

Potential for anti-angiogenic therapy targeting the receptor for advanced glycation end products/VEGF axis in ulcerative colitis (Review)

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Received August 14, 2025; Accepted December 22, 2025

DOI: 10.3892/mmr.2026.13876

Abstract. Ulcerative colitis (UC), a major form of inflammatory bowel disease, has a global incidence of ~10.6 per 100,000 individuals. The long-term side effects and dependency issues associated with conventional UC therapies have become increasingly evident, highlighting the need for more effective and safer treatment options. In previous years, clinical research on small-molecule targeted drugs against UC has achieved notable progress; however, the underlying pathogenesis and therapeutic mechanisms of UC still require deeper investigation. The receptor for advanced glycation end products (RAGE) is a pattern recognition receptor that binds both pathogen-associated molecular patterns and damage-associated molecular patterns, thereby mediating inflammatory and cellular stress responses. Concurrently, vascular endothelial growth factor (VEGF), a key regulator of angiogenesis, is markedly upregulated in patients with UC and associates with disease severity. The RAGE/VEGF signaling axis has thus emerged as a notable target for antiangiogenic therapy in UC. Interventions aimed at disrupting the interaction between RAGE and its ligands, inhibiting RAGE pathway activation or suppressing VEGF upregulation have demonstrated promising potential to alleviate symptoms and slow disease progression. The present review summarizes previous advances in UC-targeted therapeutics and elucidates the role of the

RAGE/VEGF axis in UC pathophysiology, highlighting the potential mechanisms and clinical prospects of antiangiogenic strategies targeting this pathway.

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1. Introduction

Ulcerative colitis (UC) is a chronic, non-specific inflammatory bowel disease (IBD) that is characterized by persistent inflammation and ulceration of the colonic mucosa. Patients with UC typically present with abdominal pain, diarrhea and stools containing blood and mucus (1). Although the precise pathogenesis of UC remains to be fully elucidated, it is generally understood to result from the multifactorial interplay of environmental factors, immune dysregulation, gut microbiota imbalance and genetic predispositions (2). Histopathological features include inflammatory cell infiltration within the lamina propria and excessive secretion of proinflammatory cytokines such as IL-6 and TNF- α (3). Globally, the prevalence of UC is ~10.6 per 100,000 individuals (4), driven by an aging population and improved diagnostic recognition. With disease progression, the risk of colonic malignancy also increases (5). In Asian populations, westernization of diets has been identified as a key contributor to the increasing prevalence. Evidence from a large cohort of 500,000 Chinese participants highlights two high-risk dietary patterns associated with increased risk of UC: i) The traditional Northern diet, consisting of high wheat and low rice intake; and ii) a modern diet rich in animal-based foods and fruits. Notably, frequent egg consumption was associated with increased susceptibility to late-onset UC, whereas spicy food intake

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Key words: ulcerative colitis, receptor for advanced glycation end products, vascular endothelial growth factor, angiogenesis, targeted therapies

showed a protective association (6). Similarly, a Japanese study has attributed the pathogenesis of UC to reduced intake of dietary fiber, fermented foods containing probiotics and plant-based nutrients, accompanied by higher consumption of refined carbohydrates and animal fats (7). Pan-Asian analyses further support these findings, indicating that 'Westernized' diets, characterized by elevated refined sugar, red meat and linoleic acid, promote UC development, while fiber-rich fruits and vegetables exert protective effects (8).

Mechanistically, these dietary factors are considered to impair gut barrier integrity, alter gut microbial composition and amplify proinflammatory signaling cascades. Acute severe colitis is experienced by ~15% of patients with UC, with >30% ultimately requiring colectomy (9). Therapeutically, monoclonal antibodies targeting key cytokines have been increasingly used to manage corticosteroid-refractory UC (10-12). However, their long-term efficacy is limited by adverse effects and the gradual loss of therapeutic response in some patients (13), underscoring the need for continued investigation into UC pathogenesis and the development of novel treatment strategies.

The receptor for advanced glycation end products (RAGE), first identified in 1992, is a transmembrane protein belonging to the immunoglobulin (Ig) receptor superfamily (10). Structurally, RAGE comprises three domains, extracellular, transmembrane and intracellular, and exists in both membrane-bound and soluble forms. Owing to its unique molecular configuration, RAGE is one of the few pattern recognition receptors capable of binding both pathogen-associated molecular patterns and damage-associated molecular patterns (DAMPs). Initially discovered for its ability to interact with AGEs implicated in diabetes (14), RAGE has since been shown to bind a wide array of non-glycation ligands, including protein S100 (S100) calgranulins, high-mobility group box 1 (HMGB1) and amyloid β (A β) protein (15). Although this is most abundantly expressed in lung tissue, RAGE signaling contributes to the pathogenesis of numerous chronic inflammatory diseases affecting multiple organs, including diabetic vascular complications (16), cardiovascular disease (17), cancer (18), Alzheimer's disease (AD) (19) and various infection-related and autoimmune disorders (20). Previous studies have revealed elevated RAGE expression in UC (21) and Crohn's disease (22). Furthermore, several DAMP ligands, including calprotectin (23), lactoferrin (24), S100A calgranulins (25) and HMGB1 (26), are recognized biomarkers of disease activity and prognosis in IBD. Other receptor systems implicated in UC, including toll-like receptors (TLRs) (27), C-type lectin receptors (28) and nucleotide-binding oligomerization domain-like receptors (29), have been well characterized. However, the contribution of RAGE to UC pathogenesis and its potential as a therapeutic target remain inadequately understood. The present review, therefore, highlights the pathobiological importance of RAGE in UC, summarizing previous advances in clinical and translational research and exploring its implications for targeted therapeutic intervention.

