

REVIEW

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Regulatory mechanisms, prophylaxis and treatment of vascular leakage following severe trauma and shock

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Abstract

Vascular leakage, or increased vascular permeability, is a common but important pathological process for various critical diseases, including severe trauma, shock, sepsis, and multiple organ dysfunction syndrome (MODS), and has become one of the most important causes of death for intensive care units (ICU) patients. Currently, although there has been some progress in knowledge of the pathogenesis of these vascular disorders, the detailed mechanisms remain unclear, and effective prophylaxis and treatment are still lacking. In this study, we aimed to provide a review of the literature regarding the regulatory mechanisms and prophylaxis as well as the treatment of vascular leakage in critical diseases such as severe trauma and shock, which could be beneficial for the overall clinical treatment of vascular leakage disorders.

Keywords: Clinical critical diseases, Vascular leakage, Vascular permeability, Shock, Sepsis

Background

Capillary leak syndrome (CLS) refers to a series of syndromes with clinical manifestations of serious tissue edema, such as severe hypoproteinemia, hypovolemia and hypoperfusion, which is caused by the massive leakage of plasma proteins and intravascular fluid due to injuries to the vascular endothelium as well as increased vascular permeability [1]. The high mortality of CLS patients is believed to be associated with the non-specific clinical manifestations and the rapid progression of these disorders in the acute-onset phase [2]. Dhir et al. [3] found that the 5-year survival rate in CLS patients is approximately 70% and that 75% of the deaths occur in the acute-onset phase [4]. In addition, research has indicated that the 10-year mortality of CLS patients is approximately 34%, while deaths that occur in the intensive care units (ICU) are caused by both the acute onset and the complications of CLS, which account for 80% of the total mortality [5].

Under normal physiological conditions, water and electrolytes could pass through the capillary wall into the interstitial space instead of the plasma albumin, while proteins

with molecular weight larger than 200 kD, or even 900 kD in some particularly severe circumstances, could also pass through the wall into the interstitial space. This physiological event occurs in cases of severe trauma, sepsis, cardiopulmonary bypass surgery (especially in infant cardiopulmonary bypass surgeries), reperfusion injury, venomous snake bites, acute lung injury, acute respiratory distress syndrome (ARDS), burns and drug toxicity (such as recombinant interleukin-2 and docetaxel). In certain drug toxicities, the mononuclear-phagocyte system, endothelial cells and neutrophils are excessively activated, resulting in the release of inflammatory cytokines and immune reactions, in which then produces injuries to the capillary endothelium, broken intercellular junctions and vascular leakage [6], which ultimately causes CLS. The major adverse effects of CLS include alveolar edema, restricted gas exchange and hypoxia, all of which aggravate injuries to the capillary endothelium cause edema in major organs such as the brain, the heart, the liver and the kidneys with the structures and functions that are damaged and that ultimately result in multiple organ dysfunction syndromes (MODS). Once that happens, the patient's condition becomes more serious and includes higher risk for death [7]. Therefore, investigating the pathogenesis of vascular leakage or increased capillary permeability is of great significance for

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the prophylaxis and treatment of CLS. In this review, we will focus on newly identified regulatory mechanisms, and the prophylaxis and treatment of vascular leakage in critical clinical diseases such as shock.

Pathways and regulatory mechanisms of vascular leakage

The vascular endothelium is composed of monolayer cells on the surface of vascular lumen and on the extracellular matrix in the deep layer. The vascular endothelium is a semi-permeable barrier between the vascular wall and the blood and controls the exchange of macromolecules and liquids between the interstitial fluid and blood. Generally, the occurrence of vascular leakage occurs through one of two pathways: the paracellular pathway, which refers to material that is diffused by passive transport through gap junction communication channels that are formed by intercellular junctions to the adjacent cells [8]; or the transcellular pathway, which refers to macromolecules that are transferred out of the vessel by endothelial cells instead of the intercellular junctions [9]. Although these two pathways can simultaneously exert synergistic or individual effects, previous quantitative analysis has confirmed that the paracellular pathway is the preferable pathway in cases of vascular leakage [10].

