Signaling at the Slit Diaphragm

THOMAS BENZING

Renal Division, University Hospital Freiburg, Freiburg, Germany

Diseases of the glomerular filter of the kidney are a leading cause of end-stage renal failure. Recent studies have emphasized the critical role of the slit diaphragm of podocytes for the size-selective filtration barrier of the kidney and revealed novel aspects of the mechanisms that lead to proteinuria, in both inherited and acquired diseases (1–4). Several critical structural protein components of the slit diaphragm have been identified. Recently, it has been speculated that these slit diaphragm proteins, in addition to their structural functions, participate in common signaling pathways. This review focuses on what is known about signaling at the slit diaphragm. It provides a snapshot of our current understanding of the signaling properties of slit diaphragm proteins and projects a framework for further studies necessary to delineate the function and dynamics of the slit diaphragm protein complex and the pathogenesis of nephrotic syndrome.

Ultrafiltration of plasma in the renal glomeruli is a major function of the kidney. The glomerular filter through which the ultrafiltrate has to pass consists of three layers: the fenestrated endothelium, the intervening glomerular basement membrane, and the epithelial podocyte foot processes. This filtration barrier behaves as a size-selective sieve restricting the passage of macromolecules on the basis of their size, shape, and charge (5–7). Although the glomerular filter is a primary target of a large number of progressive disorders that lead to chronic renal insufficiency, until recently, little was known about the importance of podocytes for establishing the size-selective filtration barrier of the kidney. The recent description of gene defects in hereditary nephrotic syndrome resulting in the loss of podocyte proteins has dramatically changed this situation. Together with data from various animal models, these studies have unraveled important aspects of the pathogenesis of proteinuric kidney diseases and challenged our understanding of the glomerular filter (1,8–10).

Podocytes are the visceral epithelial cells of the kidney glomerulus (11–13). They elaborate long, regularly spaced, interdigitated foot processes that completely enwrap the glomerular capillaries. Interdigitating podocyte foot processes form an ~40-nm-wide filtration slit and are connected by a continuous membrane-like structure called the slit diaphragm. When podocytes are injured, the intercellular junctions and cytoskeletal structure of the foot processes are altered and the cell takes on an "effaced" phenotype. Typical slit diaphragm structures disappear and proteinuria develops (10). Because there is no case of nephrotic syndrome without major changes in podocyte morphology, it has been speculated for many years that the slit diaphragm is an important component of the glomerular filter (14).

A milestone in glomerular research was the cloning of nephrin by the Tryggvason group in 1998 together with its localization to the slit diaphragm of podocytes (15–18). This work suggested that nephrin is a critical structural component of the slit membrane and bridges the distance between interdigitating podocyte foot processes (3,9,19). Nephrin, encoded by *NPHS1*, the gene mutated in congenital nephrotic syndrome of the Finnish type, is a transmembrane adhesion protein of the Ig superfamily (Figure 1). Both humans and mice lacking nephrin are born without typical slit diaphragms and exhibit severe podocyte abnormalities and massive proteinuria already *in utero* (20,21).

Recently, several additional components of the slit diaphragm have been identified (22–25). Mutations in the genes encoding for these proteins cause severe podocyte changes and nephrotic syndrome. *NPHS2*, the gene responsible for a steroid-resistant form of nephrotic syndrome, was cloned by the Antignac group and encodes for podocin, a stomatin family membrane protein (23). Podocin almost exclusively localizes to the slit diaphragm of podocytes and interacts with the cytoplasmic tail of nephrin (26–28). Gene disruption in mice results in a severe congenital nephrotic syndrome (29). The cytoplasmic multi-adaptor protein CD2AP was cloned by the Shaw laboratory as a CD2-interacting protein in lymphocytes (30). CD2AP also interacts with nephrin and localizes to the cytoplasmic face of the slit diaphragm (31). It is interesting that mice completely lacking CD2AP die of massive proteinuria 6 wk after birth, suggesting a critical role for CD2AP in slit diaphragm function (22). Moreover, CD2AP haploinsufficiency seems to be linked to glomerular disease susceptibility both in mice and in humans, further supporting the critical role of CD2AP for the integrity of the glomerular filter (32,33). Donoviel *et al.* (24) identified neph1, another Ig superfamily protein (Figure 1) that localizes to the slit and causes congenital nephrotic syndrome in knockout mice. Neph1 is a member of a family of Ig adhesion molecules that are expressed in podocytes and interact with podocin (34). Recently, the adhesion protein and member of the protocadherin superfamily of proteins FAT1 was shown to localize to the slit membrane of podocytes (35). Targeted deletion of the *fat1* gene in mice results in nephrotic syndrome and podocyte changes that resemble nephrin mutation (25).

Correspondence to Thomas Benzing, Renal Division, University Hospital Freiburg, Hugstetterstrasse 55, 79106 Freiburg, Germany. Phone: 49-761-270-3559; Fax: 49-761-270-6362; E-mail: benzing@med1.ukl.uni-freiburg.de
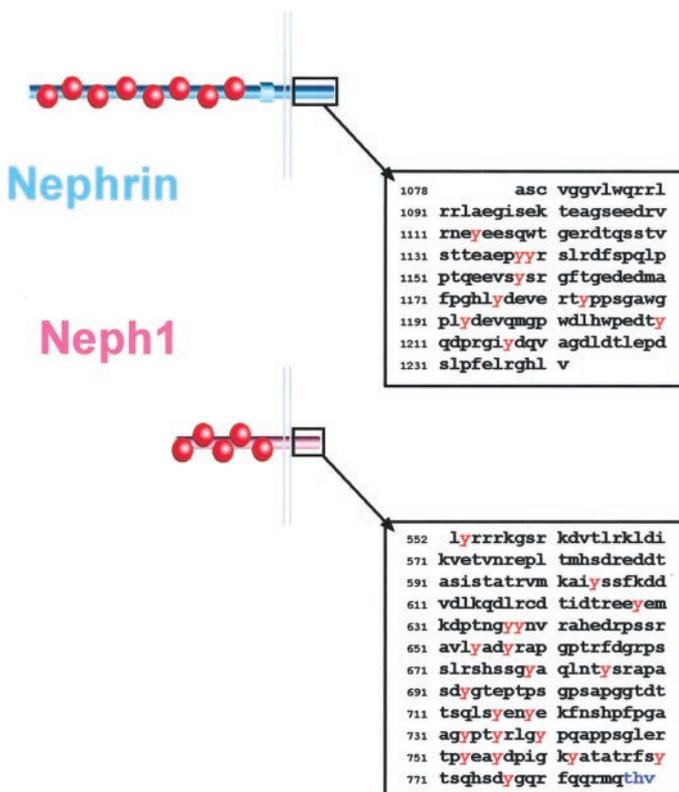
Figure 1. Nephrin and neph1 are adhesion proteins of the Ig superfamily. They contain carboxy terminal cytoplasmic tails that can be phosphorylated at tyrosine residues (red y's). Phosphotyrosine motifs of these proteins serve as docking sites for intracellular signaling adaptors.
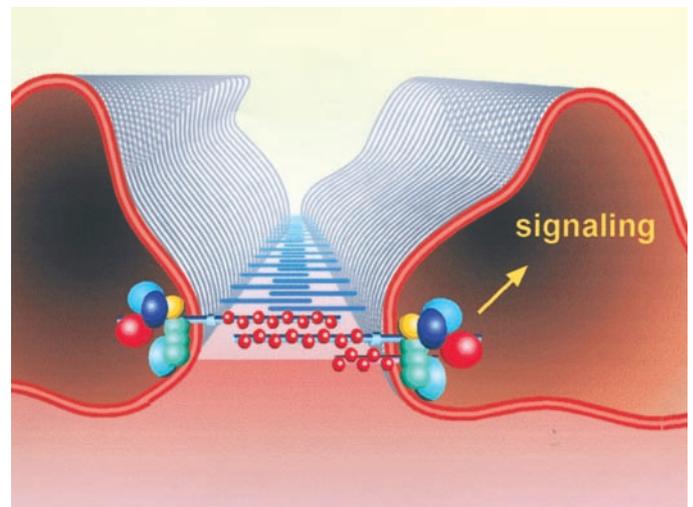