2. Other targeted therapeutic pathways in UC

Currently, the primary pharmacologic options for treating UC include corticosteroids, aminosalicylates, immunomodulators and antibiotics. However, the widespread clinical application of

these drugs is constrained by high costs, notable toxicities and frequent disease recurrence (30). Although a previous study has explored dose de-escalation strategies using immunomodulators such as thiopurines and methotrexate, these regimens have shown limited efficacy in patients with moderate-to-severe UC compared with biologic therapies and small-molecule targeted drugs (31). To address these limitations, a new generation of small-molecule targeted therapies has been developed, offering distinct advantages such as high oral bioavailability, reduced risk of immunogenicity and lower manufacturing costs (32). These agents represent a promising alternative to conventional biologics in UC management. Approaches primarily targeting cellular subsets or broad immune modulation are beyond the scope of the present discussion and are therefore not included in the classification stated in the present review.

IL-12/23. The IL-12 family has unique heterodimeric cytokines, including the IL-12, IL-23, IL-27 and IL-35 cytokines; this heterodimeric property confers a unique set of connectivity and functional interactions in these cytokines (33). Despite their similar structural features, the members of the IL-12 family have distinct properties. Among them, IL-12 and IL-23 play key roles in intestinal homeostasis and inflammation and are involved in the pathogenesis of IBD (34). The main contributions of IL-12 and IL-23 to UC pathogenesis are the induction of T helper (Th)1 and Th17 cell differentiation, respectively (35); thus, the inflammatory effects of IL-12 and IL-23 provide a theoretical rationale for the development of blocking agents targeting UC. Inhibitors targeting IL-12/23 attenuate the Th1/Th17-mediated adaptive immune response, which is a notable contributor to UC pathogenesis (36).

JAK/STAT. JAK is a non-receptor tyrosine protein kinase located downstream of different inflammatory cytokines. As an intracellular-signaling mediator, JAK interacts with STAT so as to induce phosphorylation of STAT and activate the target transcription molecules (11). The JAK/STAT pathway is an important signaling pathway that allows extracellular proinflammatory cytokines to relay inflammatory signals to the nucleus via membrane receptors. Several cytokines that are notably associated with immunity and intestinal stromal cell homeostasis, such as IL-6, IL-10, IL-2 and IL-22, as well as cytokines that act as mediators of pathological responses in UC, such as IFN- γ , IL-12, IL-23 and IL-9, are dependent on JAK/STAT-mediated signaling (37,38). When JAK/STAT signaling is blocked, the nucleus cannot receive extracellular chemical signals, which reduces inflammation. Thus, JAK inhibitors can simultaneously block multiple inflammatory pathways. Demonstrably, JAK inhibitors can broadly affect the immunopathogenesis of UC, influencing factors such as the inflammatory response, intestinal epithelial barrier and fibrosis (11).

The diversity of therapeutic targets identified thus far underscores the multifactorial nature of UC pathogenesis. Agents targeting cytokines, such as TNF- α (39-52) and IL-12/23 (40,53-56), intracellular signaling pathways, such as the JAK/STAT pathway (57-67), epithelial barrier integrity, such as mucin-2, phosphodiesterase 4 (PDE4) inhibitors (68,69) and lymphocyte trafficking, for example sphingosine 1-phosphate receptor (70-74), have demonstrated clinical efficacy

in mediating UC (11,12,72,75), with the detailed clinical trial data of these targeted agents systematically summarized in Table SI (39-56,58-74); however, these therapies typically modulate discrete components of the inflammatory cascade or adaptive immune response. By contrast, RAGE represents a distinct signaling axis, primarily activated by DAMPs generated during tissue stress and injury (76). Functioning as a sensor of persistent inflammation and cellular injury, RAGE activation amplifies oxidative stress, perpetuates chronic inflammation and contributes to fibrotic remodeling, key pathological processes not fully addressed by current biologics or small molecule inhibitors (77). The following sections examine the mechanistic role of RAGE and its ligands in UC pathogenesis and discuss the potential of targeting this axis as a novel therapeutic strategy.

