most CRCs are microsatellite stable (MSS) and derive minimal benefit from ICI monotherapy. The MSS TME is typically characterized as cold or immune-excluded. These tumors contain few neoantigens, abundant CAFs, and immunosuppressive TAMs and MDSCs. In addition, tumors can lose antigen-presentation machinery, upregulate alternative immune checkpoint molecules, or recruit Tregs following immunotherapy.⁵⁵ Lower tumor immunogenicity and impaired antigen presentation in these tumors limit the pool of tumor-reactive T cells available for reinvigoration.^{56,57} Many MSS tumors exhibit immune exclusion even after CTL activation. CAF-driven ECM remodeling, high concentrations of TGF- β , and abnormal

vasculature contribute to this phenotype by restricting immune cell trafficking and sustaining immunosuppressive cytokine programs.^{58,59} Myeloid cell dominance, hypoxia, and altered metabolism are additional mechanisms that contribute to ICI resistance in these tumors.^{60,61} A smaller subset of CRC harbors POLE/POLD1 proofreading alterations that generate an ultramutated phenotype with a high tumor mutational burden (TMB). These alterations can enhance sensitivity to ICIs even in MSS tumors.⁶² However, although TMB may enrich for treatment response, its predictive value in CRC depends on the sequencing platform, the cutoff used, and whether the hypermutated phenotype results from defective DNA repair rather than other mechanisms.⁶³

Disease site also influences immune responses and clinical outcomes. The location of the primary tumor (right- vs. left-sided colon, or rectum vs. colon) and the site of metastasis can shape the immune composition of the TME and influence therapeutic responsiveness. For instance, right-sided CRC may exhibit higher cytotoxic immune activity. In addition, increased expression of VEGF and TAM-associated signatures can markedly influence immune responses in right-sided tumors but not in left-sided tumors.⁶⁴ In particular, liver metastases are frequently associated with stronger myeloid-mediated immunosuppression and attenuated systemic antitumor immunity. These characteristics may reduce the efficacy of ICIs despite adequate systemic drug exposure.⁶⁵ Cancer vaccines and adoptive cellular therapy (ACT) are additional strategies with growing relevance in CRC.^{66,67} However, these modalities have not yet been approved for the treatment of solid tumors such as CRC in humans. Furthermore, they face several resistance mechanisms, including the presence of fibrotic, immunosuppressive, and hypoxic niches within the CRC microenvironment.⁶⁷ (Figure 2)

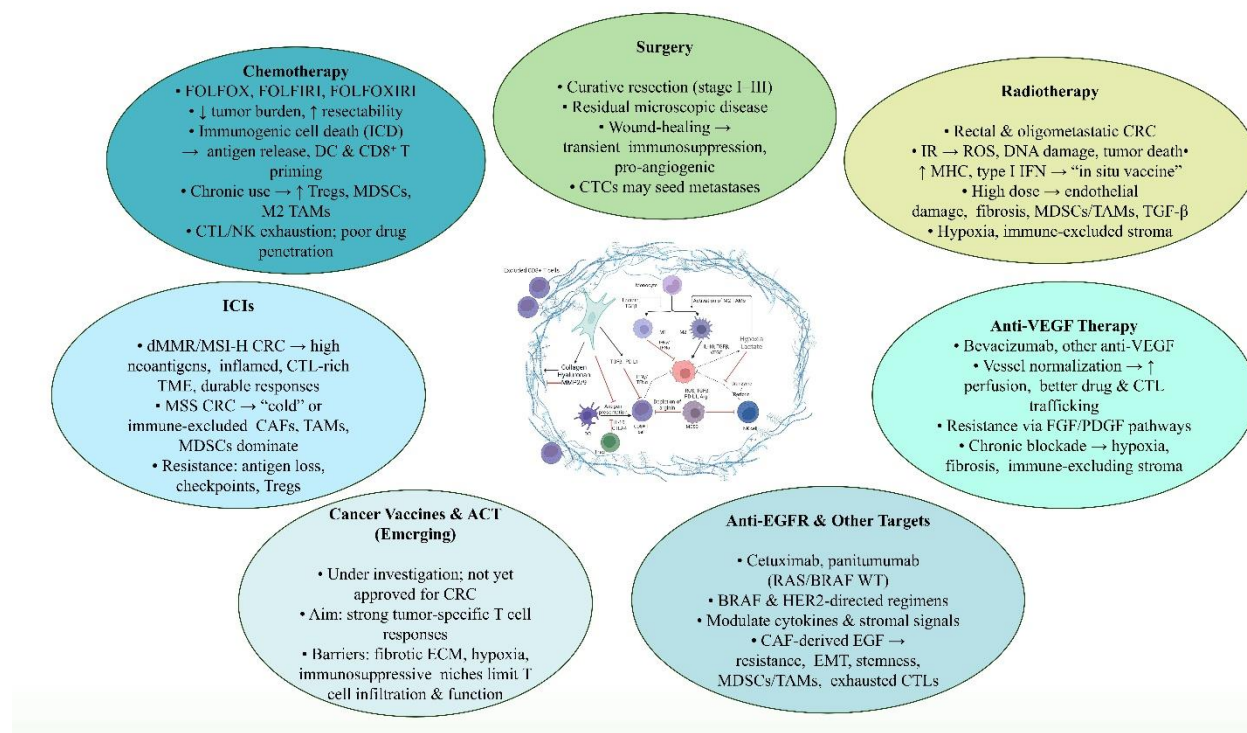


Figure 2. Various treatment modalities for CRC and their impact on the tumor stroma and antitumor immunity. (This figure is original and was not adapted or reproduced from previously published sources)

Targeting CAFs and ECM to Induce Antitumor Immunity

Several factors can activate CAFs, whereas others are secreted by CAFs and promote stemness in CRC cells or further expand the CAF population within the tumor. IL-1, TGF-β, and IL-6 are well-known factors that not only

promote CAF expansion but are also secreted by CAFs and contribute to therapeutic resistance in CRC.⁶⁸ A study showed that CAF-specific IL1R1 knockout and treatment with the IL-1 receptor antagonist anakinra remarkably reduced tumor growth in preclinical CRC models. Blockade of this pathway also resulted in reduced PD-L1 expression in CRC.⁶⁹ TGF- β and its receptor, TGFBR1, are other important therapeutic targets in CAFs. The TGF- β /TGFBR1 axis in CAFs is closely associated with IL-1 β signaling. Both IL-1 β and TGFBR1 have been shown to promote CAF recruitment and the polarization of normal fibroblasts into CAFs, leading to increased secretion of immunosuppressive cytokines and reduced production of inflammatory cytokines. IL-1 β and TGF- β activate fibroblasts through the janus kinase (JAK)/signal transducer and activator of transcription (STAT)3 and nuclear factor of kappa B (NF- κ B) signaling pathways. Blockade of either IL-1 β or TGFBR1 (using galunisertib) reduced CAF accumulation, thereby decreasing the resistance of CRC xenografts to oxaliplatin. In addition, inhibition of these pathways significantly reduced the levels of C-C motif chemokine ligand (CCL)5, IL-6, hepatocyte growth factor (HGF), and granulocyte-macrophage colony-stimulating factor (GM-CSF).⁷⁰

NADPH oxidase 4 (NOX4) is a pro-oxidant factor in CAFs that can induce apoptosis in CTLs. It is activated by TGF- β , while NOX4 activation can also stimulate TGF- β release and further promote CAF expansion. A study reported that NOX4 inhibition reversed TGF- β 1-mediated CAF activation, resulting in reduced ECM deposition, increased CTL infiltration into tumors, and an enhanced response to anti-PD-1 therapy.⁷¹ CAFs in CRC also suppress T-cell proliferation through PD-L1 expression. This molecule can be regulated by several CAF-derived secreted factors. CXCL5 is one of the key mediators. Secreted CXCL5 activates CXCR2 and phosphatidylinositol 3-kinase (PI3K)/protein kinase B (AKT) signaling in CRC cells, thereby enhancing PD-L1 expression on cancer cells and promoting immunosuppressive responses within the TME.⁷² CAFs can also regulate PD-L1 expression in CRC through the release of circEIF3K-containing exosomes. This factor suppresses miR-214 in cancer cells, resulting in PD-L1 overexpression. Since miR-214 normally acts as a negative regulator of PD-L1 in CRC cells, its suppression by CAF-derived circEIF3K enhances tumor-mediated immunosuppression.⁷³