Paracellular pathway

The paracellular pathway, also known as the interendothelial junction, refers to endothelial cells that are stimulated by an endogenous or an exogenous material. This stimulation of the paracellular pathway generates a series of variations in signal pathways to widen the intercellular gap by regulating the contraction of the endothelial cytoskeleton or by altering the intercellular junctions, which results in increased vascular permeability. There are three main types of endothelial cell junctions: tight junctions, adherens junctions between the cells, and adherens junctions between the endothelial cells and the basement membranes. Since the structure and protein composition of the tight junction and the adherens junction of endothelial cells were recently introduced in a summary report [11], we will mainly discuss the effects that these two kinds of junctions have in cases of vascular leakage.

The effect of the tight junction in vascular leakage

Tight junction proteins include the junction adhesion molecule (JAM), the occludin, the claudin, the zona occludens (ZO) and the cingulin. The JAM-1 can secure the stability of the tight junction and can regulate the permeability of the endothelial barrier by potentially mediating the construction of the reticular structure of the macromolecular complexes of the plasma membrane. Orlova et al. [12] found that the JAM plays an important role in regulating

the functions of endothelial actin and myosin, (i.e., when the *JAM* gene is knocked off, the level of actin and the activity of myosin light chain phosphatase (MLCP) decreases, which leads to an increase in the level of phosphorylated myosin light chains and the formation of actin stress fibers. Occludin is not only a major composition of the tight junction but can also regulate the functions of the tight junction. Occludin can regulate the formation and decomposition of the tight junction and can maintain the integrity of the tight junction by adjusting the activity of the transmembrane proteins (actin and myosin) through the protein kinase C (PKC), the mitogen-activated protein kinase (MAPK) and the myosin light chain kinase (MLCK). Wong et al. [13] has shown that only phosphorylated occludin can combine with the tight junction. For occludin phosphorylation, serine/threonine are usually phosphorylated at the carboxyl terminal. Most of the phosphorylated occludin is distributed in the tight junctions, while the occludin and few phosphorylated residues is mainly distributed in the basement membrane of the cytoplasm [14]. Blasig et al. [15] found an increase in the transport of uncharged molecules by the tight junction barrier after excision of the carboxyl terminals on the *occludin* gene because of cell transfection. However, no variation has been found in trans-epithelial electrical resistance (TEER) with an increased permeability of the tight junction, which indicates that the increased permeability of the barrier is caused by an interruption of the mutual effect between tight junction proteins, instead of an increase in the TEER.

There are 24 molecules with highly homologous sequences in the claudin family that are named claudin -1 to -24 and that have molecular weight ranging from 20 to 27kD [16]. Binding sequences, located in the C-terminal of all claudins, can directly incorporate other tight junction proteins in the cytoplasm [17], such as ZO-1, ZO-2, ZO-3, which are proteins with PDZ domains as well as associated PALS-1 tight junction proteins. The mutual effect between ZO-1 and ZO-2 could lead to an indirect interaction between claudins and actin [18]. The dense band, composed of claudin polymers, could accelerate the formation of barriers. Van Itallie et al. [14] found that the phosphorylated S208 locus on the C-terminal of the cytoplasm of claudin-2 can influence the location of claudin-2 without changing the binding with ZO-1 or ZO-2. Recent research has confirmed that the extracellular domain of claudin-1 can not only affect the assembly of the tight junction but can also suppress its barrier functions [19]. Interestingly, this domain of claudin-1 is closely connected to occludin, which suggests that there might be a direct mutual effect between these two proteins, and this mutual effect is expected to be confirmed in future studies.