3. RAGE signaling pathway in UC

Introduction to the RAGE molecule. The RAGE gene is located on chromosome 6 within the major histocompatibility complex class III region, which harbors numerous genes that are important to both adaptive and innate immune function (78). RAGE is a 50-55 kDa type I transmembrane glycoprotein composed of an extracellular region containing three Ig-like domains, a variable, a constant 1 and a constant 2 domain (Fig. 1). Ligand binding predominantly occurs within the variable domain (79). The extracellular region adjoins a single transmembrane segment, followed by a short, charged cytoplasmic tail, the latter being important for intracellular signal transduction (80,81). Notably, truncation of this cytoplasmic domain abolishes downstream RAGE signaling and markedly attenuates RAGE-mediated pathological effects (82,83). In addition to the membrane-bound full-length RAGE (FL-RAGE), two soluble isoforms, soluble RAGE (sRAGE) and endogenous secretory RAGE (esRAGE), have been identified. The former arises from proteolytic cleavage of membrane-bound RAGE, whereas esRAGE is produced through alternative mRNA splicing. Both soluble forms can bind circulating RAGE ligands, acting as 'decoy' receptors that prevent ligand engagement with FL-RAGE and thereby dampen inflammatory signaling (84,85).

Interactions between cell-surface RAGE and its ligands initiate a cascade of intracellular events that promote proinflammatory phenotypes both *in vitro* and *in vivo*, implicating this pathway in the pathophysiology of numerous diseases (84). In addition to binding endogenous DAMPs, RAGE can also be activated by pathogen-associated molecular patterns such as bacterial lipopolysaccharide (86), viral proteins (87), parasite-derived proteins (88) and bacterial DNA (76). Ligand engagement activates multiple downstream signaling networks, including the diaphanous-related formin 1 (89), MAPK (90), PI3K/Akt (91) and toll-interleukin 1 receptor domain-containing adaptor protein (92) pathways, culminating in NF- κ B activation. Notably, RAGE signaling forms a self-sustaining positive feedback loop with NF- κ B: Inflammatory stimuli activate NF- κ B, which subsequently upregulates RAGE expression, further amplifying and prolonging inflammatory responses (93).

RAGE expression has been detected in diverse cell types, including endothelial cells (ECs), vascular smooth muscle

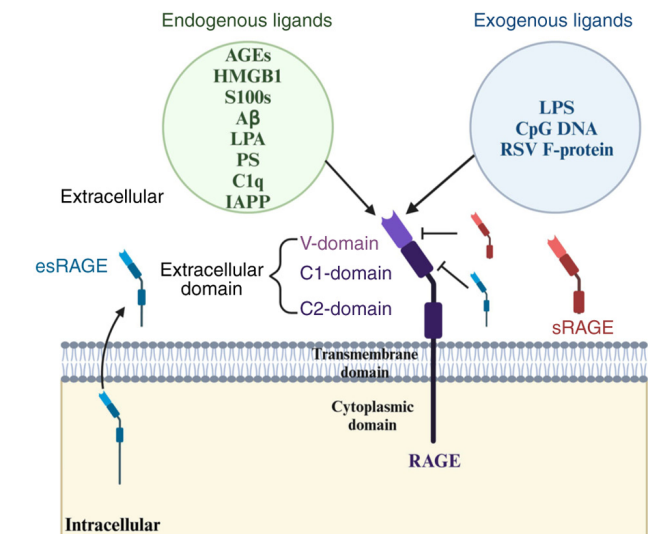


Figure 1. RAGE is a multi-ligand pattern recognition receptor. RAGE binds to a variety of ligands, including endogenous ligands (DAMPs) and exogenous ligands (pathogen-associated molecular patterns). sRAGE and esRAGE have a blocking effect on the RAGE pathway. AGEs, advanced glycation end products; RAGE, receptor for advanced glycation end products; DAMPs, damage-associated molecular patterns; sRAGE, soluble RAGE; esRAGE, endogenous secretory RAGE; HMGB1, high-mobility group box 1; S100s, protein S100s; A β , amyloid β ; LPA, lysophosphatidic acid; PS, phosphatidylserine; C1q, complement protein C1q; IAPP, islet amyloid polypeptide; CpG, 5'-C-phosphate-G-3'; RSV F-protein, respiratory syncytial virus fusion protein.

cells, monocytes and macrophages, granulocytes, adipocytes and various tumor cells (94). Aberrant RAGE expression has also been implicated in the pathogenesis of numerous diseases, such as diabetes (95), atherosclerosis (96), rheumatoid arthritis (97), AD (19), cardiovascular diseases (98) and chronic immune-mediated and inflammatory disorders (84). Furthermore, RAGE has been associated with tumor initiation and progression across multiple types of cancer (99).

Upstream activation signal of RAGE in UC. The binding of RAGE ligands to membrane-bound RAGE initiates receptor activation and triggers a cascade of intracellular signaling events. Increasing evidence identifies RAGE as an important mediator in the pathogenesis of numerous chronic inflammatory disorders (100-102). Multiple molecular mechanisms appear to contribute to disease initiation and persistence in patients with UC, particularly those amplifying proinflammatory signaling (103,104). Notably, both RAGE and its ligands exhibit elevated expression in intestinal epithelial cells from patients with UC and experimental colitis models, and are localized predominantly in inflamed mucosal regions (105-108). This interaction of RAGE and its ligands plays an important role in sustaining mucosal injury and perpetuating intestinal inflammation.

