### **REVIEW**

# Macrophages are important mediators of either tumor- or inflammation-induced lymphangiogenesis

Rui-Cheng Ji

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**Abstract** The lymphatic system provides important functions for tissue fluid homeostasis and immune response. Lymphangiogenesis, the formation of new lymphatics, comprises a series of complex cellular events in vitro or in vivo, e.g., proliferation, differentiation, and sprouting. Recent evidence has implied that macrophages act as a direct structural contributor to lymphatic endothelial walls or secret VEGF-C/-D and VEGF-A to initiate lymphangiogenesis in inflamed or tumor tissues. Bone marrow-derived macrophages are versatile cells that express different functional programs in response to exposure to microenvironmental signals, and can be identified by specific expression of a number of proteins, F4/80, CD11b, and CD68. Several causative factors, e.g., NF- $\kappa$ B, IL-1 $\beta$ , TNF- $\alpha$ , SDF-1, M-CSF, especially TonEBP/VEGF-C signaling, may be actively involved in macrophage-induced lymphangiogenesis. Alteration of macrophage phenotype and function has a profound effect on the development and progression of inflammation and malignancy, and macrophage depletion for controlling lymphangiogenesis may provide a novel approach for prevention and treatment of lymphaticassociated diseases.

**Keywords** Macrophages · Lymphangiogenesis · Lymphatic endothelial cells · Tumor · Inflammation · VEGF-A/-C/-D · VEGFR-2/-3

R.-C. Ji (⊠)

Department of Human Anatomy,

Oita University Faculty of Medicine, Oita 879-5593, Japan

e-mail: JI@oita-u.ac.jp

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#### Introduction

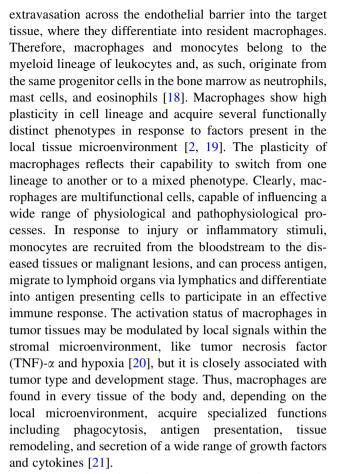
The lymphatic system orchestrates the trafficking and recirculation of immune cells including lymphocytes and antigen-presenting cells like macrophages to the regional lymph node. Macrophages within different tissues as critical cells of the innate immune response, contribute to immediate and robust defense against microbial infections and to regulation of normal cell turnover and tissue remodeling [1, 2]. Macrophage-induced lymphangiogenesis may be explained in two ways. First, macrophages and/or other bone marrow-derived cells (BMDCs) are capable of transdifferentiating or incorporating into an endothelial phenotype, thereby making a direct structural contribution to the lymphatic wall [3, 4]. Second, activated macrophages produce lymphangiogenic factors, VEGF-C/-D and VEGF-A to stimulate division of preexisting lymphatic endothelial cells (LECs) or to further influence macrophage recruitment [5–8] (Fig. 1). In human diseases and animal models, tumor- or inflammation-induced lymphangiogenesis is greatly influenced by stromal cells, and mainly dependent on macrophage recruitment and activation [9-11]. LECs may, additionally, undergo similar cellular processes like proliferation, differentiation, and formation of new networks. In the past decade, lymphangiogenesis including its molecular and functional characteristics, and macrophages including their alternative activation in tumor and inflammation have been reviewed separately [9, 12–15]. The role of macrophages in the formation of new initial lymphatics remains to be elucidated.

Recently, much effort has been made to develop new agents targeting the activity of VEGF/VEGFR signaling pathways. Some studies have shown new evidence on macrophage-induced lymphangiogenesis, especially in the experiments of high-salt diet (HSD) and herpes simplex virus-1 (HSV-1) infection [16, 17]. However, a wide spectrum of factors may influence potential sites of antilymphangiogenic intervention. This review is to highlight the functional importance of macrophages as a source of VEGFs or as a direct lymphatic contributor in tumor- or inflammation-induced lymphangiogenesis. The analysis of the events leading to macrophage-induced lymphangiogenesis may provide new understanding of therapeutic options for lymphatic-associated diseases.

# Biological features of macrophages in lymphangiogenesis

Activation and function of macrophages

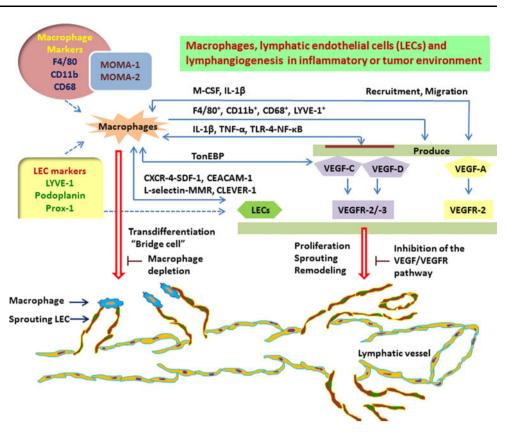
Macrophages are released from the bone marrow as immature monocytes and circulate in the blood before



On the basis of their secretory repertoire, receptor expression patterns and phenotypical criteria, macrophages are mainly divided into two subsets, classically activated and alternatively activated. Both activated macrophages can change their cellular morphology and secretory pattern as a result of appropriate stimulation. The subpopulations of activated macrophages possess different physiologies and perform distinct immunological functions [22]. Classically activated macrophages are monocytes stimulated with interferon (IFN)-γ, lipopolysaccharide (LPS), or in combination with interleukin (IL)-12 and IL-23, which differentiate into M1 macrophages. The subset of cells releases proteolytic enzymes including matrix metalloproteinase (MMP)-1, -2, -7, -9, and -12, which can degrade extracellular matrix (ECM) components like collagen, elastin and fibronectin [23, 24], and secrete nitric oxide and TNF- $\alpha$  [25]. M1 macrophages express high levels of proinflammatory cytokines and major histocompatibility complex molecules, capable of killing intracellular pathogens and tumor cells. They can induce the differentiation of T-helper (Th) 1 type responses or work as effector cells in Th1 cellular immune responses [15, 26]. Alternatively activated macrophages (M2 phenotype) are stimulated by Th2 cytokines, such as IL-4, IL-10, and IL-13. M2 macrophages actively contribute to the inflammatory response,



Fig. 1 The schema shows macrophage-induced lymphangiogenesis. Macrophages are capable of transdifferentiating into an endothelial phenotype, thereby making a direct structural contribution to the lymphatic wall. Moreover, macrophages can produce lymphangiogenic factors, VEGF-C/-D and VEGF-A to stimulate proliferation, sprouting and remodeling of preexisting lymphatics or to further influence macrophage recruitment



tumor growth, and stroma formation, and to the clearance of cell debris through producing several components involved in the synthesis of ECM [27, 28]. The molecules secreted by M2 macrophages have shown proliferative, angiogenic and antiinflammatory activities. The M2 macrophage phenotype can also produce factors that suppress T-cells proliferation and activity [29].