In addition, CAF-derived factors can induce PD-L1 upregulation in CRC cells through activation of extracellular signal-regulated kinase (ERK)5 phosphorylation.⁷⁴ CAFs can also promote PD-L1 expression in TAMs. In response to overexpression of Yes-associated protein (YAP) in CRC cells, CAFs upregulate hyaluronan synthase 2 (HAS2). This process is associated with increased secretion of connective tissue growth factor (CTGF) by cancer cells, which stimulates HAS2 production. HAS2 binds to CD44 on M2-like TAMs and promotes PD-L1 upregulation. This interaction further contributes to CTL exhaustion in CRC. Under these conditions, inhibition of HAS2 synthesis in CAFs using specific inhibitors can restore CTL activity by reducing PD-L1 expression, thereby improving the response of CRC to anti-PD-1 therapy.⁷⁵

Some other agents have also shown the potential to remodel the ECM. The ECM-modifying enzyme lysyl oxidase (LOX) may promote CRC progression, particularly in advanced-stage tumors. This enzyme can enhance tumor invasion and metastasis by increasing collagen cross-linking, thereby promoting tumor stiffness. A preclinical study demonstrated that LOX induces focal adhesion kinase (FAK) and steroid receptor coactivator (Src) phosphorylation in CRC cells, which subsequently enhances cancer cell migration and invasion. Inhibition of LOX attenuated these effects. The authors suggested that targeting LOX activity may represent a novel and effective therapeutic strategy for patients with metastatic CRC.⁷⁶ Discoidin domain receptor 1 (DDR1) is another factor involved in collagen remodeling that promotes immune exclusion in CRC. A study reported that DDR1 silencing disrupts collagen barriers and enhances CTL infiltration, revealing a novel role of the DDR1-mediated

collagen-rich matrix in tumor resistance.⁷⁷ Although ECM remodeling has shown promising results in preclinical studies, it may also facilitate metastasis. Therefore, the clinical translation of this strategy faces greater challenges than approaches targeting CAFs or other immunosuppressive cells and components.⁷⁸ (Figure 3)

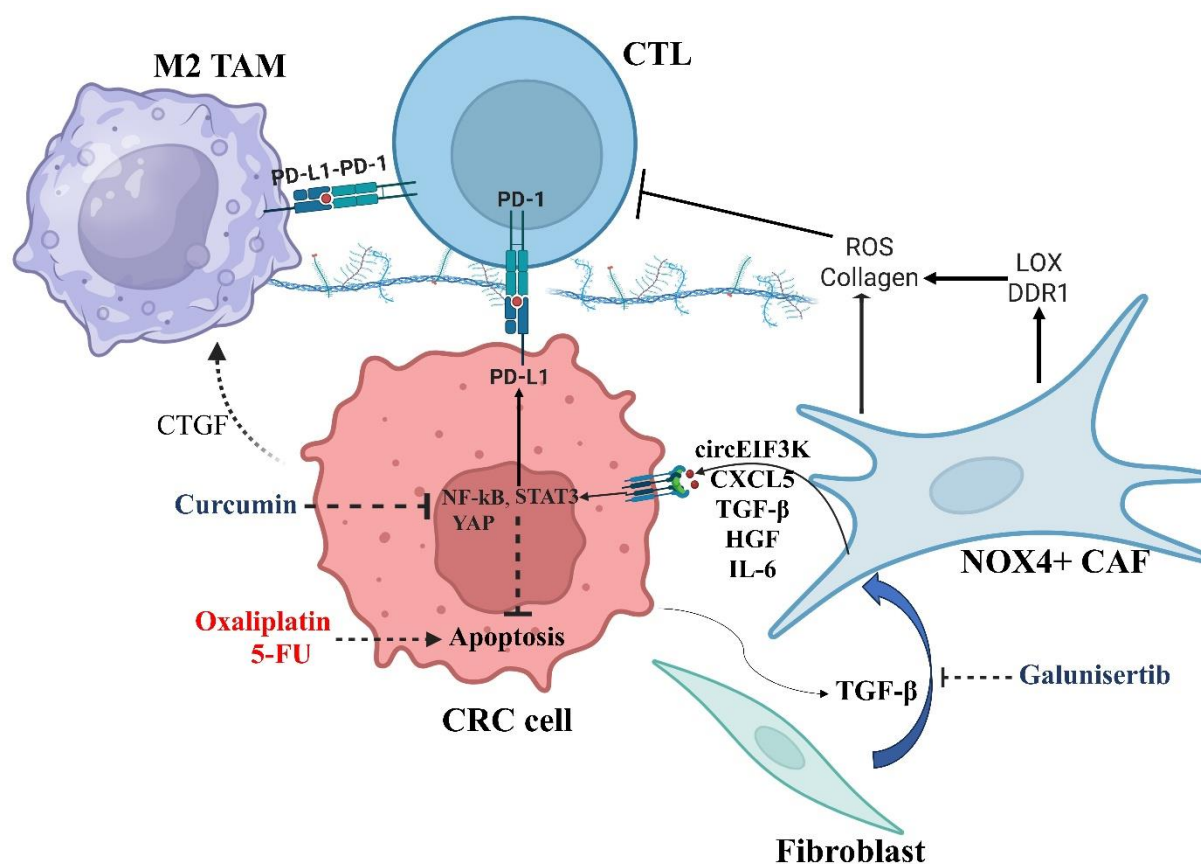


Figure 3. Mechanisms of CTL exhaustion and cancer cell resistance mediated by CAFs. As illustrated, CAFs release several factors that induce drug resistance and anti-apoptotic mediators in CRC cells. CAFs also produce collagen, which limits CTL infiltration into the tumor. In addition, CAFs stimulate CTGF release by CRC cells, thereby promoting the recruitment of M2-like TAMs and the upregulation of PD-L1 expression in these cells, ultimately leading to CTL exhaustion. Treatment with curcumin can reduce the activity of drug resistance mediators, such as NF- κ B, in CRC cells. Furthermore, blockade of TGF- β can attenuate CAF expansion and subsequently reduce resistance mechanisms in CRC. (This figure is original and was not adapted or reproduced from previously published sources)

Targeting TAMs to Induce Antitumor Immunity

Immunosuppressive TAMs express immune checkpoint molecules, engage in metabolic competition through indoleamine 2,3-dioxygenase (IDO) and arginase activity, secrete immunosuppressive cytokines and chemokines, and facilitate ECM remodeling.^{79,80} These characteristics provide several potential therapeutic targets for reducing the protumor activity of these cells. CSF-1R and CCL2 are well-established targets for depleting and reprogramming M2-like TAMs. An *in vivo* study reported that the CSF-1R inhibitor PLX3397 effectively reduced M2 TAM populations in orthotopic CRC xenograft models. When combined with anti-PD-1 therapy, this treatment significantly suppressed tumor growth. The findings also demonstrated that CAFs promote the recruitment of M2 TAMs and subsequent CTL exhaustion through CSF-1R signaling. Blockade of this pathway effectively reversed these effects in CRC.⁸¹

Another study showed that CCL2 blockade suppresses macrophage recruitment and polarization toward the M2 phenotype, thereby sensitizing CRC to 5-FU. This combination therapy reduced tumor growth approximately fivefold compared with chemotherapy alone.⁸² Interestingly, several studies have reported that MSI-H CRC tends to express high levels of PD-L1, which promotes the recruitment of M2 TAMs through the PD-L1/PD-1 axis. Moreover, sustained PD-1 overexpression on M2 TAMs reduces their phagocytic activity and contributes to CTL exhaustion. Consequently, PD-1 blockade decreases M2 TAM infiltration, promotes M1-like polarization, and enhances CTL activation in CRC.⁸³ Combining TAM-reprogramming strategies with immune checkpoint inhibitors therefore offers synergistic therapeutic potential for CRC treatment.

