REVIEW ARTICLE

Cellular Elements of the Blood-Brain Barrier

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Abstract The Blood-brain-barrier (BBB) provides both anatomical and physiological protection for the central nervous system (CNS), shielding the brain for toxic substances in the blood, supplying brain tissues with nutrients and filtering harmful compounds from the brain back to the bloodstream. The BBB is composed of four main cellular elements: endothelial cells (ECs), astrocyte end-feet, microglial cells, and perycites. Transport across the BBB is limited by both physical and metabolic barriers (enzymes, and different transport systems). Tight junctions (TJs) present between ECs form an important barrier against diffusion, excluding most blood-borne substances for entering the brain.

Keywords Blood brain barrier · Transport · Endothelial cells · Astrocytes · Perycites · Basement membrane matrix

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Introduction

The blood-brain barrier (BBB) establishes both a physical as well as a metabolic barrier isolating the Central Nervous System (CNS) from systemic circulation, creating a unique and stable environment for optimum neuronal activity [1]. It exerts bi-directional control over the passage of a large diversity of regulatory proteins, nutrients and electrolytes, as well as potential neurotoxins. This traffic is regulated through different transport mechanisms [2, 3]. In addition, the BBB exerts its defense of the CNS through the action of efflux transporters, blocking intravascular toxin entry and promoting toxic substance elimination to the bloodstream [4]. In certain regions of the CNS, classical BBB structure is replaced by a blood-cerebrospinal fluid (CSF) barrier, which, although more permeable than the BBB, still prevents free passage of serum proteins from the blood into CSF. This occurs in neurosecretory areas like the posterior pituitary, and in areas performing chemoreceptive functions like the pineal gland, the subfornical organ, the median eminence, the area postrema, the subcommissural organ and the organum vasculosum of the lamina terminalis [5]. In the blood-CSF barrier, choroid plexus blood vessels are fenestrated and form a non-restrictive barrier; however epithelial cells have apical tight junctions (TJs) restricting intercellular passage of molecules (Fig. 1a). The arachnoid barrier represents an additional barrier. It is the least studied and structurally most complex of all the brain barriers. The blood vessels of the dura are fenestrated and provide little barrier function; however, outer cells on the arachnoid membrane have TJs, and this cell layer is believed to form the physical barrier between the subarachnoid and overlaying structures. Blood vessels on arachnoid and pial surfaces have TJs similar to cerebral blood vessels, although lacking perycites and astrocytic end-feet [6] (Fig. 1b).

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Fig. 1 Schematics of different barrier interfaces. **a** The blood-CSF barrier is a barrier between choroid plexus blood vessels and the CSF. The choroid plexus blood vessels are fenestrated and form a non-restrictive barrier; however, the epithelial cells have apical tight junctions that restrict intercellular molecule passage. **b** In the arachnoid barrier, blood vessels of the dura are characterized by multiple enlarged extracellular space and few intercellular contacts, implicating a lack of structural cohesion within this layer. In contrast, outer cells of the arachnoid have numerous tight junctions, without significant extracellular space. This cell layer is therefore considered

BBB Structure

Endothelial Cells

BBB structure is conformed by cerebral endothelial cells (ECs) forming brain and spinal cord capillaries, in association with various perivascular cells such as smooth muscle cells, perycites, microglial cells and astrocytes [3, 7] (Fig. 1c). Ultrastructural cytochemistry and immunocytochemistry revealed the morphology of a functional polarity of the brain microvascular endothelium. This polarity is evidenced by asymmetric distribution of the majority of the transport-related enzymes and carriers present in the luminal and abluminal ECs plasma membranes, indicating that apical and basolateral membranes of epithelial cells are functionally distinct [8, 9].

ECs are normally connected at a junctional complex by TJs, and adherent junctions (AJs). Electron microscopy studies of the BBB have identified distinct morphologic and metabolic characteristics of these particular ECs, different to those present in peripheral tissues. The most important of these include: (a) ECs forming TJs at their adjacent margins, produced by the interaction of several transmembrane proteins projecting into the paracellular space and effectively sealing it, thus confining penetration across brain endothelium to transcellular mechanisms [10, 11]; (b) Endothelial cytoplasm lacking fenestrations typically present in peripheral-tissue capillaries [12]; (c) Fewer pinocytotic vesicles compared to peripheral endothelial cells [13]; and (d) More mitochondria, suggesting important metabolic activity [14].