Figure 2. The slit diaphragm of podocytes is a specialized cell junction with signaling properties. The slit diaphragm connects interdigitating foot processes of the podocyte (FP) and is an essential part of the glomerular filter of the kidney. Slit diaphragm proteins (nephrin and neph1) recruit cytoplasmic adaptor proteins to initiate signal transduction events that lead to the regulation of complex biologic programs.

The identification of these slit diaphragm proteins suggested that these proteins may serve important structural functions at the filtration slit necessary for establishing and maintaining an intact glomerular filter. However, accumulating evidence suggests that slit diaphragm proteins do not only serve structural functions setting up a size- and charge-selective filtration barrier but also may participate in common signaling pathways necessary to maintain the functional integrity of podocytes (27,36–38). This model proposes that the slit diaphragm protein complex is a highly dynamic protein complex that recruits signal transduction components and initiates signaling to regulate complex biologic programs in the podocyte, such as regulation of cytoskeletal rearrangements, polarized sorting and endocytosis, cell differentiation and suppression of proliferation, mechanotransduction, or podocyte viability.

Proof of Principle: Nephrin and Neph1 Are Signaling Proteins

Signal transduction is the process of converting extracellular signals into cellular responses. Transmission of an extracellular signal involves transmembrane proteins that have domains on both sides of the plasma membrane (Figure 2). The basic principle of signaling is that ligand binding on the extracellular side converts the receptor from an inactive to an active form. The process is called signal transduction because a signal has

in effect been transduced across the membrane. In general, signal transduction systems are assembled through protein–protein interactions (39). This means that signaling events that are initiated at the plasma membrane control the reversible assembly of multiprotein complexes to regulate intracellular processes. Much of this regulation is achieved through attachment of phosphate groups to (phosphorylation) or cleavage of phosphate (dephosphorylation) from serine, threonine, or tyrosine residues of crucial protein substrates (40). Phosphorylation of these residues creates binding sites for modular phosphoprotein-binding domains such as Src homology 2 and phosphotyrosine-binding domains in the case of phosphotyrosine or 14-3-3, WW domains, forkhead-associated domains, and, tentatively, WD40 repeats and leucine-rich regions in the case of phosphoserine/phosphothreonine. Thus, phosphorylation connects proteins with their upstream kinases and downstream effectors to form multiprotein complexes (40,41).

Nephrin and neph1 are adhesion proteins and members of the Ig superfamily (Figure 1). In addition to their extracellular domains that are part of the slit membrane connecting interdigitating foot processes and a single transmembrane domain, these proteins contain a short cytoplasmic tail with a number of tyrosine residues that are predicted to serve as target for dynamic phosphorylation *in vivo* (27,34). Intriguing is that tyrosine phosphorylation at the cytoplasmic face of the slit diaphragm has been observed many years before the cloning of nephrin or the description of signaling properties of slit diaphragm proteins (42). In agreement with this finding, it has recently been shown that nephrin and neph1 are phosphorylated on tyrosine residues *in vitro* and *in vivo* (28,36,37,43–45). Furthermore, recent data suggest that tyrosine phosphorylation of the cytoplasmic tail of these proteins seems to be tightly regulated (37,38).

What is the protein (kinase) responsible for tyrosine phosphorylation of nephrin and neph1? A recent study demonstrated that the Src family nonreceptor protein tyrosine kinase Fyn directly binds to the cytoplasmic tail of nephrin and mediates nephrin phosphorylation *in vitro* and *in vivo* (43). It is interesting that targeted deletion of *fyn* in mice with or without co-deletion of the tyrosine kinase gene *yes* resulted in the loss of nephrin tyrosine phosphorylation, a severe podocyte dysfunction, foot process effacement, and proteinuria, suggesting that these abnormalities may be at least partially related to altered nephrin phosphorylation (43,46).

Moreover, it could be shown that nephrin and neph1 are signaling proteins and able to stimulate transcriptional activation in a model system (27,37). Nephrin and neph1 activate the transcription factor AP-1 *via* the stimulation of a mitogen-activated protein kinase module. Direct interaction of the tyrosine-phosphorylated cytoplasmic tail of nephrin with podocin dramatically facilitated nephrin signaling, whereas inhibition of tyrosine phosphorylation of the cytoplasmic tail of nephrin abrogated nephrin-mediated signal transduction (27). It is interesting that podocin-mediated augmentation of nephrin sig-

naling required the direct interaction of the carboxy-terminal cytoplasmic domain of podocin with the cytoplasmic tail of nephrin (27,38). By contrast, in another study, neph1 signal transduction was augmented by direct interaction of the cytoplasmic tail of neph1 with the multiadaptor and scaffolding protein ZO-1 (37). Although derived from a model system, these studies provided the proof of principle that slit diaphragm proteins can initiate signal transduction.

