# Regulation of blood–testis barrier dynamics by TGF-β3 is a Cdc42-dependent protein trafficking event

# Elissa W. P. Wong<sup>a</sup>, Dolores D. Mruk<sup>a</sup>, Will M. Lee<sup>b</sup>, and C. Yan Cheng<sup>a,1</sup>

<sup>a</sup>Center for Biomedical Research, Population Council, New York, NY 10065; and <sup>b</sup>School of Biological Sciences, University of Hong Kong, Hong Kong SAR, China

Edited by Ryuzo Yanagimachi, The Institute for Biogenesis Research, University of Hawaii, Honolulu, HI, and approved May 10, 2010 (received for review January 26, 2010)

In the testis, the blood-testis barrier (BTB) is constituted by specialized junctions between adjacent Sertoli cells in the seminiferous epithelium near the basement membrane. Although the BTB is one of the tightest blood-tissue barriers in the mammalian body, it undergoes extensive restructuring at stage VIII of the seminiferous epithelial cycle to facilitate the transit of preleptotene spermatocytes. Thus, meiosis and postmeiotic germ cell development take place in the seminiferous epithelium behind the BTB. Cytokines (e.g., TGF-β3) are known to regulate BTB dynamics by enhancing the endocytosis of integral membrane proteins and their intracellular degradation. This thus reduces the levels of proteins above the spermatocytes in transit at the BTB, causing its disruption after testosterone-induced new tight junction (TJ) fibrils are formed behind these cells. By using Sertoli cells cultured in vitro with an established TJ permeability barrier that mimicked the BTB in vivo, Cdc42 was shown to be a crucial regulator that mediated the TGFβ3-induced BTB disruption. TGF-β3 was shown to activate Cdc42 to its active GTP-bound form. However, an inactivation of Cdc42 by overexpressing its dominant-negative mutant T17N in Sertoli cell epithelium was shown to block the TGF- $\beta$ 3–induced acceleration in protein endocytosis. Consequently, this prevented the disruption of Sertoli cell TJ permeability barrier and redistribution of TJ proteins (e.g., CAR and ZO-1) from the cell-cell interface to cell cytosol caused by TGF- $\beta$ 3. In summary, Cdc42 is a crucial regulatory component in the TGF- $\beta$ 3-mediated cascade of events that leads to the disruption of the TJ fibrils above the preleptotene spermatocytes to facilitate their transit.

cytokines | GTPases | protein endocytosis | seminiferous epithelial cycle | spermatogenesis

n mammalian testis, the seminiferous epithelium is segregated into the basal and apical compartments by the blood-testis barrier (BTB), which is created by coexisting tight junction (TJ), basal ectoplasmic specialization [ES, a testis-specific atypical adherens junction (AJ) type], and desmosome gap junctions between adjacent Sertoli cells near the basement membrane (1, 2). At stage VIII of the seminiferous epithelial cycle, the BTB undergoes extensive restructuring to allow the transit of preleptotene spermatocytes from the basal to the apical compartment. At the same time, preleptotene spermatocytes differentiate into leptotene and zygotene spermatocytes (3) so that meiosis and postmeiotic germ cell development can take place in the apical compartment behind the BTB (2). While the BTB undergoes this cyclic restructuring throughout spermatogenesis, the immunological barrier conferred by the BTB is maintained at all time to segregate the postmeiotic germ cell development from the host immune system to avoid the production of antibodies against germ cell-specific antigens that attack its own sperms. Previous studies have shown that cytokines (e.g., TGF- $\beta$ 2 and TGF- $\beta$ 3) and testosterone are working in concert to facilitate the transit of spermatocytes at the BTB while maintaining the immunological barrier (2, 4). For instance, testosterone maintains the immunological barrier by inducing de novo synthesis of junction proteins (e.g., claudins and occludin) (5-7) as well as transcytosis of proteins from other sites of the Sertoli cells to promote the assembly of "new" TJ fibrils behind a spermatocyte in transit (4). Conversely, cytokines enhance endocytosis of integral membrane proteins above a spermatocyte in transit and target the internalized TJ fibril proteins for intracellular degradation (4, 8), thereby destabilizing the "old" BTB ultrastructure to facilitate its transit (2). However, the regulatory component(s) that modulates these events, such as the TGF-\beta-induced enhancement in protein endocytosis, remains virtually unknown. Previous studies have implicated the Rho family small GTPase Cdc42 in regulating protein trafficking events, such as endocytosis and exocytosis, besides its roles as an actin cytoskeleton regulator (1). Although studies have shown that an alteration of Cdc42 activity, such as by overexpression of dominant-negative or constitutive-active mutant of Cdc42, induces changes in protein trafficking in cells, the upstream regulators that control Cdc42 activity in this process are unknown (1). Here, we sought to examine whether TGF- $\beta$ 3, when used at a concentration similar to the level at the BTB microenvironment in vivo (8), is an upstream physiological stimulus that activates Cdc42, and if the activation state of Cdc42 is essential for mediating TGF- $\beta$ 3-induced acceleration of protein endocytosis at the BTB. We also examined if Cdc42 determines the extent of endocytosed integral membrane proteins that are recycled and targeted to the cell surface. In short, we sought to investigate if the TGF-\u03b3-induced Sertoli cell BTB disruption is mediated by Cdc42 via its effects on protein trafficking.