ZO-1 and ZO-2, which are two intermediate connectors, can closely bind the claudin, the occludin, and the JAM with actin and is also believed to be one of the key

functions of the tight junction. Phosphorylation of the ZO-1 protein is intimately associated with the location of the intercellular tight junction and the permeability of cells, and excessive phosphorylation of the ZO-1 protein can relax the binding between occludin, leading to a decrease in function. In cells that lack the *ZO-1/ZO-2* genes, the content of tight junction-related proteins (such as claudin) is relatively low [20], and the functions of the tight junction are also affected; however, the expression of tight junction-related proteins increases and the functions of the tight junction return to normal when the cells are transfected with *ZO-1/ZO-2* genes. According to the latest research, Wang et al. [21] found that blood-brain barrier injuries caused by microwave irradiation were also associated with the decomposition of the tight junction and decreased function of the *ZO-1* gene. Tyr-phosphorylation of occludin occurs because of microwave irradiation, which weakens the mutual effect between the occludin and the ZO-1 and results in a widened gap and a decomposition of the tight junction. Further studies have revealed that this process might produce these results by activating the vascular endothelial growth factor/fetal liver kinase 1 - extracellular signal-regulated kinase (VEGF/Flk-1-ERK) pathway.

The function of adherens junctions between cells in cases of vascular leakage

The adherens junction is one of the intercellular junctions results from the interaction between cadherin and the adjacent cellular membrane. Cadherin can bind with catenin, a kind of cytoplasmic protein, which is further connected to the cytoskeleton complexes (i.e., the actin filament or the microtubules) to stabilize the intercellular junctions [22]. In particular, vascular endothelial-cadherin (VE-cadherin) refers to the endothelial cadherin that is specifically expressed by vascular endothelial cells. As the most important adhesive composition of endothelial adherens junctions, VE-cadherin can exert its functions only by way of the VE-cadherin-catenin complex, which is composed of VE-cadherin, α -catenin, β -catenin and P120-catenin, etc. The VE-cadherin-catenin complex is also mediated by the targeted molecules of substances that can increase microvascular permeability [23, 24]. Multiple substances, such as VEGF, TNF- α , platelet activating factor, and thrombin or histamine, can induce the tyrosine phosphorylation of VE-cadherin, α -catenin and β -catenin to increase the vascular permeability [25, 26]. In EDTA-treated endothelial cells, a decrease in binding activity is seen between the VE-cadherin and the cytoskeleton [27, 28], which indicates that Ca^{2+} could protect the VE-cadherin from being hydrolyzed by proteolytic enzymes.

It should be noted that the functions of tight junctions also depend upon the integrity of intercellular adherens junctions. Caused by removal of extracellular Ca^{2+} ,

loosened cables in adherens junctions will open the tight junctions [29]. However, Maier et al. [30] indicated that by blocking the binding between ZO-1 and α -catenin, the stability of the adherens junctions was not affected, but damaged the endothelial barrier functions and destroyed the assembly with variations in ZO-1 motility and the structure of the actin cytoskeleton. Thus, the results suggest that binding between ZO-1 and α -catenin might be a new coupling mechanism for adherens junctions in the endothelial barrier.

Transcellular pathway

Macromolecular substances are transferred out of the vessels through endothelial cells, instead of through the intercellular gap. Feng et al. [31] found that plasma proteins and other macromolecular substances can be diffused out of a morphologically intact capillary without any intercellular gaps. In addition, they also found alveoli with vesicles in the capillary endothelial membrane in ultrathin sections that were 14 nm in height, which could have been caused by pinocytosis. Macromolecular tracers can be rapidly diffused out of the vessel from the capillary vein through vesicular-vacuolar organelles (VVOs) [32, 33]. The protuberance, or small cavity formed by the cytoplasm of the capillary endothelial cells, is possibly associated with the regulation of focal blood velocity and flow and the exchange, synthesis, release, transformation of material and the inactivation of active substance. The angiotensin converting enzyme also exists in this small cavity. In addition, there are various proteins and enzymes distributed on the endothelial cells that express many receptors with diversified functions and structures. In addition to the vesicle transporter, aquaporin (AQP) on the endothelial membrane has been found to participate in the transcellular pathway.

