



Signaling pathways regulating blood–tissue barriers – Lesson from the testis☆



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ABSTRACT

Signaling pathways that regulate blood–tissue barriers are important for studying the biology of various blood–tissue barriers. This information, if deciphered and better understood, will provide better therapeutic management of diseases particularly in organs that are sealed by the corresponding blood–tissue barriers from systemic circulation, such as the brain and the testis. These barriers block the access of antibiotics and/or chemotherapeutic agents across the corresponding barriers. Studies in the last decade using the blood–testis barrier (BTB) in rats have demonstrated the presence of several signaling pathways that are crucial to modulate BTB function. Herein, we critically evaluate these findings and provide hypothetical models regarding the underlying mechanisms by which these signaling molecules/pathways modulate BTB dynamics. This information should be carefully evaluated to examine their applicability in other tissue barriers which shall benefit future functional studies in the field. This article is part of a Special Issue entitled: Gap Junction Proteins edited by Jean Claude Herve.

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1. Introduction

One of the major functions of blood–tissue barriers is to seal vital organs such as the brain, eye, intestine and testis from external cues and harmful substances in the environment. These barriers safeguard key physiological processes in tissue behind the tight junction (TJ)-barrier of the corresponding organ through restrictive paracellular and/or transcellular diffusion. Examples of such barriers are the blood–brain barrier (BBB), the blood–testis barrier (BTB), the blood–retinal barrier, the gut barrier and others [1–7]. However, many of these tissue barriers are not static ultrastructures. Instead, tight junctions (TJs) at the barriers undergo dynamic changes, requiring continuous disassembly, reassembly and stabilization/maintenance. In this way, for example, nutrients can be absorbed in the gut (or intestine) [8,9], and preleptotene spermatocytes in the testis, connected in clones via intercellular bridges [10,11], can be transported across the BTB at stage VIII of the epithelial cycle of spermatogenesis [12–15], without compromising the integrity of the corresponding blood–tissue barrier. Thus, it is obvious that this timely remodeling of blood–tissue barriers is under tight physiological control, involving signaling pathways which facilitate the remodeling (i.e., opening, closing, and stabilization) of the barrier. This also prevents unwanted exposure of an organ or tissue to pathogens and/or harmful substances. Studies in the past decade have made important advances in understanding the signaling pathways that play crucial roles in blood–tissue barrier dynamics [7,16]. Herein, studies based on the BTB in the testis have illustrated the involvement of several signaling complexes and pathways that are intimately involved in regulating BTB dynamics during the epithelial cycle of spermatogenesis. More important, based on these findings, it is becoming increasingly clear that these signaling pathways exert their regulatory effects downstream by targeting the F-actin- and/or microtubule (MT)-based cytoskeletons of the Sertoli cell in the seminiferous epithelium, wherein specialized junctions between adjacent Sertoli cells create the BTB. It is conceivable that these findings and concepts are applicable to other blood–tissue barriers, at least in tissue barriers that may utilize similar signaling complexes and/or pathways to modulate their function.

Understanding blood–tissue barriers garnered interest largely due to the difficulties faced by clinicians in treating diseases of the brain and the testis, since the BBB and BTB virtually block the entry of most drugs, including most chemotherapeutic drugs and male contraceptives, from exerting their effects in the target organs behind the barriers. This is possibly contributed by the presence of an extensive network of drug transporters at the BBB, and also at the BTB [3,5,17–20]. For instance, studies have shown that the testis serves as a reservoir for some viruses, mostly notably human HIV [21,22] (and Zika virus, recently shown in mice [23]). Surprisingly, although viral concentration in the serum of HIV-infected patients receiving suppressive antiretroviral therapy (ART) can be virtually undetectable, viral levels remain exceedingly high in the testis of these patients [24]. These findings thus illustrate some viruses have the ability to evade the physiological barrier conferred by the BTB or the BBB to gain entry into the testis or the brain, respectively. In fact, based on the use of human brain microvascular endothelial cells as a BBB study model, it has been demonstrated that Japanese encephalitis virus has the ability to disrupt the BBB by compromising the tight junction (TJ)-permeability barrier through changes in the host cell apoptotic protein expression [25]. Also, Hepatitis E virus has also been shown to disrupt the BBB in the brain by reducing the expression of ZO-1 at the endothelial TJ-barrier [26].

Additionally, mice transfected with Zika viruses have been shown to infect preferentially Sertoli cells, spermatogonia and primary spermatocytes in the testis [23], illustrating their ability to pass through the BTB. On the other hand, HIV-1 viruses are known to penetrate through the BBB mediated by their Tat and gp120 proteins that are capable of down-regulating the expression of adhesion proteins (e.g., occludin, claudins and ZO-1) considerably at the capillary endothelial cells, making the barrier “leaky” to facilitate their passage at the barrier [27–30]. Collectively, these findings support the notion that viruses have the ability to evade the TJ-barrier in multiple blood–tissue barriers such as the BBB and the BTB to infect an organ, creating a reservoir to harbor the viruses. There are indications that this unusual level of viruses in the brain and the testis is supported by the presence of an extensive network of drug transporters at the BBB [5,17,19] and the BTB [3,18,20,31], which prevent therapeutic drugs, that are supposed to eradicate viruses, from passing through the corresponding barrier. For instance, P-glycoprotein, an active drug transporter, is capable of pumping antiretroviral drugs (e.g., atazanavir) or male contraceptive drug (e.g., adjuvin) out of the brain or the testis, respectively [17,18,32,33]. Thus, studies have supported the concept that viruses (e.g., HIV and Zika) elect to use the testis and the brain as a viral sanctuary site [34–36]. In the testis, besides the presence of drug transporters, this is likely due to the immune tolerance properties conferred by the Sertoli cells, possibly through the immunosuppressing biomolecules secreted by these cells, making the testis an immune privileged site [37–43] in particular at the adluminal (apical) compartment behind the BTB to accommodate post-meiotic spermatid development (Fig. 1). These immunosuppressive biomolecules, coupled with the presence of an extensive network of antiretroviral drug transporters and drug metabolic enzymes in the testes of both rodents and humans [18,44,45], thus prevent the entry of anti-viral drugs into the testis, making the testis a safe haven for some viruses [34,35]. In light of these findings, a better understanding on the biology of blood–tissue barriers will have significant clinical implications in treating (or preventing) various diseases. In this brief review, we thought it pertinent to focus findings based on studies of the BTB which shall provide helpful information in designing functional studies of other blood–tissue barriers.

2. Blood–testis barrier versus other blood–tissue barriers

Most tissue barriers such as the BBB and the blood–retinal barrier are constituted by TJ-barrier of adjacent endothelial cells of microvessels supported by pericytes, surrounding the organ/tissue behind the barrier, to regulate transcellular and paracellular transports of substances across the barrier. For instance, the BBB is conferred by endothelial TJ-barrier and pericytes, and supported by astrocytes and neurons in the brain [1,46–48] (Fig. 1). It is of interest to note that the BTB, in contrast, is conferred by TJs between adjacent Sertoli cells and is restrictively located to the basal region of the seminiferous epithelium, adjacent to the basement membrane [3,4,49–53] since microvessels located in the interstitial space between the seminiferous tubules contribute virtually no barrier function to the Sertoli cell BTB [3,50,54]. This is somewhat similar to the blood–intestine (or the gut) barrier and the blood–epididymis barrier which are created by the epithelial cells of the small intestine and the epididymis [55,56]. However, besides the TJs, the BTB is supported by a testis-specific actin-rich atypical adherens junction called ectoplasmic specialization (ES) [49,57–59]. Since the BTB is anatomically localized at the basal region of the seminiferous epithelium,

towards the base of the seminiferous tubule, the ES found near the basement membrane is designated basal ES (Fig. 1). However, for other blood–tissue barriers, such as the blood–retina barrier, the TJ-barrier, in contrast to the BTB, is located the furthest away from the basement membrane, whereas the BTB is closest to the basement membrane (Fig. 1) [60]. Interestingly, the basal ES coexists with TJ, and they are further supported by gap junction (GJ), which together with the intermediate filament based desmosome all constitute the BTB, making it one of the tightest and also dynamic blood–tissue barriers in the mammalian body [3,49,52,61] (Fig. 1). Using electron microscopy, the basal ES is composed of two arrays of actin microfilament bundles that are sandwiched in between the cisternae of endoplasmic reticulum (ER) and the apposing Sertoli cell plasma membrane (Fig. 1) [3,49,62–64]. These actin microfilament bundles thus confer the BTB its unusual adhesive function.