Both M1 and M2 phenotypes are important components of the innate and adaptive immune systems, the two subsets have their own biological features. The former macrophage is devoted to elicit chronic inflammation and tissue injury, whereas the latter tends to resolve inflammation and facilitate wound healing [26, 30]. The subdivision of M2 macrophages into M2a, M2b, and M2c subgroups according to their inducing stimuli may further explain the plasticity of macrophage phenotypes [28, 31]. Macrophages are known to express several VEGFRs, including constitutive expression of VEGFR-1/-3, and inducible expression of VEGFR-2. All of these VEGFRs are implicated in macrophage recruitment during inflammation [32, 33]. VEGFR-3 expressed by some BMDCs, e.g., macrophages and monocytes [34] has been shown to regulate adaptive immunity via mediating chemotaxis of antigenpresenting cells [32]. The macrophage function mediated by the factors like VEGF-A/-C/-D, interleukin- $1\beta$  (IL- $1\beta$ ), and TNF-α, has indicated a possible link between LEC structures and macrophage differentiation. However, it remains to be validated whether the two macrophage subsets can cooperate with LECs in tumor- or inflammationinduced lymphangiogenesis.

It should be emphasized that the proliferative and patterning signals driving embryonic and pathological lymphangiogenesis are likely to be distinct. In  $PU.1^{-/-}$  and  $Csf1r^{-/-}$  mouse embryos, macrophages do not constitute the major source of prolymphangiogenic factors, including VEGF-C/-D for influencing dermal lymphatic sprouting, but instead regulate lymphatic caliber or patterning during embryonic development [35]. In addition, the cytoplasmic tyrosine kinase Syk-expressing myeloid population, which is largely comprised of M2-polarized monocytes, can stimulate lymphangiogenesis in vivo through secreting chemokines and growth factors. In Syk<sup>-/-</sup> embryos, the deregulated myeloid cells cause a lymphatic hyperplasia, leading to the formation of blood-lymphatic endothelial junctions or blood-lymphatic shunts [36]. Therefore, it is also interesting to know whether embryonic macrophages are tissue-specifically involved in morphogenetic or remodeling events, and what kind of physiological functions are being performed by these cells during embryonic lymphangiogenesis.

Macrophage mannose receptor (MMR) and LECs

MMR (also known as CD206), a 180-kDa transmembrane protein, is one of the best-characterized mannose-binding



lectins, participating in pathogen recognition, antigen preand clearance of microorganisms sentation, glycoproteins [37]. It is restricted to normal LECs including afferent and efferent lymphatics, and lymph node sinuses, but not to vascular endothelial cells [38, 39]. MMR is a ligand for L-selectin to mediate adhesion of lymphocytes to the lymphatics, suggesting that it may be involved in leukocyte trafficking. In human breast carcinomas, the intratumoral MMR expression is associated with the frequency of regional lymph node metastases via mediating entrance of tumor cells to lymphatics [40]. The uptake of phosphatidylserine-presenting liposomes by LPS-activated F4/80<sup>+</sup> macrophages upregulates the antiinflammatory phenotype and improves myocardial infarction repair, as reflected by enhanced expression of MMR and elevated secretion levels of transforming growth factor- $\beta$  (TGF- $\beta$ ) and IL-10 [41]. In MMR-deficient mice, the adhesion of both normal lymphocytes and tumor cells to lymphatics is significantly decreased. The absence of MMR impairs trafficking of CD4+, CD8+ cells and B cells into the draining lymph nodes, but does not obviously affect lymphatic morphology or phenotype [37].

Similar to MMR expression, common lymphatic endothelial and vascular endothelial receptor 1 (CLEVER-1, also known as stabilin-1), an inducible vascular adhesion molecule, is present on lymphatic and sinusoidal endothelium as well as on a subset of M2 macrophages [42]. As a scavenger receptor, CLEVER-1 is implicated in binding of lymphocytes to LECs and high endothelial venules in the lymph nodes during inflammation and tumor metastasis [40, 43]. In this respect, both CLEVER-1 and MMR may be important mediators in cancer cell adhesion to LECs. The migration of lymphocytes and dendritic cells via the lymphatics is essential for controlling the nature and magnitude of the immune response [44]. However, the precise mechanisms of leukocyte migration from peripheral tissues into afferent lymphatics and from lymphoid organs into efferent lymphatics are not fully elucidated. Blockage of these molecules for selectively reducing leukocyte migration may provide a new approach to controlling tumor metastasis and inflammation by targeting LEC function.

The LECs, although initially envisioned as a passive, inert lymphatic lining, are now considered important in the regulation of cellular growth, differentiation, and inflammatory responses. Lymphangiogenesis is a complex, multistep process that involves expression of growth factors, ECM remodeling, endothelial cell migration, proliferation, and tube formation. Current knowledge shows that lymphangiogenesis is generally secondary to angiogenesis, but occurs independently of blood vessels, which may indicate their similarity and distinction in molecular and cellular biology. Definitely, the lymphatics have several features from blood

vessels [45]. Thin-walled initial lymphatics are composed of a single layer of LECs, which are intercellularly connected by end-to-end, interdigitating, and overlapping junctions [46]. The blind-ended initial lymphatics express specific endothelial markers, responding to different growth factors, especially VEGF-C/-D, via activation of VEGFR-3. Unlike blood vessels, the lymphatics lack a basement membrane and are not surrounded by pericytes. The lymphatic endothelial layer is permeable and particularly suited for reabsorption of macromolecules. LECs with rich micropinocytotic vesicles are not only responsible for the recruitment of leucocytes into the lymphatics, but are also important in tumor cell metastasis. The pathomorphological changes in abnormal lymphatics mainly represent the size and density, and the number of sprouts, branches, and anastomoses. The dynamic alteration in dysfunctional lymphatics is usually shown in endothelial permeability, fluid absorption ability, valve movement, and lymph backflow. LEC alteration in intercellular junctions and molecular expressions, especially adhesion molecules, may provide potential morphological and functional basis for inflammatory process and tumor metastasis [47]. LECs in tumor and inflammatory tissues may express different surface markers than do "quiescent" steady state lymphatics [48]. LECs usually express three master control genes, Notch, COUP transcription factor 2, and prospero-related homeobox-1 (Prox-1), and their regulatory equilibrium in response to physiological and pathological stimuli may determine arteriovenouslymphatic cell fate specification and LEC plasticity or reprogramming [49]. A process referred to as anastomosis depends on spatiotemporal relationship between macrophages and sprouting endothelial vessels. Macrophages serve both as 'bridge cells' and as guidance posts to mediate the specialized tip cells sent from endothelial cells at the sprouting forefront, to recognize and fuse with other tip cells [50, 51]. These tissue-resident macrophages located in the vicinity of vessel branches are polarized towards the M2 type [52]. They are proposed to release signals that alter the differentiation of endothelial cells and to rely on the ECM and cell-adhesion molecules on the cell surface including the fusing cells [51]. The preparation for fusion process is independent of VEGF that only induces tip-cell formation. Ideally, macrophages with their great mobility and flexibility, and affinity for tip-cell filopodia, appear suitable to help endothelial cells on different vessel segments to establish contact [50].