Aquaporin

It had been long been believed that water could not pass through the membrane due to the hydrophobic property of the lipid bilayer in the membrane. However, it has been recently found that a 28 kD protein family on the membrane, namely, the AQP protein, that has a structure like other channel proteins, can adjust the transcellular permeability of water. The basic function of AQP is to mediate the transcellular transport of free water molecules. The major difference from other ion channels is that the osmotic pressure gradient only regulates the transport of water (i.e., the water molecules could be diffused through the AQP along the osmotic pressure gradient) instead of the so-called "turn-on" or "turn-off" phases. Thus, water molecules could be directly allowed into and out of the cells. Once the endothelial cells are injured, the expression of AQP increases, which augments capillary permeability and is believed to be closely associated with the onset of

hydrocephalus. To date, there are 13 kinds of proteins that have been identified as members of the AQP family, which include AQP0 to AQP12. These 13 AQP genes exert diversified physiological functions due to the different expression sites with similarities in permeability [34].

The transcellular pathways of water are distributed in all tissues but are mainly in epithelial and endothelial cells that have functions related to the secretion and the absorption of fluid. These proteins participate in the regulation of secreting and absorbing water as well as in the homeostasis between extra- and intracellular fluid volume.

Distributed in the outer medullary descending vasa-recta (OMDVR), the AQP1 is related to the mechanism of urinary concentration. *AQP1*^{-/-} mice showed a deficiency in urinary concentration due to the damaged water transport pathway that was energized by osmotic pressure and exhibited symptoms such as polyuria, hypotonicity of the urine, decreased response to vasopressin, significantly enlarged OMDVR and adaptive capillary wall reconstruction.

The expression of AQPs is diversified based on different places in the lung, (e.g., the *AQP1* gene is mainly expressed in the capillary endothelium; the *AQP3* gene is mainly expressed in the epithelial cells of both the nasopharynx and the airway; the *AQP4* gene is mainly expressed in the basal-lateral membrane in the epithelial cells of the airway; and the *AQP5* gene is mainly expressed in the epithelial cells in the alveoli). Both the *AQP1* and the *AQP5* genes can regulate the osmotic water transport in the capillaries of the airway, but do not affect the humidification or the liquid homeostasis on the surface of the airways.

In the thoracic tissues, the *AQP1* gene is expressed in the endothelial cells of both the visceral and cervical pleura as well as the mesothelial cells in the cervical pleura to regulate the osmotic pressure balance of fluid inside and outside the thoracic cavity. Researchers have found that the *AQP1* gene is intimately associated with the extent of cardiac necrosis in cardiopulmonary bypass and infarction models, which suggests a potential relationship between the myocardial ischemia and the maintenance of myocardial edema [35].

Expressed by hepatic cells, the *AQP8* gene is mainly located in the cellular vesical. During the process of bile secretion, the *AQP8* gene in the membrane is transported to the canalicular membranes, which are induced by cAMP and increase the water permeability of the apical membrane, thus achieving water transport [36]. In addition, Drobná Z et al. [37] found that the bile secretion by bile canaliculi is synergistically regulated by the *AQP8* gene and hepatic sinusoidal *AQP9* gene, which mediates water transport between the hepatocytes and the blood in the hepatic sinusoidal endothelium. Distributed on the basal membrane of intrahepatic

cholangiocytes, *AQP4* can maintain the equilibrium of water permeability between the apical area and the basal membrane of cholangiocytes and mainly regulates the water permeability of the basal membrane.