The BTB is also supported by two prominent signaling proteins derived from mTOR (mammalian target of rapamycin) known as mTORC1 (mammalian target of rapamycin complex 1) and mTORC2 (mammalian target of rapamycin complex 2) [65,66], as well as FAK (focal adhesion kinase) in particular p-FAK-Tyr407 [3,67]. Recent studies have shown that these signaling protein complexes also exert their regulatory effects through the F-actin and/or microtubule (MT)-based cytoskeletons [68–72], consistent with emerging evidence in the field in which mTOR was also shown to exert its regulatory effects through the cytoskeleton [73]. Anatomically, the BTB divides the seminiferous epithelium into the basal and the adluminal compartments (Fig. 1), so that meiosis I/II and post-meiotic spermatid development all take place behind the BTB, whereas undifferentiated spermatogonia (including spermatogonial stem cells), differentiated type A and type B spermatogonia, and also the newly transformed preleptotene spermatocytes from type B spermatogonia reside outside the BTB. Once formed at stage VIII of the epithelial cycle in the rodent testis, preleptotene spermatocytes are the only germ cells that are actively transported across the immunological barrier at stage VIII of the epithelial cycle in both rat and mouse testes vs. stage III in human testes [12–14,74–76]. In this context, it is of interest to note that the BTB is a highly dynamic ultrastructure since preleptotene spermatocytes connected in clones via intercellular bridges [10,11] differentiated from type B spermatogonia must be transported across the BTB between Sertoli cells at stage VIII of the epithelial cycle over the course of 20.8 and 29.1 h in mouse and rat testes [12,13] vs. 24 h at stage III in human testes [74]. Thus, the paracellular transport of preleptotene spermatocytes takes place rather rapidly, illustrating this process must be tightly coordinated and regulated, likely through the involvement of multiple signaling pathways. Interestingly, the BTB is not compromised (i.e., becoming “leaky”) during the transport of preleptotene spermatocytes across the barrier, even transiently, in order to avoid unwanted entry of harmful substances from systemic circulation to the adluminal compartment to perturb post-meiotic spermatid development. At the same time, specific antigens residing in late spermatocytes and post-meiotic spermatids behind the BTB in the adluminal compartment are sequestered from the host immune system. Taken collectively, these earlier findings have shown that the BTB has some distinctive morphological features, and its dynamic remodeling that accommodates the transport of preleptotene spermatocytes during the epithelial cycle is a cytoskeletal-dependent cellular event. Thus, its biology is likely similar to the transport of nutrients or biomolecules across the intestinal barrier during food absorption or the BBB via transcellular or paracellular pathways. It is obvious that the precise regulatory mechanism(s) underlying these events regarding transcellular and paracellular (and active) transports in different blood–tissue barriers must be carefully evaluated in future studies. In this context, it is of interest to note that ES is also found in the apical compartment where it is designated apical ES and is restrictively expressed at the Sertoli–spermatid (steps 8–19 in the rat or 8–16 in the mouse testis) interface [77,78]. Morphologically, the apical and the basal ES share virtually similar features except that

there is only a single array of actin filament bundles found in the Sertoli cell adjacent to the apposing Sertoli–spermatid plasma membranes at the apical ES vs. two arrays of actin filament bundles for basal ES (Fig. 1). However, the constituent proteins are somewhat different between the two. For instance, nectin 3 [79], JAM-C [80], $\alpha 6 \beta 1$ -integrin [81–84] and laminin- $\alpha 3$ /laminin- $\beta 3$ /laminin- $\gamma 3$ chains [85–88] are restrictively expressed at the apical ES, whereas nectin 2 [79], connexin 43 (Cx43) [89–93] are found in both the apical and basal ES. Additionally, some proteins are mostly found at the basal ES, such as N-cadherin [94–96] with its presence at the apical ES limited to only stage I–VI tubules [97].