In this context, research efforts have been made to explore whether LECs are derived from circulating progenitors by transdifferentiation or from local preexisting lymphatics by cell division in adult lymphangiogenesis. Some researchers have indicated that macrophages contribute to lymphangiogenesis by processes other than the paracrine secretion of growth factors. LECs may be derived



through incorporation of circulating BMDCs and macrophage subsets [53–55]. To date, proliferation of preexisting lymphatics mainly accounts for postnatal lymphangiogenesis, there is still lacking direct experimental evidence demonstrating the adhesive interactions between the two kinds of cells, BMDCs or macrophages, and LECs. More investigation is necessary to elucidate the relative contribution of proliferation versus progenitor cell incorporation. and the subsequent morphological evolution of lymphatic formation and remodeling in different normal and pathological tissues. It would be interesting to know whether adhesion molecules mediate integration of activated macrophages into lymphatic endothelial walls, and whether the extremely low pressure in lymphatics favors the intercellular connection between macrophages and LECs. Also, the tumor itself may produce lymphangiogenic factors, which in turn modulate LEC dynamic structures and interactions with tumor cells.

### Markers of prolymphangiogenic macrophages

For studying lymphangiogenesis, the specific markers for macrophage identification, F4/80, CD11b, and CD68 are frequently used to differentiate from LECs (Fig. 1). F4/80 is expressed in a wide range of mature tissue macrophages including Langerhans, Kupffer cells, microglia, macrophages located in the peritoneal cavity, lung, thymus and bone marrow stroma [12], suggesting that the expression is heterogeneous and varies during macromaturation and activation. F4/80-expressing macrophages with high phagocytic activity are transmigrated via local lymphatics into draining lymph nodes [56], to participate in destroying disease-producing microorganisms and removing dead tissue and other cellular debris [57]. CD11b is implicated in various adhesive interactions of myeloid cells (macrophages, monocytes, and granulocytes). CD11b monoclonal antibodies are known to modify many functions of myeloid cells. Inhibition of CD11b enhances tumor response to radiation by reducing myeloid cell recruitment [58]. CD68, the human homologue of macrosialin, is a member of the lysosomalassociated membrane protein family, and commonly regarded as a monocyte/macrophage marker [59]. Moreover, MOMA-1 (CD169) antibody against mouse metallophilic macrophage is immunohistochemically used to identify a clonogenic bone marrow progenitor specific for macrophages and dendritic cells [60]. MOMA-2 antibody is a marker for the broad detection of monocytes and macrophages in all mouse strains [61]. Other cell surface markers are for granulocytes (Gr-1), dendritic cells (CD11c) and B-lymphocytes (B220, CD45R).

Several endothelial markers are expressed by macrophages in tumor and inflammatory tissues. CD31 (platelet endothelial cell adhesion molecule-1, PECAM-1), a transmembrane glycoprotein is expressed by endothelial cells, and also expressed in certain tumors, including some vascular tumors [1, 62]. CD31 and macrophages play a key role in tissue regeneration, safely removing neutrophils, and tumor cell metastasis. The functionally important receptor in macrophage biology determines which cells will be phagocytosed through homophilic adhesion [63]. The lymphatic vascular endothelial hyaluronan receptor-1 (LYVE-1) with reproducible and highly sensitive staining characteristics, is widely used as a molecular marker for adult and embryonic LECs. LYVE-1 is also expressed in a considerable number of typical F4/80+, CD11b+ murine macrophages in tumor stroma and granulation tissue as well as in vitro [64, 65]. In the diabetic process, the occurrence of LYVE-1-expressing lymphatic compartments has been indicated to play a significant role in defective thymocyte differentiation and migration [62]. Identification of LYVE-1+ macrophages has provided evidence supporting the possibility of macrophage coordination into LECs for lymphatic formation. The macrophage subpopulations expressed with LEC markers, Prox-1, LYVE-1 and podoplanin, are essential for lymphangiogenesis in different pathological processes, e.g., acute inflammation, wound healing and tumor metastasis.

# The role of macrophages in tumor- and inflammation-induced lymphangiogenesis (Tables 1, 2)

VEGF-C/-D/VEGFR-3 signaling pathway is a crucial regulator of macrophage-induced lymphangiogenesis

Inflammatory and immune cells constitute the major cellular compartment of inflammation stroma, where intercellular communication is mediated through secretion of growth factors, chemokines, proteases, and other ECM components. Moreover, inflammatory molecules and cells are recognized as important contributors to lymphangiogenesis [13, 66]. Macrophages are a key component of inflammatory infiltrates of primary and secondary tumor tissues. The mechanisms underlying the recruitment and function of the tumor-associated macrophages (TAMs) have been an area of intense research over the past decade. Accumulating evidence in different types of human cancers and animal tumor models has indicated that TAMs receive signals from diverse cells within the tumor microenvironment in inducing angilymphangiogenesis, suppressing immunity, and in facilitating early events of the metastatic cascade [47, 67–71]. Pathological lymphangiogenesis is mainly triggered by growth factors such as VEGF-A and VEGF-C/-D, the members of VEGF family, through binding



to their receptors VEGFR-2 and VEGFR-3 [8, 72, 73] (Fig. 1). VEGF-C and -D have a similar domain structure, both undergo proteolytic processing in a similar manner and, in humans, both share the same receptor-binding specificity [74]. These secreted glycoproteins mainly signal via the tyrosine kinase receptor VEGFR-3 on the LEC surface, and result in lymphatic growth in vitro and in vivo [52, 75]. Macrophages are also a rich source of VEGF-A. Despite its initial recognition as a potent factor inducing and amplifying angiogenic response, VEGF-A has been shown to promote lymphangiogenesis, acting both indirectly via the recruitment of VEGF-C/-D-producing inflammatory cells and directly via VEGFR-2 [76, 77]. TAMs are mainly concentrated in the interphase between the tumor and normal tissue, and thus tumor-induced lymphangiogenesis is closely related with peritumoral inflammation. LYVE-1<sup>+</sup> macrophages and LECs are adjacent at the invasive edge of a metastatic melanoma with severe inflammation, and the peritumoral mononuclear inflammatory cells also express VEGF-C [5]. This suggests that the inflammation reaction and VEGF-C expressing TAMs are involved in the onset and maintenance of tumor lymphangiogenesis, phagocytosis of tumor cell debris, and immune complexes containing tumor-associated antigens [78]. Furthermore, some cytokines and chemokines are clearly implicated in the recruitment of TAMs, including macrophage colony-stimulating factor-1 (M-CSF, also known as CSF-1). Circulating monocytes are shown to be recruited by tumor-derived chemotactic factors into the tumor tissues, and differentiated into macrophages, where they exhibit a distinct phenotype similar to alternatively activated macrophages, and switch on de novo synthesis of VEGF-C/-D [69, 79].

Macrophages play a critical role in the emergence and resolution of inflammation and in the maintenance of tissue homeostasis through remodeling and repair. These cells display a high degree of heterogeneity and can adapt or alter their phenotype to suit the microenvironment in which they reside [18]. In human diffuse alveolar damage and onchocerca nodule, CD68<sup>+</sup>/VEGF-C<sup>+</sup> or CD68<sup>+</sup>/LYVE-1<sup>+</sup> macrophages are aggregated around newly formed lymphatics or even colocalized with LECs in the proliferative stage [80, 81]. In murine chronic respiratory tract and peritoneal infection models, abundant macrophage infiltration is closely associated with upregulated expression of VEGF-C/-D and increased vessel density [10, 82]. Under the circumstances, lymphangiogenesis may provide effective conduits for removal of excess interstitial fluid and leaked proteins derived from blood vessels. Impaired lymphangiogenesis combined with inflammatory fibrosis may interfere with interstitial clearance and lead to sluggish lymph flow, and even lymphedema [14, 83]. However, it still remains unsolved whether the lymphangiogenesis is the sole determinant to compensate for increased leakage.