Intracellular Signaling Adaptors: The Functional Slit Diaphragm Complex Assembles through Dynamic Protein–Protein Interactions

Signal transduction from cellular receptors requires intracellular adaptor proteins (Figure 3). Adaptor proteins are noncatalytic polypeptides that contain one or more protein interaction modules that mediate protein interactions (47). As described above, many of the protein interactions are regulated through phosphorylation and dephosphorylation of crucial protein and lipid substrates (40,48).

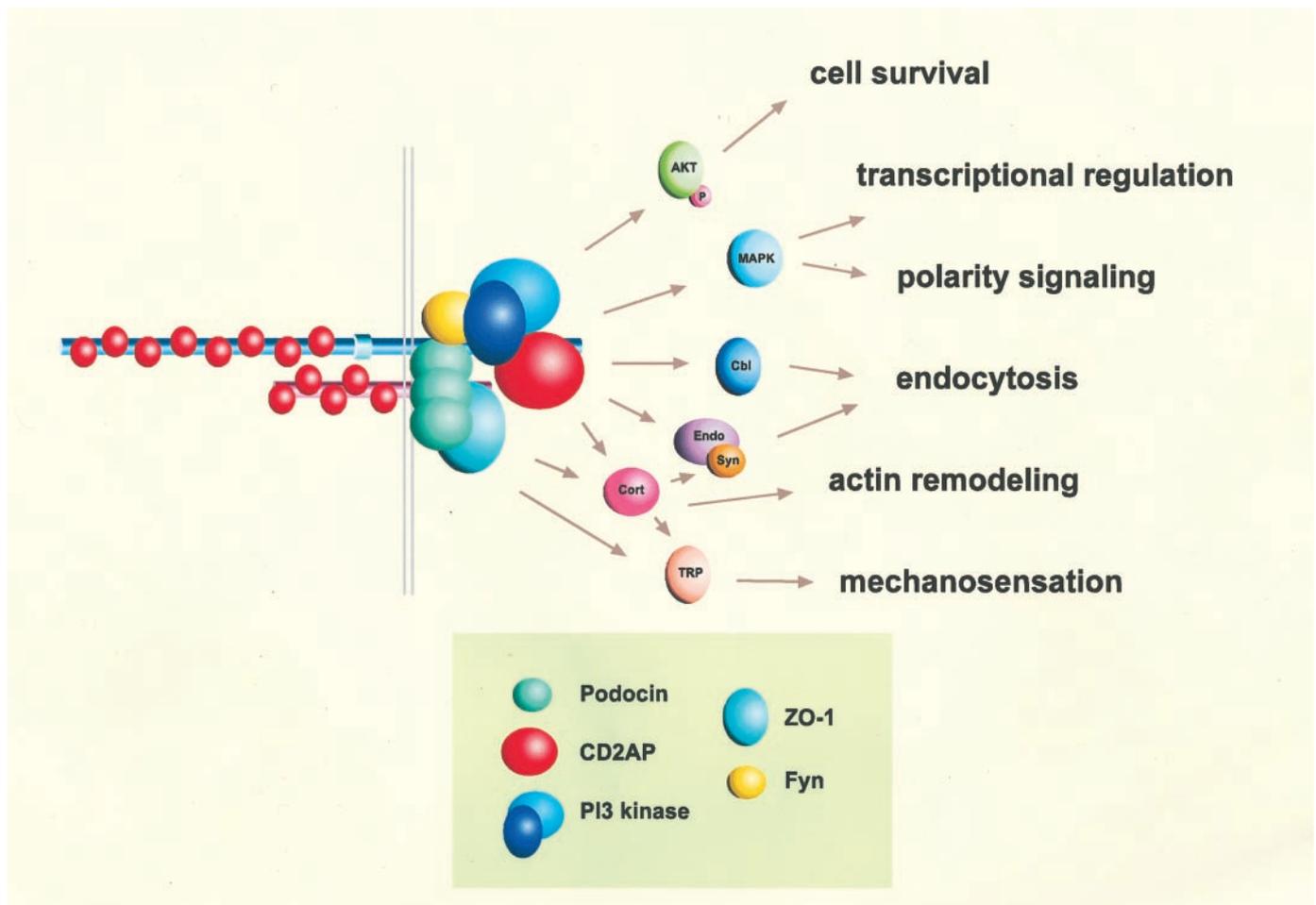By screening phosphotyrosine-binding proteins for their in-

Figure 3. Signaling at the slit diaphragm. Hypothetical signaling pathways involved in the regulation of podocyte biology and glomerular function. AKT, AKT/protein kinase B; Cbl, Casitas B-lineage lymphoma; Cort, cortactin; Endo, endophilin; MAPK, mitogen-activated protein kinase family; Syn, synaptojanin; TRP, hypothetical TRP channel.

teraction with the tyrosine-phosphorylated cytoplasmic tail of nephrin, the protein p85 was the first SH2 domain-containing protein to be identified that binds to the tyrosine-phosphorylated cytoplasmic tail of nephrin *in vivo* (36). p85 is the regulatory subunit of class Ia phosphoinositide 3-OH (PI3) kinase. PI3 kinase activity is responsible for the phosphorylation of lipids at the inner leaflet of the plasma membrane (49). Recruitment of the regulatory p85 subunit to the cytoplasmic tail of nephrin induced the activation of the p110 catalytic subunit, which converts the membrane lipid phosphatidylinositol-4,5-biphosphate to phosphatidylinositol-3,4,5-triphosphate. Thus, lipids at the cytoplasmic side of the filtration slit are phosphorylated by nephrin-activated PI3 kinase, which may initiate a cascade of events in the podocyte foot process (36).

Signaling proteins with pleckstrin-homology (PH) domains accumulate at sites of PI3 kinase activation by directly binding to these phosphorylated lipids. These proteins themselves regulate a variety of crucial cellular programs such as cell survival, actin cytoskeletal dynamics, endocytosis, and cell metabolism (49). Of particular interest in the podocyte is the PH domain–containing serine-threonine kinase AKT (36). Other PH domain proteins that are activated by PI3 kinase and could play a role in podocyte biology include GDP-GTP exchange factors for Rac and ARF6 and protein tyrosine kinases of the Bruton's tyrosine kinase (Btk) and Tec family. Binding of PI3 kinase–generated phospholipids to the PH domain of AKT leads to the translocation and activation of AKT. Among a wealth of effects, AKT activity has been found to be required for the growth factor–dependent survival of a wide variety of cell types ranging from fibroblasts to neurons by blocking apoptosis (50). Consequently, nephrin-mediated activation of PI3 kinase and AKT activity has been shown to inhibit podocyte apoptosis and to increase the threshold for podocyte cell death induced by apoptotic stimuli (36).