As discussed earlier, the CRC stroma contains a broad spectrum of TAM populations with diverse functional states. Human single-cell RNA sequencing and spatial profiling studies have further refined the macrophage landscape in CRC. These analyses have identified multiple TAM programs beyond the traditional M1/M2 classification, including antigen-presenting/inflammatory macrophages, monocyte-like macrophages, and immunoregulatory macrophages. These distinct macrophage states are associated with differences in phagocytic capacity, angiogenesis, and ECM remodeling.⁸⁴ Spatial mapping studies have also shown that immunosuppressive myeloid programs frequently colocalize with CAF-rich, TGF- β -associated stromal niches and are depleted in T cell-inflamed regions of digestive tumors.⁸⁵ These human CRC atlases support a therapeutic strategy that combines targeting TAM recruitment and polarization pathways with stromal modulation and immune checkpoint blockade.

Targeting MDSCs for Inducing Antitumor Immunity

Several therapeutic strategies have been proposed to target MDSCs and restore antitumor immunity. Experimental studies suggest that these approaches include promoting the differentiation of MDSCs into mature myeloid cells, blocking their recruitment, directly inhibiting their immunosuppressive functions, and targeting their metabolic pathways.⁸⁶ As explained, GM-CSF, VEGF, IL-6, IL-10, TGF- β , and prostaglandin E2 (PGE2) can expand MDSCs by inducing STAT3/6 phosphorylation in these cells. In addition, CSF-1, CCL2, and CCL5 can enhance the recruitment of MDSCs. These factors form an interactive communication network promoting MDSC accumulation. These factors can be suggested as promising targets for inhibiting MDSCs. Maraviroc, a C-C chemokine receptor (CCR)5 antagonist, combined with pembrolizumab, is being evaluated in metastatic CRC.⁸⁷ However, its effects on MDSCs in these patients need to be determined. Histamine dihydrochloride (a NOX2 inhibitor) has been shown to reduce MDSC accumulation in MC-38 cell-bearing mice. This effect resulted in improved tumor response to anti-PD-1/PD-L1 therapy.⁸⁸ Similarly, embelin, an inhibitor of X-linked inhibitor of apoptosis protein (XIAP), significantly decreased MDSC populations in both peripheral lymphoid organs and tumor tissues by reducing ROS production and arginase-1 expression. Furthermore, naringin suppressed colitis-associated CRC development by regulating the immunosuppressive activity of MDSCs through inhibition of the NF- κ B/IL-6/STAT3 signaling pathway. TLR7/8 agonist resiquimod (R848) is another agent that can induce an inflammatory response in CRC. Treatment with this agent can sensitize CRC to oxaliplatin by reducing MDSCs within tumors and polarization of these toward M1 TAM.⁸⁹ (Figure 4)

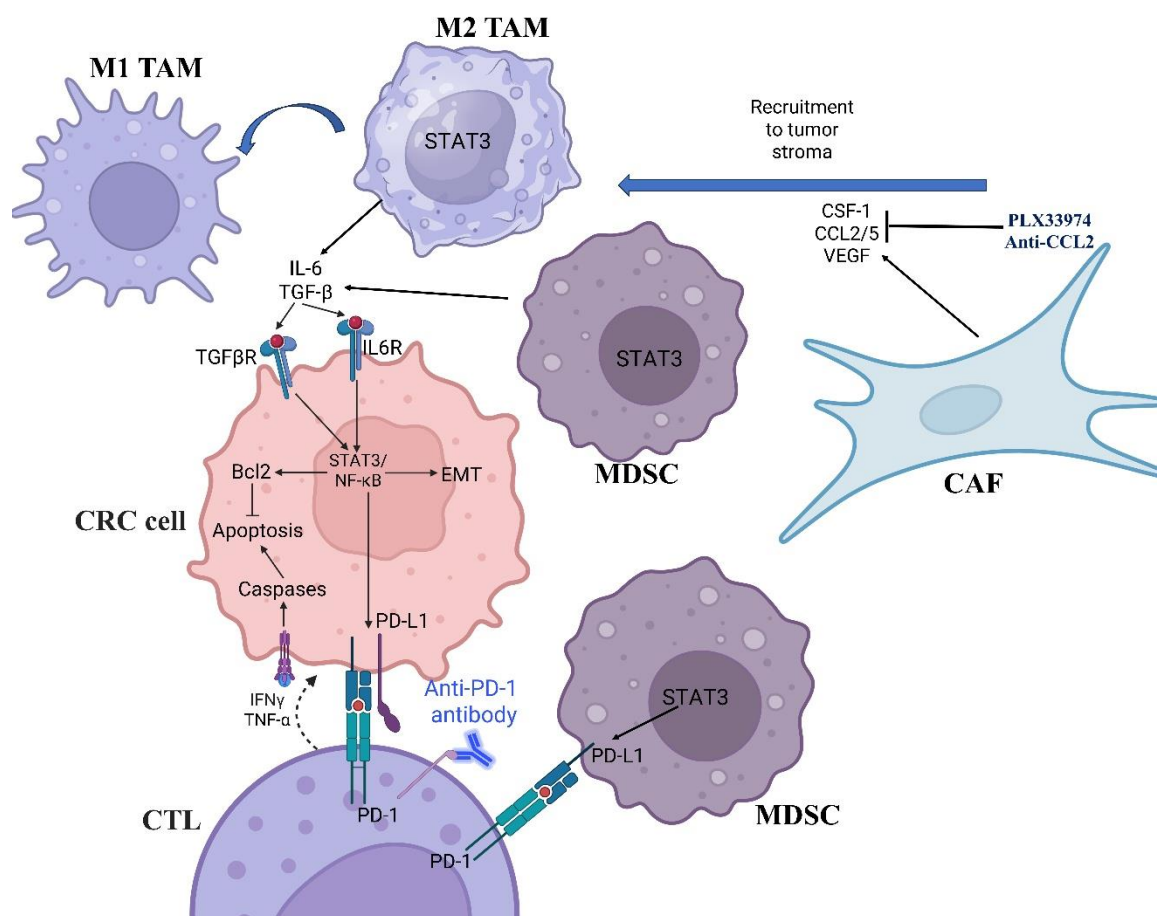


Figure 4: Targeting TAMs and MDSCs in CRC for boosting antitumor immunity. Chemokines such as CSF-1 and CCL2/5 can induce the recruitment of MDSCs and M2 TAMs. These cells induce CTL exhaustion by expressing PD-L1 and enhance drug resistance in CRC by releasing IL-6 and TGF-β. As illustrated, the blockade of CCL2/5 and CSF-1 can reduce the recruitment of these cells and subsequent resistance to therapy. (This figure is original and was not adapted or reproduced from previously published sources)

Targeting Tregs for inducing antitumor immunity

Tregs are potent immunosuppressive cells and represent a promising target for enhancing antitumor immunity. CCR8 has emerged as an attractive target for selective Treg depletion because its expression distinguishes tumor-infiltrating Tregs from those residing in lymphoid organs. CCR8-expressing Tregs migrate into tumors in response to the CCL1 ligand secreted by CAFs and M2-polarized TAMs. Selective CCR8 depletion has been reported to preserve peripheral immune tolerance while eliminating tumor-infiltrating Tregs.⁹⁰ Targeting CCR8 in CRC models has also been shown to enhance the expansion and activation of Th1 CD4⁺ cells and CTLs.⁹¹ This improvement in antitumor immunity has been associated with enhanced responses to anti-PD-1 therapy and vaccine-based strategies in murine CRC models.^{92,93}

