REVIEW

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Occludin: a gatekeeper of brain Infection by HIV-1

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Abstract

Compromised structure and function of the blood-brain barrier (BBB) is one of the pathological hallmarks of brain infection by HIV-1. BBB damage during HIV-1 infection has been associated with modified expression of tight junction (TJ) proteins, including occludin. Recent evidence indicated occludin as a redox-sensitive, multifunctional protein that can act as both an NADH oxidase and influence cellular metabolism through AMPK kinase. One of the newly identified functions of occludin is its involvement in regulating HIV-1 infection. Studies suggest that occludin expression levels and the rate of HIV-1 infection share a reverse, bidirectional relationship; however, the mechanisms of this relationship are unclear. In this review, we describe the pathways involved in the regulation of HIV-1 infection by occludin. We propose that occludin may serve as a potential therapeutic target to control HIV-1 infection and to improve the lives of people living with HIV-1.

Keywords Occludin, HIV, Blood brain barrier, Virus

Introduction

Human immunodeficiency virus (HIV-1) infection leads to a weakened immune system, causing people living with HIV-1 (PLH) to become susceptible to other pathogens. When the immune system becomes ineffective, an individual may develop acquired immunodeficiency syndrome (AIDS). In 2022, ~39 million people were living with HIV-1 and approximately 630,000 individuals had AIDS-related deaths. Since the start of the HIV-1 epidemic, tens of millions of people have died from HIV-1 and AIDS-related complications [1]. Due to the development of antiretroviral therapy (ART) in 1996, HIV-1

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infection is now classified as a chronic, rather than fatal, disease, and the majority of affected individuals have manageable infections without AIDS development [1-3].

Early after infection, HIV-1 enters the central nervous system (CNS) [4] (Fig. 1A). While the mechanisms of this process are still not fully understood, the most likely is a "Trojan horse" mechanism via HIV-1 infected monocytes or T-cells, which act as carriers, allowing the virus to pass the blood-brain barrier (BBB) and infect cells of the CNS. Among the CNS cells, microglial cells, perivascular macrophages, astrocytes, and pericytes have been identified as possible reservoirs for HIV-1 [5-10]. Although the use of ART suppresses the replication of the HIV-1 virus, the main limitations of this therapy arise due to limited ability to effectively bypass the BBB. In addition, antiretroviral drugs are being transported out of the brain parenchyma by transporter systems. This inability of ART to accumulate in the CNS contributes to HIV-1 infection in the brain, the formation of viral reservoirs.



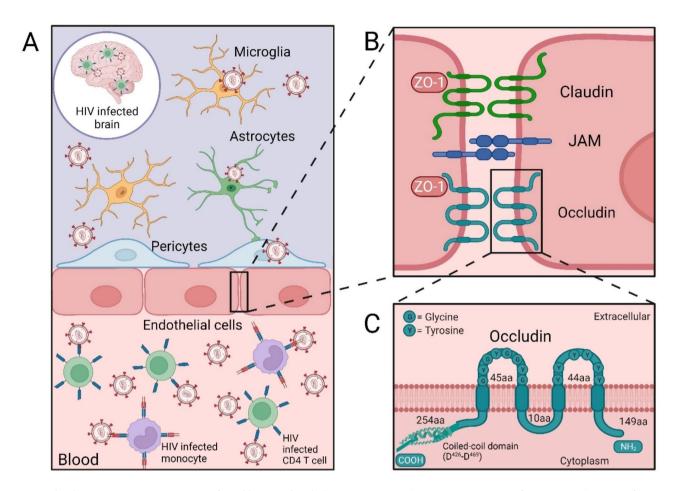


Fig. 1 Blood Brain Barrier (BBB) in HIV-1 infected brain and occludin structure. (A) Schematic representation of CNS invasion by HIV-1. After infecting leukocytes in the blood (monocytes and T-cells), HIV-1 can cross the BBB via the Trojan horse mechanism and infect various CNS cells, such as astrocytes, pericytes, and microglia cells. Moreover, brain infection by HIV-1 is associated with a disruption of the BBB integrity by altering tight junction (TJ) protein expression and function. (B) Schematic representation of the TJs formed by transmembrane proteins (e.g., occludin, claudins, and junctional adhesion molecules [JAM]). (C) Schematic representation of occludin structure, showing the domains and phosphorylation residues

and the development of cerebrovascular comorbidities [11, 12].