3. mTOR: mTORC1 vs. mTORC2 and BTB dynamics

3.1. Introduction

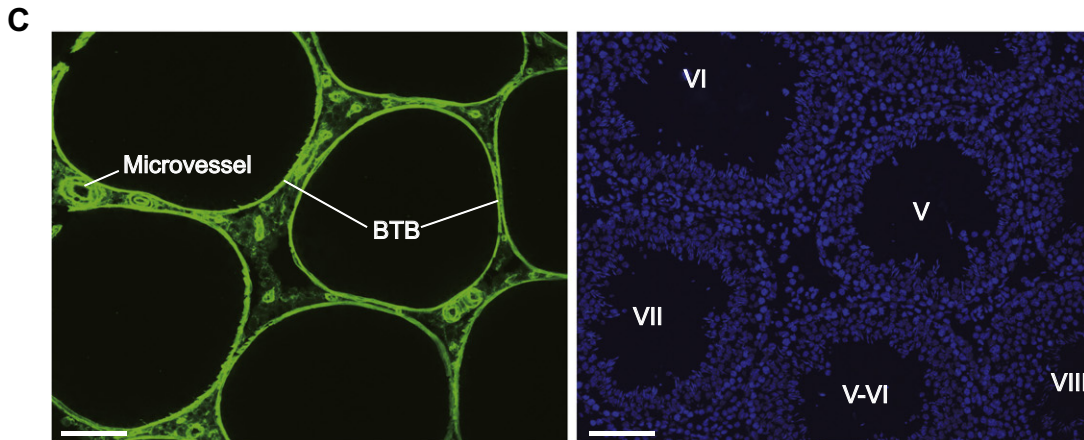
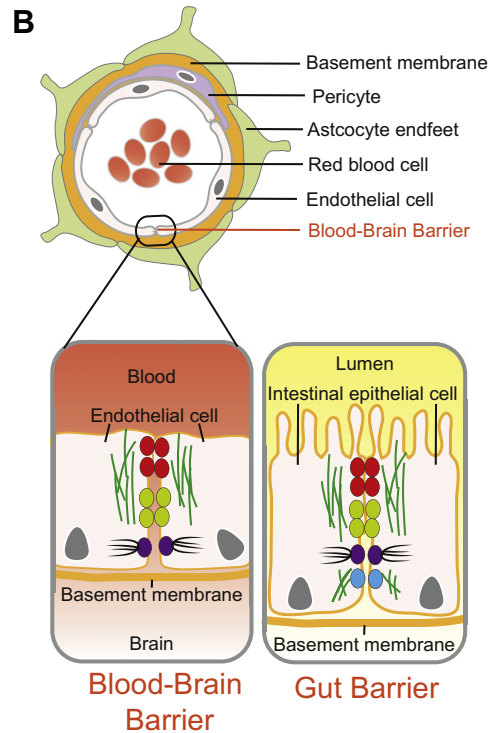
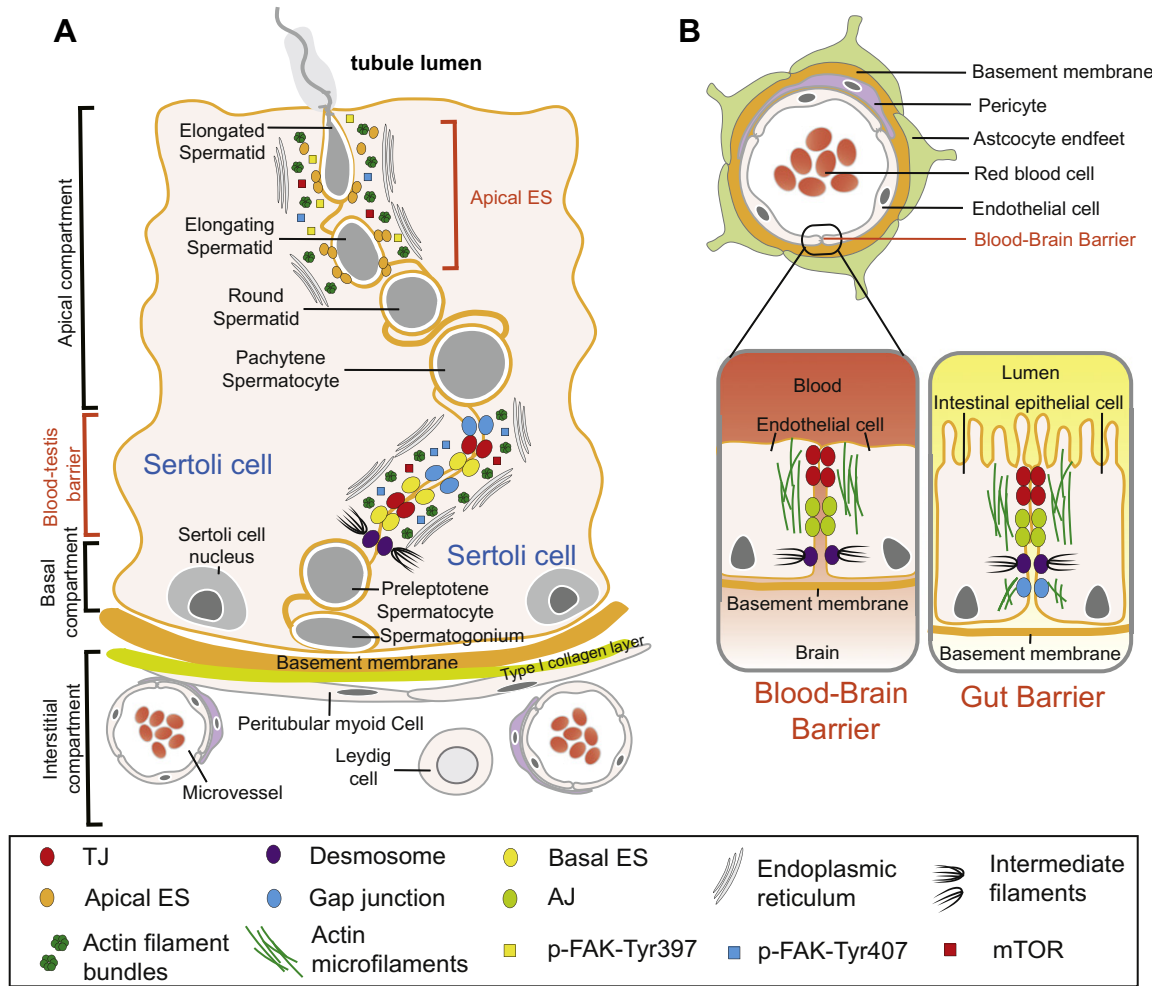
mTOR is a 290 kDa Ser/Thr protein kinase first found in yeasts, and its intrinsic kinase activity can be rapidly blocked by antibiotic rapamycin (also known as sirolimus) [98,99]. Subsequent studies have shown that mTOR is an almost indispensable signaling protein and it is found in virtually all mammalian cells, playing an important role in regulating cell energy status, growth, pathogenesis of many diseases including diabetes and carcinogenesis, and also cytoskeletal function and organization [73,98,100–103]. It is now known that mTOR exists in two distinct and functionally different forms depending on its binding partners, creating two separate signaling complexes called mTORC1 and mTORC2 [73,98,99,104]. In short, when mTOR associates with adaptor protein Raptor (regulatory-associated protein of mTOR), the mTOR/Raptor complex creates the mTORC1 signaling complex which is a rapamycin sensitive regulatory protein kinase. When mTOR associates with adaptor protein Rictor (rapamycin-insensitive companion of mTOR), the mTOR/Rictor complex creates mTORC2 which is rapamycin insensitive. The most important downstream signaling proteins of mTORC1 are p70S6K (ribosomal protein S6 kinase), rpS6 (ribosomal protein S6) and Akt1/2 vs. PKC- α (protein kinase C- α) and SGK1 (serum/glucocorticoid regulated kinase 1, a Ser/Thr protein kinase) signaling proteins for mTORC2 [66,103,105]. Studies have shown that treatment of spermatogonia in vitro with rapamycin, which blocks mTORC1 function through the mTORC1/p70S6K pathway, is known to reduce spermatogonial mitotic proliferation, illustrating mTORC1 is involved in the maintenance of germline pool in the rodent testis [106]. Inhibition of mTORC1 by rapamycin in vivo leads to atrophy of seminiferous tubules, associated with reduced sperm count, confirming the notion that mTORC1 is involved in spermatogenesis [106]. In this context, it is of interest to note a conditional knockout (KO) mouse model to eliminate Raptor was prepared by deleting mTORC1 in the Wolffian duct during development [107]. These *Raptor^{fl/fl};Ksp-Cre* mice are infertile, displaying defects in the epithelial cells of their epididymis, vas deferens, and seminal vesicles due to extensive organ regression with advancing age [107]. For instance, the epididymal epithelial cells of these *Raptor^{fl/fl};Ksp-Cre* mice have defects in metabolism and a considerable reduction in protein secretion [107]. Furthermore, these epithelial cells are also found to actively engulf and destroy epididymal spermatozoa in the epididymis which are not detected in the corresponding age-matched control (*Raptor^{fl/fl}*) mice [107]. In short, these findings thus illustrate the significance of mTOR in testis function but also other accessory male reproductive organs such as the epididymis, vas deferens and the seminal vesicles.

3.2. mTOR and stage-specific expression/localization of its component proteins in the testis

Studies in the testis by immunohistochemistry and/or immunofluorescence microscopy have shown that mTOR [70], and the signaling proteins of mTORC1 such as p-rpS6 (the activated form of rpS6) [69, 72], and p-Akt1 and p-Akt2 (the signaling partners of rpS6) [71], and also Rictor (the adaptor/partner protein that creates mTORC2 when

binding to mTOR) [70], are all localized stage-specifically at the basal ES/BTB, and the apical ES [69–72] during the epithelial cycle. For instance, mTOR is found at the basal ES in virtually all stages of the epithelial cycle in the rat testis, but also at the apical ES at stages I–VIII of the cycle until late VIII when spermiation takes place and its staining re-appears at the apical ES in stages XIII–XIV [70]. For p-rpS6, it is predominantly expressed at the basal ES/BTB in stage VIII and IX tubules and virtually undetectable in other staged tubules; its expression at the apical ES is most predominant in stage VII tubules but considerably diminished in stage VIII and other staged tubules [71,72]. For Rictor, its expression at the basal ES/BTB is predominant at stage V–VII tubules

but virtually undetectable at VIII and other stages [70]. These findings regarding their differential expression at the basal ES/BTB thus suggest that the mTORC1/rpS6 and mTORC2/Rictor signaling complexes may have different effects on the Sertoli cell BTB function. Indeed, studies in vitro and/or in vivo using different research tools have demonstrated mTORC1 and mTORC2 have antagonistic effects on the Sertoli cell BTB function. Such tools include overexpression of a constitutively active quadruple mutant of rpS6, namely a p-rpS6 mutant, which was generated by converting S235, S236, S240 and S244 (S, Ser) to E235, E236, E240 and E244 (E, Glu) [71]; the use of rpS6-specific shRNA to silence rpS6 to impede mTORC1 function [69]; and the use of Rictor-specific siRNA



duplexes to silence Rictor to impede mTORC2 function [70]. In brief, mTORC1 is now known to promote Sertoli cell BTB remodeling by making the BTB “leaky” based on studies *in vitro* and also *in vivo* [69,71,72], whereas mTORC2 promotes BTB integrity by “tightening” the Sertoli cell TJ-barrier [70] to confer integrity of the BTB. These findings are important, since the presence of these two signaling complexes that have antagonistic effects at the basal ES/BTB, their differential spatiotemporal expression at the microenvironment of the BTB thus fine-tunes the timely restructuring of the Sertoli cell-cell junction to accommodate the transport of preleptotene spermatocytes across the barrier (Fig. 2). Below is a brief critical review of these findings.