#### Results

Localization of Cdc42 at the BTB Is Stage-Specific with Considerably Diminished Expression at Stage VII to VIII of the Epithelial Cycle, Coinciding with BTB Restructuring. To understand whether Cdc42 is involved in regulating BTB dynamics, its localization in rat testis was first characterized by immunohistochemistry. Frozen testis cross-sections from adult rats were stained with an anti-Cdc42 antibody (Fig. 1A, i-vii). This antibody specifically detected Cdc42 by immunoblotting using lysates obtained from rat testes and Sertoli cells (Fig. 1A, vii). Cdc42 was ubiquitously expressed in the entire seminiferous epithelium (Fig. 1A, i). This finding is consistent with earlier studies which have shown that Cdc42 regulates various cellular processes, such as actin dynamics and cell polarity (1). At higher magnifications, Cdc42 was found to be prominently expressed near the basement membrane, consistent with the localization of the BTB (Fig. 1A, *ii*, black arrowheads). Furthermore, a stage-specific expression pattern was observed (Fig. 1A, i-v). Notably, the staining of Cdc42 at the BTB in stage V tubule was weaker compared with tubules at stage X-XIII

<sup>1</sup>To whom correspondence should be addressed. E-mail: y-cheng@popcbr.rockefeller.edu.

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(Fig. 1*A*, *iii*, is a magnified view of the boxed area shown in Fig. 1*A*, *iii*). However, this diminished staining was most obvious and drastic at stage VII-VIII (Fig. 1*A*, *i* and *iv*) when the BTB undergoes extensive restructuring to facilitate the transit of preleptotene spermatocytes. When the anti-Cdc42 antibody was replaced with normal chicken IgY, no positive signal was observed (Fig. 1*A*, *vi*) illustrating the specificity of the staining results in Fig. 1*A*, *i–v*. To further validate the localization of Cdc42 at the BTB, dual-labeled immunofluorescence analysis was performed to colocalize Cdc42 with a known BTB marker. Consistently, Cdc42 (Fig. 1*B*, *i*, red) was shown to colocalize with the basal ES marker N-cadherin (Fig. 1*B*, *ii*, green) at the BTB (Fig. 1*B*, *iii* and *iv*).

Cdc42 Is Activated in Sertoli Cell Epithelium upon TGF-β3 Stimulation. TGF- $\beta$ 3 is a known regulator of BTB (2). In order to test the possibility that Cdc42 is a downstream mediator of TGF- $\beta$ 3, we first examined if TGF-\u03b33 affects the activation of Cdc42 in a Sertoli cell culture system known to establish functional and structural barrier that mimics the BTB in vivo (9). As Cdc42 switches between active (i.e., GTP-bound) and inactive (i.e., GDP-bound) states, we performed a pull-down assay using GSTp21-binding domain (i.e., PBD) of PAK-1 to precipitate active Cdc42 (Cdc42-GTP). Isolated Sertoli cells were cultured in F12/ DMEM for 4 d to form an intact cell epithelium before being stimulated with 4 ng/mL TGF- $\beta$ 3, at a concentration similar to its level at the BTB microenvironment in vivo (8). It was found that TGF-β3 transiently activated Cdc42 at 5 and 20 min after Sertoli cells were exposed to TGF- $\beta$ 3 (Fig. 2 A and B). However, prolonged stimulation by TGF-\beta3 for 60 min significantly decreased the level of active Cdc42 versus its basal level at 0 min (Fig. 2 A and B). In addition, the inactivation of Cdc42 at 60 min was accompanied by a mild but significant decrease in the total Cdc42 (Fig. 2 A and C). Previous studies have shown that TGF- $\beta$ 3 disrupts the Sertoli cell TJ barrier (10). However, it is not known if TGF-β3 disrupts the TJ barrier within 24 h after cells are exposed to TGF-\beta3. Thus, 4 ng/mL TGF-\beta3 was added to the Sertoli cell epithelium on day 4 when functional TJ had been established (Fig. 2D). Interestingly, the TJ barrier was not disrupted when the transepithelial electrical resistance (TER) was quantified at 15 and 60 min after the addition of TGF- $\beta$ 3 (Fig. 2D) when Cdc42 was activated before this time at 5 to 20 min (Fig. 2A vs. Fig. 2D). Instead, the TJ barrier was visibly disrupted by 3 h and thereafter (Fig. 2D). These findings implicate that