CCL5 is another important chemoattractant for Tregs in CRC. Increased CCL5 expression promotes the expansion of TGF-β⁺ Tregs, thereby inducing CTL apoptosis.⁹⁴ Immunosuppressive mediators such as TGF-β are major drivers of Treg expansion. Therefore, reducing TGF-β levels within the tumor microenvironment may decrease Treg accumulation. TGF-β produced and secreted by TAMs has been shown to promote Treg expansion in CRC.⁹⁵ Moreover, TGF-β expression in CRC is positively correlated with Foxp3 expression and distant metastasis.⁹⁶ Similar to MDSCs, Treg populations can also be reduced following treatment with certain chemotherapeutic

agents. Low-dose cyclophosphamide has been reported to deplete Tregs in CRC.⁹⁷ Tregs are major suppressors of CTL activity in cancer and can also impair DC function. Colon cancers contain CCR4⁺CTLA4^{hi}Foxp3 Tregs that may serve as therapeutic targets for restoring antitumor immunity.⁹⁸

Several studies have suggested that targeting CTLA-4 with monoclonal antibodies is an effective strategy for depleting or reducing Treg populations.⁹⁹ However, other studies have reported limited efficacy or even increased Treg expansion following CTLA-4 blockade.^{100,101} In preclinical models, treatment of CRC-bearing mice with an anti-CTLA-4 antibody significantly reduced tumor-infiltrating Tregs.¹⁰² Clinical trials have also demonstrated improved antitumor immunity in patients with CRC following treatment with anti-CTLA-4 antibodies.^{103,104} Nevertheless, experimental studies indicate that cells within the CRC stroma can express alternative immune checkpoint molecules that diminish the efficacy of anti-CTLA-4 therapy. Therefore, Treg depletion using anti-CTLA-4 antibodies in combination with other agents, such as anti-PD-1 or anti-PD-L1 antibodies, may further improve therapeutic efficacy.¹⁰⁵

Targeting Hypoxia for Inducing Antitumor Immunity

Targeting hypoxia, HIF-1 α signaling, metabolic pathways, and tumor oxygenation has emerged as a promising strategy for remodeling antitumor immunity in CRC. Treatment with PX-478, a HIF-1 α inhibitor, has been shown to enhance oxaliplatin sensitivity by suppressing the HIF-1 α /miR-338-5p/IL-6 feedback loop in CRC xenograft models. The findings demonstrated that IL-6 is a direct target of miR-338-5p and mediates STAT3/Bcl-2 activation under hypoxic conditions. Moreover, the HIF-1 α /miR-338-5p/IL-6 signaling loop was found to be essential for the development of chemoresistance, and disruption of this pathway restored chemosensitivity.¹⁰⁶ Hypoxia also promotes the secretion of TGF- β 2 by CAFs, thereby enhancing chemoresistance in CRC. Consequently, alleviating tumor hypoxia may attenuate the immunosuppressive effects of CAFs and improve therapeutic responses.¹⁰⁷ Collectively, these findings indicate that targeting hypoxia-related pathways can reverse immunosuppression and enhance the efficacy of anticancer therapies in CRC.

Targeting Tumor Acidity and Altered Metabolism for Inducing Antitumor Immunity

The Warburg effect promotes excessive lactate production, resulting in acidification of the tumor stroma. This acidic milieu suppresses antitumor immunity and contributes to resistance against multiple anticancer therapies. Therefore, targeting this acidic stroma with pH-modulating drugs can modulate antitumor efficacy against CRC. A study showed that cariporide treatment induced TNF- α production and improved antitumor immunity, although it was also associated with elevated IL-6 levels.¹⁰⁸ Inhibition of monocarboxylate transporters (MCTs) reduces lactate export and accumulation, thereby sensitizing CRC cells to chemotherapy.¹⁰⁹ Similarly, proton pump inhibitors have been reported to improve the survival of patients receiving FOLFOX.¹¹⁰

Additional metabolic targets have also been proposed for remodeling the immunosuppressive microenvironment. In human CRC, CAFs are known as the prominent CD73^{hi} population. These cells can be expanded through an adenosine–A2B receptor-mediated feedforward loop. Inhibition of CD73 has therefore been shown to restore antitumor immunity.¹¹¹ TAMs has also emerged as an attractive therapeutic strategy. The STING agonist GB2 induces metabolic remodeling of TAMs by enhancing the glycolysis–ROS–HIF-1 α axis while suppressing oxidative phosphorylation (OXPHOS), thereby promoting M1 polarization and increasing macrophage phagocytic activity. These changes restore CTL function and enhance the therapeutic efficacy of anti-PD-1

immunotherapy.¹¹² Metformin is another promising metabolic modulator that affects both TAMs and MDSCs. Metformin activates adenosine monophosphate-activated protein kinase (AMPK) while inhibiting mechanistic target of rapamycin (mTOR) signaling in these immunosuppressive cells. In addition, it suppresses the mevalonate pathway, which plays a critical role in tumor metabolism. Treatment with metformin has also been shown to reduce Treg frequencies in murine CRC models without significantly affecting peripheral lymphoid tissues.¹¹³

Targeting CTLs and NK Cells

In addition to strategies aimed at suppressing immunosuppressive mechanisms within the TME, direct activation of NK cells and CTLs has also attracted considerable attention. Therapeutic cancer vaccines represent a promising approach for enhancing antitumor immunity while minimizing systemic toxicity. Current CRC vaccine platforms include whole tumor cell-based vaccines, DC-based vaccines, peptide vaccines, nucleic acid vaccines, and viral vector-based vaccines.¹¹⁴ Among these approaches, the ELI-002 2P vaccine has demonstrated a favorable safety profile in a Phase I clinical trial involving patients with KRAS-mutated CRC (NCT05726864). Recent findings showed that most patients developed robust antigen-specific immune responses characterized by activation of CD4⁺ Th1 cells and CTLs.

Furthermore, patients with stronger CTL responses experienced prolonged relapse-free periods. The vaccine also generated durable antitumor immunity, suggesting its potential to prevent or delay cancer recurrence in high-risk patients.¹¹⁵ Some other vaccine platforms, including *Listeria monocytogenes*-based immunotherapy and ADX-NEO, which combines a *L. monocytogenes* platform with neoantigens, have demonstrated acceptable safety profiles in Phase I clinical trials (NCT03189030 and NCT03265080). These approaches are currently being evaluated as monotherapies or in combination with other anticancer agents for the treatment of solid cancers.¹¹⁶ Gemogenovatulcel-T (Vigil) is another promising vaccine that has demonstrated the ability to induce durable adaptive immune responses when combined with FOLFOX-6 chemotherapy. The available evidence suggests that this vaccine is safe and exhibits potential antitumor activity in patients with advanced CRC.¹¹⁷ Messenger RNA (mRNA)-based vaccine technology has recently emerged as a promising therapeutic strategy, offering greater specificity, enhanced efficacy, and fewer adverse effects than traditional approaches.¹¹⁸ Results of clinical trials investigating novel ICIs, vaccines, and combination treatment strategies is presented in Table 1. (Table 1)

Table 1: Summary of Clinical Trials Evaluating Immunomodulatory Strategies in CRC

Population	Design	Key Efficacy	Safety	
mKRAS PDAC/CRC; MRD+ (AMPLIFY- 201)	Phase 1 (N=25; 5 CRC); ELI-002 2P vaccine	• 84% biomarker reduction; 24% clearance • mRFS: 16.3 mo • T cell response: 84% • mOS: 16.3 mo	• No grade ≥ 3 AEs • No DLTs/CRS • Fatigue (24%)	¹¹⁹
pMMR/MSS mCRC	Phase 2 (N=114) serplulimab plus	• PFS: 17.2 vs. 10.7 • OS wasn't reached to the aim of study	Grade ≥ 3 TRAEs: 65.5% vs 56% ¹	¹²⁰