In UC, chronic inflammation and mucosal damage promote the accumulation of AGEs, which interact with RAGE to exacerbate inflammatory signaling. AGEs are naturally formed during aging however, their formation is accelerated under conditions of hyperglycemia and oxidative stress, such as in diabetes mellitus (81). The binding of AGEs to RAGE activates the NF- κ B and MAPK signaling pathways (90), stimulating the release of proinflammatory cytokines, including IL-6

and TNF- α , thereby aggravating mucosal inflammation and driving UC progression (21). AGEs are generated through the Maillard reaction, a non-enzymatic process in which reducing sugars react with proteins, lipids or DNA (109). This reaction proceeds from the formation of reversible Schiff bases and Amadori intermediates to stable, irreversible AGEs via oxidative rearrangements (110). Given that diabetes is a frequent comorbidity among patients with UC (111), strategies aimed at glycemic control, through dietary interventions, hypoglycemic agents or inhibition of glycation reactions, may effectively suppress AGE production and attenuate intestinal inflammation. Inhibitors of AGE synthesis, including aminoguanidine, which has been evaluated in acetic acid- (112) and TNF- α -induced rat and murine colitis models (113), metformin, tested in oxazolone- (114), acetic acid- (115) and dextran sulfate sodium (DSS)-induced models (116), and pioglitazone, previously assessed in acute and chronic DSS-driven murine colitis (117,118), consistently alleviate inflammation and reduce colonic mucosal injury across experimental settings. Although some clinical evidence supports these findings, translational validation remains limited (119).

Another therapeutic strategy involves preventing AGE-RAGE binding, which can be achieved via soluble receptor analogs, receptor antagonists or post-receptor signaling inhibitors. In UC, blockade of this binding suppresses inflammatory cascades, preserves mucosal integrity and modulates immune responses (120). Statins, for instance, interrupt the positive feedback loop between the AGE-RAGE axis and C-reactive protein expression, thereby reducing inflammation and oxidative stress (121). Statins, as a potential preventive and therapeutic strategy for UC, have been shown to attenuate colitis severity in animal models (122-124). However, clinical investigations evaluating the disease-modifying and preventive potential of statins in UC have yielded limited and inconsistent findings (125-127). Current epidemiologic evidence is insufficient to support the use of statins for the prevention or treatment of UC (128).

Low-molecular-weight heparin acts as a competitive RAGE antagonist by displacing AGE ligands, leading to notable anti-inflammatory and antioxidant effects in UC, as supported by clinical evidence (129-131). Collectively, AGEs contribute to UC pathogenesis through multiple mechanisms that sustain inflammation and tissue injury. Elucidating these pathways may yield novel therapeutic targets and provide mechanistic insight into AGE-RAGE-mediated intestinal pathology.

HMGB1 was the second ligand identified to bind RAGE following the discovery of AGEs (132). HMGB1 is a highly-conserved nuclear protein comprising two N-terminal DNA-binding domains and an acidic C-terminal domain. It is broadly expressed in multiple tissues, including the brain, heart, lungs, liver, spleen, kidneys and lymphatic organs, and can be localized in the nucleus, cytoplasm and extracellular milieu (133). Under resting conditions, HMGB1 predominantly resides within the nucleus; however, upon stimulation by lipopolysaccharide, 5'-C-phosphate-G-3' DNA, TNF- α or IL-1, various immune cells, particularly monocytes and neutrophils, actively secrete HMGB1 (134). Passive release also occurs from necrotic cells (134). Both actively and passively released HMGB1 can bind high-affinity receptors such as TLR2, TLR4 and RAGE on target cells (135-137). These interactions drive

immune cell activation, cytokine release and downstream inflammatory cascades (138,139). RAGE-HMGB1 binding activates multiple tumor-associated signaling pathways, including the ERK1/2, p38 MAPK and NF- κ B pathways, thereby promoting cancer progression and metastasis (140).

In the context of UC, blockade of HMGB1/TLR4 or HMGB1/RAGE signaling markedly attenuates inflammation in experimental models (141,142). Clinically, fecal HMGB1 levels correlate strongly with disease severity and mucosal activity in UC (143-145), highlighting its promise as a non-invasive biomarker for both overt and subclinical intestinal inflammation (26,146). Therapeutic strategies targeting HMGB1 remain in early development, but preclinical evidence suggests potential efficacy. Pharmacological agents such as dapagliflozin (141) and several natural compounds, including isoliquiritin (147), 20(S)-protopanaxadiol saponins (148) and matrine (149), have demonstrated anti-HMGB1 effects in experimental models. Nonetheless, the majority of these interventions remain confined to animal experimental stages (147,148,150), and rigorous clinical validation is required to confirm their safety, pharmacokinetics and therapeutic benefit. To date, HMGB1-targeted therapies have not entered routine clinical practice, although ongoing advances warrant close attention to emerging evidence.