The interplay between macrophages and lymphangiogenic regulators reflects complex changes in inflammation and tumor microenvironment

Proinflammatory cytokine-induced activation of macrophages reciprocally interacts with VEGF-C/-D/VEGFR-3 or VEGF-A/VEGFR-2 signaling. The activity of IL-1 $\beta$  is mediated by upregulation of VEGF-C/-D and VEGF-A, together with macrophage recruitment in response to inflammatory stimuli [84]. IL-1 $\beta$  and TNF- $\alpha$  can activate the transcription factor nuclear factor- $\kappa B$  (NF- $\kappa B$ ) by inducing phosphorylation, ubiquitination, and subsequent degradation of IkB by the proteasome pathway [85]. NFκB is a master mediator of many cellular processes to regulate various pathways that impact on the function of TAMs. NF- $\kappa$ B-induced expression of inflammatory cytokines, e.g., IL-6, by macrophages may contribute to tumor cell survival and proliferation in inflammationlinked tumor onset, but modulation of NF-κB activation in TAMs in established tumors maintains their immunosuppressive and tumor-promoting phenotype [31]. Local tissue inflammation may cause lymph nodes to undergo a transient but profound remodeling, with volume expansion, lymphoid hyperplasia, and markedly increased lymph node lymphangiogenesis [86]. Lymph node lymphangiogenesis is induced by VEGF-A secreted from inflamed tissues rather than regional draining lymph nodes [87]. B lymphocyte accumulation is also suggested to be a major reason for lymph node lymphangiogenesis and increased lymph flow [44, 88]. However, extensive infiltration of TAMs may potentially contribute to signaling of lymphangiogenesis within the draining lymph nodes.

Contribution of ECM to lymphangiogenesis and tumor metastasis has been supported by comprehensive clinical data and experimental tumor models [11]. The cytokines produced by macrophages interact with appropriate target cells for lymphatic proliferation in a favorable environment, in which ECM remodeling is regulated by macrophage secretion of proteinases, e.g., MMP-2 and MMP-9 [11]. Interactions between stromal components and tumor or inflamed cells may serve as a crucial mediator for initiating lymphangiogenesis. Tumor-associated stromal cells are different from their counterparts in normal tissues. The fibroblasts can produce growth factors and ECM proteins for proliferation and survival of tumor cells [89]. Fibroblast elimination in vivo has profound effects on immune polarization that is associated with decreased tumor lymphangiogenesis and suppression of spontaneous breast cancer metastasis [90]. Hyaluronic acid constitutes a major part of ECM and provides a favorable microenvironment for cell proliferation and migration in tissue injury and repair [11]. A hyaluronan-rich tumor stroma has greatly



Table 1 Tumor-associated macrophages (TAMs) and tumor-induced lymphangiogenesis

Animal models or human diseases	Macrophages (F4/80 <sup>+</sup> , CD11b <sup>+</sup> , CD68 <sup>+</sup> , LYVE-1 <sup>+</sup> ) and other biological features (cytokine/chemokine/growth factor)	References	
VEGF-C-overexpressing human melanomas /female Swiss/c	VEGF-C induces macrophage chemotaxis and recruitment, revealing a potential function of VEGF-C as an immunomodulator  CD11b <sup>+</sup> , F4/80 <sup>+</sup> macrophages and all LYVE-1 <sup>+</sup> lymphatics express VEGFR-3		
(nu/nu) nude mice			
	Increased densities of peritumoral macrophages in the skin surrounding VEGF-C-transfected melanomas are correlated with the extent of tumor growth suppression		
Squamous carcinoma/human uterine cervix	VEGF-C and VEGF-D are produced by activated macrophages with expression of a panel of specific markers including CD68		
	VEGF-C-expressing macrophages produce VEGFR-3 and induce peritumoral lymphangiogenesis		
Primary cutaneous malignant	LYVE-1 <sup>+</sup> macrophages express VEGF-C in metastatic tumors		
melanoma/human	The low levels of VEGF-C expression by tumor cells are complimented by stromal sources like peritumoral macrophages		
Intradermal tumor models/C57BL/6 mice Malignant melanoma/human	LYVE-1 expression occurs in a subset of CD11b <sup>+</sup> , F4/80 <sup>+</sup> tissue macrophages that preferentially co-express stabilin-1 and contribute to lymphatic vessel count		
Ç	Double labeling with macrophage and LEC markers can clearly differentiate LYVE-1 <sup>+</sup> lymphatics from LYVE-1 <sup>+</sup> tumor-infiltrating macrophages		
Ovarian cancer /CbyJ.Cg-Foxn1nu/J mice	VEGF-C/-D and VEGF-A from CD11b <sup>+</sup> /LYVE-1 <sup>+</sup> macrophages induce dysfunctional lymphangiogenesis		
	Infiltrating macrophages are not involved in LEC incorporation		
Osteosarcoma/osteopetrotic (op/op) mice	<ul> <li>M-CSF contributes to the appearance of LYVE-1<sup>+</sup> macrophages and postnatal lymphangiogenesis</li> <li>M-CSF deficiency reduces the abundance of LYVE-1<sup>+</sup> and LYVE1<sup>-</sup> macrophages, resulting in defects in vascular and lymphatic development</li> </ul>		
	M-CSF inhibition effectively suppresses tumor angiogenesis and lymphangiogenesis		
	Retinal macrophages express high levels of MMP-2 and MMP-9 but not VEGF		
Insulinoma / Rip1Tag2 transgenic mice	About 80% GFP <sup>+</sup> BMDC within the tumors are F4/80 <sup>+</sup> macrophages		
TRAMP-C1 prostate cancer	F4/80 <sup>+</sup> /LYVE-1 <sup>+</sup> macrophages exist in the tumor periphery		
transplantation/C57Bl/6 mice	BMDC integrate into tumor-associated lymphatic vessels in vivo		
	Macrophages contribute to tumor lymphangiogenesis by processes rather than the secretion of lymphangiogenic factors		
	Macrophages can convert into LECs and integrate into cord-like structures formed by LECs in vitro		

promoted intratumoral lymphangiogenesis [91]. LYVE-1<sup>+</sup> macrophages preferentially coexpressing the hyaluronan receptor-like molecule CLEVER-1, have been found to mimic sprouting and collapsed lymphatics in murine tumor models and excisional wound healing [64]. M-CSF contributes to the appearance of LYVE-1<sup>+</sup> macrophages in the osteosarcoma and its deficiency will result in defects in lymphatic development [92]. Clearly, differentiation of LYVE-1<sup>+</sup> lymphatics from LYVE-1<sup>+</sup> tumor-infiltrating macrophages should be undertaken by double immunohistochemical staining in addition with individual-specific markers (Fig. 1).