3.3. mTORC1 and BTB dynamics

In mammalian cells and tissues, mTORC1 is activated by growth factors (e.g., insulin, IGF-1), nutrients (e.g., amino acids) or cellular energy status (e.g., high ATP/AMP ratio), involving PI3-K (phosphoinositide 3-kinase) and Akt/PKB upstream [66,108]. This in turn activates ribosomal protein S6K (S6 protein kinase, also known as p70 S6K) and rpS6 (ribosomal protein S6) downstream via phosphorylation to modulate anabolic metabolism and other cellular function. It is now known that Hippo, Notch, and Wnt signaling pathways also contribute to modulating mTORC1 signaling function [104]. Studies in the testis have shown that mTORC1/rpS6 signaling complex regulates BTB dynamics by promoting BTB remodeling, making the BTB “leaky” [65,66]. This conclusion is reached based on the following observation. First, a knockdown of rpS6 by RNAi (by effectively blocking mTORC1 function) promotes the Sertoli cell TJ-barrier by making it “tighter” *in vitro* or *in vivo* using either rpS6-specific siRNA or shRNA for transfection in Sertoli cells cultured *in vitro* or by administering into the testis *in vivo*, respectively [69]. Second, treatment of Sertoli cells with an established TJ-permeability barrier that mimics the BTB *in vivo* with rapamycin (mTORC1 is rapamycin sensitive) that blocks mTORC1 function also causes the Sertoli cell TJ-barrier to become “tighter” *in vitro* [69]. Third, overexpression of an rpS6 cDNA (wild-type) in Sertoli cells (i.e., by activating/promoting mTORC1 function) perturbs the Sertoli cell TJ-barrier, making it “leaky” [71,72]. However, overexpression of p-rpS6 mutant (the constitutively activated form of rpS6) in Sertoli cells causes the Sertoli TJ-barrier to be “leakier” than overexpression of wild-type rpS6 [71,72]. More important, mTORC1/rpS6 complex is known to exert its disruptive effects on the Sertoli cell BTB integrity by perturbing F-actin organization at the apical and basal ES [69], through a considerable reduction in actin bundling activity, thereby perturbing actin bundle organization at the ES [72]. In short, these findings support the notion that mTORC1/rpS6

signaling complex promotes BTB remodeling by disrupting F-actin organization at the basal ES, causing the BTB to become “leaky”, which is what occurs at stage VIII of the epithelial cycle. Additionally, these findings are supported by the stage-specific expression of p-rpS6 at the basal ES/BTB wherein p-rpS6 S235/S236 and p-rpS6 S240/S244 expression was found to be up-regulated considerably at late stages VIII–IX [69,71,72] during BTB remodeling to facilitate the transport of preleptotene spermatocytes at the immunology barrier.

It is increasingly clear that mTORC1 modulates BTB dynamics through two signaling pathways (Fig. 2). First, an activation of rpS6 through an up-regulation of p-rpS6 (i.e., an induction of mTORC1 signaling function) leads to a down-regulation of p-Akt1/2, which in turn induces an increase in the association of Arp3 and its upstream activator N-WASP (neuronal Wiskott–Aldrich syndrome protein) [72]. This thus causes actin nucleation at the barbed ends of a linear actin microfilament (i.e., branched actin polymerization), re-organizing actin filaments from a bundled to a branched/un-bundled network, destabilizing cell adhesion protein complexes at the BTB (e.g., occludin-ZO-1, N-cadherin- α -catenin which utilize F-actin for attachment) due to a loss of actin filament bundles as the basal ES/BTB. Indeed, there is considerable reduction in actin bundling activities in Sertoli cell epithelium following overexpression of the constitutively active quadruple phosphomimetic mutant p-rpS6 [72]. This latter change thus contributes to destabilizing the arrays of actin microfilament bundles at the basal ES necessary to maintain BTB integrity, making the immunological barrier “leaky”. In this context, it is of interest to note that the ability of the Sertoli cell to organize the actin microfilaments between their bundled and un-bundled/branched configuration is crucial to BTB dynamics. For instance, a Sertoli cell-specific knockout (KO) of N-WASP was shown to cause male infertility in both *Drosophila* and mouse [109], and a detailed analysis has shown that this is due to the inability of the testis to confer plasticity to the F-actin network at the ES to support meiosis and spermiogenesis, leading to irreversible disruption of the basal ES/BTB to support spermatogenesis [110]. Second, overexpression of the rpS6 phosphomimetic (and constitutively active) mutant p-rpS6 in Sertoli cell epithelium that leads to a down-regulation of Akt1/2 is shown to induce MMP-9 (matrix metalloproteinase 9) production by Sertoli cells, which in turn induces proteolysis of TJ and/or basal ES adhesion protein complexes at the BTB, contributing to a “leaky” immunological barrier [71]. This mTORC1 based p-rpS6-p-Akt1/2-MMP-9 signaling pathway that modulates BTB function is confirmed by studies using MMP-9 inhibitor 1 (a specific MMP-9 inhibitor) since this MMP-9 inhibitor effectively blocks the p-rpS6 mutant-induced Sertoli cell TJ-barrier disruption [71]. Also, a knockdown of p-Akt1/2 by RNAi using

Fig. 1. A schematic diagram illustrating the layout of various junction types at the blood–testis barrier (BTB) versus other blood–tissue barriers. (A) In the testis, the Sertoli cell BTB physically divides the seminiferous epithelium inside a seminiferous tubule, such as a stage VII tubule in an adult rat testis, into the apical (adluminal) and the basal compartments as shown herein. Preleptotene spermatocyte differentiated from type B spermatogonium in late stage VII of the cycle is the only spermatocyte that is being transported across the immunological barrier at stage VIII of the cycle. The most notable adherens junction (AJ), a cell–cell actin-based anchoring junction type, is the testis-specific atypical AJ called ectoplasmic specialization (ES). The ES is either found in the adluminal compartment at the Sertoli–spermatid (step 8–19 spermatids in the rat testis) interface called apical ES or at the Sertoli cell–cell interface called the basal ES, adjacent to the basal compartment. The ES is typified by the presence of an array of actin filament bundles in the Sertoli cell that is sandwiched in between the endoplasmic reticulum and the adjacent Sertoli–spermatid plasma membranes (apical ES) or the adjacent Sertoli cell–cell plasma membranes (basal ES). Unlike other blood–tissue barriers, the BTB is closest to the basement membrane and it is constituted by co-existing TJ, gap junction and desmosome (a cell–cell intermediate filament-based anchoring junction). As noted herein, a pachytene spermatocyte differentiates further into diplotene spermatocyte so that it can undergo meiosis I/II to form round spermatids which will be further developed into sperm via spermiogenesis. In the rat and mouse testis, apical ES, once formed between Sertoli cells and step 8 spermatids, is the only anchoring device that supports spermatid adhesion. This is also the anchoring device that supports spermatid transport across the adluminal compartment so that spermatozoa line-up against the tubule lumen to prepare for their release at spermiation at late stage VIII of the epithelial cycle. The seminiferous epithelium composed of only Sertoli and germ cells at different stages of their development lying on the basement membrane which is a modified form of extracellular cell matrix [86,144]. Behind the basement membrane is the type I collagen layer, to be followed by the peritubular myoid cell layer. Microvessels and Leydig cells are found in the interstitial space. (B) Other blood–tissue barriers, such as the blood–brain barrier are constituted mostly by endothelial TJ-barrier between endothelial cells or the TJ-barrier between epithelial cells as shown in the gut barrier herein. These TJ-barriers, unlike the BTB, are furthest away from the basement membrane and AJ that form the adherens plaque always located behind the TJ, which together form the junctional complex, to be followed by desmosome and/or gap junction. In short, the different cell junction types in other blood–tissue barriers do not mix as co-existing ultrastructures as seen at the BTB. Pericytes are also an integrated component of the BBB, which is also supported by astrocytes and neurons. (C) A functional assay to illustrate the relative location of the BTB in the rodent testis and the ability of this immunological barrier to block the diffusion of biotin across the Sertoli cell TJs is shown herein. The functional BTB integrity assay *in vivo* was performed as detailed elsewhere [147]. Herein, a membrane impermeable biotin (EZ-Link Sulfo-NHS-LC-biotin, Mr. 556.59 obtained from Thermo Fisher Scientific) was administered to the testis under the tunica albuginea when the rat was under anesthesia using Ketamine HCl/xylazine as described [147]. About 30 min thereafter, rats were euthanized by CO₂ asphyxiation, frozen sections of the testis were obtained and biotin was detected by Alexa Fluor 488-streptavidin (green fluorescence). In this normal rat testis as shown in the *left panel*, the BTB residing near the basement membrane, as annotated, blocked the diffusion of the biotin (see green fluorescence) across the barrier in all tubules as noted herein. However, the microvessels found in the interstitial space were not effective in blocking the diffusion of biotin to the seminiferous tubules. *Right panel* is the corresponding DAPI (4',6-diamidino-2-phenylindole) image (stained for the cell nuclei) of the *left panel* illustrating the different staged tubules. Scale bar, 100 μ m.