The molecular biology of TJs is quite complex [15], and their proteins, as well as their adaptor molecules, which

an effective morphological and functional barrier between circulating blood in the dura and the CSF in the subarachnoid space. **c** The bloodbrain-barrier is a barrier between the lumen of cerebral blood vessels and brain parenchyma. In the brain, endothelial cells form tight junctions at their margins, sealing off paracellular pathways between cells. Perycites are vascular cells adjacent to capillaries that share a common basement membrane with endothelial cells, and have many cytoplasmic processes encircling capillaries. Endfeet processes from astrocytes form a network surrounding capillaries, and microglial cells represent the immunocompetent cells of the brain

link TJs to the cytoskeleton, are often affected during acute or chronic brain disease. Figure 2 shows the molecular organization of BBB TJs, critical determinants of BBB restrictiveness. They are composed of a network of intracellular and trans-membrane proteins linked to an active cytoskeleton base, causing TJs to form a seal while retaining capacity for rapid modulation and regulation. Two major trans-membrane protein components of TJs have now been identified, occludin [16] and claudins [17].

Occludin

Occludin was the first integral membrane protein discovered in endothelial cell TJs, including the BBB. It is composed of four trans-membranous domains with carboxyl and amino-terminals oriented towards the cytoplasm and two extracellular loops spanning the intracellular cleft [18]. Multiple phosphorylation sites have been identified its serine and threonine residues, and the phosphorylation state of occludin regulates its association with both cell membrane and barrier permeability [19]. Recent data have shown that occludin phosphorylation regulates TJs permeability in a G-protein dependent or -independent manner, depending on the receptor involved, regardless of cytoskeleton changes [20]. Both external loops as well as trans-membrane and C terminal cytoplasmic occludin domains are important for para-cellular permeability regulation [21]. The N terminal cytoplasmic domain of occludin regulates trans-epithelial migration of neutrophils, and has an important role in maintaining TJs assembly and barrier function [22]. Deletion constructs lacking N terminus or extracellular domains exert a dramatic effect on TJs integrity [22]. In addition, recent studies have



Basement membrane

Fig. 2 Molecular organization of tight and adherent junctions. The main transmembrane molecules mediating cellular contact at the tight junction are occludin and the endothelial claudins. Other transmembrane molecules with leukocyte trafficking functions include junctional adhesion molecules (JAMs) and the endothelial selective adhesion molecule (ESAM), both members of the immunoglobulin superfamily. These molecules bind to the cytoskeleton via first-order (ZO-1-3 and CASK) and second-order (cingulin, and JACOP) adaptor

demonstrated that occludin regulates epithelial cell differentiation [23].

Claudins

Claudins are a multigene family of more than 20 members forming TJ strands through homophilic claudin-claudin interactions, mediated by claudin's second extracellular loop [24]. These proteins share all four trans-membrane domains of occludin, but do not contain any sequence homology to occludin. Claudins are believed to be the major trans-membrane proteins of tight junctions, as occludin knockout mice are still capable of forming these inter-endothelial connections, while claudin knockout mice are nonviable [25–28]. Claudin-3, -5 and -12 are localized on the BBB [29], whereas the presence of claudin-1 seems to vary among species, though this has not been fully clarified [30]. New findings point to a promoter function for claudin-5 in promatrix metalloproteinase (MMP)-2 activation through a membrane-type matrix metalloproteinase. This new function described for claudin may be important in angiogenesis, and in disease processes with increased vessel permeability [31].

molecules. Signaling and regulatory proteins include MAGI-1-3, PAR3-6, ZONA-B, RGS5, AF6, and MUPP1 (details on these proteins are provided in the text). These adaptor/signaling proteins control interaction between the membranous component and the cytoskeleton. Contact in adherent junctions is established mainly through vascular endothelial cadherin (VE-cadherin) and platelet-endothelial cell adhesion molecule (PECAM), coupled to the cytoskeleton via catenins and/or desmoplakin

Other Junction Proteins

A third group of TJ-associated molecules recently identified include junctional adhesion molecules (JAMs) [32], and the endothelial selective adhesion molecule (ESAM or 1G8 antigen) [33]. These belong to the immunoglobulin (Ig) gene superfamily, and mediate homophilic and probably heterophilic interactions. They have a single transmembrane domain and the extracellular portion has two immunoglobulin-like loops that are formed by disulphide bonds. Three JAM-related proteins have been investigated in rodent brain sections. It has been observed that JAM-1 is expressed in endothelial and epithelial cells, whereas JAM-2 and JAM-3 are expressed in most vascular endothelial cells [34–36]. Investigators believe altered expression of JAMs, in addition to affecting tight junctional structure, may also affect leukocyte trafficking, with implications for immune status in CNS disease.