	HLX04 and serplulimab vs placebo			
pMMR/MSS mCRC	Phase 2 (N=201) FOLFOXIRI plus bevacizumab alone or in combination with atezolizumab	No improvement in PFS compared to conventional therapy	No additional TRAEs was reported for immunotherapy arm compared to FOLFOXIRI plus bevacizumab	121
dMMR/MSI-H mCRC; ≥ 1 prior line (CheckMate 142)	Phase 2 (N=74); Nivolumab	• ORR: 31.1% • 12-mo PFS: 50%; 12-mo OS: 73% • Responses in all subgroups	• Grade 3-4: 20% • No treatment-related deaths	103
MSI-H/dMMR mCRC; first-line (KEYNOTE-177)	Phase 3 (N=307); Pembrolizumab vs Chemotherapy	• PFS: 16.5 vs 8.2 mo • ORR: 45% vs 33%	• Grade ≥ 3 TRAEs: 22% vs 66% • No pembrolizumab-related deaths	122
MSI-H/dMMR mCRC; first-line (CheckMate 8HW)	Phase 3 (N=303); Nivo+Ipi vs Chemotherapy	• 24-mo PFS: 72% vs 14% • Benefit across all subgroups	• Grade 3-4: 23% for Nivo+Ipi vs 48% for chemotherapy • 2 treatment-related deaths for Nivo+Ipi	123
Refractory CRC; all standard therapies (CO.26 studies)	Phase 2 (N=180); Durva+Treme+BSC vs BSC	• OS: 6.6 mo for Durva+Treme+BSC vs 4.1 mo for BSC only	• Grade ≥ 3: 64% for combination therapy vs 20% for BSC only	124
Refractory mCRC (BACCI study)	Phase 2 (N=128); Cape+Bev+Atezo vs Cape+Bev+Placebo	• PFS: 4.4 for Cape+Bev+Atezo vs 3.6 mo for Cape+Bev+Placebo	• Similar AE rates • 1 treatment-related death	125
Advanced solid tumors, including MSS-CRC	Phase 1 (N=192; 42 CRC); Oleclumab alone or with Durvalumab	• CRC: ORR 2.4% (1 CR) • mPFS: 5.4 mo	• TRAEs: 60% • CRC: grade 3-4 19%	126

MSS-CRC; recurrence after chemo	Phase 1 (N=6); Personalized vaccine (Neoantigen Vaccine)	• Immune response: 67% • PFS: 19 vs 11 mo (responders vs non)	• Grade 1 injection reactions, rash, headache	127
Advanced CRC; ≥ 2 prior lines	Phase 1 (N=6); NKG2D CAR- NK $\pm$ anti-PD-1	• Best: SD (1 patient) • 2 patients OS >700 days	• TRAEs: 100% • Hematologic toxicities (lymphodepletion)	128

Abbreviations: AE, adverse event; AESI, adverse event of special interest; Atezo, atezolizumab; Bev, bevacizumab; BICR, blinded independent central review; BSC, best supportive care; Cape, capecitabine; CI, confidence interval; CR, complete response; CRC, colorectal cancer; CRS, cytokine release syndrome; ctDNA, circulating tumor DNA; DLT, dose-limiting toxicity; dMMR, deficient mismatch repair; DOR, duration of response; Durva, durvalumab; EGFR, epidermal growth factor receptor; FOLFIRI, folinic acid + fluorouracil + irinotecan; FOLFOX, folinic acid + fluorouracil + oxaliplatin; FOLFOXIRI, folinic acid + fluorouracil + oxaliplatin + irinotecan; HLX04, bevacizumab biosimilar; HR, hazard ratio; Ipi, ipilimumab; IRRC, independent radiology review committee; ITT, intention-to-treat; mCRC, metastatic colorectal cancer; mKRAS, mutant KRAS; MRD, minimal residual disease; MSI-H, microsatellite instability-high; MSS, microsatellite stable; MTD, maximum tolerated dose; Nivo, nivolumab; NR, not reached; NSCLC, non-small cell lung cancer; OR, odds ratio; ORR, objective response rate; OS, overall survival; PD-1, programmed cell death protein-1; PD-L1, programmed death-ligand 1; PDAC, pancreatic ductal adenocarcinoma; PFS, progression-free survival; pMMR, proficient mismatch repair; PR, partial response; Q2W, every 2 weeks; Q3W, every 3 weeks; Q4W, every 4 weeks; QOL, quality of life; RFS, relapse-free survival; RMST, restricted mean survival time; RP2D, recommended phase 2 dose; SAE, serious adverse event; SD, stable disease; TEAE, treatment-emergent adverse event; TMB, tumor mutational burden; TRAE, treatment-related adverse event; Treme, tremelimumab; WT, wild-type; XELOX, capecitabine + oxaliplatin.

The findings from clinical trials reveal a clear dichotomy based on the molecular status of the tumor. In total, these findings suggest that ICIs are the standard of care for MSI-H/dMMR CRC. These trials have shown that nivolumab plus ipilimumab provides the most durable disease control. No immunotherapy strategy has demonstrated a transformative benefit in patients with MSS/pMMR CRC. The modest signals from combinations and emerging data on vaccines suggest that converting MSS tumors to an immune-responsive state requires more sophisticated approaches, including better patient selection using biomarkers such as TMB and ctDNA dynamics.

Natural products for boosting antitumor immunity in CRC

Natural products, particularly polyphenol-rich compounds, have been investigated as immunomodulatory candidates for CRC, mainly in preclinical models. Agents such as curcumin, resveratrol, quercetin, and epigallocatechin gallate (EGCG) have been reported to influence inflammatory signaling (e.g., NF- κ B and STAT3), cytokine profiles, and immunosuppressive pathways within the TIME. These modulatory effects are associated with changes in CTL activity and reduced MDSCs or Treg programs in experimental systems.¹²⁹ However, the strength of evidence varies substantially across compounds and model systems, and findings from in vitro assays should not be extrapolated to clinical efficacy without exposure and pharmacokinetic support.

Curcumin is the most frequently studied compound for CRC immunomodulation. Preclinical studies suggest that curcumin can attenuate immunosuppressive signaling in the TIME (including TGF- β - and NF- κ B signaling pathways) and may reduce immunosuppressive TAMs and Treg-associated features in CRC models.¹³⁰⁻¹³² Curcumin has been shown to attenuate M2 TAMs by lowering IL-10 secretion and arginase-1 expression. These effects reversed the M2 polarization of TAMs and attenuated CRC cell invasion.¹³³ Curcumin treatment has been shown to polarize MDSCs toward an M1-like phenotype by inhibiting STAT3 and NF- κ B and subsequently

attenuating IL-6 release by MDSCs.¹³⁴ Some phytochemicals like curcumin, Cucurbitacin B, and Astragaloside IV suppress M2 polarization of TAMs by inhibiting NF- κ B/STAT3. These agents can also block VEGF/HIF-1 α -induced angiogenesis and restore antitumor immunity by downregulating PD-L1.¹³⁵⁻¹³⁷

In a limited clinical investigation, curcumin was associated with immunological changes consistent with reduced Treg activity and enhanced Th1-type responses. However, clinical efficacy outcomes remain insufficiently defined.¹³⁸ Resveratrol and EGCG have also shown immunomodulatory effects in CRC-related models. These products have shown the ability to suppress tumor-promoting stromal/metabolic interactions and attenuate signaling pathways involved in angiogenesis and hypoxia responses.¹³⁹⁻¹⁴¹ Additional natural compounds, including luteolin, piceatannol, glycyrrhizin, tanshinone IIA, and acriflavine, have been reported to affect TAM/MDSC/Treg-associated pathways or HIF-related signaling in preclinical CRC models.¹⁴²⁻¹⁴⁶ All-trans retinoic acid (ATRA) promotes MDSC differentiation into mature cells, thereby attenuating their immunosuppressive effects.¹⁴⁷ However, most studies mentioned have limited validation in immune-competent CRC models and lack human evidence. (Figure 5)