Fig. 1. Stage-specific expression of Cdc42 at the BTB in adult rat testis. (A, i-v) Immunohistochemistry was performed using frozen testis sections and a specific anti-Cdc42 antibody (Table S1) with a negative control shown in vi. The specificity of this antibody in testis (T) and Sertoli cell (SC) were illustrated in vii using immunoblot analysis with the corresponding protein lysates (~25  $\mu g$  protein). (i) Cdc42 was localized in the seminiferous epithelium with stage-specific expression at the BTB but it was absent in stage VIII tubules. (ii) Magnified micrograph shows that Cdc42 was detected in the Sertoli cell cytoplasm that extended toward the edge of the tubule lumen. Nevertheless, Cdc42 was predominantly localized at the BTB (black arrowheads). (iii) Magnified view of the boxed area in ii showing Cdc42 was highly expressed at the BTB with its expression began to diminish at stage V. (iv and v) Reduced level of Cdc42 at the BTB persisted from stage VI to VIII. At stage VIII, Cdc42 at the BTB was virtually undetectable. (vi) Control section in which normal chicken IgY was replaced with the anti-Cdc42 antibody. [Scale bars: i, 100 µm; ii (applies to vi), 40 µm; iii (applies to iv and v), 20 µm.] (B) Colocalization of Cdc42 (red, i) with basal ES protein N-cadherin (green, ii) at the BTB (iii). Nuclei were stained with DAPI (blue, *iv*). [Scale bars: 10  $\mu$ m in *i* (applies to *ii-iv*).]

Cdc42 activation maybe necessary for the subsequent effects of TGF- $\beta$ 3 on the Sertoli cell TJ barrier function.

Cdc42 Is Required to Mediate TGF- $\beta$ 3–Induced Activation of p38 MAPK. The findings that Cdc42 is localized at the BTB (Fig. 1) and TGF- $\beta$ 3 regulates its activation state (Fig. 2) implicates that Cdc42 is a crucial mediator of TGF- $\beta$ 3–induced BTB disruption. To test this hypothesis, we altered the activation state of Cdc42 by expressing full-length Cdc42 or dominant-negative Cdc42 mutant T17N in primary Sertoli cells and investigate if there is



**Fig. 2.** TGF-β3 activates Cdc42 in Sertoli cells. (A) Sertoli cells were cultured for 4 d, thereafter, cells were stimulated with TGF-β3 (4 ng/mL) for 5 to 60 min. GTP-bound Cdc42 (active form) was quantified. Equal amount of proteins were probed with an anti-Cdc42 antibody to estimate total Cdc42, and the same blot was stripped and probed with an anti-actin antibody to assess equal protein loading. TGF-β3 transiently stimulated Cdc42 at 5 and 20 min after treatment. At 60 min, both total and active Cdc42 were significantly decreased versus controls. Composite data from three experiments for Cdc42 GTP (*B*) and total Cdc42 (*C*) are shown. Protein level at 0 min was arbitrarily set at 1. Each bar is a mean  $\pm$  SD; \*\**P* < 0.01. (*D*) Sertoli cells were cultured at 1.2 × 10<sup>6</sup> cells/cm<sup>2</sup> on Matrigel-coated bicameral units and the TJ barrier function was monitored by quantifying the TER across the cell epithelium. TGF-β3 (4 ng/mL) was added to the units on day 4.5 (arrow). This experiment was repeated three times. Each data point is a mean  $\pm$  SD; \*\**P* < 0.01.