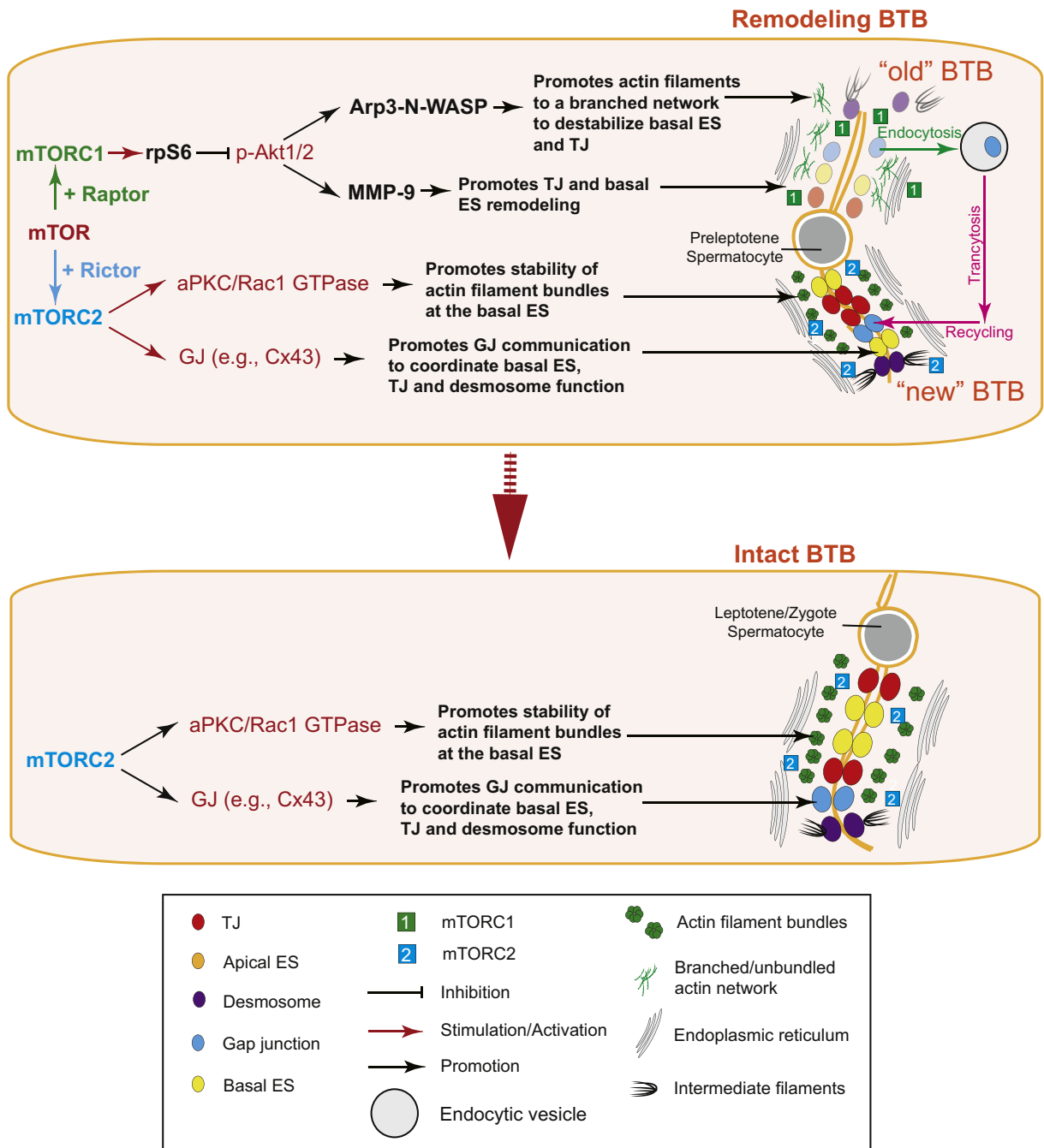


Fig. 2. A schematic diagram illustrating the involvement of mTORC1 and mTORC2 in BTB dynamics. mTORC1 and mTORC2 are known to promote BTB remodeling and BTB integrity, respectively. It is through the antagonistic effects of these two mTOR signaling proteins, mTORC1 and mTORC2 can rapidly modulate the opening and/or closing of the BTB across the microdomains of the BTB during the transport of preleptotene spermatoocytes connected in clones across the immunological barrier. mTORC1 (a complex formed by mTOR and Raptor) exerts its effects through rpS6 and the p-Akt1/2 signaling molecule involving both the Arp2/3 complex and its upstream activator N-WASP, and MMP9 which affect the actin organization and the relative stability of adhesion protein complexes at the BTB. mTORC2 (a complex formed by mTOR and Rictor) exerts its effects through aPKC (atypical protein kinase C)/Rac1 GTPase, and gap junction (GJ, such as Cx43-based GJ communication channels). See text for further details.

specific siRNA duplexes also mimics findings of p-rpS6 mutant overexpression in Sertoli cells by perturbing the Sertoli cell TJ-permeability barrier function [71]. More important, a knockdown of p-Akt1/2 by RNAi in Sertoli cells also leads to an increase in Arp3-N-WASP association, analogous to overexpression of p-rpS6 mutant in Sertoli cells [72]. Taken collectively, these findings provide compelling evidence that mTORC1/rpS6 signaling complex exerts its disruptive effects on the Sertoli TJ-permeability barrier through p-rpS6/Akt1/2/Arp3-N-WASP or p-rpS6/Akt1/2/MMP-9 signaling pathways. Nonetheless, some of these findings remain to be confirmed and expanded to studies

in the adult rat testes *in vivo* to assess if an overexpression of the p-rpS6 phosphomimetic mutant (or an inactivation of the Akt1/2 signaling protein) would impede BTB function as seen in the studies *in vitro*.

3.4. mTORC2 and BTB dynamics – an involvement of GJ function?

Studies have shown that mTORC2 promotes BTB integrity, keeping the BTB “tight” in the testis [65,66], based on the following observations. First, a knockdown of Rictor (Rictor binds to mTOR to form the mTORC2 complex, and thus its knockdown effectively blocks mTORC2 function)

by RNAi perturbs the Sertoli cell TJ-barrier *in vitro*, making it “leaky” [70]. Second, Rictor knockdown in the testis *in vivo* by RNAi also makes the BTB “leaky”, mediated through disruptive organization of F-actin at the ES in the testis [70]. Furthermore, Rictor knockdown by RNAi in Sertoli cells with an established TJ-permeability barrier also perturbs the interaction of the basal ES adaptor protein α -catenin with actin, as well as TJ adaptor protein ZO-1 with actin [70]. These observations are physiologically important since it is known that α -catenin and ZO-1 anchor the corresponding basal ES integral membrane protein N-cadherin and TJ integral membrane protein occludin (also JAM-A and claudin 11) to F-actin, respectively, for attachment. A loss of Rictor (i.e., mTORC2 function) by RNAi would lead to changes in N-cadherin- α -catenin and occludin-ZO-1 association, this thus illustrates that mTOR/Rictor (i.e., mTORC2) plays a crucial role in modulating protein–protein interactions of cell adhesion protein complexes at the BTB. Furthermore, specific inactivation of mTORC2 in Sertoli cells using a genetic model by deleting *Rictor* in Sertoli cells in *Rictor^{flox/flox};Amh-Cre* mice, led to infertile mice with defects in actin and MT organization in Sertoli cells across the seminiferous epithelium. Loss of cytoskeletal organization thereby impeded Sertoli cell polarity and BTB function, resulting in spermatogenic arrest, in which the tubules of these adult mice were devoid of elongating/elongated spermatids [111]. Findings from the genetic model thus confirm the notion that mTORC2 is supporting Sertoli cell function including BTB integrity through its effects to promote cytoskeletal organization in Sertoli cells. Besides these observations, it was shown that a Rictor knockdown also impeded Sertoli cell-cell GJ-based channel communication based on FRAP (fluorescence recovery after photobleaching) analysis [70], suggesting the possibility that mTORC2 may exert its regulatory effect through GJs.