Carboxi-terminal cytoplasmic tails present in occludin, claudins and JAMs are linked to a number of first order cytoplasmic adaptor proteins such as zonula occludens -1 (ZO-1), ZO-2, ZO-3, and Ca²⁺-dependent protein serine kinase (CASK) [37–39]. ZO-1, ZO-2, and ZO-3 share three

defined core regions: (a) a SH3 domain important in signal transduction and in anchoring transmembrane TJs to cytoskeleton, (b) a guanylate kinase-like domain that catalyses ATP-dependent transformation of GMP to GDP, and (c) a PDZ-domain mediating specific binding to carboxy-terminal cytoplasmic ends of transmembrane proteins. Second order adaptor molecules include cingulin, afadin (AF6) and function-associated coiled-coil protein (JACOP). These two groups of adaptor proteins have sequence similarity with each other and belong to the membrane-associated guanylate kinase (MAGUK) protein family. Importantly, actin, the primary cytoskeleton protein binds to the carboxi-terminal of ZO-1 and ZO-2, a complex cross-linking trans-membrane elements, and thus providing structural support to ECs [38]. Adaptor proteins also interact with different signaling and regulatory molecules such as MAGI-1, MAGI-2, and MAGI-3, the partitioning defective proteins PAR-3 and PAR-6, MUPP-1, the binding protein ZONA B, and the regulator of G-protein signaling (RGS5), all of which control interactions between the membranous component and the actin/vinculin-based cytoskeleton [40-42]. Thus, modulation of TJ-associated proteins and cytoskeletal organization may be controlled through local chemical signals, thereby providing BBB permeability regulation.

Cell-cell interactions in the functional zone are also stabilized by AJs, typically found intermingled with TJs (Fig. 2). These junctions are composed of membrane protein cadherin joined to actin cytoskeleton via intermediary proteins named catenins forming adhesive contact between cells.

VE-Cadherin (cadherin-5)

Among AJs, the endothelial-specific integral protein VE-cadherin is linked to cytoskeleton via catenins. At the BBB, the cytoplasmic domain of cadherins binds to the sub-membrane plaque protein β - or γ -catenin, which is linked to actin cytoskeleton via α -catenin. The role of catenins in AJs bears resemblance to that of zonula occludens proteins in TJs. Recently, a new p120 catenin family was identified whose role remains controversial [43]. High affinity binding of p120 catenin to VE-cadherin suggests it may be engaged in vascular permeability regulation, thus affecting BBB function in some way. Recent in vitro and in vivo studies show that VE-cadherin is required for endothelial integrity in quiescent vessels and in organization of new vessels [44]. VE-cadherin may regulate EC function through different mechanisms: (a) activation of signaling molecules with a role in cytoskeleton organization; (b) transcription factor regulation; (c) formation of complexes with growth factor receptors, and modulation of their signaling [45]. In contrast to VE- cadherin, immunoreaction for N-cadherin indicated that this molecule is located abluminally. Thus, presumably VE-cadherin, which is located in interendothelial junctions promotes interaction between ECs, whereas N-cadherin may be responsible for anchorage to other cell types such as perycites or vascular smooth muscle cells [46].

PECAM-1

Platelet-endothelial cell adhesion molecule (PECAM), also known as CD31, is concentrated at the apical domain of the intercellular junction, and is not structurally associated with TJs [47]. PECAM-1 is involved in cell-cell adhesion through either homophilic interactions with other PECAM molecules or heterophilic interactions with other proteins, such as integrin $\alpha_{\rm v}\beta_3$ [48]. Recently, altered vascular permeability has been observed in PECAM-1 deficient mice [49], and PECAM-1 has shown an important role in monocyte transmigration through CNS endothelia [50]. During pathological insults, the BBB is capable of modulating its own cyto-architecture, increasing permeability while retaining structural integrity, and hence protecting the brain and maintaining homeostasis; however, this function may be lost under extreme conditions, causing TJs along the BBB to dissociate, which in turn leads to edema, decreased neuronal function and brain damage.