any change in steady-state levels of integral membrane proteins at the BTB in the presence or absence (control) of TGF- $\beta$ 3. The dominant-negative mutant of Cdc42 contained a site-specific mutation that converted amino acid residue 17 from Thr (T) to Asn (N). This thereby sequesters guanine nucleotide exchange factors to prevent endogenous Cdc42 from being activated (11). Transfection was performed 2 d after Sertoli cell isolation to allow functional TJ barrier and ultrastructures of BTB to form (12). Overexpression of Cdc42 and T17N in primary Sertoli cells was confirmed by RT-PCR (Fig. 3A, i) and immunoblotting (Fig. 3A, ii). An approximately 8-fold and 2.5-fold increase in Cdc42 mRNA and protein versus vector pCIneo control were observed, respectively. Two days after transfection, cell lysates were harvested to examine protein levels of several BTB-associated proteins by immunoblotting. It was found that levels of several TJ (e.g., occludin, JAM-A, CAR, and ZO-1) and basal ES proteins (e.g., N-cadherin,  $\alpha$ -catenin,  $\beta$ -catenin, and  $\gamma$ -catenin) remained unaltered after overexpression of Cdc42 and T17N versus pCIneo vector control (Fig. 3 B-D). Furthermore, when transfected cells were treated with TGF- $\beta$ 3 (4 ng/mL) for 1 h, no significant changes in protein levels were noted (Fig. 3 B-D). Collectively, these findings suggest that overexpression of Cdc42 or its dominantnegative mutant T17N in Sertoli cells did not affect the steady-state levels of integral membrane proteins at the BTB. It is noted that TGF-β3 perturbs the Sertoli cell BTB function via p38 MAPK (10, 13). Therefore, we examined the phosphorylation level of p38 MAPK after overexpression of Cdc42 or T17N in the presence or absence of TGF- $\beta$ 3 (Fig. 3 *E* and *F*). Consistent with the previous findings, TGF- $\beta$ 3 enhanced phosphorylation of p38 MAPK after TGF- $\beta$ 3 stimulation in vector control cells. Unexpectedly, overexpression of Cdc42 alone also activated p38 MAPK, possibly as a result of the increased level of Cdc42 to transduce signal in the p38 MAPK pathway. However, the level of phosphorylated-p38 MAPK was not affected by T17N overexpression. Significantly, inhibition of endogenous Cdc42 by T17N blocked TGF- $\beta$ 3-induced p38 MAPK phosphorylation (Fig. 3 *E* and *F*).

Active Cdc42 Is Essential for the TGF-β3–Enhanced Protein Endocytosis at the BTB. TGF- $\beta$ 3 is known to disrupt Sertoli cell BTB function by enhancing endocytosis of integral membrane proteins at the BTB (8). To address whether TGF- $\beta$ 3 induces protein internalization via activation of Cdc42, we performed an endocytosis assay using Cdc42- or T17N-expressing Sertoli cells in the presence or absence of TGF- $\beta$ 3 using Sertoli cells cultured for 4 d with an intact epithelium. Cell surface proteins of Sertoli cells expressing vector control (pCIneo), Cdc42, or T17N were biotinylated with approximately equal amounts of biotinylated proteins (e.g., occludin and CAR) were found on the cell surface in these cells (Fig. S1). Sertoli cells were then incubated with or without TGF-β3 (4 ng/mL) for 5, 20, and 60 min. Internalized proteins were evaluated by recovering cell surface biotinylated proteins on streptavidin beads. We quantified the rate of protein internalization by calculating the percentage of endocytosed protein, which is defined as the level of internalized proteins over



+TGF-β3 (4 ng/ml)

Fig. 3. Activation of p38 MAPK by TGF- $\beta$ 3 is mediated by Cdc42. (A) Sertoli cells were cultured at  $0.5 \times 10^6$  cells/cm<sup>2</sup> for 2 d to establish a functional TJ barrier with the ultrastructures of TJ, basal ES and desmosome when examined by electron microscopy as earlier described (12). Thereafter, these Sertoli cells were transfected with vector control (pCineo), full-length Cdc42 (Cdc42), or dominant-negative mutant of Cdc42 (T17N). (i) Total RNA was extracted 12 h posttransfection and treated with DNase I to remove any possible genomic DNA contamination, and the steady-state level of Cdc42 mRNA was monitored by RT-PCR with S16 served as a loading control (Upper). (ii) Immunoblotting using a specific anti-Cdc42 antibody was performed 2 d after transfection to assess the increase in Cdc42 and T17N protein levels with the actin served as a loading control. Lower panels in *i* and *ii* are composite results of the corresponding RT-PCR and immunoblot analysis from three experiments. Cdc42 mRNA and protein levels were normalized against S16 and actin, respectively, wherein the mRNA and protein level from cells transfected with pCIneo arbitrarily set at 1. (B) Protein lysates were harvested 2 d after transfection. Before termination, cells were treated with or without TGF-B3 (4 ng/mL) for 60 min. Steady-state levels of BTB-associated proteins (25 µg of protein) were then assessed by immunoblotting. (C, D) Bar graphs (mean  $\pm$  SD) of composite results of three independent immunoblotting experiments such as those shown in B with the protein levels normalized against actin, wherein the protein level for each specific BTB marker from cells transfected with pCIneo (vector alone) was arbitrarily set at 1. (E) Phosphorylation of p38 MAPK was quantified by immunoblotting using an anti-phospho-p38 antibody. Addition of TGF- $\beta$ 3 in vector control (pClneo) cells or overexpression of Cdc42 alone resulted in an increase in phosphorylation of p38 MAPK. Activation of p38 MAPK by TGF-<sub>β3</sub> was Cdc42-dependent as overexpression of the dominant-negative mutant T17N prevented its activation (i.e., phosphorylation) induced by TGF- $\beta$ 3. Total p38 MAPK level remained unchanged in all groups. (F) Bar graphs (mean  $\pm$  SD) show composite results of three experiments. Protein levels were normalized against actin with the protein level from cells transfected with pCIneo (vector alone) arbitrarily set at 1; \*\*P < 0.01.