However, nephrin is not the only slit diaphragm protein to associate with p85 and activate PI3 kinase. Recently, it was demonstrated that CD2AP directly interacts with p85 (36). Together with nephrin, CD2AP strongly activates PI3 kinase in podocytes. Targeted disruption of the *cd2ap* gene dramatically reduces AKT activity in podocytes and is associated with an increased susceptibility to podocyte apoptosis (36). These findings are particularly interesting in the context of the pathogenic steps that lead to glomerulosclerosis (51–54). Podocyte death and podocyte depletion have been proposed as hallmarks of both primary and secondary forms of glomerulosclerosis for many years and are now considered a key step in the development of progressive renal disease (51,55–57). Thus, the structural and functional integrity of the slit diaphragm proteins and signaling at the slit diaphragm may be required for the inhibition of apoptosis and for cell survival in podocytes. In support of this hypothesis, $cd2ap^{+/-}$ heterozygous mice are haploinsufficient and develop severe glomerular changes at 9 mo of age with a histologic pattern similar to that in human focal segmental glomerulosclerosis (32,33).

Although the underlying mechanism of CD2AP-mediated PI3 kinase activity at the molecular level is not completely understood, recent evidence suggests that by directly interacting with several target proteins, CD2AP may orchestrate PI3 kinase effectors to amplify efficient PI3 kinase signaling (T. Benzing, unpublished data). In analogy to CIN85, CD2AP may also be involved in the recycling and endocytosis of transmembrane receptors (*e.g.*, nephrin), thereby regulating signal transduction from the slit diaphragm (32,58). An additional function of the PI3 kinase downstream effector AKT is to repress collagenase expression and to induce the synthesis of laminin and type IV collagen chains (59,60); both are key components of the glomerular basement membrane. Because basement membrane abnormalities are involved in the development of several forms of proteinuria, it is tempting to speculate that AKT activation may contribute to the synthesis and/or maintenance of an intact glomerular basement membrane. These data further support the concept that signal transduction at the slit diaphragm is critical for podocyte function, viability, and integrity of the glomerular filter.

It's All about Location: Signaling at the Slit Diaphragm Needs a Lipid Raft Surrounding

As mentioned above, nephrin-mediated signaling is facilitated by the direct interaction with the *NPHS2* gene product podocin (27). Podocin, a member of the stomatin protein family with a short amino terminal domain, a transmembrane region, and a cytosolic carboxy terminal domain, is exclusively expressed in podocytes of the developing and mature glomeruli and predicted to form a membrane-associated hairpin-like structure with the N- and C-terminal domains facing the cytosolic side of the slit diaphragm (26). A functional interaction of nephrin with podocin was indirectly confirmed in patients with hereditary nephrotic syndrome. In an interesting study, Koziell *et al.* (61) could show a functional interrelationship between *NPHS1* and *NPHS2*, the genes encoding for nephrin and podocin. However, until recently, the question remained how podocin by directly interacting with nephrin may facilitate nephrin signaling. Some light has been shed on the mechanism through which podocin can augment nephrin signaling by a recent study that demonstrated that podocin-mediated recruitment of nephrin to so-called lipid raft microdomains of the plasma membrane is required for efficient nephrin signaling (38).

Multiple pieces of evidence suggest that the plasma membrane of the filtration slit has a special lipid composition (28,43,44,62). Lipid rafts are specialized microdomains of the plasma membrane with a unique lipid content and a concentrated assembly of signal transduction molecules (63). Rafts have been proposed to form platforms for many important cellular processes, such as polarized sorting of membrane proteins and signal transduction (64–66). Mundel and co-workers (28,44) could show that podocin is a lipid raft–associated protein at the filtration slit. Subsequently, Huber *et al.* (38) demonstrated that podocin serves to recruit nephrin into lipid raft microdomains. Lipid raft targeting of nephrin was required for the proper initiation of nephrin signaling. Disease-causing podocin mutations failed to target nephrin to rafts and lost their ability to augment nephrin signal transduction (38).

Thus, not only the protein components but also a correct lipid composition of the plasma membrane at the slit diaphragm is important for proper signal transduction at the filtration slit.

Talking about the Ligands: What Can We Learn from Model Organisms?

As detailed above, the basic principle of signal transduction is that ligand binding on the extracellular side converts the receptor (in our case, nephrin) from an inactive to an active form. Consequently, an important question is, "What could be the ligand that binds to the extracellular domain of the proteins at the slit diaphragm inducing the activation of signaling cascades as described above?" Early work suggested that nephrin may engage in homophilic interactions (16). Moreover, cross-linking of nephrin molecules was sufficient to induce an increase in tyrosine phosphorylation of the cytoplasmic tail of nephrin (45). Although subsequent studies confirmed homophilic binding of nephrin molecules (67–69), these homophilic interactions may not be the only interactions occurring *in vivo*. Recently, neph1 was shown to serve as a binding partner of the extracellular domain of nephrin (67,69,70). Although these interactions were surprisingly promiscuous, these data suggested that *cis* and *trans* interactions involving at least nephrin and neph1 Ig superfamily proteins are required to set up an intact slit diaphragm structure and induce efficient signal transduction. The identification of neph1 led to the description of a family of neph proteins in humans and mice (neph1, neph2, neph3/filtrin), all expressed in the podocyte (34,71). Whether these proteins act as additional ligands of nephrin at the filtration slit is not clear to date.

These data are strongly supported by experimental results derived from various model organisms. Nephrin and neph proteins can be found in different species ranging from worm and fly to mice and humans. Although the fruit fly *Drosophila melanogaster* and the nematode *C. elegans* lack structures comparable to a mammalian kidney glomerulus, some cells engage in specialized cell–cell contacts that closely resemble the specialized cell junction of podocytes. The *Drosophila* homologues of nephrin (hibris [*hbs*] and sticks-and-stones [*sns*]) interact with homologues of mammalian neph1 (dumbfounded [*duf*] and roughest/irreC [*rst*]) (72–74) to engage in intimate cell junctions that are required for myoblast fusion during embryonic muscle development. During skeletal muscle development and regeneration after injury, mononucleated myoblasts fuse to form multinucleated muscle fibers. This process of myoblast fusion is amenable to genetic dissection in the fly, in which muscle formation involves a well-defined temporospatial sequence of events that are remarkably conserved also in mammalian myogenesis. Recognition and fusion require the formation of intense cell–cell contacts, so-called prefusion complexes, that are based on neph and nephrin proteins and comparable to the slit diaphragm cell junctions of podocytes (75–77). Loss of one of the nephrin or neph homologues in this system disrupts the cellular program required for myoblast fusion. Intriguing is that *in vivo* mapping of the functional protein domains required for myoblast fusion re-

vealed that the intracellular domain mediates their activity (77), suggesting that intact signal transduction is required for the proper function of these proteins.