While the testis is known to express almost a dozen GJ proteins during the epithelial cycle including the testis-specific connexin 33 [112, 113], connexin 43 (Cx43) is one of the most important and the best studied GJ proteins in the testis in both rodents and humans [89–91, 114, 115]. In fact, a specific knockout (KO) of Cx43 leads to male infertility [92, 116, 117]. In these Sertoli specific-Cx43 KO mice, spermatogonia fail to differentiate into spermatocytes to initiate meiosis I/II, and Sertoli cells also fail to become terminally differentiated to support the establishment of a functional BTB [116]. Since Sertoli cells remain proliferative, the Cx43-specific KO in Sertoli cells leads to a surge in Sertoli cell population, and clusters of Sertoli cells are persistently found in tubule lumen in adult mouse testes, failing to support spermatogenesis [116, 118]. These findings also suggest that other connexins found in the testis fail to supersede the loss function of Cx43 following its specific deletion in Sertoli cells. However, in these earlier studies [92, 116, 117], the expression of other connexins found in the testis (e.g., Cx33) has not been examined so that it is not known if other connexin genes were affected following Sertoli cell-specific deletion of Cx43. Nonetheless, subsequent studies have shown that germ cell-specific deletion of Cx43 fail to induce any phenotypic changes in the seminiferous epithelium of these mouse testes since Sertoli cells in these mice express Cx43, displaying normal spermatogenesis and fertility even though the steady-state level of Cx43 in these mutant mouse testes is considerably reduced since contribution of Cx43 to the testis pool by germ cells has been voided [119]. Collectively, these findings thus support the notion that Cx43-based GJ communications between Sertoli cells (perhaps also at the Sertoli-germ cell interface through hemi-channel) are more important to support spermatogenesis instead of functional Cx43-based GJ channels between germ cells. Besides this genetic model, we also noted that adult rats treated with a single acute dose of adjuvant, 1-(2,4-dichlorobenzyl)-1H-indazole-3-carbohydrazide, at 250 mg/kg b.w. via oral gavage, was found to induce irreversible male infertility due to permanent BTB disruption [120]. Interestingly, the testes in these rats also displayed a phenotype similar to Sertoli cell-specific Cx43 KO mice except that Sertoli cells in these rats were not mitotically active and a considerable down-regulation and disruptive localization of Cx43 were found [121]. While the population of

spermatogonia was unaffected in these rats, spermatogonia failed to restart spermatogenesis due to meiotic arrest since spermatogonia could not differentiate into preleptotene spermatocytes [120, 121]. Furthermore, F-actin organization in the seminiferous epithelium of these rats was grossly disrupted [121]. However, overexpression of Cx43 in the testis of adjuvant treated rats at acute dose was able to reboot spermatogenesis since meiosis was detected in many of the affected tubules, but spermatids failed to undergo complete spermiogenesis [121]. Nonetheless, in tubules that had signs of spermatogenesis with meiosis, F-actin organization in the epithelium was re-established, making them indistinguishable from control/normal tubules [121]. These findings are important since they illustrate the crucial role of Cx43-based GJ to support normal F-actin organization. Based on the study that a knockdown of Rictor function would impede GJ-channel communication [70], it is tempting to speculate that the homeostasis of F-actin organization in the seminiferous epithelium during the epithelial cycle is supported by chemical signals mediated by intercellular GJ-based channels with the intimate involvement of mTORC2. In fact, earlier studies have also demonstrated the role of GJs in organizing other cell junctions such as desmosome, TJ and basal ES at the immunological barrier to maintain BTB dynamics (i.e., assembly, disassembly and stabilization) [93, 122].

Additionally, a recent study using a conditional knockout approach to delete mTOR in Sertoli cells using *mTOR^{flox/flox};Amhr2-Cre* mice has shown that these mice are infertile, associated with considerable disorganization of seminiferous epithelium including a loss of Sertoli cell polarity, an increase in germ cell apoptosis, defects in germ cell adhesion that lead to specific loss of pachytene spermatocytes and spermatids [123]. In short, spermatocytes fail to advance beyond pachytene spermatocytes to enter meiosis I/II. However, specific KO of mTOR in Sertoli cells in *mTOR^{flox/flox};Amhr2-Cre* mice did not appear to affect the basal ES/BTB function [123] since no apical ES could be found in these adult mice due to the absence of elongating/elongated spermatids. However, due the lack of data based on electron microscopy and the use of a functional BTB integrity assay in this report [123], it remains to be determined if the BTB integrity of these mice were in fact compromised. Interestingly, Sertoli cell-specific deletion of mTOR also leads to a considerable increase in p-rpS6 and mis-localization of Cx43 so that Cx43 no longer localizes at the base of the epithelium near the BTB but diffusively distributed across the entire epithelium [123]. Findings from this genetic model thus support the notion that mTOR is involved in GJ dynamics such as in the Rictor knockdown model by perturbing mTORC2 function which in turn perturbs GJ communication function [70]. In this context, it is of interest to note that since studies in other mammalian cells and/or epithelia have demonstrated the transport of miRNAs across GJs to modulate (or coordinate) cellular function [124–129], and germ cells are known to express a large number of miRNAs [130, 131], it is thus likely that GJ in the testis including Cx43-based hemichannels may be used to modulate Sertoli cell function by germ cells through the transport of miRNAs under the influence of mTORC2. In short, mTORC2 may work with other signaling molecules and/or pathways downstream such as Akt1/2 to modulate GJ communication function, which in turn determines the transport of miRNAs into the Sertoli cell to regulate cytoskeletal function as schematically shown in Fig. 2. This possibility must be carefully evaluated in future studies.

4. FAK: p-FAK-Tyr407 versus p-FAK-Tyr397 on BTB dynamics

4.1. Introduction

FAK (focal adhesion kinase, also known as PTK2, protein tyrosine kinase 2, a 125 kDa polypeptide), a substrate of Src, is an extensively studied signal transducer downstream of integrin receptors that transmit signals at the cell-ECM (extracellular matrix) interface called focal adhesion complex (FAC or focal contact) to modulate epithelial and/or endothelial cell function [67, 132–135]. In short, FAK is an important signaling

molecule at the FAC, an actin-based anchoring junction at the cell-matrix interface. However, there are no actin-based focal adhesion ultrastructures in the testis except the intermediate filament-based cell-matrix anchoring junction called hemidesmosome [51]. There are six putative phosphorylation sites along the FAK polypeptide: at Tyr-397, -407, -576, -577, -861 and -925 [67,136]. Tyr-397 is the auto-phosphorylation site of FAK, involved in its initial activation, and when it is phosphorylated (i.e., activated), this promotes Src binding, leading to conformational activation of Src and results in a dual-activated FAK-Src signaling complex [137]. On the other hand, FAK-Tyr407 phosphorylation suppresses Tyr397 phosphorylation to negatively regulate the overall function of FAK regarding its intrinsic kinase and biological activities, such as contact inhibition and cell cycle arrest [138], illustrating the antagonistic effects of p-FAK-Tyr397 vs. p-FAK-Tyr407. Interestingly, FAK was first detected in 2001 in adult rat testes at the basal ES/BTB site (in stage I–XIV tubules) but apparently limited to the cytoplasm of early spermatogenic cells, and also at the apical ES (mostly in stage IV–VIII tubules) using an anti-FAK monoclonal antibody by immunofluorescence microscopy [84]. Subsequent studies by immunofluorescence microscopy and/or immunohistochemistry, and co-immunoprecipitation using multiple antibodies from different sources have shown that FAK is an integrated component of the ES in 2003 which is a testis-specific actin-based cell-cell atypical adherens junction [139]. For instance, FAK is mostly expressed by the basal ES/BTB, but p-FAK-Tyr397 was predominantly localized at the apical ES and virtually undetectable at the basal ES/BTB [139,140]. In fact, the expression of p-FAK-Tyr397 persisted at the apical ES at the Sertoli-step 19 spermatid interface until the time sperm are released into the tubule lumen at spermiation [68,140], thus p-FAK-Tyr397 has been implicated to be involved in spermiation [141]. It is now known that p-FAK-Tyr397 forms a multi-protein signaling complex with β 1-integrin, p130Cas, DOCK180, RhoA, vinculin, PI 3-kinase, and PKB, possibly creating a signaling platform at the apical ES to regulate spermiation [141–143]. Interestingly, FAK nor any of its activated forms is detected at the focal adhesion complex (or focal contacts, a cell-ECM (extracellular matrix) anchoring junction type) at the Sertoli cell-basement membrane interface (note: basement membrane is a modified form of ECM in the testis [86,144]). Subsequent studies have shown that, unlike p-FAK-Tyr397, p-FAK-Tyr407 is localized at the apical ES and also basal ES/BTB, but not at the basement membrane [68]. These observations in the testis are important because they illustrate the significance of FAK, an FAC protein found in virtually all epithelia, in adherens junctions since virtually all the earlier studies focus on the role of FAK as a cell-ECM regulator. In fact, it is now known that FAK, in particular p-FAK-Tyr397 is an important regulator of spermiation [141]. Studies using different constitutively active phosphomimetic mutants of FAK, such as p-FAK-Y397E and p-FAK-Y407E vs. constitutively inactive (i.e., non-phosphorylatable) phosphomimetic mutants of FAK, such as p-FAK-Y397F and p-FAK-Y407F to overexpress either in Sertoli cells cultured *in vitro* that mimic the Sertoli cell BTB or in the testis *in vivo* have shown that p-FAK-Tyr397 and p-FAK-Tyr407 have antagonistic effects on the Sertoli cell barrier in which p-FAK-Tyr397 promotes BTB remodeling by making it “leaky” whereas p-FAK-Tyr407 promotes BTB integrity by making it “tighter”. These findings also suggest that, similar to mTORC1 and mTORC2, p-FAK-Tyr397 and p-FAK-Tyr407 serve as molecular “switches” to induce BTB disassembly or reassembly (Fig. 3).