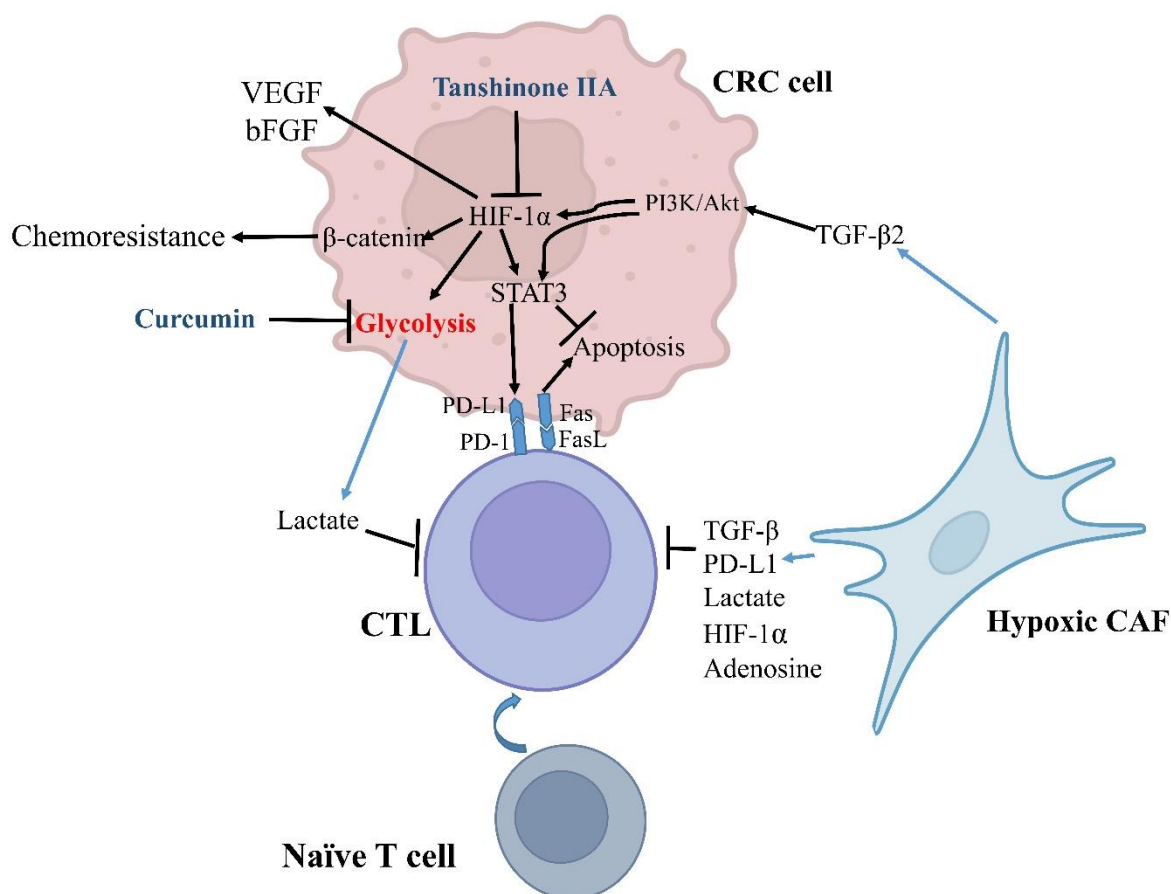


Figure 5: Natural products can remodel the TIME in CRC by modulating hypoxia and metabolism. Hypoxia can potentiate both glycolysis and lactate production. Hypoxia can induce the release of TGF- β 2, lactate, and adenosine, which not only suppress CTLs but also induce chemoresistance in CRC cells. The modulation of HIF-1 or glycolysis by natural products can mitigate these effects. (This figure is original and was not adapted or reproduced from previously published sources)

From a pharmaceutical-development perspective, the translation of natural products faces serious challenges, including poor aqueous solubility, extensive first-pass metabolism, short systemic half-life, and limited and

variable oral bioavailability.^{148,149} These limitations can prevent achieving intratumoral exposures comparable to those used in mechanistic in vitro studies. In addition, variability in formulation and product standardization (extracts vs. purified compounds) causes significant obstacles. Other limitations include potential drug–drug interactions, enhanced normal tissue toxicity by anticancer drugs, and the absence of consistent biomarker-driven clinical studies.^{150–152} Overall, natural products are best viewed as adjunct immunomodulatory candidates or lead structures rather than an alone anticancer approach in CRC. Future studies should prioritize standardized formulations, exposure–response relationships, immune-competent CRC models with defined endpoints, and biomarkers. Appropriate endpoints, such as CTL infiltration/function, can predict the direct immunomodulatory effects of different natural products. This can also facilitate the comparison of the potential of various products in different forms. Biomarker-stratified clinical investigations are also needed to determine whether these immunological effects translate into clinically meaningful benefit.^{153,154}

Nanomedicine for boosting antitumor immunity in CRC

Nanomedicine platforms can improve the intratumoral delivery of immunomodulatory agents, including cytotoxic drugs that induce immunogenic cell death, targeted inhibitors, natural products, and ICIs. Nanoparticles can accumulate in tumors through the enhanced permeability and retention (EPR) effect. This effect results from tumor vasculature.¹⁵⁵ However, the magnitude of the EPR is heterogeneous and frequently less pronounced in patients than in murine models. Accordingly, active targeting (e.g., ligand- or antibody-mediated binding to tumor or stromal markers) and stimulus-responsive release (pH-, redox-, or enzyme-triggered systems) are commonly explored to enhance tumor retention. Specific polymers in nanoparticles can provide controlled release within the acidic or enzyme-rich tumor stroma. This can amplify local killing and prevent severe side effects in normal tissues.¹⁵⁶ Nanocarriers also enable the co-delivery of combination payloads (e.g., antigen plus immune stimulant or chemotherapy plus immunomodulator). These formulations can carry ECM-degrading enzymes or stromal-targeting moieties that reduce tumor rigidity and improve drug penetration into the stroma of the tumor.^{157,158} These properties provide opportunities for remodeling the TIME in different malignancies, including CRC.

Nanoformulations have been investigated to improve the pharmacological performance of poorly soluble natural products and support immune activation by various immunomodulators. For example, delivery systems such as liposomes, micelles, gold nanoparticles, and polymeric or chitosan nanoparticles have been used to increase the efficacy of curcumin against CRC.¹⁵⁹ In an SW620 xenograft model, gold nanoparticles reduced α -SMA⁺ CAF features and ECM-associated mediators, including collagen I and CTGF. Nanoparticles also inhibited TGF- β 1 and VEGF, which was associated with improved vascular function and reduced hypoxia.¹⁶⁰ Several nanomedicine systems have also been designed to reprogram suppressive myeloid programs in immune-competent CRC models. A study by Mao et al. developed lentinan-ursolic acid polymeric nanomedicine to target CRC in mice. This nanocomplex promoted M2 to M1 polarization by inducing ICD in the tumor. In addition, mannose-modified erythrocyte membrane-wrapped nanoparticles loaded with artesunate and chloroquine repolarized M2 TAMs to M1 TAMs, thereby inhibiting the immunosuppressive effects of TAMs.¹⁶¹ Aptamer-conjugated-2c-loaded nanoparticles (Apt-2cNP) and retinoic acid-loaded PLGA nanoparticles are other nanocomplexes that have been utilized to modulate TAM polarization within colorectal TME by inhibiting NF- κ B/STAT3 signaling pathway associated with M2 polarization.^{162,163}

Despite these opportunities, the translation of immuno-nanomedicine faces substantial barriers. The major challenges include variable tumor delivery (due to tumor heterogeneity), uptake by the reticuloendothelial system, and potential immunotoxicity. Furthermore, challenges in scalable manufacturing, reproducibility, and regulatory characterization add another layer of barriers to the clinical translation of nanoparticles. Therefore, comparative reporting of carrier composition, physicochemical properties, pharmacokinetics, toxicity, and model quality is essential for each type of nanomedicine. The results of important factors and modulatory effects of different nanoparticles for remodeling antitumor immunity in CRC are summarized in Table 2. (Table 2)