Formed by endothelial cells (EC), astrocytes, neurons, pericytes and microglia cells, the BBB forms a highly specialized barrier that selectively divides the brain parenchyma from the systemic blood circulation [13]. One of the main structural features of the BBB is the presence of tight junctions (TJs) formed by transmembrane proteins, such as occludin, junctional adhesion molecules (JAMs), and claudins (Fig. 1B) that interact with TJ-associated proteins, such as the scaffolding proteins zonula occludens (ZO) 1 or 2. During HIV-1 infection, structural modifications of the BBB have been associated with changes in the expression of TJ proteins. Recently, occludin has attained additional importance, not only for its role in maintaining the integrity of TJs, but also for its influence on cellular metabolism and regulation of HIV-1 infection [10, 14–16].

Occludin structure

Occludin was the first transmembrane TJ protein identified [17]. Occludin is a member of the TJ-associated-MARVEL (Myelin/lymphocyte And Related proteins for VEsicle trafficking and membrane Link) proteins (TAMPs) family of TJ proteins containing a MARVELmotif which consists of four transmembrane helices [18, 19]. Occludin is known as MARVEL D1, and additional proteins in this family are MARVEL D2 (tricellulin) and MARVEL D3 [20, 21]. Studies propose that the MAR-VEL motif may be responsible for occludin dimerization and localization to the basolateral membrane [18]. Although the MARVEL proteins have not been found to be essential to TJ formation, they appear to be important for maintaining the permeability properties of the BBB [22]. Although usually classified as being important to TJ assembly, function, and regulation, its various roles in cellular activities are unclear. For example, occludin-deficient mice maintain normal paracellular permeability and normal TJs [23]. Occludin is a 65-kDa integral plasma

membrane protein containing 522 amino acids (aa) [17, 24]; however, there is evidence of additional isoforms formed by alternative splicing [25]. Occludin exhibits distinct domains: (a) a long C-terminal cytoplasmic domain (257 aa); (b) four transmembrane domains, including TM1 (23 aa), TM2 (25 aa), TM3 (25 aa), and TM4 (22 aa); (c) two extracellular loops, EL1 (46 aa), which is enhanced with tyrosine and glycine residues, and EL2 (48 aa), which includes two cysteines; (d) one intracellular loop (10 aa); and (e) a short N-terminal cytoplasmic domain (66 aa) [16, 21] (Fig. 1C). The long C-terminal domain accounting for almost 50% of its weight and which ends in the coiled coil, structurally distinguishes occludin from claudins. The N- and C-terminal regions are locations for key occludin phosphorylation residues and provide the functional variability of occludin at TJs [26]. The N-terminal domain bears a Type I WW binding motif (PPXY) and interacts with ITCH, an E3 ubiquitin protein ligase [27]. Modifications near the N-terminus affect TJ localization [28] and barrier properties [29]. The C-terminal domain contains an α -helical coiled-coil structure of approximately 426-469 aa, interacting as a dimerized four-helical bundle. This structure allows one occludin molecule to interact with another and establishes specific interactions with other regulatory proteins. Reportedly, C-terminal interactions with regulatory molecules play an important role in TJ assembly and function [30]. Despite some in vitro evidence indicating occludin N-terminal phosphorylation [31], more evidence supports the existence of C-terminal phosphorylation [26].

Cells and organs expressing occludin

Occludin is ubiquitously expressed; however, it is present in various amounts in different tissues and cells. For example, a mouse study showed that occludin mRNA is expressed at similar levels in the duodenum, ileum, liver, and lung, with lower amounts in the brain, and higher amounts in the colon. Protein and mRNA expression levels were found to be mostly consistent across tissues, except that kidney cells produced significantly lower levels of occludin than other organs, including the brain [32]. In the human brain, elevated occludin expression in astrocytes, oligodendrocytes, and cerebral cortex pyramidal neurons was detected in both Alzheimer's disease and vascular dementia [33]. Occludin levels were found to be inducible by TNF- α treatments in a variety of cell types [34, 35], suggesting the existence of common molecular pathways for occludin upregulation upon inflammatory stimuli. Additionally, a high degree of homology in occludin was reported across animal species [21]. Examples of other cell types expressing occludin include mouse hepatocytes [36] and activated T-lymphocytes [37]. A lowlevel mRNA occludin expression was also detected in HEK293 cells [38].

Regarding the BBB, occludin is expressed primarily in brain endothelial cells. Moreover, occludin expression was found to be enhanced in mouse brain endothelial cells when cocultured with resting microglia [39, 40]. Similarly, occludin levels were significantly increased in cocultures of rat endothelial cells with astrocytes [41]. Occludin is also expressed in mouse astrocytes and neurons, in addition to epithelial and endothelial tissue [42]. Several studies have shown that human brain pericytes express occludin [6, 9, 14, 43]. In addition, rat pericytes induce the expression of occludin through the release of angiopoietin via the pericyte-derived multimeric angiopoietin-1/Tie-2 pathway [39]. Taken together, occludin expression shares significant relationships among cells from various tissues, including the cells composing the BBB.