In agreement with this concept, *syg-1*, the *C. elegans* homologue of *neph3*, has been shown to be required as a guidepost signal in neuronal synapse formation in *C. elegans* (78), a process that also requires tightly regulated signal transduction events. Thus, from these data, the concept is emerging that members of the neph and nephrin protein families form specialized cell junctions that are involved in pathfinding, orientation, formation of prefusion complexes, and the intimate organization of cell extensions in various cells and organisms, including the mammalian kidney. All of these programs are strictly dependent on intracellular signaling networks.

Hanging on a Scaffold: The Role of Actin Cytoskeleton and PDZ Domain Proteins in the Organization of Signaling Proteins at the Filtration Slit

Although many of the key proteins of the slit diaphragm have now been identified, the fundamental question remains how the different proteins are organized at this specialized cell junction. Given the fluid nature of plasma membranes, restriction of podocyte proteins to the slit diaphragm protein complex at the base of the filtration slit requires anchoring mechanisms. Obviously, this restriction is a critical prerequisite for the maintenance of a sieve as well as efficient signal transduction at the filtration slit. In addition to the function of podocin, which recruits nephrin into specialized lipid raft microdomains of the plasma membrane at the slit diaphragm, two crucial mechanisms seem to be important for the assembly of slit diaphragm components. First, it has been shown that slit diaphragm proteins are associated with the cortical actin cytoskeleton in the podocyte *in vitro* and *in vivo* (79–81). This interaction seems at least in part to be mediated by CD2AP (82). Each foot process is equipped with a microfilament-based contractile apparatus composed of actin, myosin-II, α-actinin, talin, paxillin, and vinculin (83–85). The slit diaphragm protein complex is linked to the actin cytoskeleton and seems to modify actin dynamics. CD2AP has been shown to associate with WASp, the Arp2/3 complex, the actin-capping protein CAPZ, and cortactin, proteins involved in actin filament assembly (86–88). Actin fiber formation is a highly dynamic process that is governed by continuous assembly and disruption of filaments. It is well known that the dynamics of the submembranous actin meshwork of podocytes is profoundly changed in effaced foot processes (1). The current belief is that loss of the organized structure of the actin cytoskeleton in podocytes is a prerequisite for podocyte foot process effacement and proteinuria. These findings assign a central role to the submembranous actin cytoskeleton for maintaining the stability of the podocyte's shape and the integrity of the slit diaphragm protein complex. Moreover, it seems that loss of the integrity of the slit diaphragm complex has a dramatic effect on the actin cytoskeleton leading to foot process effacement and proteinuria (1). Work by the Shimizu, Salant, and Chugh

groups showed that injection of antisera directed against the extracellular domains of nephrin or neph1 results in rapidly developing proteinuria, disorganization of the actin cytoskeleton, and foot process effacement (70,89–91). The critical importance of an intact submembranous actin skeleton is highlighted by the fact that mutations in the actin-bundling protein α-actinin-4 have been detected in an autosomal dominant hereditary form of focal segmental glomerulosclerosis (92). Patients with mutations in the *ACTN4* gene as well as mice with targeted disruption of *ACTN4* or transgenic overexpression of a mutated form of α-actinin-4 display effaced podocyte foot processes and a steroid-resistant form of focal segmental glomerulosclerosis (93,94). Although a critical role of signaling at the slit diaphragm for active actin remodeling and the maintenance of the podocyte structure is highly conceivable, little is known about the effectors of slit diaphragm proteins involved in transmitting these signals to the actin meshwork (95,96). It is interesting that α-actinin-4 has been shown to bind to densin-180 in the postsynaptic density in neurons (97). Densin-180 has recently been localized to the slit diaphragm of podocytes by Holthöfer *et al*. (98) and may provide one important link of slit diaphragm proteins to the actin cytoskeleton.

The second anchoring mechanism that restricts podocyte proteins to the slit diaphragm protein complex is binding to scaffolding proteins. The first of these scaffolding proteins localized to the cytoplasmic face of the filtration slit by Farquhar and colleagues (42,99) was a protein called zonula occludens 1 (ZO-1). ZO proteins are membrane-associated multidomain proteins that are usually localized at sites of intercellular junctions. They contain several protein interaction modules, namely three PDZ domains, a Src homology 3 (SH3) domain, and a guanylate kinase (GUK) domain (100). PDZ domains are protein-binding modules that recognize short peptide motifs within their protein targets (101). In most cases, the last three to five residues at the extreme carboxy terminus of a transmembrane protein represent the target sequence. Genetic evidence from invertebrate systems demonstrates a role for ZO proteins in facilitating signal transduction, and evidence from vertebrate systems demonstrates a structural role in organizing transmembrane protein complexes (102,103). In a recently published functional study, it was shown that ZO-1 directly binds to the cytoplasmic tail of neph proteins (37). This interaction was mediated by the first PDZ domain of ZO-1 and the last three amino acids of the carboxy terminal domain of neph proteins and induced a dramatic increase in tyrosine phosphorylation of the cytoplasmic tail of neph1. Thus, in addition to clustering neph proteins, ZO-1 alters the phosphorylation state of Neph1 and its ability to induce signal transduction. It has been suggested that ZO-1 in addition to its signaling function interacts with the actin cytoskeleton and components of the paracellular seal (104). Although the functional implications of ZO-1/actin association have not yet been established *in vivo*, ZO-1 could link Neph1 and its associated binding proteins to the actin cytoskeleton and contribute to the organization of the foot processes of podocytes. It is interesting to note that the interaction of the cytoplasmic tail of neph1 with PDZ domain proteins seems to be regulated by phosphorylation of a critical

threonine residue (C. Reinhardt, T.B. Huber, T. Benzing, unpublished data), which suggests that the specificity for PDZ domain binding at the slit diaphragm is regulated by signaling events.

Signaling Effectors: Highway to He(alth)ll

How can we put all of this together? In this article, I have summarized data suggesting that signaling at the slit diaphragm is critical for the regulation of podocyte function, maintenance of foot process structure, and possibly podocyte survival (Figure 3). Although many aspects of this concept have yet to be addressed in various animal models, recent studies clearly indicate that nephrin and neph proteins are signaling proteins. However, the regulation of dynamics and kinetics of signaling is completely unclear. The recent generation of mouse strains that allow for podocyte-specific gene targeting will greatly aid the study of signaling *in vivo* (105–107).