The permeability of the blood-brain barrier in brain tissues is also associated by some subtypes of AQP. Teng et al. [38] found a significant and positive correlation between the expression of *AQP4* mRNA and the permeability of the blood-brain barrier in mice after cerebral hemorrhage. Ke et al. [39] identified focal changes in the expression of *AQP4* mRNA in cases hydrocephalus with concomitantly damaged blood-brain barriers, while there were no significant changes in cases of hydrocephalus that were caused by diffuse brain injuries without any damage to the blood-brain barriers. In addition, the research by Liu et al. [40] indicated that overexpressed *AQP9* gene after a cerebral hemorrhage was closely associated with the damage of the blood-brain barrier and the formation of hydrocephalus. The possible explanatory mechanism is that, while in an ischemic and hypoxic environment, the Na⁺-K⁺-ATPase of the membrane in the brain tissues is destroyed and the balanced ion exchange in the membrane is broken, thus activating the expression of the *AQP9* gene, which perceives changes in osmotic pressure.

Vesicle

Under normal physiological conditions, the transport of bio-macromolecules in the blood is strictly restricted by the endothelial barrier, which makes the paracellular pathway only permeable to small molecular substances, such as glucose or blood urea nitrogen, while it is impossible for macromolecular substances like albumin to pass through the membrane directly. The transport of such macromolecular substances depends on the vesicles, a kind of cellular structure, by which the molecules awaiting transport will be absorbed and then delivered to the organelles of the target cell or extracellularly. This pathway plays a crucial role in maintaining the normal colloid osmotic pressure of the tissues. Plasmalemmal vesicles that include the caveolae and fenestrae are currently being studied.

Like the subcellular structure, the caveola is a flask-shaped, cave-like invagination specifically spread on the surface of the cytoplasmic membrane with a diameter that ranges from 50 to 100 nm. Caveolae are widely spread throughout various cells but are rich in endothelial, epithelial and smooth muscle cells with the existence of the Caveolin molecule as the representative feature [41]. Caveolae mainly participate in the endocytosis and pinocytosis of macromolecular substances and in signal transduction [42]. As a kind of integrin membrane protein with a molecular weight that ranges from 21 to 24 kD, caveolin plays important roles in maintaining the morphological integrity, structure and