Occludin and HIV-1 Infection

Impairment in TJ expression levels and damage to BBB permeability are associated with infection by a variety of viruses, such as Zika virus [44], human T-cell leukemia virus (HTLV-1) [45], mouse adenovirus type 1 (MAV-1) [46], and HIV. Besides its role in maintaining BBB integrity, occludin has also been characterized to play important roles in the entry and progression of several viral infections. In influenza/H1N1 [47] and HIV [14] infections, a decrease in occludin levels has been shown to increase infection. On the other hand, the opposite effect has been observed in Hepatitis C infection, where occludin was demonstrated to be an essential factor for viral entry and allowing cells to be infected [48–50]. In this review we will focus on the role of occludin in HIV infection.

Recent evidence indicates a bidirectional connection between HIV-1 infection and changes in occludin protein expression levels, pointing to occludin as a critical regulator in HIV-1 infection [14]. In this regard, the effect of the HIV-1 transactivator protein (Tat), which recruits elongation factors for RNA polymerase II, has been shown to decrease occludin expression levels in human endothelial cells [51–53]. Additional studies have used transgenic rats to demonstrate that HIV-1 proteins decrease occludin levels in the hippocampus and in epithelial cells [54, 55]. In human brain pericytes, a dual-stage response pattern has been identified, characterized by a significantly decreased occludin expression in pericytes 48 h post-infection, i.e., at the peak of active infection in these cells, followed by subsequent increased occludin levels during the development of latent infection [7, 9, 14]. The involvement of occludin in the regulation of HIV-1 replication has been confirmed in human monocytic U-937 cells, human macrophages, and HEK 293 cells [14]. To illustrate this effect, occludin silencing resulted in a 75% and 250% increase in HIV-1

replication in human primary macrophages and differentiated monocytic U937 cells, respectively [56]. In contrast, occludin overexpression in HIV-infected human brain pericytes decreased the rate of HIV-1 infection as measured by p24 levels by approximately 50% [9].

The findings reported above suggest that occludin may be a potential target for preventative and pharmacological intervention aimed to eliminate viral reservoirs in PLH. In addition, this data raises the prospect that patients with inflammatory diseases with lower occludin expression may be more susceptible to HIV-1 infection. However, the mechanisms involved in the regulatory interaction between occludin and HIV-1 infection remain largely unknown. At present, two complementary molecular pathways of occludin regulating HIV-1 infection have been identified in human brain pericytes. They include (a) the regulation of the SIRT1 expression by modulation of NAD+and (b) modulation of the antiviral 2'-5'-oligoadenylate synthetase (OAS) gene family through STAT-1 signaling pathway [14, 56, 57] (Fig. 2).

Occludin regulation of HIV-1 Infection through the SIRT1 pathway

SIRT1 is a highly conserved, nicotinamide adenine dinucleotide-dependent class III histone deacetylase [58]. The SIRT1 enzyme deacetylates histone proteins at H3K9, H3K14, H4K16 [59], and H1K26 [60] to control chromatin formation [61]. SIRT1 also deacetylates other proteins [62], with the subsequent modulation of their activity [63]. Examples of such proteins include p53 [62],

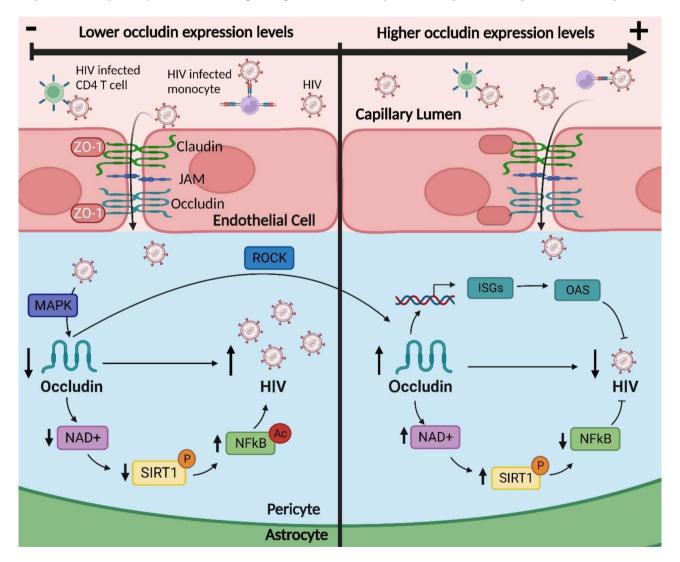


Fig. 2 HIV-1 infection in human brain pericytes under low (left panel) and high (right panel) occludin levels. A decrease in occludin leads to NAD + depletion, decreasing SIRT1 phosphorylation and increasing NF-κB acetylation, which leads to an increase in HIV-1 replication. In contrast, elevated occludin levels act as an HIV-1 inhibitor by increasing NAD+, following with an increase in phosphorylation of SIRT1 and a decrease in NF-κB acetylation. Moreover, elevated occludin levels increase the expression of interferon-stimulates genes (ISGs) such as the antiviral OAS gene family which degrades viral RNA and provides antiviral protection