It is reasonable to speculate that the slit diaphragm protein complex is highly dynamic. Protein components of the complex are endocytosed, recycled, and returned back to the cell surface. In this regard, it is conceivable that nephrin or neph1 molecules that enter the complex may be dephosphorylated and inactive. Interaction with their respective ligand at the slit diaphragm may then induce tyrosine phosphorylation and initiation of signaling. This could be a way of sensing repair and turnover of slit diaphragm components. In conjunction with ion channels, this system could also serve to monitor pressure at the filtration slit (108,109). It is interesting to note that the closest homologue of podocin in *C. elegans*, a stomatin family protein called MEC-2, is involved in mechanosensation in the worm (110). Thus, it is tempting to speculate that podocin has similar functions in the mammalian kidney.

An interesting question is whether podocyte foot processes are able to regulate the width of the filtration slit, slit diaphragm permeability, and glomerular ultrafiltration. Although experimental data are almost completely lacking, it seems that this could be the case. The slit diaphragm is a robust structure with a fairly constant width. However, it is increasingly appreciated that the width may vary and that the slit diaphragm has to be partially elastic and highly dynamic in nature (3,111). In addition to acting as a molecular sieve, it has been suggested that the slit diaphragm may impose substantial resistance to liquid flow across the glomerulus (112). Thus, fine tuning of the width of the slit diaphragm may have an impact on the hydraulic resistance and thus contribute to the regulation of glomerular ultrafiltration and permeability of the filter.

It is clear that the slit diaphragm is not the only membrane domain where signaling takes place in the podocyte. Recent experimental evidence suggests a critical role for integrin signaling at the sole of the podocyte foot process (113), for growth factors such as vascular endothelial growth factor (114) or basic fibroblast growth factor (115), protein tyrosine phosphatases (116), and chemokines (117,118) in podocyte development and glomerular pathophysiology.

However, it is clearly more and more appreciated that (*1*) the slit diaphragm protein complex does not only serve as static molecular sieve but rather is a highly dynamic functional

protein complex and (*2*) signaling at the slit diaphragm may be critical for maintaining the integrity of the podocyte architecture and the function of the glomerular filter of the kidney. A better understanding of the mechanisms involved in signal transduction at the slit diaphragm will definitively provide valuable insights into important aspects of glomerular diseases in general. Progress in research on podocyte biology and signaling will greatly help to improve our understanding of the pathophysiology not only of inherited but also of the more common acquired diseases, namely minimal change disease, primary focal segmental glomerulosclerosis, and membranous or diabetic nephropathy. From this perspective, at some point patients will benefit from the progress that has been made in the exciting field of podocyte cell biology and signal transduction.

Acknowledgments

References

1. Kerjaschki D: Caught flat-footed: Podocyte damage and the molecular bases of focal glomerulosclerosis. *J Clin Invest* 108: 1583–1587, 2001
2. Somlo S, Mundel P: Getting a foothold in nephrotic syndrome. *Nat Genet* 24: 333–335, 2000
3. Tryggvason K, Wartiovaara J: Molecular basis of glomerular permselectivity. *Curr Opin Nephrol Hypertens* 10: 543–549, 2001
4. Miner JH: A molecular look at the glomerular barrier. *Nephron Exp Nephrol* 94: e119–e122, 2003
5. Brenner BM, Hostetter TH, Humes HD: Molecular basis of proteinuria of glomerular origin. *N Engl J Med* 298: 826–833, 1978
6. Brenner BM, Hostetter TH, Humes HD: Glomerular permselectivity: Barrier function based on discrimination of molecular size and charge. *Am J Physiol* 234: F455–F460, 1978
7. Rennke HG, Venkatachalam MA: Glomerular permeability of macromolecules. Effect of molecular configuration on the fractional clearance of uncharged dextran and neutral horseradish peroxidase in the rat. *J Clin Invest* 63: 713–717, 1979
8. Antignac C: Genetic models: Clues for understanding the pathogenesis of idiopathic nephrotic syndrome. *J Clin Invest* 109: 447–449, 2002
9. Tryggvason K, Ruotsalainen V, Wartiovaara J: Discovery of the congenital nephrotic syndrome gene discloses the structure of the mysterious molecular sieve of the kidney. *Int J Dev Biol* 43: 445–451, 1999
10. Mundel P, Shankland SJ: Podocyte biology and response to injury. *J Am Soc Nephrol* 13: 3005–3015, 2002
11. Kriz W, Lemley KV: The role of the podocyte in glomerulosclerosis. *Curr Opin Nephrol Hypertens* 8: 489–497, 1999
12. Kreidberg JA: Podocyte differentiation and glomerulogenesis. *J Am Soc Nephrol* 14: 806–814, 2003
13. Pavenstadt H, Kriz W, Kretzler M: Cell biology of the glomerular podocyte. *Physiol Rev* 83: 253–307, 2003
14. Rodewald R, Karnovsky MJ: Porous substructure of the glomerular slit diaphragm in the rat and mouse. *J Cell Biol* 60: 423–433, 1974
15. Kestila M, Lenkkeri U, Mannikko M, Lamerdin J, McCready P, Putaala H, Ruotsalainen V, Morita T, Nissinen M, Herva R, Kashtan CE, Peltonen L, Holmberg C, Olsen A, Tryggvason K: Positionally cloned gene for a novel glomerular protein—nephrin—is mutated in congenital nephrotic syndrome. *Mol Cell* 1: 575–582, 1998
16. Ruotsalainen V, Ljungberg P, Wartiovaara J, Lenkkeri U, Kestila M, Jalanko H, Holmberg C, Tryggvason K: Nephrin is specifically located at the slit diaphragm of glomerular podocytes. *Proc Natl Acad Sci U S A* 96: 7962–7967, 1999
17. Holthofer H, Ahola H, Solin ML, Wang S, Palmen T, Luimula P, Miettinen A, Kerjaschki D: Nephrin localizes at the podocyte filtration slit area and is characteristically spliced in the human kidney. *Am J Pathol* 155: 1681–1687, 1999
18. Holzman LB, St John PL, Kovari IA, Verma R, Holthofer H, Abrahamson DR: Nephrin localizes to the slit pore of the glomerular epithelial cell. *Kidney Int* 56: 1481–1491, 1999
19. Tryggvason K: Unraveling the mechanisms of glomerular ultrafiltration: Nephrin, a key component of the slit diaphragm. *J Am Soc Nephrol* 10: 2440–2445, 1999
20. Holmberg C, Antikainen M, Ronnholm K, Ala Houhala M, Jalanko H: Management of congenital nephrotic syndrome of the Finnish type. *Pediatr Nephrol* 9: 87–93, 1995
21. Putaala H, Soininen R, Kilpelainen P, Wartiovaara J, Tryggvason K: The murine nephrin gene is specifically expressed in kidney, brain and pancreas: Inactivation of the gene leads to massive proteinuria and neonatal death. *Hum Mol Genet* 10: 1–8, 2001
22. Shih NY, Li J, Karpitskii V, Nguyen A, Dustin ML, Kanagawa O, Miner JH, Shaw AS: Congenital nephrotic syndrome in mice lacking CD2-associated protein. *Science* 286: 312–315, 1999
23. Boute N, Gribouval O, Roselli S, Benessy F, Lee H, Fuchshuber A, Dahan K, Gubler MC, Niaudet P, Antignac C: NPHS2, encoding the glomerular protein podocin, is mutated in autosomal recessive steroid-resistant nephrotic syndrome. *Nat Genet* 24: 349–354, 2000
24. Donoviel DB, Freed DD, Vogel H, Potter DG, Hawkins E, Barrish JP, Mathur BN, Turner CA, Geske R, Montgomery CA, Starbuck M, Brandt M, Gupta A, Ramirez-Solis R, Zambrowicz BP, Powell DR: Proteinuria and perinatal lethality in mice lacking NEPH1, a novel protein with homology to NEPHRIN. *Mol Cell Biol* 21: 4829–4836, 2001
25. Ciani L, Patel A, Allen ND, Ffrench-Constant C: Mice lacking the giant protocadherin mFAT1 exhibit renal slit junction abnormalities and a partially penetrant cyclopia and anophthalmia phenotype. *Mol Cell Biol* 23: 3575–3582, 2003
26. Roselli S, Gribouval O, Boute N, Sich M, Benessy F, Attie T, Gubler MC, Antignac C: Podocin localizes in the kidney to the slit diaphragm area. *Am J Pathol* 160: 131–139, 2002
27. Huber TB, Kottgen M, Schilling B, Walz G, Benzing T: Interaction with podocin facilitates nephrin signaling. *J Biol Chem* 276: 41543–41546, 2001
28. Schwarz K, Simons M, Reiser J, Saleem MA, Faul C, Kriz W, Shaw AS, Holzman LB, Mundel P: Podocin, a raft-associated component of the glomerular slit diaphragm, interacts with CD2AP and nephrin. *J Clin Invest* 108: 1621–1629, 2001
29. Roselli S, Heidet L, Sich M, Henger A, Kretzler M, Gubler MC, Antignac C: Early glomerular filtration defect and severe renal