The S100 protein family constitutes one of the largest subgroups of calcium-binding proteins, exhibiting distinct biological functions and tissue-specific expression patterns (151). Extracellular S100 proteins interact with several receptors, including RAGE, TLR4, fibroblast growth factor receptor 1 and G-protein coupled receptors (152). Through these interactions, they promote the transcription of proinflammatory mediators such as TNF- α , IL-1 β , IL-6 and IL-8, induce reactive oxygen species generation and regulate apoptosis (102). Although RAGE binding is considered a common feature of numerous S100 proteins (153), only specific members, including S100A1, S100A2, S100A4-9, S100A11-13, S100B and S100P, have been experimentally validated as RAGE ligands *in vivo* (154). Among these, S100A8/A9, also known as calprotectin, is predominantly expressed by neutrophils and is markedly elevated in IBD. The notable stability of calprotectin in fecal samples has established it as a robust biomarker of intestinal inflammation (155,156). Functionally, calprotectin contributes to epithelial barrier dysfunction by disrupting cytoskeletal organization and tight junction integrity via TLR4- and RAGE-dependent pathways in endothelial and epithelial cells (157). Calprotectin further compromises EC integrity by downregulating junctional proteins and increasing vascular permeability (158). The quinoline-3-carboxamide derivative ABR-215757 binds S100A9 and S100A8/A9 complexes, blocking their interactions with TLR4 and RAGE, thereby exerting potent anti-inflammatory effects across several experimental models (159-161). Localized targeting of calprotectin in UC mucosa using monoclonal antibodies represents a promising therapeutic strategy, supported by successful outcomes in preclinical models of atherosclerosis (162).

Beyond HMGB1 and S100 proteins, several other endogenous RAGE ligands have been identified, including A β (15), lysophosphatidic acid (LPA) (163), phosphatidylserine (164),