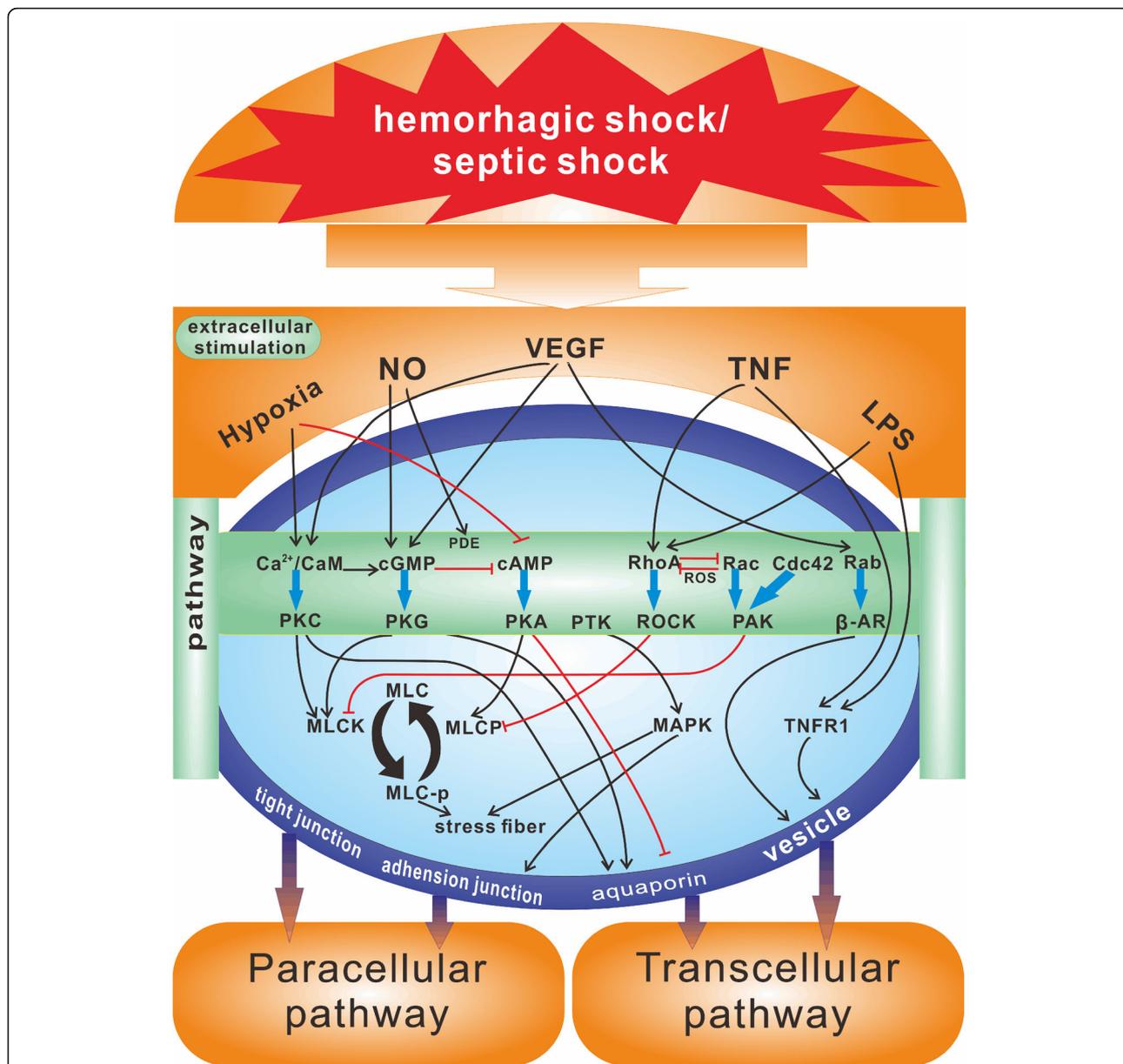


Fig. 1 The mechanism of signaling transduction of vascular permeability. NO, Nitric Oxide; VEGF, vascular endothelial growth factor; TNF, Tumor necrosis factor; PKC, Protein kinase C; PDE, Phosphodiesterase; cGMP, Cyclic guanosine monophosphate; PKG, Protein kinase G; cAMP, Cyclic adenosine monophosphate; PKA, Protein Kinase A; PTK, Protein Tyrosine Kinase; RhoA, Ras homolog gene family member A; ROCK, Rho-associated coiled-coil-containing protein kinase; ROS, Reactive oxygen species; Rac, Ras-related C3 botulinum toxin substrate 1; PAK, p21-Activated Kinase; Cdc42, Cell division control protein 42; AR, Androgen receptor; MLC, Myosin light chain; MLCP, Myosin light chain phosphatase; MLCK, Myosin Light Chain Kinase; MAPK, Mitogen-activated protein kinase; TNFR1, Tumor necrosis factor receptor 1. a) Ca^{2+} -PKC/CaM pathway, the vascular permeability is regulated in the tight junction by controlling the phosphorylation level of MLC by MLCK; b) cGMP-PKG pathway, the vascular permeability is regulated by AQP activity and tight junctions through controlling the phosphorylation level of MLC by MLCK; c) cAMP-PKA pathway, the vascular permeability is regulated by adjusting the activity of MLCP and AQP; d) PTK-MAPK pathway, the vascular permeability is affected by regulating the tight junctions by FAK; e) SGP pathway (small G protein), the vascular permeability is regulated by adjusting the tight junction, the adherens junctions and the vesicles by Rho and Rac GTPases and by CDC42

pathways. VEGF destroys the intercellular adherens junction and tight junction to increase vascular permeability and can promote the phosphorylation of Y658 and Y731, VE-cadherin, to destroy the mutual junction between VE-

cadherin and β -catenin [53]. In addition, VEGF can break the intercellular tight junctions through the VEGFR-2 pathway, which precipitates vascular leakage [54–56]. Moreover, VEGF can increase vascular permeability by

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