BBB Transport Systems

In addition to structural elements assuring BBB tightness, drug- and nutrients-metabolizing enzymes as well as transport systems provide additional barriers. These enzymes include γ -glutamyl transpeptidase (γ -GT), alkaline phosphatase (AP) aromatic acid decarboxylase, and several cytochrome 450 enzymes. They metabolize neuroactive bloodborne solutes and their concentration is significantly higher in cerebral microvessels compared to non-neuronal capillaries, endowing this dynamic interface with metabolic activity [1].

Nutrients and water-soluble compounds such as ions, amino acids, vitamins and proteins necessary for brain function possess specific transport systems embedded in BBB plasma membranes that allow entry into the brain. Various physiological transport processes are present at the BBB level [45, 51].

Carrier-Mediated Transport

Relies on molecular carriers present at both the apical (blood) and basolateral (brain) membranes of the BBB. These carriers tend to be highly stereospecific, and function in the selective transport of small molecules, such as hexoses, amino-acids, monocarboxylic acids, nucleosides, amines and vitamins [1]. Nutrient concentration gradients generally follow a direction from blood to brain, regulated according to CNS metabolic needs as well as by substrate concentration in plasma.

Ion Transporters

The sodium pump is localized in the abluminal membrane [52] and regulates sodium influx into the brain interstitial space in exchange for potassium. This pump maintains a high Na^+ gradient at the BBB, allowing Na^+ dependent transport to occur. The sodium–potassium-two chloride co transporter resides predominantly in the luminal BBB membrane [53]. Finally, the sodium-hydrogen exchanger is expressed in the luminal membrane, whereas the chloride-bicarbonate exchanger is expressed on each side. These two transporters play critical roles in regulating the intracellular pH of the endothelium.

Active Efflux

Efflux of molecules from ECs can be initiated at the luminal membrane, as in the case of ATP-binding cassette (ABC) transporters [54]. The multidrug resistance transporter P-glycoportein (P-gp) is an ATP-dependent efflux pump which prevents the passage of drugs and toxins across the BBB into the brain and may facilitate their transport from brain to blood [55]. First described in certain tumor cells that are protected against anticancer agents as a result of P-glycoprotein overexpression, it is now established that P-glycoprotein is expressed constitutively in many normal non-tumorous tissues [56, 57]. In addition to Pgp, several mutidrug resistance-associated proteins (MDRs) are expressed in brain microvessels, and are responsible for reducing the penetration of different drugs into the brain and increasing their efflux from the brain. Recent studies in rat and human brain tissue have shown that Pgp is expressed on both luminal and abluminal membranes as well as in perycites, microglia, and astrocytes [58]. The second efflux transport subfamily, which belongs to the ABC protein superfamily and can confer multidrug resistance is the MRP family. Thus far, the mammalian MRP family consists of nine proteins [59], and most cells appear to express multiple MRP family members. MRP1 and MRP5 appear to be ubiquitous and are both expressed at the BBB [60]. Similar to P-gp, MRP6 is also expressed on BBB endothelium and upregulated in response to glial signals [61].

Receptor Mediated Transport

BBB ECs express several transport systems for neuroactive peptides such as arginine-vasopressin, enkephalins, luteinizing-hormone-releasing hormone, and some cytokines and chemokines. Influx of large proteins into the brain, such as transferrin, low density lipoprotein (LDL), IgG, insulin and insulin growth factor occurs through a transcellular receptor-mediated transport mechanism known as transcytosis [1]. A circulating ligand interacts with a specific receptor at the apical plasma membrane of the ECs. Once bound to ligand, the process of endocytosis is initiated, with receptor-ligand complexes forming intracellular vesicles [62]. During transcytosis these vesicles travel to the basolateral side of the polarized endothelial cell, where they are released.

Caveolae are vesicular invaginations of the plasma membrane 50- to 100-nm in size involved in molecular transport, cell adhesion, and signal transduction [63]. Caveolin, a 21- to 24-kDa protein, is the principal structural component of caveolae, and three caveolin genes (caveolin-1, -2, and -3) have been identified. Endothelial cells are known to express the highest levels of caveolin-1 [64]. Moreover, caveolin-1 and -2 are found in rat microvessels, and caveolin-1 is expressed in the human BBB [65]. Transcytosis is one of the first functional roles proposed for caveolae. Molecules such as albumin and insulin are known to undergo endothelial transcytosis in peripheral tissue, perhaps through different subsets of caveolae [64]. Caveolar membranes contain receptors for transferring, insulin, albumin, ceruloplasmin, RAGE, LDL, HDL, IL-1 and vesicle-associated membrane protein-2 [15].