total cell surface proteins that were biotinylated without stripping. As shown in Fig. 4A, B, and E, Sertoli cells expressing full-length Cdc42 displayed an increase in endocytosis of occludin and CAR versus vector control. In contrast, expression of T17N in Sertoli cells did not change the rate of endocytosis significantly versus control cells (Fig. 4 A, B, and E). Similar to the previously published results (8), TGF-\beta3 promoted endocytosis of occludin and CAR (Fig. 4 A, C, and F). Besides, we found that by overexpressing Cdc42 and stimulating the cells with TGF- $\beta$ 3, it has an additive effect on enhancing protein endocytosis (Fig. 4A, D, and G). Importantly, Sertoli cells lacking active Cdc42, by expressing dominant-negative mutant T17N, was shown to eliminate the stimulatory effect of TGF- $\beta$ 3 on protein endocytosis (Fig. 4 A, D, and G). Collectively, these data demonstrated that the disruptive effects of TGF-\u00b33 on BTB dynamics via an increase in protein endocytosis at the BTB is mediated by Cdc42. Furthermore, these findings also illustrated that, although protein endocytosis at the Sertoli cell BTB per se under basal condition is not entirely de-



Fig. 4. TGF-β3-mediated acceleration of protein endocytosis at the BTB requires active Cdc42. (A) Sertoli cells expressing vector control (pClneo), Cdc42, or dominant-negative Cdc42 (T17N) were used for endocytosis assay 2 d after transfection. Cells were biotinylated at 4 °C and incubated in the presence or absence of TGF-B3 (4 ng/mL) for 0, 5, 20, or 60 min at 35 °C to allow protein endocytosis. At specified time points, biotin on cell surface proteins that were not internalized were stripped. Cell lysates were harvested in RIPA lysis buffer. Biotinylated proteins that were endocytosed were recovered by using NeutrAvidin beads for immunoblotting. Half of the total cell surface biotinylated proteins, without stripping with MESNA buffer, were used to estimate the percentage of endocytosed protein. The blots for occludin and CAR shown herein are representative of three experiments. Actin served as a loading control. B-D and E-G are the corresponding data for occludin and CAR. (B and E) Results were expressed as the percentage of endocytosed protein normalized against total cell surface biotinylated protein. Transient overexpression of Cdc42 enhanced protein endocytosis whereas overexpression of T17N did not affect kinetics of protein internalization versus vector control, illustrating that Cdc42 facilitated but was not essential for protein endocytosis at the BTB under normal physiological conditions. (C and F) Addition of TGF-<sub>β3</sub> increased the rate of protein endocytosis versus vector control. Each time point is mean  $\pm$  SD; \*\*P < 0.01 (pCIneo vs. Cdc42, T17N or pCIneo+TGF-β3). (D and G) Treatment of Sertoli cells overexpressing Cdc42 with TGF-<sub>β3</sub> further enhanced endocytosis. However, overexpression of T17N abolished TGF-<sub>β</sub>3-induced enhancement of protein endocytosis. Each time point is a mean  $\pm$  SD; \*\*P < 0.01 (Cdc42 vs. Cdc42+TGF-β3); n.s., no significant change (T17N vs. T17N+TGF-β3).

pendent on Cdc42, the TGF- $\beta$ 3-induced protein endocytosis is dependent on Cdc42.

Protein Recycling to the Cell Surface Is Impaired by an Inactivation of Cdc42. The amount of proteins that remains at the intercellular junctions is the net result of protein endocytosis, recycling, transcytosis, and intracellular degradation. Thus, we next investigated if Cdc42 affects recycling of endocytosed proteins to cell surface. Cell surface proteins were biotinylated and cells were incubated at 18 °C for 2 h to allow accumulation of endocytosed proteins in early or sorting endosomes (14). Biotin that remained on cell surface proteins that were not endocytosed was removed by 2-mercaptoethanesulfonate (MESNA) stripping buffer. Biotinylated proteins that were internalized into cell cytosol were allowed to recycle back to the plasma membrane for 1 h, which was subsequently extracted to track the amount of recycled biotinylated proteins on the cell surface. Fig. S2 illustrates that an equal amount of protein was used for the recycling assay shown in Fig. 5. In line with the previously published results, TGF-\u00b33 impaired targeting of endocytosed proteins back to the cell surface (4). Instead, they underwent endosome-mediated protein degradation (Fig. 5A), which eventually led to a disruption of Sertoli cell TJ barrier (Fig. 5A and Fig. 2D). However, in this study, it was shown that overexpression of T17N alone also inhibited protein recycling but to a lesser extent versus control cells treated with TGF- $\beta$ 3 (T17N vs. pCIneo+TGF- $\beta$ 3; Fig. 5 A and B). Interestingly, it is noted that there was no significant change in recycling of CAR when T17N-expressing cells were treated with TGF-β3.