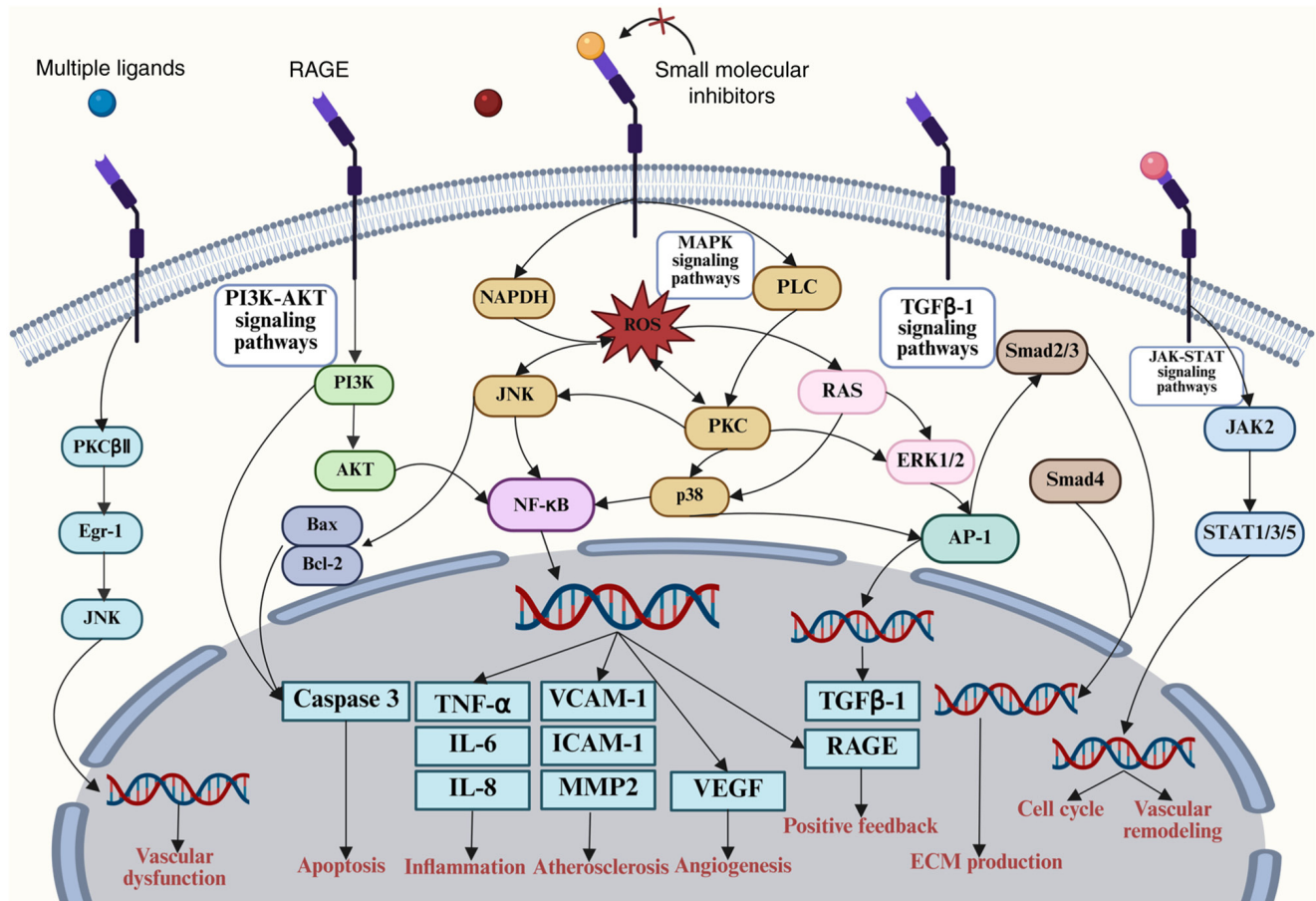


Figure 2. Schematic diagram of RAGE signaling. The interaction of RAGE with ligands leads to the activation of the NADPH, ROS, PI3K/AKT, RAS/ERK, MAPK, TGFβ-1 and JAK/STAT pathways, which further activate intracellular transcription factors such as NF-κB, Egr-1, AP-1 and STAT3. Transcription factors cause a series of functional changes in the nucleus such as vascular dysfunction, apoptosis, inflammation, atherosclerosis, angiogenesis, ECM production, cell cycle and vascular remodeling. RAGE, receptor for advanced glycation end products; PKCβII, protein kinase C βII; Egr-1, Early growth response-1; JNK, c-Jun N-terminal kinase; PI3K, Phosphatidylinositol-3 kinase; AKT, Protein kinase B; Bax, Bcl-2-associated X protein; Bcl-2, B-cell lymphoma/leukemia-2; NADPH, Nicotinamide adenine dinucleotide phosphate; ROS, Reactive oxygen species; MAPK, Mitogen-activated protein kinase; PLC, Phospholipase C; PKC, Protein kinase C; TNF-α, Tumor necrosis factor-α; NF-κB, Nuclear factor kappa B; IL-, Interleukin; ERK1/2, Extracellular signal-regulated kinase 1/2; JAK, Janus kinase; STAT, Signal transducer and activator of transcription; VCAM-1, Vascular cell adhesion molecule-1; ICAM-1, Intercellular adhesion molecule-1; MMP-2, Matrix metalloproteinase-2; VEGF, Vascular endothelial growth factor; TGF-β, Transforming growth factor-β; ECM, Extracellular matrix.

complement protein C1q (165) and islet amyloid polypeptide (166). Although the involvement of DAMPs in UC remains insufficiently characterized, emerging evidence suggests that they contribute to disease pathogenesis or to comorbid conditions associated with UC. For instance, modulation of adrenergic receptor signaling can preserve intestinal barrier integrity in UC partly through the presenilin 1/β-secretase-1/Aβ axis, conferring antioxidant, anti-inflammatory and antifibrotic effects (164). Similarly, bamboo leaf flavonoids downregulate Aβ expression in the brain, ameliorating both AD and UC-like inflammation (167). Furthermore, inhibition of the autotaxin/LPA axis reduces chronic intestinal inflammation by suppressing Th17 cell differentiation (168,169). Despite these insights, to the best of our knowledge, no current studies have directly demonstrated that these ligands exert anti-UC effects specifically through RAGE signaling. Further mechanistic and translational investigations are therefore warranted to delineate their roles within RAGE-dependent inflammatory networks.

Downstream pathways of RAGE in UC. Ligand binding to RAGE activates multiple downstream signaling cascades implicated in the pathogenesis of UC (Fig. 2). These include the Ras/MEK/ERK1/2S (170), stress-activated protein kinase/JNK (171), MAPK/p38 (172), PI3K/AKT (173), JAK/STAT (174), Rho GTPase (175) and vascular endothelial growth factor (VEGF) (176) pathways. Collectively, these cascades activate the transcription factors NF-κB, STAT3, activator protein 1 and early growth response-1, which subsequently induce the synthesis and secretion of vascular cell adhesion protein 1, intercellular adhesion molecule 1, matrix metalloproteinase-2, IL-1, IL-6 and TNF-α (15,177-180). DAMP-mediated RAGE activation drives UC pathogenesis via three interconnected mechanisms: i) Rho GTPase modulation alters gut microbiota composition and metabolites, promoting disease progression (175); ii) JAK/STAT signaling regulates inflammatory mediators and immune cell activation (181); and iii) MAPK pathway activation induces mitochondrial dysfunction (182), autophagy (183), oxidative stress (184) and apoptosis (185). Collectively, these pathways underscore the

central role of RAGE in UC pathogenesis by orchestrating inflammation, disrupting intestinal barrier integrity and dysregulating immune responses. Thus, identifying and characterizing RAGE-associated downstream targets may offer novel insights into UC pathophysiology and reveal new therapeutic strategies.

4. RAGE-angiogenesis-UC

Angiogenesis as a new component of UC pathogenesis. Angiogenesis, the formation of new capillaries from pre-existing blood vessels in adult tissues, is a multistep process involving EC proliferation, migration, differentiation, lumen formation and maturation, ultimately expanding the microvascular network (186,187). This process represents a double-edged sword: While important for wound healing and tissue repair, it also contributes to pathological tissue remodeling in cancer and chronic inflammatory diseases. Beyond oncology, angiogenesis plays a key role in several chronic inflammatory disorders such as atherosclerosis, rheumatoid arthritis and psoriasis (188-193). Although angiogenesis has been implicated in UC (194), quantitative characterization of mucosal vascular remodeling during active inflammation remains limited. However, increasing evidence from clinical and experimental studies demonstrates notable angiogenesis in UC and Crohn's disease, with elevated vascular density associating with IBD severity (195-200).