4.2. p-FAK-Tyr397 promotes BTB remodeling vs. p-FAK-Tyr407 which promotes BTB integrity

Studies using various p-FAK mutants have shown that p-FAK-Tyr397 promotes BTB remodeling by making the Sertoli cell TJ-barrier “leaky”. For instance, overexpression of p-FAK-Y397F (a non-phosphorylatable/constitutively inactive p-FAK-Tyr397 mutant) or p-FAK-Y407E (a constitutively active p-FAK-Tyr407 mutant) in Sertoli cell epithelium both promotes the integrity of Sertoli cell TJ-barrier,

making it “tighter” [68]. However, overexpression of p-FAK-Y407F (a non-phosphorylatable/constitutively inactive p-FAK-Tyr407 mutant) or p-FAK-Y397E (a constitutively active p-FAK-Tyr397 mutant) promotes the Sertoli cell TJ-barrier remodeling, making it “leaky” [68]. Taken collectively, these findings are important since they illustrate that changes in the spatiotemporal expression of these two p-FAK proteins at the BTB microenvironment can possibly induce the immunological barrier to become either “leaky” or “tighter” at specific domains, such as at the site above or below the preleptotene spermatocytes connected in clones being transported across the BTB. In short, by increasing the level of p-FAK-Tyr407 and/or reducing the level of p-FAK-Tyr397 at the BTB microenvironment, this promotes BTB integrity by tightening the immunological barrier in non-stage VIII tubules (Fig. 3A). These changes also facilitate the establishment of a “new” BTB, such as at the rear end of the preleptotene spermatocytes during the transport of these germ cells across the immunological barrier (Fig. 3). On the other hand, by reducing the level of p-FAK-Tyr407 and/or increasing the level of p-FAK-Tyr397 at the BTB microenvironment promotes BTB remodeling by making the barrier “leaky” in stage VIII tubules (Fig. 3B). Studies have also shown that p-FAK-Tyr407, which is crucial to maintain BTB integrity, is likely working in concert with other regulatory proteins to modulate BTB dynamics (Fig. 3C). This notion is supported by use of a different animal study model, in which a biologically active peptide called F5-peptide was administered to the testis *in vivo*, and was shown to induce BTB remodeling, concomitant with a considerable down-regulation of the expression of p-FAK-Tyr407 in the testis [145]. Studies have shown that F5-peptide produced in the testis at the apical ES during spermiation is through activation of MMP-2 that cleaves laminin- γ 3 chains [87,145–147]. The laminin- γ 3 chain breakdown is essential for the release of sperm at spermiation since laminin- γ 3 is also an integrated component of the apical ES [85, 87,88]. For instance, laminin- γ 3 forms a functional ligand with laminin- α 3 and laminin- β 3 chains and this trimeric laminin ligand [88], also an elongated spermatid-based apical ES protein, in turn interacts with the Sertoli cell-specific α 6 β 1-integrin receptor to create a bona fide adhesion complex at the apical ES [87,88]. A recent report has shown that the release of biologically active F5-peptide from the laminin- γ 3 chain at the apical ES promotes further ES breakdown to facilitate the release of sperm at spermiation [147]. However, F5-peptide also considerably perturbs the spatial expression of p-FAK-Tyr407 since its expression at the basal ES/BTB during F5-peptide induced BTB disruption was found to be considerably down-regulated [145]. For instance, p-FAK-Tyr407 no longer prominently localized at the BTB near the basement membrane in the seminiferous epithelium when the BTB was found to be “leaky” based on an *in vivo* integrity assay [145]. These findings are important, since it demonstrates that p-FAK-Tyr407 is being used by the testis to promote F5-peptide-induced BTB restructuring, illustrating the physiological relevance of the earlier study using phosphomimetic mutants of p-FAKs [68]. Based on these findings, we now propose a model shown in Fig. 3C, which is similar to the model depicted in Fig. 2, illustrating that the mTORC1 and p-FAK-Tyr397 may be working in concert to promote BTB remodeling, by making the immunological barrier “leaky”, such as at stage VIII of the epithelial cycle to support the transport of preleptotene spermatocytes across the immunological barrier. On the other hand, mTORC2 and p-FAK-Tyr407 may also be working in concert to promote BTB integrity, making the immunological barrier “tighter”, such as in non-stage VIII tubules (Figs. 2 and 3). In this context, it is of interest to note that while the events of apical ES degeneration to support the release of sperm at spermiation vs. remodeling of the BTB to support preleptotene spermatocyte transport take place at the opposite ends of the seminiferous epithelium – at the apical (adluminal) near the tubule lumen vs. the site near the basement membrane – these two events are still functionally connected within a single Sertoli cell (or a single layer of Sertoli cells in the seminiferous epithelium) through integrin-based signaling function. At present, the signaling molecule(s) that elicit