Inactivation of Cdc42 Blocks TGF-β3–Induced Disruption of Cell Junctions at the BTB. We next characterized if an inactivation of Cdc42 would lead to any phenotypic changes in the Sertoli cell TJ barrier and protein distribution at the cell-cell interface (Fig. S3). Overexpression of dominant-negative T17N was performed on day 2 by transfecting Sertoli cells with an established TJ barrier. On day 4.5, 4 ng/mL TGF- $\beta$ 3 was added in both the apical and basal compartments of the bicameral units for 24 h (Fig. 6A). In vector control cells, TGF- $\beta$ 3 significantly perturbed the TJ barrier by 3 h which persisted until the end of the experiment. Conversely, T17N expression prevented TGF-β3-induced TJ barrier disruption (Fig. 6A). We next determined if these changes in TJ barrier disruption would be reflected by an alteration in the localization of junction proteins at the cell-cell interface. Transfected cells were denoted by vectors that were fluorescently labeled by Cy3 (Fig. 6B and C, red). CAR (Fig. 6B, green) and ZO-1 (Fig. 6C, green) was localized at the cell-cell interface in control cells without treatment of TGF-\u03b33 that formed an almost undisrupted barrier. However,



**Fig. 5.** Inactivation of Cdc42 in Sertoli cell epithelium perturbs protein recycling. (*A*) Recycling of proteins from cytosol to plasma membrane was assessed as described in *Materials and Methods*. Overexpression of T17N resulted in a decrease in recycling of proteins, such as CAR, back to cell surface. Also, treatment of Sertoli cell BTB with TGF- $\beta$ 3 perturbed CAR protein recycling. However, inactivation of Cdc42 neither blocked nor potentiated TGF- $\beta$ 3-induced disruption of protein recycling. (*B*) Composite data of *A* is shown.

cells that were treated with TGF-\beta3 (4 ng/mL) displayed a disruption of CAR and ZO-1 staining at the Sertoli cell junctions (Fig. 6B and C). In cells with Cdc42 overexpression, a mild disruption of CAR localization (Fig. 6B) at the cell junction was noted, and more ZO-1 also redistributed near the cell surface (yellow arrowheads in Fig. 6B) to cytosol (white arrowheads in Fig. 6B). These findings are consistent with the results indicating that both TGF-\beta3 treatment and Cdc42 overexpression resulted in enhanced endocytosis as shown in Fig. 4 A-G. However, both CAR and ZO-1 remained at the cell-cell interface in Sertoli cells overexpressing T17N (Fig. 6 B and C and Fig. S3). In agreement with the additive effect in endocytosis by treating Cdc42-expressing cells with TGF- $\beta$ 3, a more severe disruption in CAR and ZO-1 localization was noted (Fig. 6 B and C, green). Based on results shown in Fig. 4 A and D-G, TGF- $\beta$ 3-induced enhancement in endocytosis was abolished when Cdc42 was inactivated. This finding was confirmed by data shown in Fig. 6 A and B in which overexpression of T17N in the epithelium would render these cells nonresponsive to the disruptive effects of TGF- $\beta$ 3. For instance, the disruptive effect of TGF-B3 in redistributing CAR and ZO-1 from the cell surface to cytosol was blocked when Cdc42 was inactivated (Fig. 6 *B* and *C*).