In order to exploit endogenous receptor mediated transport systems at the BBB for drug delivery, different molecules that normally do not cross the BBB can be conjugated to a molecule with capability of targeting receptor mediated transport. These molecules could be either natural or artificial ligands, such as monoclonal antibodies or peptides [51], which can in turn be used to carry conjugated neuro-therapeutic substances across the BBB [66]. Classical examples of receptors involved in receptor mediated transports are: the insulin receptor, the transferrin receptor, and the transporters for low-density lipoprotein and insulin-like growth factors [51, 67, 68].

Absorptive Mediated Endocytosis

While receptor-mediated transcytosis systems require binding of a ligand to a specific receptor, absorptive mediated endocytosis is initiated by polycathionic molecules binding to negative charges on the plasma membrane. This process lacks specific targeting and may lead to widespread absorption [69].

Astrocytes

Among the glial cells of the CNS, the role of astrocytes remained enigmatic. In the late 1980s, experiments

demonstrating astrocytes expressed voltage-gated channels and neurotransmitter receptors generated interest in these cells as potential participants in intercellular communication. However, only recently have certain astrocyte functions been revealed, these include the control of cerebral vascular tone and of synapse formation and function, and adult neurogenesis. Astrocytes show a number of different morphologies, depending on their location and association with other cell types. Of the 11 distinct phenotypes distinguished, 8 involved specific interactions with blood vessels. Evidence from cell culture studies indicate astrocytes upregulate many BBB features, leading to tighter TJs, expression as well as polarized distribution of transporters, and of specialized enzyme systems [70–74].

Ninety percent of the abluminal surface of cerebral microvasculature endothelium is ensheathed by astrocytic end-feet, which play an essential role in determining different BBB features. These specialized structures show high density of purinergic P2Y receptors, of potassium channel Kir4.1, and of water-channel protein aquaporin-4 (AQP4), indicating key roles in gliovascular signaling and in regulation of brain water and electrolyte metabolism under normal and pathological conditions [75].

AQP4 is a type III transmembrane protein regulating water entry to and from multiple types of tissue epithelia, but it also has a critical role when expressed by astrocytes, which regulate water and ion movement in the brain. AQP4 mRNA riboprobe revealed a remarkable prevalence of AQP4 in multiple periventricular areas. These include the dorsal hypothalamic area, the dorsomedial hypothalamic nucleus, and the suprachiasmatic nucleus lining the third ventricle, the paraventricular thalamic nucleus and subfornical organ lining the dorsal third ventricle. In addition, strong AQP4 hybridization signal was found in the most dorsal part of the lateral ventricle, in the dorsal raphe contacting the aqueduct, and in the choroid plexus of the lateral ventricles [76, 77]. Interestingly, the strongest hybridization signal was observed at the pial surface, where the brain is in contact with the CSF in the subarachnoid space. This preferential location of AQP4 mRNAexpressing cells in periventricular areas is reminiscent of that seen for the atrial natriuretic peptide, suggesting that the presence of AQP4 channels in these nuclei may be of critical importance in detecting alterations in CSF homeostasis preceding neurosecretory processes [77]. In addition, it is worthy to note the co-localization of AQP4 with the inward-transporting potassium channel Kir4.1 in astrocytes at the BBB interface, suggesting a functional relationship between both proteins (Fig. 3). It has been suggested that the presence of a water channel could facilitate excess K+ clearance, generated during high neuronal activity [78, 79]. Supporting this hypothesis, mice with reduced perivascular expression of AQP4, show



Fig. 3 Astroglial-endothelial signaling interactions. The BBB is formed by endothelial cells surrounded by basal membrane, and astrocytic perivascular endfeet. Astrocytes are strongly implicated in induction of certain BBB characteristics such as tighter TJs, specialized enzyme systems, and polarized transporter localization (1). In addition they also play key roles in gliovascular signaling and in the regulation of brain water and electrolyte metabolism under normal and pathological conditions (2). *GDNF* Glial cell line-derived neurotrophic factor, *IL-6* Interleukin-6, *bFGF* basic fibroblast growth factor, *TGF-β1* transforming growth factor β 1, *A1* angiopoietin, *LIF* Leukemia inhibitory factor, γGT γ -glutamil transpeptidase, *AAD* aromatic acid decarboxylase. *AP* alkaline phosphatase; Aquaporin-4; ∞ Agrin; \bigotimes potassium channel Kir4.1

alterations in K+ homeostasis with delayed clearance after neuronal stimulation [80].