disease in podocin-deficient mice. *Mol Cell Biol* 24: 550–560, 2004

30. Dustin ML, Olszowy MW, Holdorf AD, Li J, Bromley S, Desai N, Widder P, Rosenberger F, van der Merwe PA, Allen PM, Shaw AS: A novel adaptor protein orchestrates receptor patterning and cytoskeletal polarity in T-cell contacts. *Cell* 94: 667–677, 1998

31. Shih NY, Li J, Cotran R, Mundel P, Miner JH, Shaw AS: CD2AP localizes to the slit diaphragm and binds to nephrin via a novel C-terminal domain. *Am J Pathol* 159: 2303–2308, 2001

32. Kim JM, Wu H, Green G, Winkler CA, Kopp JB, Miner JH, Unanue ER, Shaw AS: CD2-associated protein haploinsufficiency is linked to glomerular disease susceptibility. *Science* 300: 1298–1300, 2003

33. Wolf G, Stahl RA: CD2-associated protein and glomerular disease. *Lancet* 362: 1746–1748, 2003

34. Sellin L, Huber TB, Gerke P, Quack I, Pavenstadt H, Walz G: NEPH1 defines a novel family of podocin interacting proteins. *FASEB J* 17: 115–117, 2003

35. Inoue T, Yaoita E, Kurihara H, Shimizu F, Sakai T, Kobayashi T, Ohshiro K, Kawachi H, Okada H, Suzuki H, Kihara I, Yamamoto T: FAT is a component of glomerular slit diaphragms. *Kidney Int* 59: 1003–1012, 2001

36. Huber TB, Hartleben B, Kim J, Schmidts M, Schermer B, Keil A, Egger L, Lecha RL, Borner C, Pavenstadt H, Shaw AS, Walz G, Benzing T: Nephrin and CD2AP associate with phosphoinositide 3-OH kinase and stimulate AKT-dependent signaling. *Mol Cell Biol* 23: 4917–4928, 2003

37. Huber TB, Schmidts M, Gerke P, Schermer B, Zahn A, Hartleben B, Sellin L, Walz G, Benzing T: The carboxyl terminus of Neph family members binds to the PDZ domain protein zonula occludens-1. *J Biol Chem* 278: 13417–13421, 2003

38. Huber TB, Simons M, Hartleben B, Sernetz L, Schmidts M, Gundlach E, Saleem MA, Walz G, Benzing T: Molecular basis of the functional podocin-nephrin complex: Mutations in the NPHS2 gene disrupt nephrin targeting to lipid raft microdomains. *Hum Mol Genet* 12: 3397–3405, 2003

39. Endy D, Yaffe MB: Signal transduction: Molecular monogamy. *Nature* 426: 614–615, 2003

40. Yaffe MB: Phosphotyrosine-binding domains in signal transduction. *Nat Rev Mol Cell Biol* 3: 177–186, 2002

41. Yaffe MB, Elia AE: Phosphoserine/threonine-binding domains. *Curr Opin Cell Biol* 13: 131–138, 2001

42. Kurihara H, Anderson JM, Farquhar MG: Increased Tyr phosphorylation of ZO-1 during modification of tight junctions between glomerular foot processes. *Am J Physiol* 268: F514–F524, 1995

43. Verma R, Wharram B, Kovari I, Kunkel R, Nihalani D, Wary KK, Wiggins RC, Killen P, Holzman LB: Fyn binds to and phosphorylates the kidney slit diaphragm component Nephrin. *J Biol Chem* 278: 20716–20723, 2003

44. Simons M, Schwarz K, Kriz W, Miettinen A, Reiser J, Mundel P, Holthofer H: Involvement of lipid rafts in nephrin phosphorylation and organization of the glomerular slit diaphragm. *Am J Pathol* 159: 1069–1077, 2001