#### Discussion

TGF-<sub>b</sub>3–Accelerated Protein Endocytosis That Leads to BTB Disruption Is Mediated by Cdc42. Cdc42 was shown to be a downstream effector necessary for the TGF-β3-induced BTB restructuring. TGF-β3 appears to exert its effects by first activating Cdc42 to its GTP-bound form, which in turn enhances protein endocytosis at the BTB to disrupt the TJ barrier. Although overexpression of Cdc42 in Sertoli cells facilitates protein endocytosis, its inactivation in Sertoli cells, such as by overexpressing T17N, did not affect the kinetics of protein endocytosis at the BTB or the distribution of CAR and ZO-1 at the cell surface as reported herein. This illustrates that the function of Cdc42 on endocytosis under normal physiological conditions can be superseded by other GTPases, as several GTPases are involved in endocytic vesiclemediated protein trafficking (15, 16). However, Cdc42 is absolutely needed for TGF-<sub>β</sub>3-mediated Sertoli cell BTB disruption and this effect cannot be superseded by other GTPases, as supported by several observations. First, Cdc42 was activated by TGF-β3 preceding the TJ barrier disruption. Second, inactivation of Cdc42 via an overexpression of T17N in Sertoli cells would render a loss of response of the cell epithelium to TGF-\beta3induced acceleration in protein endocytosis. Third, perhaps most importantly, an inactivation of Cdc42 would lead to a loss of response of the Sertoli cells to the disruptive effects of TGF-B3 regarding the TJ barrier function. These findings are further supported by immunofluorescence analysis, which showed that TGF-β3 was effective to induce relocation of CAR and ZO-1 from the cell-cell interface to cytosol, but it failed to induce similar redistribution of CAR and ZO-1 in Sertoli cells when Cdc42 was inactivated when T17N was overexpressed in the Sertoli cell epithelium. Collectively, these data demonstrate unequivocally the pivotal role of Cdc42 in mediating the regulatory function of TGF- $\beta$ 3 in BTB dynamics. However, it is of interest to note that the expression of Cdc42 in the seminiferous epithelium as demonstrated by immunohistochemistry using an antibody against total Cdc42 is stage-stage, where its expression at the BTB is lowest at stage VIII with TGF- $\beta$ 3 expression at this site is highest at this stage (13). If Cdc42 is so crucial to TGF-B3 action at stage VIII, why would its expression level be reduced at the BTB at this stage? We offer the following explanation. The antibody used in our study stained total Cdc42, yet most of the Cdc42 at the BTB at this stage would have been activated by TGF- $\beta$ 3, as shown in Fig. 2Å, when TGF- $\beta$ 3 expression was highest at the BTB site at stage VIII as reported earlier (13). As activated Cdc42 would have a different antigenic configuration,



Fig. 6. Sertoli cell junction disruption induced by TGF-B3 is blocked by inactivation of Cdc42. (A) Sertoli cells were cultured at  $1.2 \times 10^6$  cells/cm<sup>2</sup> on bicameral units and transfected with vector control pCineo or T17N on day 2 after plating; 2.5 d thereafter (i.e., on day 4.5), cells were treated with or without TGF-β3 (4 ng/mL) and the TJ barrier function was monitored by TER measurement. Expression of T17N alone did not result in change in TER versus vector control (pCIneo). Addition of TGF-<sub>β</sub>3 in vector control cells resulted in a significant decrease in TER, illustrating TJ barrier disruption. Conversely, overexpression of T17N blocked the disruptive effect of TGF-<sub>β</sub>3 on the TJ barrier. (B and C) Sertoli cells transfected with vector control (pClneo), Cdc42, or T17N were treated with or without 4 ng/mL of TGF- $\beta$ 3 for 60 min. Transfected cells were tracked by fluorescently labeling plasmids with Cy3 (red). Cells were fixed and stained with either an anti-CAR antibody (green) (B) or an anti-ZO-1 antibody (green) (C). Nuclei were visualized by DAPI (blue). Overexpression of Cdc42 caused a mild redistribution of CAR (B) and ZO-1 (C) from the Sertoli-Sertoli cell interface to cytosol versus pCIneo. Treatment of control cells with TGF-<sub>β</sub>3 disrupted the localization of CAR (B) and ZO-1 (C) at the cell-cell interface in both control and Cdc42overexpressed cells, causing them to relocate from the cell surface (yellow arrowhead) to cytosol (white arrowhead). Whereas overexpression of Cdc42 worsened junction damage induced by TGF-β3, inactivation of Cdc42 by overexpressing T17N blocked the TGF-<sub>β</sub>3-induced junction disruption, confirming results in A.

this makes it possibly unrecognizable by the anti-total Cdc42 antibody. These findings are analogous to an earlier report illustrating total FAK is localized mostly at the BTB, but its active phosphorylated forms (e.g., p-FAK-Tyr<sup>397</sup> and p-FAK-Tyr<sup>576</sup>) are restricted to the apical ES (17), where the anti-total FAK failed to detect these two activated forms at this site. Additionally, germ cells, in particular preleptotene spermatocytes, may regulate the expression and/or the activation of Sertoli cell Cdc42 in the seminiferous epithelium microenvironment, such as the BTB.

**Cdc42** Is Not Involved in TGF-β3–Mediated Protein Recycling Events. In the present study, Cdc42 was shown to be involved in protein recycling, analogous to earlier studies in MDCK cells reporting that a deletion (18) or inactivation of Cdc42 (19) would impede protein recycling back to the cell surface. However, Cdc42 is not essential in basal and TGF-β3–mediated protein recycling. For instance, cell–cell junctions remain intact in T17N-expressing cells despite a decrease in recycling of CAR back to the cell surface. Furthermore, when control cells were treated with TGF-β3, a disruption of CAR and ZO-1 localization was observed when there is an increase in endocytosis and a decrease in protein recycling. This conclusion is further strengthened from the immunofluorescence staining and TER measurement data, which show that overexpression of T17N is able to reverse the disruptive effects of TGF-B3 on the TJ barrier by blocking the increase in TGF-β3-mediated endocytosis. These results collectively reveal that the role of Cdc42 on mediating TGF-β3induced protein endocytosis is more profound and is able to supersede its effect on recycling of proteins to cell surface. Conversely, if protein recycling at the BTB is dependent entirely on Cdc42, the TJ barrier function would have been disrupted after overexpression of T17N in Sertoli cells because of the impairment in protein recycling. These findings are consistent with earlier studies that show an inactivation of Cdc42 did not result in morphological changes in TJ fibrils in MDCK cells (19, 20). It is likely that, although Cdc42 activity is needed for protein recycling at the BTB, other small GTPases, such as Rab proteins (e.g., Rab13) (21, 22) play a more dominant role on protein recycling, and TGF-β3 can also mediate its effects on recycling via one of these other GTPases.