Table 2. Comparison of Nanoparticle-Based Immunomodulatory Strategies in CRC Preclinical Models

Formulation & Targeting	Mechanism of Action	In Vivo Model & Efficacy	PK Profile	Safety & Manufacturing	Ref.
M1EVs + OXA, RA, LF (Intrinsic EV homing)	M2→M1 repolarization; STAT3/NF- κ B/AKT $\downarrow$; $\uparrow$ CD8 $^{+}$ T cells; $\downarrow$ IL-10, PD-L1; $\downarrow$ MDR1/survivin	CT-26 syngeneic (flank + peritoneal); $\downarrow$ primary tumor & metastases; $\uparrow$ apoptosis	Not reported	Safety: Basic H&E only. Manufacturing: Ultracentrifugation	¹⁶⁴
Nanocurcumin + resveratrol (320 nm) + mEHT	ICD via HSP70/CRT; $\uparrow$ CD3 $^{+}$ T cells & F4/80 $^{+}$ macrophages; apoptosis activation	CT-26 syngeneic (flank); $\downarrow$ tumor volume & weight; $\uparrow$ T-cell infiltration	Mean concentration: CUR nanoparticle: 7.85 vs 0.7 ng/mL for free at 1 h; and 646 for resveratrol nanoparticle vs 76 ng/mL for free at 15 min	Safety: Not reported. Manufacturing: Physical grinding	¹⁶⁵
PLGA + Betulinic acid analogue (2c) (EpCAM DNA aptamer)	$\uparrow$ M1 macrophages; $\uparrow$ CD8 $^{+}$ T cells; $\uparrow$ Bax/caspase-3; $\downarrow$ Bcl-2; $\downarrow$ NF- κ B	DMH-induced carcinogen model (immunocompetent); $\downarrow$ tumor burden (67.5%); $\uparrow$ tumor accumulation	T $_{1/2}$: 36 h (vs 6 h free); AUC: increased by 2.58 fold	Safety: Hemolysis <5%; liver/kidney histology improved in H&E study. Manufacturing: PLGA (FDA-approved); aptamer costly. Regulatory: Clear path for PLGA.	¹⁶⁶
AuNPs (15 nm) + Cisplatin	Vessel decompression: $\downarrow$ CAFs, $\downarrow$ collagen I, $\downarrow$ TGF- β /VEGF;	SW620 xenograft (BALB/c nude) – immunodeficient (major limitation); $\downarrow$	AuNP PK not reported; enhanced cisplatin	Safety: No weight loss; no organ injury in H&E staining. Manufacturing: Simple 15 nm synthesis; scalable. Regulatory:	¹⁶⁷

	↑ perfusion; ↓hypoxia; enhances cisplatin delivery	tumor growth; perfusion ↑23→43%	accumulation in the tumor	AuNPs have FDA precedent.	
PLGA-lecithin- PEG + Curcumin (EpCAM RNA aptamer)	Targeted endocytosis → apoptosis; ↑ intracellular curcumin	In vitro only (HT29/HEK293T); no in vivo efficacy data (major gap)	T _{1/2} : ~5.93 h (vs 1.07 h free); AUC enhanced by 2.2 fold; sustained release 24 h	Safety: Not reported (PK only in healthy rats). Manufacturing: Nanoprecipitation; RNA aptamer costly but scalable. Regulatory: No in vivo data limits regulatory path.	¹⁶⁸
LNT-UA (carrier- free; LNT as carrier + immunoadjuvant)	UA → ICD; LNT → DC maturation & M2→M1 repolarization; ↑CD8 ⁺ /CD4 ⁺ ; ↑IFN-γ/TNF-α; ↓IL-10	CT-26 syngeneic (flank + bilateral); AOM/DSS spontaneous CRC (best model); ↓ primary & distant tumors; 2.2× survival extension	Not quantified; oral bioavailability assumed improved	Safety: No weight loss; normal ALT/AST/BUN/creatinine; H&E staining. Manufacturing: Simple nanoprecipitation. Regulatory: LNT-UA are GRAS; path as botanical supplement simpler.	¹⁶¹
Cholesterol- coated PLGA + RA (Cholesterol membrane targeting)	IL- 10R/STAT3/NF- κB↓; M2-TAM repolarization; ↓EMT; ↓PD-L1; synergy with αPD-L1	CT-26 syngeneic (flank) + mice model; ↓ tumor growth & metastasis	Not reported	Safety: Assumed standard. Manufacturing: PLGA (FDA-approved); cholesterol/RA approved; simple formulation. Regulatory: Highly feasible; all components approved.	¹⁶⁹

Abbreviations: AUC, area under the curve; CAFs, cancer-associated fibroblasts; CUR, curcumin; DC, dendritic cell; DMH, dimethylhydrazine; EPR, enhanced permeability and retention; GMP, Good Manufacturing Practice; GRAS, generally recognized as safe; ICD, immunogenic cell death; LNT, lentinan; mEHT, modulated electro-hyperthermia; M1EVs, M1 macrophage-derived extracellular vesicles; OXA, oxaliplatin; PLGA, poly(lactic-co-glycolic acid); RA, retinoic acid; SEC, size-exclusion chromatography; TMA, tissue microarray; UA, ursolic acid.

Preclinical evidence for nanoparticle-based immunomodulation demonstrates considerable promise. However, significant translational gaps remain in this field. Among the formulations mentioned in Table 2, M1 macrophage-derived extracellular vesicles, lentinan-ursolic acid, and PLGA-betulinic acid exhibited the most robust immunological activity. Pharmacokinetic profiling remains a critical limitation in this field. Future studies should focus on pharmacodynamic and safety profile factors.

Limitations and future perspectives

Many findings on CRC microenvironment targeting are based on cell lines or short-term murine experiments. However, clinical validation of these models is limited. Preclinical models cannot replicate the complexity of human stroma. This issue is a serious limitation in translating these findings into clinical practice. The reported effects are also sensitive to model choice, dosing schedule, and tumor implantation site. Consequently, the apparent consistency across studies may reflect methodological similarity rather than biological robustness.¹⁷⁰ Publication bias is an additional concern. Negative or neutral findings are rarely reported in detail.¹⁷¹ This distorts the perceived efficacy of the strategies discussed above. Therefore, the strength of evidence differs markedly between intervention classes. For instance, ICIs in dMMR/MSI-H tumors have been adopted clinically and show durable activity in prospective CRC trials.¹⁷² However, most stromal, myeloid, and metabolic modulation strategies remain preclinical or early phase. Furthermore, natural products and nanoformulations are predominantly at the discovery stage.¹⁷³ Therefore, we should weigh these differences by comparing different approaches. Uniform reporting of model type, exposure, comparator, and immune endpoints would improve their comparability. Without such standardization, translational prioritization remains subjective.