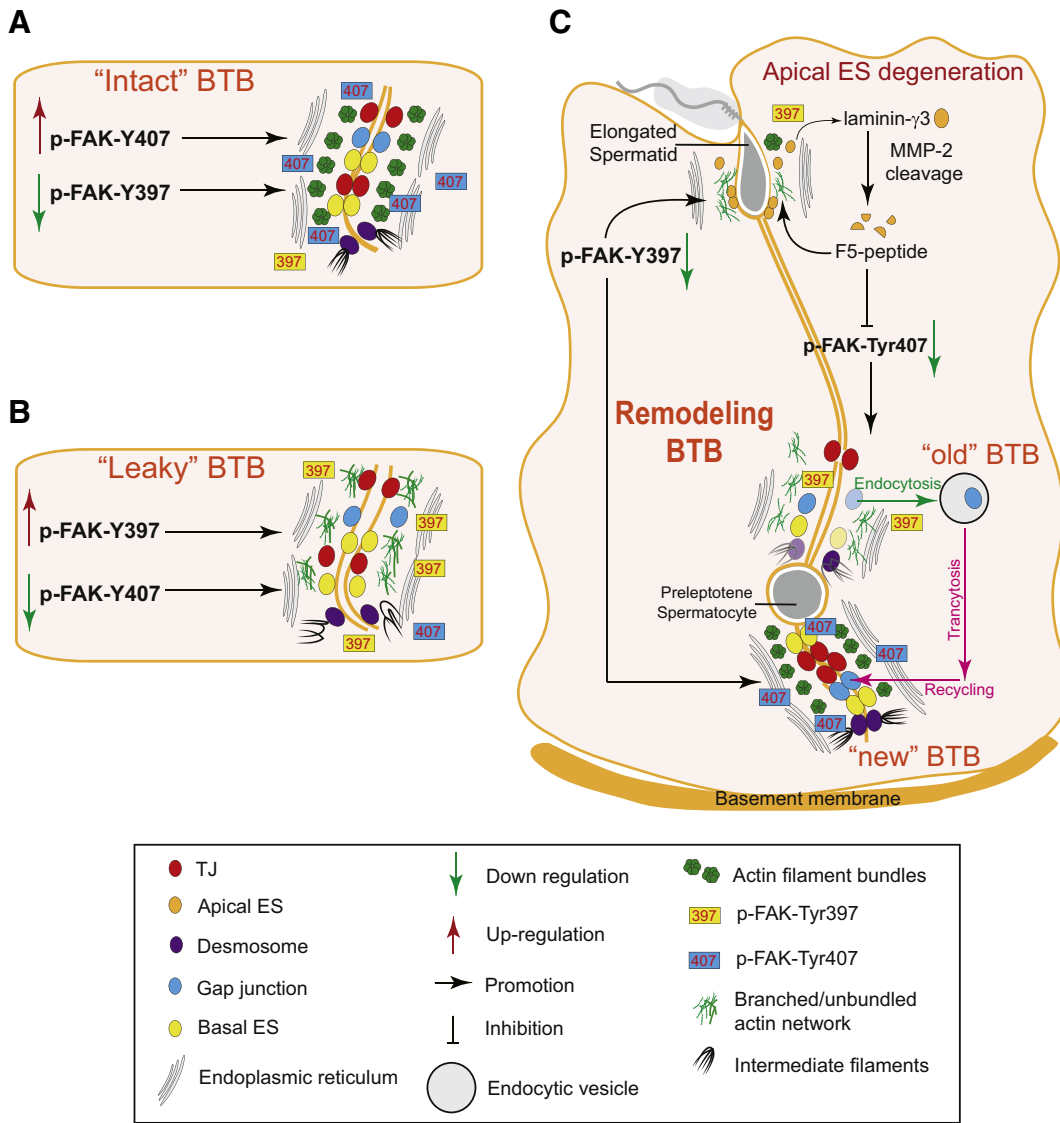


Fig. 3. A schematic diagram illustrating the involvement of p-FAK-Tyr397 and p-FAK-Tyr407 in BTB dynamics. p-FAK-Tyr397 and p-FAK-Tyr407 are the phosphorylated/activated form of FAK known to (A) promote BTB remodeling and (B) support BTB integrity, respectively. (C) These two signaling molecules work as molecular switches that turn “on” and “off” the immunological barrier by making it either “leaky” or “tighter” across the microdomains of the BTB to support the transport of preleptotene spermatocytes across the immunological barrier. Studies have shown that p-FAK-Tyr407 is also working in concert with F5-peptide generated at the apical ES just shortly before spermiation takes place to modulate the disassembly of the “old” BTB and the assembly of the “new” BTB above and below the preleptotene spermatocytes being transported across the immunological barrier. See text for further details.

these events remain unclear, but studies in other epithelia have shown that this likely involves integrin-based signaling molecules [148–150]. Studies using the F5-peptide model has also shown that F5-peptide likely exerts its effects, possibly mediated by a down-regulation on the expression of p-FAK-Tyr407, through inside-out and outside-in signaling in the testis [145], similar to other epithelia [151–153].

5. Concluding remarks and future perspectives

As briefly summarized above, we have critically evaluated findings based on studies at the BTB in rodents, illustrating that mTORC1 and p-FAK-Tyr397 signaling complexes and their corresponding signaling pathways promote BTB remodeling, leading to the immunological barrier to become “leaky”. However, mTORC2 and p-FAK-Tyr407 signaling complexes and their corresponding pathways promote BTB integrity, making the barrier “tighter”. In short, these two pairs of signaling proteins, namely mTORC1 vs. mTORC2, and p-FAK-Tyr397 vs. p-FAK-Tyr407, have antagonistic effects on the BTB integrity, by serving as

molecular switches to turn “off” or “on” the immunological barrier, thereby supporting the transport of preleptotene spermatocytes across the barrier during spermatogenesis. However, it is not known at present the molecules and or signaling pathways that connect mTORC1 and mTORC2 with p-FAK-Tyr397 and p-FAK-Tyr407 to work in concert to modulate BTB dynamics. It is also likely that p-FAKs are working in concert with the c-Src/c-Yes non-receptor protein kinases which are recently shown to play a role in modulating BTB dynamics [154–156] since FAK and Src are signaling partners known to regulate mammalian cell physiology. More important, the respective up-stream molecule(s) that trigger either mTORC1/mTORC2 and/or p-FAK-Tyr397/p-FAK-Tyr407 activation is not fully elucidated. However, recent studies have suggested that the local regulatory axis that connects the basement membrane and the BTB [157] may be utilizing mTOR to modulate basal ES/BTB function. For instance, laminin α 2 chain in the basement membrane adjacent to the BTB, possibly through the 80 kDa fragment from its C-terminus, was found to promote the BTB function, making the BTB tighter, since the knockdown of laminin α 2 by RNAi using

laminin $\alpha 2$ -specific shRNA (small hairpin RNA) vs. control non-targeting shRNA was shown to perturb the Sertoli cell TJ-barrier function via its disruptive effects on F-actin organization in Sertoli cells [157,158]. More important, the laminin $\alpha 2$ knockdown was associated with an up-regulation of p-rpS6 expression [158], and rpS6 is the downstream signaling molecule of mTORC1 which is known to promote BTB disruption as discussed herein. Furthermore, the use of rapamycin, a specific inhibitor of mTORC1 [103], was found to block the laminin $\alpha 2$ shRNA-mediated disruptive effects on F-actin organization in Sertoli cells [158]. Collectively, these recent findings support the notion that laminin $\alpha 2$ chain and/or its biologically active fragment(s) may be the upstream regulatory of the mTORC1/mTORC2 regulatory signaling molecules to modulate BTB dynamics.

On the other hand, the local functional axis that connects the apical ES and the BTB [146] may be utilizing FAK to regulate BTB function. It has been shown that F5-peptide, a biologically active 50-amino acid residue fragment generated from the laminin- $\gamma 3$ chain at the apical ES (i.e., at the Sertoli-late spermatid interface) at stage VIII of the cycle, exerts its effects by perturbing the spatiotemporal expression of p-FAK-Tyr407 at the apical and basal ES/BTB, associated with gross disruption on the organization of F-actin network across the seminiferous epithelium [145]. These changes in turn perturbed adhesion function at the apical and basal ES, leading to spermatid exfoliation and BTB disruption based on studies *in vitro* and *in vivo* [145,147]. In fact, overexpression of the p-FAK-Tyr407 phosphomimetic (and constitutively active) mutant p-FAK-Y407E was shown to block the disruptive effects of F5-peptide on Sertoli cell TJ-barrier function [145]. In short, the laminin $\alpha 2$ chain and the F5-peptide derived from laminin $\gamma 3$ may be the corresponding upstream molecule that triggers the mTORC1/mTORC2 and p-FAK-Tyr397/p-FAK-Tyr407 activation and/or inactivation of these signaling molecules. It is obvious that much work is needed to further expand these findings.

Nonetheless, it is likely that germ cells, such as preleptotene spermatocytes in the basal compartment and elongated spermatids in the adluminal (apical) compartment are playing an important role by serving as the upstream regulators to modulate BTB dynamics, such as through the production of laminin $\alpha 2$ chain-derived peptide(s) in the basement membrane [157,158] or F5-peptide from the laminin- $\gamma 3$ chain at the apical ES [145–147] as briefly discussed above. In fact, this possibility is also supported in a recent report based on a study *in vitro* wherein germ cells cocultured with Sertoli cells are found to modulate Sertoli TJ-permeability barrier function [159]. On the other hand, proteins that are expressed at the apical ES and TJ as well as small GTPases can also modulate the barrier function as shown in other epithelia and/or endothelia as recently reviewed [7,160,161]. Emerging evidence has also supported the involvement of Frizzled receptors in BBB formation and maintenance [162]. Collectively, the findings reviewed herein have supported our beliefs that the hypothetical model depicted in Figs. 2 and 3 provides the framework for investigators to design functional experiments in future years to study BTB biology, and to assess the applicability of this information in studying other blood–tissue barriers.

Declaration of conflicts of interest

Nothing to declare.

Transparency document

The Transparency document associated with this article can be found in the online version.

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