## Cdc42 Are Working with Polarity Proteins to Regulate BTB Dynamics.

During the infiltration of Neisseria meningitidis across the bloodbrain barrier that causes meningitis, an activation of Cdc42 was detected that induced protein endocytosis in the microvessel endothelium to increase TJ permeability to facilitate the bacterial entry (23). To prevent hemorrhage, the bacterial pili also activated Cdc42 behind their entry site to recruit polarity complex Par3/Par6/aPKC to reestablish the endothelial barrier by relocating the endocytosed TJ and AJ proteins via transcytosis to the site (23). In fact, Cdc42 is known to be involved in targeting of proteins to the basolateral domain of epithelial cells (19, 24). Together with the previously published results in which Par6 and 14-3-3 (also known as Par5) were shown to be involved in endocytic vesicle-mediated protein trafficking at the BTB (25), it is likely that Cdc42 is working in concert with Par6 and 14-3-3 to play a dual role in regulating BTB dynamics. First, Cdc42 facilitates TGF-β3-enhanced endocytosis to disrupt "old" TJ-fibrils above the migrating spermatocytes. Second, it also helps to target the endocytosed proteins to the "new" BTB site below the spermatocytes via transcytosis, likely working with Par6 and 14-3-3. This thus maintains the immunological barrier integrity during the transit of spermatocytes at the BTB.

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## **Materials and Methods**

Animals and Antibodies. The use of Sprague-Dawley rats was approved by the Rockefeller University Animal Care and Use Committee (protocols 06018 and 09016). Antibodies used in this study are listed in Table S1.

**General Methods.** Primary Sertoli cell cultures, DNA transfection, cell staining, preparation of cDNA constructs, Cdc42 activation assay, immunohistochemistry, dual-labeled immunofluorescence analysis by fluorescence microscopy, TJ barrier function assessment, and statistical analysis are described in *SI Materials and Methods*.

**Endocytosis Assay.** Endocytosis assay was performed as described (4, 25). Cell lysates were harvested in RIPA buffer (50 mM Tris/HCl, 150 mM NaCl, 5 mM EGTA, 0.2% SDS, 1% Triton X-100, 1% sodium deoxycholate, and 2 mM N-ethylmaleimide, pH 8), with 1  $\mu$ g/mL aprotinin, 1  $\mu$ g/mL leupeptin, 2 mM PMSF, and 15  $\mu$ L/mL each of phosphatase inhibitor mixtures 1 and 2 (Sigma). Biotinylated proteins were recovered by Ultralink Immobilized NeutrAvidin Plus beads (Pierce) and subjected to SDS/PAGE and immunoblotting.

Recycling Assay. Cell surface proteins were biotinylated at 4 °C as described (4). Cells were then incubated at 18 °C for 2 h to allow internalization and accumulation of biotinvlated proteins in early or sorting endosomes (14). Biotinylated proteins that were not endocytosed were stripped by 50 mM 2-mercaptoethanesulfonate (MESNA) buffer (15). F12/DMEM with or without TGF-β3 (4 ng/mL) was added for 1 h at 35 °C and plasma membrane was extracted. In brief, cells were scraped from 100-mm plates in 250 mM sucrose, 20 mM Tris-HCl, 2 mM EGTA, pH 7.5, freshly supplemented with protease and phosphatase inhibitors (lysis buffer). Cells were sonciated and unbroken cells and nuclei were removed by centrifugation at  $3,000 \times q$ for 5 min. Postnuclei supernatant was centrifuged at  $17,000 \times q$  for 20 min, and the pellet was resuspended in 100 µL of lysis buffer and overlaid on 1 mL of 1.12 M sucrose solution. Ultracentrifugation was performed at 100,000  $\times$  g (at 4 °C) for 1 h and the top layer of the sucrose cushion was enriched with plasma membrane. Subsequently, the top layer was collected and centrifuged at 40,000  $\times$  g for 30 min, and the pellet (plasma membrane) was dissolved in RIPA buffer (~150-200 µg of protein) for affinity precipitation by NeutrAvidin Plus beads.

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