Macrophages and VEGF ligands, however, may not be the sole lymphangiogenic modulators. The process of lymphatic formation may be independent of the VEGFR-3 ligands VEGF-C and -D or of macrophage infiltration. In HSV-1-induced lymphangiogenesis, macrophage recruitment and increased TGF- $\beta_1$  have shown no effect on VEGF-C or VEGF-D expression in LECs, and macrophages are not a detectable source of VEGF-A [17]. TGF- $\beta$  signaling negatively regulates lymphangiogenesis in inflammatory and certain tumor tissues. A high level of TGF- $\beta$ 1 expression is associated with abnormal lymphatic architecture and dilated lymphatics, and its inhibition significantly accelerates lymphangiogenesis during wound repair [93]. TGF- $\beta$  blockade may thus prevent abnormality of diaphragmatic lymphatics and improve ascites drainage in orthotopic human ovarian carcinoma model [94]. Also, inhibition of endogenous TGF- $\beta$  signaling by T $\beta$ R-I inhibitor induces early lymphatic development in mouse



Table 2 Inflammatory macrophages and inflammation-induced lymphangiogenesis

Animal models or human diseases	Macrophages (F4/80 <sup>+</sup> , CD11b <sup>+</sup> , CD68 <sup>+</sup> , LYVE-1 <sup>+</sup> ) and other biological features (cytokine/chemokine/growth factor)	References	
Suture-induced inflammatory corneal model/transgenic mice	CD11b <sup>+</sup> F4/80 <sup>+</sup> macrophages in inflamed corneas release lymphangiogenic factors VEGF-C/-D	[76]	
for VEGF-A <sup>164/164</sup> or VEGF-A <sup>188/188</sup>	VEGF-A-recruited macrophages upregulate VEGF-C/-D to induce inflammatory lymphangiogenesis		
	Macrophage recruitment is an essential mediator of the (indirect) lymphangiogenic effect of VEGF-A		
Corneal transplantation/BALB/c and CB17 SCID mice	Bone marrow-derived CD11b <sup>+</sup> macrophages with expression of LYVE-1 and <i>Prox-1</i> in inflamed corneal stromata physically contribute to pathological lymphangiogenesis	[4]	
	Macrophages alone can form LYVE-1/podoplanin-positive tube-like structures and transdifferentiate into LECs		
Chronic respiratory tract infection	Airway macrophages express VEGFR-3 ligands VEGF-C or VEGF-D	[10]	
with Mycoplasma pulmonis/ C3H or C57BL/6 mice	VEGFR-3 signaling is the principal driving force for lymphatic growth		
Renal transplants/human	Macrophages may serve as lymphatic endothelial progenitors or as a major source of VEGF-C and other lymphangiogenic factors	[53]	
	Once integrated into the lymphatic endothelial layer, the donor- derived endothelial cells do not retain any macrophage markers, such as CD11b or CD68		
	VEGFR-3 <sup>+</sup> macrophages with high developmental plasticity may transdifferentiate into LECs		
Impaired diabetic wound healing/ db/db mice	F4/80 <sup>+</sup> macrophages promote lymphatic formation during the early stages of wound healing	[147]	
	The mRNA levels of VEGFR-3 and its ligands VEGF-C and VEGF-A are reduced in db/db-derived macrophages		
	IL-1 $\beta$ stimulation can rescue diabetic macrophage function that induces lymphatic formation and accelerates wound healing via increased VEGFR-3 and VEGF-C expression		
Inflamed cornea (corneal micropocket assay)/C57BL/6	IL-1 $\beta$ -induced lymphangiogenesis is mediated by upregulation of VEGF-C/-D and VEGF-A, together with recruitment and activation	[84]	
mice	of F4/80 <sup>+</sup> macrophages, and can be suppressed by NF- $\kappa$ B inhibition with suppression of VEGF-C/-D and VEGF-A expression		
Excisional wound healing/C57B6 mice	Increased infiltration of F4/80 <sup>+</sup> macrophages is associated with decreased scarring	[93]	
	Increased TGF- $\beta_1$ is associated with abnormal lymphatic architecture and dilated lymphatics		
	TGF- $\beta_1$ inhibition directly promotes lymphangiogenesis and macrophage infiltration, independent of VEGF-C/-D		
LPS-induced peritoneal inflammation/C3H/HeN (HeN,	CD11b <sup>+</sup> /F4/80 <sup>+</sup> macrophages that infiltrate into diaphragmatic lymphatics can induce lymphangiogenesis by secreting VEGF-C/-D	[137]	
normal TLR4 signaling), C3H/ HeJ (HeJ, TLR4 gene missense mutation)	TLR-4 signaling in LECs is a critical initiator of LPS-induced inflammatory lymphangiogenesis by chemotactic recruitment of activated macrophages		
Bacteria-induced acute ear skin inflammation/GFP <sup>+</sup> (C57BL/6J	Lymphangiogenesis is related with recruitment of CD11b <sup>+</sup> /Gr-1 <sup>+</sup> macrophages in the inflamed skin and draining lymph nodes	[138]	
genetic background) and K14- VEGF-C transgenic mice	VEGF-C/-D and VEGF-A are derived from the CD11b <sup>+</sup> /Gr-1 <sup>+</sup> macrophages		
	A subset of CD11b <sup>+</sup> /Gr-1 <sup>+</sup> /F4/80 <sup>+</sup> macrophages, and VEGF-C/-D and VEGF-A are major mediators for pathogen clearance and inflammation resolution through lymphatic expansion and enhanced lymph flow		



Table 2 continued

Animal models or human diseases	Macrophages (F4/80 <sup>+</sup> , CD11b <sup>+</sup> , CD68 <sup>+</sup> , LYVE-1 <sup>+</sup> ) and other biological features (cytokine/chemokine/growth factor)	References	
Idiopathic pulmonary fibrosis/ human	Activated CD11b <sup>+</sup> alveolar macrophages can transdifferentiate into LECs to form podoplanin/LYVE-1-positive lymphatic-like vessels in vitro	[54]	
	VEGF-C and -D are not the driving molecules of lymphangiogenesis in idiopathic pulmonary fibrosis		
Onchocerciasis (Onchocerca nodule)/human	CD68 <sup>+</sup> /LYVE-1 <sup>+</sup> macrophages are recruited to lymphangiogenic area and integrated into endothelial lining of the nodule lymphatics	[80]	
HSD/male Sprague–Dawley rats and Swiss-129 Sv mice	HSD increases TonEBP, VEGF-C mRNA and protein expression in macrophages		
	TonEBP binds promoter of the gene encoding VEGF-C and causes VEGF-C secretion by macrophages		
	TonEBP-VEGF-C signaling in MPS cells is a major determinant of lymphangiogenesis and extracellular volume		
LPS-induced peritonitis/FVB/N and GFP <sup>+</sup> mice (C57BL/6J genetic background)	CD11b <sup>+</sup> macrophage-derived VEGF-C/D play a key role in LPS- induced aberrant lymphangiogenesis, and lymphatic remodeling in a paracrine manner	[82]	
Corneal infection with HSV-1/ C57BL/6 mice (GFP expression	HSV-1 directly induces lymphangiogenesis through VEGF-A/ VEGFR-2 signaling	[17]	
under chicken $\beta$ -actin promoter)	VEGF-A is derived from HSV-1-infected epithelial cells rather than F4/80 <sup>+</sup> macrophages		
	BMDCs do not transdifferentiate into LECs		