Astrocytes are also strongly implicated in induction of other BBB characteristics such as tighter TJs, specialized enzyme systems, and polarized localization of transporters [72, 73, 81-83] (Fig. 3). Using heterologous culture, and allowing only astrocytic end-feet to contact umbilical vein endothelial cells, Hayashi and co-workers showed that a number of specific BBB markers such as glucose transporters, transferrin receptor (TfR), y-glutamil transpeptidase, and P-glycoprotein undergo transcription upregulation [72]. Interestingly, astrocytic end-feet membranes show unique aggregates of intramembrane particles packed in orthogonal arrays (OAPs) developed in parallel with endothelial TJs [84]. When the BBB breaks down, this high number of orthogonal particles in end-feet membranes is greatly reduced or even absent [85]. Such observations suggest a specific role for these particles in astrocyte/ endothelium interactions, particularly during BBB development. Interestingly, OAPs and AQP4 correlate with the expression of agrin, a heparin sulfate proteoglycan of the basal lamina [86, 87]. Agrin accumulates in brain microvessels at the time of BBB tightening, and is required for the segregation of AQP4 to perivascular astrocytic end-feet, a process mediated by agrin binding to α -dystroglycan [75].

Moreover, other culture systems have shown that transplanted astrocytes induce BBB properties in non-neural vascular ECs, indicating that astrocytes represent a major source of the neural tissue inductive influence [88]. Finally, selective elimination of reactive astrocytes using suicide gene strategies causes BBB disruption, inhibiting its repair [89]. There is still debate about the factors involved in this differentiation, but it is likely they are multiple, involving some that are soluble and others depending on cell-to-cell contact [90]. Several molecules, e.g., transforming growth factor- β 1 (TGF β 1), glial cell line-derived neurotrophic factor (GDNF), basic fibroblast growth factor (bFGF) and interleukin-6 (IL-6), and angiopoietin 1 (Ang-1), have all been associated with the regulation of different aspects of BBB phenotype. For example, studies in mice lacking or over-expressing ang-1 have revealed that ang-1 is responsible for recruiting and sustaining periendothelial support cells and for contributing to the impermeability of blood vessels [91]. The secretion of ang-1 from perivascular astrocytes can bind its receptor Tie-2 onto endothelial cells. On the other hand, endothelial cells can also modulate astrocyte phenotype by secreting growth factors, such as the leukemia inhibitory factor [71]. In addition, endothelial cells, pericytes and astrocytes further contribute to extracellular matrix structure, which in turn influences EC differentiation [71].

Perycites

Perycites are vascular cells adjacent to capillaries that share a common basement membrane with endothelial cells, and have many cytoplasmic processes encircling capillaries. The lineage and identity of perycites is still not fully characterized. These cells seem to be morphologically, biochemically and physiologically heterogeneous [92]. They express non-muscle actins and they also contain α -smooth muscle actin which is characteristic of vascular smooth muscle cells. Perycite to endothelia ratio in the brain is 30-fold higher compared to that of striated muscles [93]. Through long cytoplasmic processes that extend over and encircle the endothelial tube, pervcites make focal contact with ECs through specialized junctions [94]. It is believed that recruitment and further interaction of perycites along the microvascular endothelial wall are essential for the formation, maturation, and maintenance of normal microvascular structure and function. In the CNS perycites contribute to microvessel stability covering a major part of the abluminal endothelial surface [94]. In addition, they influence vessel stability through matrix deposition and activating signals promoting ECs differentiation [95]. Their distribution and degree of coverage of the vascular endothelium vary among different vessel types. During embryonic angiogenesis, PDGF- β produced by ECs appears to be critical in recruitment pervcites to the forming blood vessels. Thus, PDGF- β deficient mutant mice develop defective capillary endothelial structures. These abnormalities contribute to structural instability of the capillary wall leading to microvascular hemorrhage and other vascular damage [96, 97]. On the other hand, perycites release different growth factors and angiogenic molecules which regulate microvascular permeability, remodeling and angiogenesis (e.g., TGF- β , ang-1 and 2, PDGF, and sphingosine-1 phosphate; [98]). Thus, the active form of TGF- β 1 secreted from perycites appears to at least partially mediate perycite effects on actin expression and organization on ECs [99, 100]. Perycites migrate away from brain microvessels in response to hypoxia [101] or brain trauma [102], conditions associated with increased BBB permeability and disorganization of actin filaments in ECs. A lack of perycites results in endothelial hyperplasia and abnormal vascular morphogenesis in the brain. Moreover, rich expression of the contractile protein α -smooth muscle actin in perycites associated with brain capillaries suggests perycites may also control blood flow [92, 103], functioning similarly to vascular smooth muscle cells in arterioles and small pial arteries in the brain, which regulate cerebral blood flow responses [104]. Some BBB perycites might be of macrophage lineage, possessing capacity to phagocytize exogenous proteins and present antigens [105].