In UC, the colonic mucosa undergoes recurrent cycles of ulceration and regeneration. This dynamic process increases local neovascularization and enhances the recruitment of leukocytes, nutrients and oxygen to inflamed regions (194,201). The expansion of the vascular network during inflammation is accompanied by notable structural and functional changes in blood vessels. Functionally, these changes promote inflammation through several mechanisms: i) Enhanced leukocyte infiltration; ii) augmented nutrient delivery that sustains metabolically active immune responses; and iii) EC activation, which drives local cytokine, chemokine and metalloproteinase production (202). Consequently, angiogenesis and inflammation form a self-perpetuating, chronic cycle.

Hypoxia serves as a central trigger in inflammation-induced angiogenesis. Inflammatory and immune cells migrate to hypoxic sites, where they release angiogenic mediators, including growth factors, cytokines, proteases and nitric oxide, which stimulate EC activation and vascular remodeling. The resulting neovascularization amplifies inflammation by increasing the delivery of oxygen, nutrients and inflammatory mediators to affected tissues (203,204). In UC, this excessive angiogenesis enlarges the endothelial surface area and enhances vascular permeability, promoting plasma extravasation and worsening IBD severity (199). Notably, the neovessels formed during active UC differ from those generated during normal physiological angiogenesis. UC-induced vessels are structurally immature, highly permeable, poorly perfused, prone to stenosis and thrombosis and display hypersensitivity to growth factors, features that exacerbate mucosal injury and sustain chronic inflammation (205,206). Collectively, inflammation and angiogenesis in UC exist in a reciprocal, self-amplifying relationship that drives disease progression (207-210).

RAGE mediates UC angiogenesis. Angiogenesis is coordinated through a balance of pro- and anti-angiogenic molecules. Although the VEGF family is a central player, the angiogenic cascade in UC involves the complex interplay of multiple factors, receptors and isoforms (211). VEGF is the most extensively studied angiogenic factor in IBD, with elevated levels in circulation and the intestinal mucosa associating with disease activity (212,213). The VEGF family comprises several isoforms, such as VEGF-A, -B, -C, -D and -E, and placental growth factor (PlGF), which exert their effects primarily by binding to three tyrosine kinase receptors: VEGFR1, VEGFR2 and VEGFR3 (214). Although VEGFR2 is the primary mediator of pathological angiogenesis, driving EC proliferation, permeability and survival, the roles of other receptors and isoforms are increasingly recognized. VEGFR1, which has a higher affinity for VEGF-A than other isoforms but weaker tyrosine kinase activity than other VEGFRs, acts as a decoy receptor, thereby fine-tuning the availability of VEGF for VEGFR2 (215). The VEGF2 ligands, VEGF-B and PlGF, are upregulated in inflammation and modulate VEGFR1-specific signaling, influencing monocyte recruitment and inflammatory angiogenesis (216). Furthermore, the neuropilin (NRP) co-receptors NRP1 and NRP2, which bind specific VEGF-A isoforms, enhance VEGFR2-signaling complex formation and signaling potency (217).

The specific splice variants of VEGF-A are notably important. The pro-angiogenic VEGF-A_{xxx} isoforms, such as VEGF-A₁₆₄, dominate in the inflammatory milieu of UC (218). By contrast, the anti-angiogenic VEGF-A_{xxx}b isoforms, such as VEGF-A₁₆₄b, are often downregulated, creating a permissive environment for neovascularization (57). Previous evidence suggests that restoring the balance of isoforms toward VEGF-A₁₆₄b can ameliorate experimental colitis (57). VEGF-C, primarily known for lymphangiogenesis via VEGFR3, can also contribute to blood vessel angiogenesis in chronic inflammation (219).

Under the inflammatory environment of UC, cytokines such as TNF- α and IL-1 β can activate the RAGE-signaling pathway, which, in turn, promotes the expression and release of VEGF (21). Alterations in the extracellular matrix and oxidative stress, both hallmarks of UC, further amplify RAGE activation and its downstream pro-angiogenic signals (77,177,220). The downstream signaling of VEGFR2 exhibits notable crosstalk with RAGE-activated pathways. VEGFR2 activates the ERK1/2/MAPK pathway via Ras, which is important for EC proliferation and migration (221). VEGFR2 also activates PI3K, leading to the activation of AKT, a central regulator of cell survival, and small GTPases such as Rac, which guides cytoskeletal dynamics and EC motility (222,223). Notably, both RAGE and VEGFR2 signaling converge on NF- κ B activation, creating a feed-forward loop that amplifies the production of proinflammatory cytokines and sustains the angiogenic response (224). Supporting this interconnection, neutralizing RAGE has been shown to markedly inhibit AGE-induced activation of both the VEGF and NF- κ B pathways (224), while RAGE silencing also inhibits VEGF expression and angiogenesis in colorectal cancer models (225).

Beyond VEGF, other angiogenic factor families are active in UC. The angiopoietin (Ang)/Ang-1 receptor (Tie2) system is important for vascular maturation and stability. Ang-1,

produced by pericytes, activates Tie2 to promote vessel quiescence and integrity (226). In UC, the balance is shifted toward Ang-2, which is stored in and released from endothelial Weibel-Palade bodies upon inflammatory stimuli. Ang-2 acts as a context-dependent antagonist of Tie2, destabilizing vessels, priming them to be more responsive to VEGF and promoting vascular leakage and inflammation (227). Platelet-derived growth factors (PDGFs), particularly PDGF-BB produced by ECs and platelets, are important for recruiting pericytes and vascular smooth muscle cells in order to stabilize newly formed vessels. PDGF-BB is also associated with M1 macrophages and has demonstrated notable potential diagnostic value for active IBD (228).