the RelA/p65 subunit of nuclear factor kappa-light-chain enhancer of activated B cells (NF- κ B) [61], forkhead box O transcription factors O4 (FOXO4) [64], O3 (FOXO3) [59], O1 (FOXO1) [65], peroxisome proliferator-activated receptor-γ coactivator-1 alpha (PGC-1α) [66], PGC-1β [67], BMAL1:CLOCK heterodimer [59], and endothelial NOS (eNOS) [68]. SIRT1 also regulates genes related to mitochondrial uncoupling protein 2 (UCP2) [69]. SIRT1 activity decreases PI3K-AKT signaling [70], while increasing AKT-glycogen synthase 3 (GSK3) signaling pathway [71]. Interestingly, SIRT1 can induce AKT activity, while AKT activity may be inhibited by SIRT3/6 [72]. Finally, SIRT1 represses peroxisome proliferator-activated coreceptor gamma (PPAR- γ) transcription [73, 74] and regulates androgen and estrogen receptor responses [75].

SIRT-1 works in concert with AMP-activated protein kinase (AMPK), and it has been reported that occludin levels promote AMPK expression and activation in human pericytes [56]. A study from our laboratory on human brain pericytes showed that occludin, acting as a NADH oxidase, can regulate SIRT1 activity, which influences HIV-1 transcription [14]. Specifically, we identified that occludin has a putative NADH binding site in a pocket formed by complementation of the CC-domain binding site, and can convert NADH to NAD⁺. This process is enhanced upon occludin overexpression and its importance stems from the fact that NAD⁺ is a cofactor regulating SIRT1 activity, which can deacetylate (and thus inactivate) NF-κB, an important stimulator of HIV-1 transcription (Fig. 2). The opposite processes occur when occludin is depleted, which results in a decrease in NAD+levels, decreased p-Ser47 phosphorylation of SIRT1, diminished SIRT1 activity, and enhanced activity of NF-κB, which drives HIV-1 transcription [14] (Fig. 2). Indeed, phosphorylation of Ser²⁷ emerged as central to SIRT1-based activation mechanisms [76], and also correlated with AMPK activation [77]. In support of the described mechanisms, it was reported that HIV-1 Tat protein can decrease NAD+levels, leading to the deactivation of SIRT1 and the activation of p53 [78]. Moreover, SIRT1 downregulation was linked to increased astrocyte NF-KB activation through Tat upregulation of microR-NAs miR-34a and miR-138 [79] and increased levels of SIRT1 functioned as an inhibitor to Tat by upregulating AMPK [80]. Interestingly, higher SIRT1 levels were detected after treatment with anti-HIV integrase transfer inhibitors [81]. It was also demonstrated that the SIRT1 inhibition leads to inflammatory responses in T cells via hyperactivation of NF-KB [82]. SIRT1 can reduce the expression of occludin by impairing the recovery of occludin expression in human brain pericytes [14]. Indeed, SIRT1 overexpression was consistently found to negatively regulate occludin expression in several cell types [83, 84].

Occludin modulation of HIV-1 replication through STAT-1 molecular pathway

Recently, another study has identified a novel regulatory pathway involving occludin as a regulator of the STAT-1 pathway. The Janus kinase/signal transducer and activator of transcription (JAK/STAT) signaling pathway is a membrane-nucleus signaling involved in the transduction of antiviral genes such as the OAS gene family [85]. After being phosphorylated by the receptor-associated kinases, the STAT family members assemble into homoor heterodimers that translocate to the nucleus [86]. In the context of HIV-1 infection, STAT-1 was shown to regulate HIV-1 promoter activity and was implicated in the immunopathogenesis of HIV-1 infection and its inflammatory responses [87-90]. Studies have reported that the JAK/STAT signaling pathway could be inhibited by HIV-1 viral gene products, which involve Vif, Vpu, Nef, and Tat, in order to avoid the immune system; however, HIV-1 infection increases STAT-1 expression and overall phosphorylation [88, 91–94].