Basement Membrane Matrix

The basement membrane separates ECs from neighboring cells, namely perycites and astrocytes. It is composed of different extracellular matrix (ECM) structural proteins such as collagen, fibronectin, heparan sulfate, proteoglycans, chondroitin sulfate proteoglycans and laminin. Matrix adhesion receptors are expressed on vascular cells, neurons, and supporting glial cells (i.e., astrocyte end feet and microglia; [106]). Integrins play a key role in mediating endothelial signaling, cell migration and brain capillary formation during angiogenesis [107]. Growth factors such as vascular endothelial growth factor are bound to ECM proteins and can be activated in situ by MMPs [108]. Disruption of the ECM is strongly associated with increased BBB permeability in pathological states, such as brain tumors and cerebral ischemia [109, 110].

Microglia Cells

In addition to astrocytes and perycites, the development and maintenance of the BBB probably involves other cell populations. Another cell type in close contact with cerebral blood vessels is the cerebral perivascular macrophage, also referred to as perivascular cell, or perivascular microglia. This cell occupies a strategic position in the BBB allowing control of innate and adaptive immune responses in the brain. Microglial cells derive from leptomeningeal mesenchymal cells, which transform into microglia on entry into the brain [111]. Circulating monocytes provide another important source of microglia in the brain [112]. Studies in rodents and humans have shown that these cells are bone marrow derived and regularly replaced by monocytic precursor cells, therefore representing tissue macrophages of the brain [113]. Indeed, perivascular macrophages are recognized by markers for peripheral macrophages, confirming their origin from monocyte lineage [114]. Recent studies have shown that non-contact culture of confluent brain capillary ECs with human blood-derived macrophages, substantially decreases paracellular permeability, indicating an active role of these cells in BBB physiology [115]. In addition, perivascular microglia in the human brain express molecules involved in antigen recognition, antigen presentation and co-stimulation, supporting a possible role for these cells in perivascular inflammation regulation in the human CNS [116]. This link between microglia in the brain, circulating monocytes, and bone marrow cells has changed our preconception of the brain as an immune privileged site.

Concluding Remarks and Future Perspectives

Knowledge of BBB biology has advanced significantly in recent years. Application of modern molecular and cell biology techniques, together with traditional structural studies, enables us to appreciate the BBB not only as a static anatomical barrier, but also as a highly complex and metabolically active bi-directional interface. Nevertheless, several key questions related both to physiology and pathology of the BBB remain unanswered. Challenges for the future include, understanding crosstalk between glial cells, vessel cells (such as endothelial cells and perycites) and neurons. Better knowledge of human BBB transport systems is essential in order to translate findings from animal models or tissue culture systems to humans. Also, better ways of imaging and monitoring functions of in vivo barrier activity will be need in the future. Finally, better understanding of cellular proteomics and metabolism will have to be devised before BBB-targeted therapies can be developed. Over the coming years, emerging information may help to understand the role of the BBB in the pathogenesis of different neurological diseases. Early treatment of barrier dysfunction could reduce neuropathological symptom severity and facilitate recovery. Future studies should therefore explore the translational potential of different approaches currently at the preclinical development level. Overall, understanding the structure and physiology

of the BBB will open new future directions for diagnosis and therapy of several neurological disorders.

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