embryonic stem cells, and promotes lymphangiogenesis in mouse models of chronic peritonitis and pancreatic cancer [95]. T cell-secreted interferon-y reduces the number of Prox-1+ LECs and directly inhibits lymph node lymphangiogenesis without prolymphangiogenic stimulation from macrophages [96]. Obviously, the main factors and mediators governing inflammation-induced lymphangiogenesis are not well defined. In recent few years, animal cornea has been widely used for studying inflammatory lymphangiogenesis, because it is an avascular, alymphatic, and immune privileged tissue. The optimum experimental conditions in the transparent cornea can be easily determined, and the results can be analyzed under stereo and dynamic observation. In a mouse corneal transplant model, both BMDCs and a subpopulation of CD11b<sup>+</sup> macrophages have been shown to contribute to the induction of lymphangiogenesis. Bone marrow-derived CD11b<sup>+</sup> macrophages, which coexpress LEC markers like LYVE-1 and Prox-1, can coalesce with LECs in inflamed corneal stromata, and have the ability to assemble into lymphatic-like structures in vitro [4], although LECs may show a downregulation of LYVE-1 expression during inflammation [97]. Dynamic regulation of inflammatory cascade will require intervention at multiple levels simultaneously targeting a variety of cytokines, chemokines, and growth factors, which influence lymphangiogenesis and macrophage recruitment to the inflamed tissues. The development of animal models concerning LEC and macrophage

plasticity will lead us to understand the mechanisms that are involved in lymphangiogenesis regulation.

A novel idea for lymphangiogenesis: macrophages act as a direct structural contributor to lymphatics

Noteworthily, some studies have indicated that coexpression of macrophage and lymphatic markers and, incorporation of CD11b<sup>+</sup> macrophages into newly formed lymphatics occur during the early stage of lymphatic formation [4, 64, 76]. The cell incorporation into LECs most likely occurs in the diseased condition rather than in the normal tissues. Bone marrow derived endothelial precursor cells with VEGFR-2 or VEGFR-3 expression are extravagated from blood vessels and subsequently incorporate into newly formed lymphatics, and irradiation of bone marrow can remarkably suppress lymphatic growth in a mouse corneal model [98]. Myeloidderived suppressor cells originate in the bone marrow from common myeloid progenitor and often differentiate into CD11b<sup>+</sup> Gr1<sup>med</sup> F4/80<sup>low/-</sup> IL-4R $\alpha$ <sup>+</sup> cells [31]. With tumor growth, these cells increase in the blood and some of them are recruited to the tumor site, where they often express the macrophage marker F4/80 and differentiate into TAMs [99, 100]. When cocultured in vitro with LECs, bone marrowderived macrophages incorporate predominantly at the tips and branch points of growing cord-like structures, suggesting they may instigate lymphatic sprouts after being recruited to LECs [55]. In the bronchoalveolar lavage fluid



from subjects with idiopathic pulmonary fibrosis, short-fragment hyaluronic acid enhances LEC migration and proliferation, and CD11b<sup>+</sup> alveolar macrophages can transdifferentiate into LECs and form lymphatic-like vessels in vitro [54]. In human renal transplants, recipient-derived lymphatic progenitor cells directly transdifferentiate into LECs, contributing to *de novo* lymphangiogenesis. The potential candidates for lymphatic progenitors are considered to be VEGFR-3<sup>+</sup> tissue macrophages with developmental plasticity [53].

In the few years, progress has been made in understanding the link between precursor cells or macrophages and LECs, but there is still controversy concerning cell incorporation in lymphangiogenesis, even for the same tumor cell lines. Actually, some issues still remain to be solved, (1) Does the LEC incorporation from migrated macrophages occur in either initial or collecting lymphatics?; (2) How do the incorporating cells participate in functional intercellular junctions, valve formation, and arrangement of perilymphatic elements in the surrounding tissue?; (3) When do the anchoring filaments, a characteristic feature of initial lymphatics appear to attach LECs to interstitial collagen fibrils? Macrophages belong to the myeloid cell lineage and derive from myeloid progenitor cells. If macrophages physically contribute to LECs or differentiate into lymphatic prototype in tumor and inflammatory tissues, they are assumed to eventually lose their phenotype upon integration.

# New insights into macrophage-induced lymphangiogenesis

Recently, some studies have revealed an unexpected evolutionary link between macrophages and lymphangiogenesis, which may help to mediate and coordinate the functions of many other signaling factors and pathways.

## HSD and lymphangiogenesis

Lymphangiogenesis is physiologically required for the maintenance of interstitial fluid balance and diffusion of protein molecules. Interstitial fluid flow and migration of LECs with VEGF-C expression are supposed to modulate or even direct lymphangiogenesis [101]. It is known that extracellular fluids in the intravascular and interstitial compartments are normally in equilibrium. Sodium-potassium-ATPase activity in the cell membrane can be rapidly adjusted in response to environmental changes like sodium intake in maintaining the balance. Mononuclear phagocyte system (MPS) including macrophages may also regulate various homeostatic processes. Extracellular accumulation of Na<sup>+</sup> may inevitably lead to retention of interstitial fluid.

VEGF-C as an osmosensitive, hypertonicity-driven gene is intimately involved in extracellular volume and blood pressure homeostasis. Tonicity-responsive enhancers play a crucial role in hypertonicity-induced transcriptional stimulation of the sodium/myo-inositol cotransporter, sodium/ chloride/betaine cotransporter, and aldose reductase. The tonicity-responsive enhancer binding protein (TonEBP) is a transcription factor that stimulates transcription through its binding to sequences of the tonicity-responsive enhancers via a Rel-like DNA binding domain [102]. A recent study reported that HSD leads to interstitial hypertonic Na<sup>+</sup> accumulation and volume retention in the rat skin, where TonEBP/VEGF-C signaling in infiltrating MPS cells provide a buffering mechanism for modulating interstitial Na<sup>+</sup> clearance and increasing endothelial nitric oxide synthase (eNOS) protein expression [16]. TonEBP binds the promoter of the gene encoding VEGF-C and causes VEGF-C secretion by macrophages [16], indicating a Na<sup>+</sup>-induced hyperplasia of the lymphatic network [9]. Thus, VEGF-C secretion exposed to osmotic stress does not stem from an inflammatory response. MPS/TonEBP/VEGF-C activity shows a "M2 feature" of MPS cell function. The dermal interstitium in which MPS cells reside, represents a separate tissue-specific, extracellular microenvironment that is not necessarily reflected by changes in serum electrolyte concentrations [103]. MPS-driven and VEGF-C-mediated lymphatic network modification has an important role in the extrarenal regulation of interstitial electrolyte and volume balance.