We reported that occludin levels directly influence the expression of the antiviral interferon stimulated genes (ISGs), such as the OAS genes in human brain pericytes, by regulation of the JAK/STAT-1 molecular pathway. Indeed, overexpression of occludin markedly elevated mRNA levels of ISGs genes such as OAS1, OAS2, OAS3 and OASL, with subsequent protein upregulation and a decrease in HIV replication. Moreover, silencing of occludin (but not silencing of ZO-1) induced an opposing impact, highlighting the importance of occludin in the innate immune regulation to provide antiviral protection [57].

Occludin phosphorylation as a possible target for HIV-1 Infection in the brain

The occludin function as a BBB structural protein is regulated by phosphorylation processes [95]. Because altering occludin phosphorylation can trigger TJ assembly or disassembly, there is likely a delicate balance between kinase and phosphatase activities acting on occludin. Several protein kinases (PKs) were shown to alter the occludin phosphorylation. Specifically, serine, threonine, and tyrosine occludin residues have been recognized as phosphorylation sites for these kinases [96, 97]. Table 1 summarizes the locations of phosphorylation sites and the kinases that have been identified to modify occludin phosphorylation status. Interestingly, the modification of occludin phosphorylation determines its dimerization and membrane location [98].

Table 1 Occludin phosphorylation sites

Kinase	Phosphorylation Site	Model	Mutational analysis	Physiological changes	Refer- ences
c-Src	Tyr ³⁹⁸ , Tyr ⁴⁰² ,	Rat-1, MDCK (Cell culture	Yes	Regulation of ZO-1, -2, -3.	[99– 101]
	Tyr ⁴⁷³	MDCK (Cell culture)	No	p85a recruitment.	[102]
CK2	Thr ⁴⁰⁰ , Thr ⁴⁰⁴ , Ser ⁴⁰⁸	Caco-2, MDCK (Cell culture)	Yes	CK2-mediated barrier regulation. Regulation of ZO-2.	[103] [104]
	Thr ³⁷⁵ , Ser ³⁷⁹	Xenopus laevis	Yes	-	[105]
сРКС	Ser ³³⁸	MDCK (Cell culture)	No		[106]
	Ser ⁴⁹⁰	BREC (in vivo)	No	Inhibits TJ trafficking	[107]
nPKCη	Thr ⁴⁰³ , Thr ⁴⁰⁴ , Thr ⁴³⁸	Caco-2, MDCK (Cell culture)	Yes	Delays assembly at the TJs	[108, 109]
аРКСζ	Thr ⁴²⁴ , Thr ⁴³⁸ , Thr ⁴⁰³ , Thr ⁴⁰⁴	Rat-1, MDCK, Caco-2 (Cell culture)	Yes	Delays assembly at the TJs	[110] [108]
ROCK	Thr ³⁸² , Ser ⁵⁰⁷	COS-7 (Cell culture), BMEC (in vivo)	No		[111]
VEGF	Ser ⁴⁹⁰	BREC (Cell culture)	Yes	Inhibits TJ trafficking	[112]

Abbreviations. Ser, serine; Thr, threonine; Tyr, tyrosine; c-Src, cellular tyrosine-protein kinase Src; CK2, casein protein kinase 2; cPKC, conventional protein kinase C; nPKC, novel protein kinase C; aPKC, atypical protein kinase C; VEGF, vascular endothelial growth factor; ROCK, Rho-associated protein kinase; MDCK, Madin Darby canine kidney cells; Caco-2, human colorectal epithelial adenocarcinoma cells; T84, human colon carcinoma cells; BMEC, brain microvascular endothelial cell; BREC, regulatory B cell; COS-7, African green monkey kidney cells (SV40 transformed)

Src kinases in occludin phosphorylation and HIV-1 Infection

Src kinases are known regulators of occludin phosphorylation (Fig. 3) [28]. For example, c-Src was shown to phosphorylate tyrosine^{398/402,473} on the C-terminus of occludin [99, 101, 102]. Another member of this family of Src kinases is c-Yes, which can also phosphorylate occludin. c-Yes inhibition can lead to occludin redistribution in the cell membranes and altered membrane permeability [113, 114]. Interestingly, some studies reported that c-Src-kinase can regulate HIV-1 infection of immature monocyte-derived dendritic cells [115]. In contrast, other studies have suggested that c-Src activation in HIV-1 infection can prevent early CD4 T-cells infection [116]. An association between the extracellular vesicle-associated c-Src and an increase in latent HIV-1 activation via the PI3K/AKT/mTOR pathway in monocytes and T cells was recently reported [117].