Patient selection and biomarker gaps are other important issues. Molecular stratification is essential for interpreting the immunotherapeutic potential in CRC. Mismatch repair status remains the dominant clinical biomarker in CRC. POLE/POLD1 alterations may extend the benefit to selected MSS tumors. Tumor mutational burden adds information.¹⁷⁴ However, considering assay thresholds are inconsistent at this moment. Anatomical variables also influence the response to therapy. These differences may suggest diverse treatment options for tumors at different locations. Liver metastases, prior chemotherapy, and radiotherapy alter immune responses.¹⁷⁵ These variables are unevenly reported in published studies. However, all of these factors can significantly affect the response of CRC to anticancer modalities. Emerging spatial and single-cell analyses of human CRC have revealed significant heterogeneity across the CRC stroma. These findings demonstrate that CAFs, TAMs, and MDSCs occupy specific tumor neighborhoods. On the other hand, CTLs are often confined to peripheral regions.^{176,177} This unique organization of stromal and immune cells may explain resistance despite adequate systemic drug exposure. However, spatial assays have not yet been standardized for routine clinical use. Cost, throughput, and interpretation remain other important barriers. Simplified multiplex panels may prove more feasible. Prospective validation is required before spatial metrics can guide therapy selection or trial enrollment in CRC.¹⁷⁸

Stromal and ECM-directed strategies face significant challenges. Targeting CAFs and ECM remains conceptually attractive. However, the clinical translation of these strategies is complex. Fibroblast populations in the tumor stroma are heterogeneous and have diverse functions. Some CAF subsets prevent tumor progression. These subsets promote antigen presentation and CTL activation. Therefore, broad depletion of CAFs may be harmful.¹⁷⁹ Marker-based targeting of these cells is also imperfect because FAP and α -SMA are expressed in normal tissues. ECM modification carries additional risks. Reducing tumor stiffness can improve perfusion and drug delivery. However, it may simultaneously facilitate invasion or dissemination.¹⁸⁰ The timing and degree of remodeling are likely critical. Similar concerns exist regarding pathway inhibition. For instance, TGF- β signaling regulates immunity, epithelial homeostasis, and cardiovascular function. Therefore, sustained systemic blockade can cause serious side effects.¹⁸¹ Localized or tumor-restricted delivery of TGF- β may mitigate these side effects. However, evidence for such approaches in CRC is limited. Furthermore, most stromal interventions have been evaluated as

monotherapies in preclinical studies. The efficacy of these interventions within multimodal regimens is poorly defined. Sequencing relative to chemotherapy, radiotherapy, or ICIs requires systematic studies rather than empirical combinations.

Suppressive myeloid cells are also compelling targets in CRC. However, the translation has been disappointing. CSF-1R inhibition efficiently reduces TAMs. However, compensatory recruitment of TAMs or MDSCs through alternative chemokine axes reduces the efficacy of this strategy. Myeloid plasticity further complicates the interpretation.¹⁸² Treg targeting raises different concerns. Systemic depletion may precipitate autoimmune toxicity. CTLA-4-directed antibodies illustrate this trade-off, particularly in combination regimens.¹⁸³ Selective approaches, such as CCR8-directed depletion, appear more attractive mechanistically. However, clinical findings on this strategy are limited.¹⁸⁴ Pharmacodynamic monitoring is another unresolved issue. Peripheral measurements do not necessarily capture the multi-compartment tumor–stroma–immune interactions that determine intratumoral function and repeated on-treatment tumor biopsies are difficult to scale in routine practice.¹⁸⁵

Nanomedicine-based approaches have been proposed to overcome stromal barriers. However, the clinical translation of these approaches is constrained by variable tumor accumulation, reticuloendothelial clearance, and potential immunotoxicity. Manufacturing complexity is an additional obstacle. In addition, regulatory characterization requirements are correspondingly demanding.¹⁸⁶ Similar considerations apply to natural products. However, poor solubility, extensive metabolism, and inconsistent standardization limit their reproducibility. The interaction potential with anticancer agents is insufficiently characterized.¹⁷³ Consequently, both approaches require rigorous pharmacokinetic and toxicological evaluations before efficacy claims can be substantiated in patients with CRC.

The progress of current approaches will depend on disciplined prioritization rather than broader exploration. Near-term opportunities are relatively evident. Checkpoint blockade has shown promising results and should continue to be optimized for dMMR/MSI-H CRC. Combination strategies for MSS tumors should be considered with regard to specific barriers. For instance, specific strategies should be considered for myeloid-rich or stromal-rich tumors.¹⁸⁷ In addition, particular combinations may be needed for vascular normalization.¹⁸⁸ These hypotheses should be tested prospectively. The trial design must evolve according to these challenges and perspectives. Biomarker-defined cohorts can overcome challenges by reducing heterogeneity. Furthermore, biomarker-based strategies can facilitate adaptive therapies to refine treatment doses and sequences.¹⁸⁹ Preclinical standards also require improvements. Immunocompetent, orthotopic, and metastatic models should be prioritized. Patient-derived systems incorporating immune and stromal components deserve wider adoption in the future. The reporting of exposure, toxicity, and comparator selection should be routine in these studies.^{170,190} Finally, translational success will require realistic framing of the results. Microenvironment modulation is unlikely to produce durable responses alone. Integrating pharmacology, formulation science, and immunological biomarkers can provide the most credible route to meaningful clinical benefits in CRC.

Conclusion

CRC remains a therapeutically challenging disease, particularly in tumors with an immunosuppressive microenvironment. In such settings, CAF/ECM remodeling, suppressive myeloid programs, Tregs, hypoxia, and metabolic remodeling converge to limit CTLs and NK cell function. These features also reduce drug penetration

and blunt responses to chemotherapy, targeted therapy, and ICIs. The strength of evidence supporting TIME-modulating strategies in CRC is uneven and should guide prioritization. The most mature and clinically validated approach is immune checkpoint blockade in dMMR/MSI-H CRC. Clinical trials and combination regimens (e.g., PD-1 ± CTLA-4 blockade) have confirmed that this strategy can provide durable responses in patients. In contrast, most interventions aimed at stromal remodeling (CAF/ECM), myeloid reprogramming (TAM/MDSC), adenosine/metabolic pathways, and hypoxia remain supported mainly by preclinical studies or early-phase trials. Accordingly, these strategies should be interpreted as hypothesis-generating unless corroborated by biomarker-stratified clinical data. Some strategies can also be suggested as near-term clinical options. These options either have regulatory approval in defined CRC subsets or rely on agents with established clinical availability that can be rationally combined. According to the reviewed studies, biomarker-guided ICI use in dMMR/MSI-H tumors can be suggested as a promising option for CRC patients. In addition, combination strategies for pMMR/MSS CRC that aim to convert cold tumors into hot tumors can be classified into this category. Chemotherapy or radiotherapy to trigger inflammatory responses, anti-angiogenic therapy for vascular normalization, and carefully selected ICIs in combination with stroma/myeloid targeting are promising approaches. Immune-priming approaches with early human safety signals, including selected therapeutic vaccine platforms in molecularly defined settings, can be suggested as another option. Importantly, success in MSS CRC will likely require matching combinations to the dominant resistance mechanisms.

Several approaches have shown limited clinical translation, despite a strong mechanistic rationale. Monotherapy with immune checkpoint blockade is largely ineffective in pMMR/MSS CRC. In addition, depletion or broad inhibition of MDSCs or TAMs (e.g., CSF-1/CSF-1R-axis strategies) has not consistently produced durable benefits. This highlights pathway redundancy, compensatory recruitment, and diverse TAM functions. Similarly, although aggressive ECM-modifying strategies may improve drug perfusion, they may trigger invasion, side effects, or unpredictable stromal remodeling. These findings emphasize that TIME targets should be prioritized not only by biological plausibility but also by human feasibility, safety margins, and biomarker-defined vulnerability.

Other strategies remain in the early stage or preclinical phases. Selective stromal reprogramming, spatially informed strategies that disrupt CAF–myeloid suppressive neighborhoods, and targeting of adenosine, lactate transports, and hypoxia-associated pathways can be classified into this category. Furthermore, nanomedicine-based approaches can be suggested as another example that has been designed to improve intratumoral exposure and boost immune priming by ICIs. These approaches remain promising but require rigorous validation in immunocompetent and clinically relevant CRC models. These strategies face remarkable challenges, such as the need for standardized immune endpoints and careful toxicology and manufacturability assessments prior to clinical translation. Natural products and nutraceutical candidates have shown immunomodulatory activity in experimental CRC models. However, their clinical relevance is limited by bioavailability, variability in formulation, and limited controlled trial data.

In summary, advancing CRC immunotherapy will require biomarker-stratified and mechanism-matched combinations. Integration of human single-cell/spatial evidence to identify dominant suppressive niches is essential for targeting the TIME. In addition, development programs that explicitly address pharmacokinetics, toxicity, and translational feasibility are crucial for future preclinical studies and clinical trials. Such a

prioritization framework can separate clinically actionable strategies from early exploratory concepts and may accelerate durable immune control in CRC.

Competing Interests

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