Despite the central role of VEGF and its synergistic partners in UC angiogenesis, drug development targeting VEGF has predominantly focused on oncology. The majority of mechanistic insights into the RAGE/VEGF axis are derived from diabetes-related lesions and tumors (229-231). Consequently, there is a notable gap in the comprehension of the precise mechanisms and therapeutic potential involved in targeting the RAGE/VEGF network and its associated angiogenic factors, specifically in UC. Future research should therefore explore multi-target strategies that co-regulate RAGE, specific VEGF isoforms and parallel pathways such as the Ang-2/Tie2 pathway to achieve effective vascular normalization in UC.

Therapeutic strategies targeting angiogenesis in UC. RAGE knockdown is safe in animal models, supporting the feasibility of developing RAGE-targeted drugs (232). However, to the best of our knowledge, no anti-RAGE drug has been approved for the treatment of UC to date. Several investigations are exploring strategies that interfere with RAGE activation, including antagonistic ligands, RAGE gene deletion or small-molecule inhibitors (120,233,234). Among these, FPS-ZM1 (77,235) binds to the V-type domain of RAGE, thereby preventing its interaction with multiple ligands such as AGEs (84,236-238), HMGB1 (84,239-241), S100B (84,242) and A β (243). Other RAGE antagonists or inhibitors (Table SII) (84,236-244), including azeliragon, alagebrium and Tanshinone IIA (241,243,244), have been primarily developed for other RAGE-related conditions, such as neurodegenerative disorders, diabetes, tumors and inflammatory diseases (237,245,246). As aforementioned, angiogenesis is a multifactorial process involving numerous cells, molecules and signaling pathways, all of which may serve as potential therapeutic targets in UC (21,208,210). Beyond conventional anti-inflammatory agents, such as 5-aminosalicylic acid derivatives, glucocorticoids and biologics, which indirectly modulate VEGF-mediated angiogenesis (247,248), direct anti-VEGF therapies have gained attention as potential adjunctive treatments. Representative agents include receptor tyrosine kinase inhibitors, such as axitinib and sunitinib, and monoclonal antibodies such as bevacizumab, as well as investigational compounds such as rapatinib, hesperidin and sorafenib (249-251). These agents inhibit VEGF activity, suppress new vessel formation and consequently reduce vascular density and permeability in the colonic mucosa, leading to attenuation of inflammatory responses and tissue injury (247-251). Despite these

promising mechanisms, clinical outcomes of antiangiogenic drugs in UC remain suboptimal, and further preclinical and clinical studies are warranted to validate their efficacy and safety.

5. Outlooks

Although numerous innovative drugs and biologics have been approved for UC treatment in previous years, the complex multifactorial pathogenesis of UC continues to limit therapeutic efficacy. Furthermore, individualized therapy in UC remains underdeveloped, and the lack of reliable prognostic biomarkers complicates the selection of optimal therapeutic regimens (40,47,50,54). Although sRAGE and esRAGE function as both biomarkers and natural inhibitors of RAGE-mediated pathology, their large recombinant protein structures hinder their practical use as therapeutic agents. Consequently, current research is increasingly focused on developing small-molecule inhibitors that can selectively target the extracellular ligand-binding domains of RAGE or its intracellular signaling cascades (252-254).

Nevertheless, several key questions remain regarding the long-term safety, pharmacodynamics and physiological impact of RAGE blockade in humans. Further studies are required to elucidate the molecular properties of potent RAGE inhibitors and to clarify the systemic consequences of chronic RAGE inhibition. In parallel, although VEGF-based antiangiogenic therapies have been successfully used in clinical trials against various tumors (255-257), their application in chronic inflammatory diseases such as UC is still in its infancy. Antiangiogenic therapy may represent a promising adjunctive approach to preventing inflammation recurrence and persistence in UC. Given that angiogenesis involves multiple interdependent steps, regulated by growth and survival factors, adhesion molecules and proteases, intestinal angiogenesis in UC provides a multidisciplinary array of potential pharmacological targets (258-260). Despite being generally considered low in toxicity, antiangiogenic agents warrant comprehensive evaluation to determine their effects on normal physiological angiogenesis and mucosal healing dynamics. Consequently, combined targeting of RAGE ligands and VEGF may offer a synergistic and effective therapeutic strategy for UC. Translation to clinical applications will require careful evaluation of human tolerability and maintaining an appropriate physiological-pathological angiogenesis balance.

Acknowledgements

Not applicable.

Funding

The present article is supported by the Anhui Provincial Health Research Program (grant nos. AHWJ2023A20431 and AHWJ2023A20431) and Clinical Research Project of Anhui University of Chinese Medicine (grant no. 2024YFYLCZX35).

Availability of data and materials

Not applicable.

Authors' contributions

CX designed the manuscript concept. CX and YL wrote the manuscript. KH, LW, YH, DZ and FH participated in writing and reviewing the manuscript. All authors read and approved the final version of the manuscript. Data authentication is not applicable.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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