PKC kinases in occludin phosphorylation and HIV-1 Infection

Various PKC isoforms can participate in occludin phosphorylation (Fig. 3) [118, 119]. Occludin Ser³³⁸ has been identified as a potential phosphorylation site for these kinases [106, 120]. PKC α , which can phosphorylate this residue, can also regulate occludin expression [121–123]. In addition, PKC β activation can also induce occludin phosphorylation [124]. Of the novel PKCs, PKC η targets Thr^{403,404,438} occludin residues. Phosphorylation of more of these target residues increases the presence of occludin in cells membranes [108, 109, 125]. Furthermore, PKC ϵ -mediated phosphorylation can dissociate

the ZO-1-occludin complex, thereby disrupting TJ complexes [126]. Atypical PKC ζ has also been associated with phosphorylation of occludin and its subsequent reorganization. PKC ζ is believed to phosphorylate occludin Thr^{403,404,424,438} residues [108, 110, 127–129].

Interestingly, PKC modulators were being studied to eliminate HIV-infected cells by reactivating latent HIV-1, and then destroying it in an approach named "shock and kill". Unfortunately, these approaches were not fully successful. While PKC agonists can function as latency-reversing agents to reactivate the virus, they increase cellular resilience to apoptosis [130]. Furthermore, modulators of PKC activation, such as phorbol myristate acetate, can result in the nuclear translocation of NF- κ B and enhanced HIV-1 transcription via activation of the HIV-1 long terminal repeat (LTR) [131, 132].

Rho and ROCK signaling in occludin phosphorylation and HIV-1 Infection

The Rho–ROCK signaling pathway is formed by Rho GTPase and its downstream effector, Rho-associated kinase (ROCK). The ROCK family contains two isoforms, ROCK1 and ROCK2. The Rho GTPase family contains three subfamilies, Rho (RhoA, RhoB, and RhoC), Rac (Rac1, Rac2, and Rac3), and cell division cycle 42 (Cdc42). Active GTPases are bound to GTP and associated with cell proliferation [133]. Several studies have shown the critical role of the Rho–ROCK pathway in modulating TJs [134–138], including phosphorylation of occludin (Fig. 3) [139]. In mice, occludin residues Thr³⁸² and

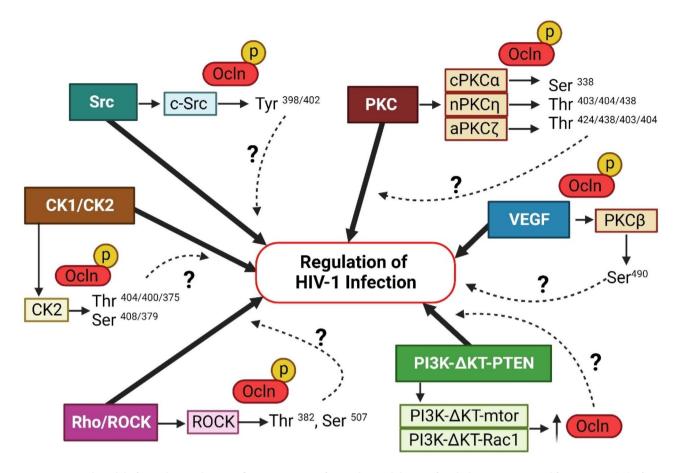


Fig. 3 Proposed model of signaling pathways influencing HIV-1 infection by modulation of occludin expression and function. Occludin functions are regulated by phosphorylation processes. Src, PKC, Rho-ROCK, VEGF, and PI3K-AKT-PTEN kinases can both alter occludin phosphorylation status and influence HIV-1 infection in several cell types. We propose that occludin phosphorylation may serve as one of the targets to modulate HIV-1 infection

Ser⁵⁰⁷ were the target sites of GST–ROCK [111]. Also, ROCK signaling caused re-localization and regulation [140] [141] of occludin, which suggests that inhibiting the RhoA–ROCK2 pathway can reverse occludin downregulation [141]. However, other investigators indicated that inhibition of ROCK can upregulate occludin [142]. Nevertheless, different ROCK1 and ROCK2 isoforms, as well as different experimental models, may account for this discrepancy.

Interestingly it has been demonstrated that inhibition of Rho-ROCK played a protective role in the BBB maintenance by limiting occludin downregulation in endothelial cells after HIV-1 Tat-treatment [52]. Recently, a potential role of Rho/ROCK in Tat-induced occludin dysregulation, among other TJ proteins, has been shown in C57BL/6 mouse brains [143].