The lymphatic system collects excess tissue fluid, macromolecules, and cells from the ECM and transports them back into the blood circulation. The connection between stromal matrix and slender lymphatics is directly influenced by interstitial fluid pressure (IFP). Several factors contribute to an increased IFP in tumor tissues, e.g., vascular abnormalities, fibrosis, and contraction of the interstitial matrix. Increased IFP in many solid tumors forms an obstacle in tumor treatment as it results in inefficient uptake of therapeutic agents [104]. Lymphatic permeability is considered to be a crucial factor for modulating IFP and interstitial environment. Increased lymphatic vessel density and area fraction, and high IFP within tumor tissues may facilitate access of tumor cells into the peripheral lymphatics [46]. Netrin-4, a lamininrelated secreted protein for lymphangiogenesis, can stimulate lymphatic permeability in vitro and in vivo by activating small GTPases and Src family kinases/FAK and down-regulating tight junction proteins, thus promoting to tumor dissemination [105]. Indeed, high IFP prevailing in the tumor tissues may affect lymphangiogenesis via integrin-mediated signal transduction [106]. After an excessive salt intake, local hypertonicity is sensed by macrophages that stimulate lymphatic growth via inducing VEGF-C



secretion, creating a third fluid compartment that buffers the increased body Na<sup>+</sup> and volume [107]. It should be noted that macrophages are exposed to high Na<sup>+</sup> concentrations, where the uniquely stored sodium is not free but supposedly bound to proteoglycans. Therefore, several issues need to be addressed in the future, (1) How can osmotically inactive Na<sup>+</sup> induce a hypertonic state that is sensed by macrophages [107]?; (2) Do macrophages have a limited capacity to produce VEGF-C in interstitial hypertonic Na<sup>+</sup> environment?; (3) Does the TonEBP/VEGF-C regulatory axis exist in the kidney?

### HSV-1 and inflammatory lymphangiogenesis

HSV-1, differing from other viruses, does not encode molecular mimics of any known angiogenic factors. Herpes simplex keratitis results from an infection with HSV-1, depending on aberrant host responses to antigen within the immune-privileged cornea. HSV-1 infection induces the production of many angiogenic factors, e.g., VEGF, IL-6, MMP-9, and platelet-derived growth factor [108–110], suggesting that normal equilibrium may be disrupted between proangiogenic and antiangiogenic stimuli to induce an angiogenic switch [111].

In contrast to established inflammatory models, however, HSV-1-induced lymphangiogenesis occurs independently of macrophage recruitment and VEGF-C/-D expression, but dependently on VEGF-A/VEGFR-2 signaling, indicating that BMDCs do not transdifferentiate to LECs after corneal HSV-1 infection [17]. Furthermore, continuous cytokine exposure is not required for the maintenance of mature lymphatics, whereas withdrawal of lymphangiogenic stimuli may elicit destruction of immature lymphatics [74, 112]. In comparison with VEGF-C/-D-induced lymphangiogenesis, the newly formed lymphatics induced by VEGF-A/VEGFR-2 have some structural and functional characteristics, showing a relatively dilated, leaky, and poorly functional phenotype [77, 113, 114]. However, HSV-1-induced lymphatics remain intact and functional well beyond resolution of the infection. The molecular mechanism that explains the phenotype of LECs is still unknown.

## M-CSF and CEACAM-1

Numerous tumor-derived chemoattractants interacting with tyrosine kinase receptors, such as M-CSF and VEGFs, are thought to ensure the recruitment of macrophages into tumor tissues [12]. M-CSF signaling through its receptor CSF1R (CD115, c-fms) is a critical regulator of the differentiation, proliferation and survival of macrophages and monocytes, and the expression of specific cell surface markers [115, 116]. M-CSF receptor signaling contributes to myeloid cell-mediated angiogenesis through regulating

the recruitment of CD11b<sup>+</sup>F4/80<sup>+</sup> TAMs [117]. M-CSFinduced VEGF secretion has suggested its direct role in monocyte/macrophage-mediated angiogenesis. M-CSF functions as an angiogenic switch for promoting the formation of high-density vessel networks in the primary breast tumor [115]. Recombinant M-CSF can induce tube and network formation in human umbilical vein endothelial cells, through transcriptional regulation [118], M-CSF and VEGF have close overlapping functions in the support of osteoclastic bone resorption. In the op/op mouse (ablated for M-CSF), the osteopetrotic phenotype is rescued by a single injection of human recombinant VEGF-A, showing that VEGF-A can substitute for M-CSF in vivo [119]. Moreover, TNF has been found to induce M-CSF-dependent cells, including osteoclast precursors and monocytes, to produce VEGF-C through NF-kB, leading to significantly increased lymphangiogenesis [120]. M-CSF inhibition effectively suppresses tumor lymphangiogenesis, but the continuous inhibition does not affect the healthy lymphatics outside tumors [92]. Modulation of the signaling molecules in the recruitment and function of distinct subsets of tumor-infiltrating myeloid cells will improve the cancer treatment.

The carcinoembryonic antigen-related cell adhesion molecule-1 (CEACAM-1), a member of the immunoglobulin superfamily, has been implicated in various intercellular adhesion and intracellular signaling, for controlling growth and differentiation of normal and cancer cells, especially for regulating both lymphoid and myeloid cell types [121]. CEACAM-1 acts as a potent angiogenic factor and as a major morphogenic effector for VEGF [122]. Recently, CEACAM-1 has been reported to trigger reprogramming of vascular endothelial cells to lymphangiogenesis. The switch factor is colocalized with podoplanin in LECs of tumor tissues, and its expression appears earlier in the lymphatics than in tumor-associated blood vessels and before tumor invasion [123]. CEACAM-1 overexpression in human umbilical vein endothelial cells leads to an upregulation of VEGF-C/-D and VEGFR-3, and interestingly, the endothelial cells transfected with CEACAM-1 show enhanced expression of lymphatic markers Prox-1, podoplanin, and LYVE-1 [123]. In experimental cutaneous leishmaniasis, B6.Ceacam-1<sup>-/-</sup> mice show impairment of lymphangiogenesis, indicating that lymphatic formation is affected by the loss of CEACAM-1<sup>+</sup>/CD11b<sup>high</sup> cells. The myeloid cells do not constitute definite LEC precursors, and thereby can neither fuse nor transdifferentiate into lymphatics [48]. Therefore, the issue has been debated as to how macrophages contribute physically to the developing lymphatic wall, resulting from lack of dynamic data to support the cellular integration mechanism.

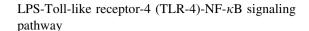


#### SDF-1-CXCR-4 axis

The chemokine, stromal cell-derived factor-1 (SDF-1, also called CXCL-12) is critical to bone marrow stem cell development, and its receptor CXCR-4 is moderately expressed in some subsets of leukocytes including monocytes/macrophages [124]. Murine embryos lacking SDF-1 or CXCR-4 show multiple lethal defects, including impaired bone marrow lymphoid and myeloid hematopoiesis [125, 126]. The SDF-1-CXCR-4 axis regulates the adhesion of hematopoietic cells to fibronectin and other ligands, and the interaction of hematopoietic cells with endothelial and stromal cells, through stimulating VEGF secretion and activating integrins in the bone marrow microenvironment [127]. SDF-1 acts as a chemoattractant for human CD34<sup>+</sup> progenitor cells [128], which may explain the mobilization of hematopoietic progenitors to peripheral blood. CD31expressing endothelial cells have been suggested to be a source of SDF-1. SDF-1 gene expression is regulated by the transcription factor hypoxia-inducible factor-1 in endothelial cells, resulting in selective in vivo expression of SDF-1 in ischemic tissue in the direct proportion to reduced oxygen tension [129].