PI3K-AKT-PTEN signaling in occludin phosphorylation and HIV-1 Infection

The PI3K–AKT pathway is involved in the regulation of several cell functions, such as cell survival, growth, proliferation, motility, metabolism, angiogenesis, and immune

responses [144]. This regulation is, in part, facilitated by AKT-mediated activation of the protein kinase complex, which is the mammalian target of rapamycin (mTOR) [145, 146]; moreover, AKT1, AKT2, and AKT3 have unique functions in cell growth [147].

PI3K is a family of lipid kinases capable of phosphorylating the inositol ring 3'-OH group in inositol phospholipids. Class I PI3Ks are heterodimers formed by a catalytic subunit (p100) and a regulatory subunit (p85) that together catalyze the phosphorylation of phosphatidylinositol 4,5-bisphosphate (PIP3) to phosphatidylinositol 3,4,5-triphosphate (PIP₃) [148, 149]. PIP₃ promotes the translocation of the serine/threonine protein kinase AKT to the cell membrane, where it is activated by phosphorylation at the Thr³⁰⁸ site by phosphoinositidedependent kinase 1 (PDK1), while PDK2 phosphorylates the Ser⁴³⁷ site [150, 151]. PDK1 is also activated by PIP₃ since PDK2 is part of the mTORC2 complex [152]. PIP3 can be dephosphorylated by phosphatase and tensin homolog (PTEN), which inhibits AKT activity [153-155]. Meanwhile, AKT can also be directly dephosphorylated at Thr³⁰⁸ by protein phosphatase 2 (PP2A) [156] and at Ser⁴⁷³ by the PH domain and leucine-rich-repeat-containing protein phosphatases 1 and 2 (PHLPP1/2) [157].

Active AKT is involved in regulating many downstream targets, including mTOR, p21 proteins, Bad, caspase-9, the Wnt– β -catenin pathways, a p53 inhibitor, glycogen synthase kinase (GSK-3 β), mouse double minute 2 homolog (MDM2), NF- κ B, FOXOs, and cyclic adenosine monophosphate responsive element binding protein 1 (CREB-1) [158–164]. The PI3K-AKT pathway has been described as being involved in TJ alterations [165, 166], and the PI3K regulatory p85 subunit can, among other targets, directly bind to the C-terminus of occludin [167, 168].

The p85 subunit of PI3K is involved in several functions, such as PTEN regulation [169] and phosphorylation of p70S6K [170]; however, it largely serves to regulate PI3K activity. Specifically, phosphorylation of the p85 subunit can enhance PI3K signaling [171]. In contrast, p85 may have primarily inhibitory effects on PI3K signaling in hepatocytes [172]. Binding of PI3K to occludin during oxidative stress was shown to reduce transepithelial electrical resistance (TEER) [168]. However, whether PI3K can directly phosphorylate occludin and the identity of the amino acid targets involved in this phosphorylation both remain unknown. The PI3K-AKT-mTOR pathway of cascading phosphorylation may lead to enhanced occludin production [173], and it has been shown that inducers of this pathway (e.g., celastrol) [174] can prompt occludin expression. It was demonstrated that activation of the PI3K-AKT-Rac1 pathway with acidic fibroblast growth factor (aFGF) can upregulate occludin [175]. Likewise, basic FGF (bFGF) can enhance occludin expression by activating the downstream signaling pathway PI3K-AKT-Rac-1 [176]. In addition, inhibition of PI3K-AKT activity by LY294002 suppressed occludin expression in response to anticancer drugs [177], ferulic acid [178], and/or resveratrol [179]. In human brain microvascular endothelial cells (HBMEC), PI3K inhibition was shown to negate occludin upregulation after silent information regulator 5 (SIRT5) silencing [180], suggesting that PI3K upregulation of occludin may be dependent upon SIRT5 deacetylase activity.

Activation of the PI3K-Akt pathway was demonstrated to induce HIV-1 transcription by activating latent HIV-1 in monocytes and T cells [181]. In addition, PI3K-Akt can prevent the formation of latent HIV-1 reservoirs. As such, PI3K-Akt inhibitors and subsequent downregulation of the PTEN protein resulted in the death of HIV-infected macrophages [182]. Moreover, exposure to HIV-1 Tat protein leads to increased inflammatory cytokine production through the PI3K/Akt and ERK1/2 pathways in astrocytes [183]. Finally, a cross-talk between STAT1 and PI3K-Akt can result in BBB dysfunction in human brain microvascular endothelial cells (Fig. 3) [184].

Occludin expression and HIV-1 Infection in response to stimulation by vascular endothelial growth factor (VEGF) and the cell cycle regulators

Vascular endothelial growth factor (VEGF) is an angiogenic factor that was shown to induce phosphorylation and downregulation of occludin [119, 185, 186]. The Ser⁴⁹⁰ occludin residue is the downstream phosphorylation site responsible for inducing ubiquitination of this protein [107, 112, 187, 188]. Interestingly, VEGF can lead to PKCβ activation, with target Ser⁴⁹⁰ occludin phosphorylation. Indeed, it has been shown that inhibition of VEGF blocks occludin Ser490 phosphorylation downstream of PKCβ activation [107] (Fig. 3). Additionally, occludin Ser⁴⁹⁰ phosphorylation was demonstrated to be associated with mitotic entry, in which occludin facilitates the process and increases cell proliferation [189]. Recently, research has also suggested that activating the VEGF-Flk-1-ERK pathway causes occludin tyrosine phosphorylation [190].

VEGF has been characterized to have neuroprotective effects and was present at higher levels during neurocognitive disorders [191, 192]. This was possibly due to its role in maintaining proper functions of neurons and glial cells, as well as in blood vessel formation [193]. On the other hand, VEGF is a strong proinflammatory factor. In PLH, T cells have been shown to upregulate VEGF due to inflammatory signals [194]. An inverse relationship was observed between blood VEGF-D concentrations and amnestic mild cognitive impairment in older people with HIV-1 [191]. In patients with HIV encephalopathy, the serum concentration of VEGF was increased in comparison to PLH without this comorbidity [192]. In addition, the HIV-1 Tat protein was found to damage microvessels and reduce VEGF levels, suggesting a possible role in neurocognitive decline in HIV-1 infection [195].

The casein kinase 1 and 2 (CK1 and CK2) are serine/ threonine kinases that, among other proteins, phosphorylate occludin. There may be multiple regulatory regions on occludin that are affected by CK1- ε ; at the same time, the C-terminal region of occludin can inhibit CK1- ε phosphorylation [196]. However, much more is known about the involvement of CK2 in occludin phosphorylation. CK2 phosphorylates three amino acid residues- Thr404, Ser408, and Thr400 - in the human occludin C-terminus. Thr375 and Ser379 have also been described in Xenopus laevis as potential CK2 phosphorylation sites [103–105, 197]. Also, inhibiting CK2 leads to overexpression of occludin [103]. Several papers have described a link between CK2 and HIV-1 replication proteins [198]. While the substrate of this interaction remains unknown, it has been shown that HIV-1 Rev can activate CK2, which then can induce HIV-1 Rev phosphorylation [199]. Moreover, it also has been described that multiple HIV-1 gene products can be phosphorylated by CK2 [198, 199].

Concluding remarks and future perspectives

Occludin plays a key role in maintaining the integrity and permeability of the BBB [200] and it has been reported that modification or loss of occludin expression levels are associated with increase neurological damage in several diseases such as ischemic stroke [201, 202] or status epilepticus [203]. A recent study has also shown an increase in serum zonulin and ocln levels in people with bipolar disorder [204] and children with autism spectrum disorder [205]. Importantly, structure and function alterations of the BBB are characteristics hallmarks in brains infected by HIV-1. In fact, alterations in occludin expression levels have been associated with BBB damage during HIV infection.

Traditionally, occludin has been considered a multifunctional TJ protein regulating endothelial and epithelial structure and function. However, occludin is ubiquitously expressed in several cells and tissues, which suggests much broader functions than those assigned to regulating the integrity of tissue barriers. In fact, although is mainly known for its role as a TJ, occludin protein is also a multifunctional protein that can influence cellular metabolism acting as a NADH oxidase.

Recently, occludin has attracted importance due to its newly discovered metabolic functions and its role in controlling HIV-1 infection. Various mechanistic pathways have been proposed to be involved in this effect, such as regulating the expression of the OAS gene family through the STAT-1 signaling pathway, or by regulating the SIRT1 activity through NAD+. Occludin functions appear to be influenced by its phosphorylation, and several signaling pathways can be involved in this process including Src, PKC, CK2, Rho-ROCK, VEGF, and PI3K-AKT-PTEN (Table 1). Importantly, the kinases involved in occludin phosphorylation can also influence HIV-1 infection (Fig. 3). The present review describes the cross-talks between phosphorylation of occludin and regulation of HIV-1 infection; however, it is not fully understood whether these are unrelated or causative associations. Unfortunately, no preclinical study has focused on occludin as a possible target in HIV-1 infection. We propose that a better understanding of the occludin-HIV-1 infections may identify occludin as a possible target to control HIV-1 infection and improve the life of people living with HIV-1.

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Data Availability

Available upon request.

Declarations

Competing interests

The authors declare no competing interests.

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