The tumor cells expressing CXCR-4 for specific LEC-secreted SDF-1 may approach and invade preexisting or newly formed lymphatics [130]. In extramammary Paget's disease, LECs of subcapsular sinuses and lymph node-resident macrophages have an ability to produce SDF-1. The epithelial-mesenchymal transition-related features may promote lymphatic metastasis by activating SDF-1-CXCR4 axis [131]. In human breast carcinoma, stromal fibroblasts promote tumor growth and angiogenesis through elevated SDF-1 secretion [132]. Blocking the SDF-1-CXCR4 interactions with neutralizing anti-CXCR4 or anti-SDF-1 antibodies can significantly impair these migratory responses, indicating that SDF-1 is one of the main chemotactic factors for cancer cells in the ECM [133].

Recently, SDF-1 has been described to induce recruitment, infiltration and ongoing retention of bone marrow-derived LYVE-1<sup>+</sup> macrophages in regulating formation of vascular networks [21], suggesting that the reciprocal relationship between CXCR4-expressing macrophages and SDF-1-expressing vascular-stromal cells is involved in angiogenesis. Moreover, proteolytic enzymes such as MMP-9 play a role in the process by degrading SDF-1 in bone marrow, increasing expression of CXCR-4 and mobilizing maturing leukocytes, progenitors, and stem cells [134]. Macrophage function, which is potentially coordinated by SDF-1-CXCR-4 signaling, may contribute to enhanced regional lymphangiogenesis.



Macrophages and endothelial cells are pivotal components in the development of innate immune responses against invading microorganisms. LPS or endotoxin is a potent activator of cells including macrophages, monocytes, and endothelial cells in the inflammatory process [135]. Bacterial LPS induces actin reorganization, increased paracellular permeability, and disruption of endothelial monolayer integrity and survival signaling events in vitro through caspase cleavage of adherens junction proteins [136]. In LPS-induced peritonitis of mice, CD11b<sup>+</sup> macrophage-derived VEGF-C and -D induce abnormal and dysfunctional lymphangiogenesis, exhibiting an impaired peritoneal fluid drainage [82]. The substantial increase in lymphatic vessel density is resulted from preexisting LECs and reversible remodeling [137], but not from transdifferentiation of BMDCs. LPS-induced recruitment of CD11b<sup>+</sup>/ Gr-1<sup>+</sup> macrophages that are demonstrated to be F4/80<sup>+</sup> cells, is also involved in inflammation resolution [138].

Endothelial cells of lymphatics and blood vessels express TLR-4 and respond to LPS. Bacterial LPS activates NF-κB through TLR-4 in the cultured human dermal microvessel endothelial cells [139]. TLR-4 expression in LEC intracellular region can enhance recruitment and infiltration of CD11b<sup>+</sup> macrophages around lymphatics. However, LPS-TLR4 signaling in LECs does not directly promote cell proliferation, migration, and tube formation, and expression of lymphangiogenic molecules [137]. NFκB-dependent mediator, LPS increases VEGFR-3 expression and responsiveness of LECs to VEGFR-3 ligands. Inflammation-induced NF-kB signaling precedes lymphatic-specific upregulation of VEGFR-3 in vivo, and NF-κB activates VEGFR-3 transcription in cultured LECs [140]. This suggests that LEC stimulation by NF-κB-dependent cytokines has the potential to amplify lymphangiogenic signaling by increasing VEGFR-3 expression. Thus, LPS-TLR4-NF-κB signaling in LECs may be a crucial pathway that conveys LPS-induced inflammation and lymphangiogenesis, but the mechanistic basis of its regulation of lymphatic-specific genes has not been well defined.

In addition, eNOS and IL-6 have been indicated to mediate macrophage-induced lymphangiogenesis. eNOS expressed in LECs regulates the initial lymph flow by acting on collecting lymphatics in vivo [141], and mediates VEGF-C-induced lymphangiogenesis, peritumor lymphatic hyperplasia and tumor metastasis, through VEGFR-2/-3 signaling dependent on PI3 K-mediated Akt activation [142]. The virus-induced expression of cytokines and chemokines is primarily due to stimulation of one or more of the depicted signal transduction cascades [143]. In



human cytomegalovirus-infected LEC cultures, many of these factors are involved in the physiological regulation of endothelial cell properties. The lymphangiogenesis is supposed to be through an indirect mechanism that relies on the stimulation of IL-6 and secretion of granulocytemacrophage colony-stimulating factors from infected cells, but is independent of VEGF [144].

### Macrophage depletion and its prospective use

Either systemic depletion of all BMDCs by irradiation or local depletion of macrophages with administration of clodronate liposomes prior to tissue injury can significantly inhibit lymphangiogenesis. In combination with blockage of VEGF/VEGFR signaling pathways, macrophage depletion may provide a potent target for upcoming gene or protein therapy in controlling tumor- or inflammation-induced lymphangiogenesis to prevent tumor metastasis and attenuate inflammatory responses.

In an ovarian cancer model, selective depletion of macrophages with additional inhibition of VEGF-C/-D and VEGF-A signaling with soluble VEGFR-3 and VEGF-Trap has indicated that VEGF-A/-C/-D from CD11b+/ LYVE-1<sup>+</sup> macrophages are responsible for mediating aberrant lymphangiogenesis [145]. During acute skin inflammation, depletion of macrophages CD11b<sup>+</sup>/Gr-1<sup>+</sup> macrophages and, blockade of VEGF-C/-D or VEGF-A result in delayed antigen clearance and inflammatory cell migration, and decreased LPS-induced lymphangiogenesis and regional lymph flow [138]. In organ and tissue transplantation, lymphatics are thought to be important mediators of immune processes, acting as a conduit for foreign antigens and antigen-presenting cells, such as macrophages. Preexisting blood vessels and lymphatics are an established risk factor for the immune rejection. Absence of lymphatics in the recipient bed prior to transplantation is suggested to promote subsequent graft survival. The local depletion of VEGF-C/-D expressing macrophages leads to substantial inhibition of corneal lymphangiogenesis [76]. Moreover, integrin  $\alpha 5\beta 1$  plays an important role in VEGFR-3-mediated lymphangiogenesis in vivo, and its functional inhibition by small molecule antagonists has significantly blocked the outgrowth of new lymphatics into the cornea in a dose-dependent manner [146]. In diabetic macrophages, on the other hand, the mRNA levels of VEGFR-3 and its ligands VEGF-C/-A are notably decreased, resulting in delayed lymphangiogenesis. Application of IL-1 $\beta$ -treated db/db-derived macrophages to diabetic wounds induces new lymphatic formation and accelerates the healing process [147]. During the past decade, increasing evidence has indicated that macrophages surrounding tumor or inflamed tissues are actively involved in pathological lymphangiogenesis, and thus alteration of macrophage phenotype and function has a significant impact on LEC proliferation and sprouting. This may reveal the potential of specific anti-lymphangiogenic therapy in the treatment of lymphatic-associated diseases.

#### **Conclusions**

Recent advances have been made in understanding the mechanisms of macrophages as a direct result of secreted growth factors, VEGF-C/-D and VEGF-A, or even as integrated cells to fuse with LECs in lymphangiogenesis (Fig. 1). However, multiple macrophage phenotypes have differential functions and exert divergent effects on surrounding cells. Further study of the factors that stimulate or inhibit macrophages and that accelerate or delay regression of newly formed lymphatics may offer novel therapeutic approaches for lymphedema formation, inflammatory process, and tumor metastasis.

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