45. Lahdenpera J, Kilpelainen P, Liu XL, Pikkarainen T, Reponen P, Ruotsalainen V, Tryggvason K: Clustering-induced tyrosine phosphorylation of nephrin by Src family kinases. *Kidney Int* 64: 404–413, 2003

46. Yu CC, Yen TS, Lowell CA, DeFranco AL: Lupus-like kidney disease in mice deficient in the Src family tyrosine kinases Lyn and Fyn. *Curr Biol* 11: 34–38, 2001

47. Pawson T: Protein modules and signalling networks. *Nature* 373: 573–580, 1995

48. Yaffe MB, Smerdon SJ: PhosphoSerine/threonine binding domains: you can't pSERious? *Structure (Camb)* 9: R33–R38, 2001

49. Cantley LC: The phosphoinositide 3-kinase pathway. *Science* 296: 1655–1657, 2002

50. Downward J: Mechanisms and consequences of activation of protein kinase B/Akt. *Curr Opin Cell Biol* 10: 262–267, 1998

51. Kriz W, Lemley KV: The role of the podocyte in glomerulosclerosis. *Curr Opin Nephrol Hypertens* 8: 489–497, 1999

52. Rennke HG: How does glomerular epithelial cell injury contribute to progressive glomerular damage? *Kidney Int Suppl* 45: S58–S63, 1994

53. Kim YH, Goyal M, Kurnit D, Wharram B, Wiggins J, Holzman L, Kershaw D, Wiggins R: Podocyte depletion and glomerulosclerosis have a direct relationship in the PAN-treated rat. *Kidney Int* 60: 957–968, 2001

54. Schiffer M, Bitzer M, Roberts IS, Kopp JB, ten Dijke P, Mundel P, Bottinger EP: Apoptosis in podocytes induced by TGF-beta and Smad7. *J Clin Invest* 108: 807–816, 2001

55. Elger M, Kriz W: Podocytes and the development of segmental glomerulosclerosis. *Nephrol Dial Transplant* 13: 1368–1373, 1998

56. Fries JW, Sandstrom DJ, Meyer TW, Rennke HG: Glomerular hypertrophy and epithelial cell injury modulate progressive glomerulosclerosis in the rat. *Lab Invest* 60: 205–218, 1989

57. Kriz W, Gretz N, Lemley KV: Progression of glomerular diseases: Is the podocyte the culprit? *Kidney Int* 54: 687–697, 1998

58. Soubeyran P, Kowanetz K, Szymkiewicz I, Langdon WY, Dikic I: Cbl-CIN85-endophilin complex mediates ligand-induced downregulation of EGF receptors. *Nature* 416: 183–187, 2002

59. Li X, Talts U, Talts JF, Arman E, Ekblom P, Lonai P: Akt/PKB regulates laminin and collagen IV isotypes of the basement membrane. *Proc Natl Acad Sci U S A* 98: 14416–14421, 2001

60. Mawal-Dewan M, Lorenzini A, Frisoni L, Zhang H, Cristofalo VJ, Sell C: Regulation of collagenase expression during replicative senescence in human fibroblasts by Akt-forkhead signaling. *J Biol Chem* 277: 7857–7864, 2002

61. Koziell A, Grech V, Hussain S, Lee G, Lenkkeri U, Tryggvason K, Scambler P: Genotype/phenotype correlations of NPHS1 and NPHS2 mutations in nephrotic syndrome advocate a functional inter-relationship in glomerular filtration. *Hum Mol Genet* 11: 379–388, 2002

62. Sorensson J, Fierlbeck W, Heider T, Schwarz K, Park DS, Mundel P, Lisanti M, Ballermann BJ: Glomerular endothelial fenestrae in vivo are not formed from caveolae. *J Am Soc Nephrol* 13: 2639–2647, 2002

63. Simons K, Toomre D: Lipid rafts and signal transduction. *Nat Rev Mol Cell Biol* 1: 31–39, 2000

64. Simons K, Ikonen E: Functional rafts in cell membranes. *Nature* 387: 569–572, 1997

65. Smart EJ, Graf GA, McNiven MA, Sessa WC, Engelman JA, Scherer PE, Okamoto T, Lisanti MP: Caveolins, liquid-ordered domains, and signal transduction. *Mol Cell Biol* 19: 7289–7304, 1999

66. Kurzchalia TV, Parton RG: Membrane microdomains and caveolae. *Curr Opin Cell Biol* 11: 424–431, 1999

67. Gerke P, Huber TB, Sellin L, Benzing T, Walz G: Homodimerization and heterodimerization of the glomerular podocyte proteins nephrin and NEPH1. *J Am Soc Nephrol* 14: 918–926, 2003

68. Khoshnoodi J, Sigmundsson K, Ofverstedt LG, Skoglund U, Obrink B, Wartiovaara J, Tryggvason K: Nephrin promotes cell-cell adhesion through homophilic interactions. *Am J Pathol* 163: 2337–2346, 2003

69. Barletta GM, Kovari IA, Verma RK, Kerjaschki D, Holzman LB: Nephrin and Neph1 co-localize at the podocyte foot process intercellular junction and form cis hetero-oligomers. *J Biol Chem* 278: 19266–19271, 2003

70. Liu G, Kaw B, Kurfis J, Rahmanuddin S, Kanwar YS, Chugh SS: Neph1 and nephrin interaction in the slit diaphragm is an important determinant of glomerular permeability. *J Clin Invest* 112: 209–221, 2003

71. Ihalmo P, Palmen T, Ahola H, Valtonen E, Holthofer H: Filtrin is a novel member of nephrin-like proteins. *Biochem Biophys Res Commun* 300: 364–370, 2003

72. Dworak HA, Charles MA, Pellerano LB, Sink H: Characterization of Drosophila hibris, a gene related to human nephrin. *Development* 128: 4265–4276, 2001

73. Strunkelnberg M, Bonengel B, Moda LM, Hertenstein A, de Couet HG, Ramos RG, Fischbach KF: rst and its paralogue kirre act redundantly during embryonic muscle development in Drosophila. *Development* 128: 4229–4239, 2001

74. Ramos RG, Igloi GL, Lichte B, Baumann U, Maier D, Schneider T, Brandstatter JH, Frohlich A, Fischbach KF: The irregular chiasm C-roughest locus of Drosophila, which affects axonal projections and programmed cell death, encodes a novel immunoglobulin-like protein. *Genes Dev* 7: 2533–2547, 1993

75. Ruiz-Gomez M, Coutts N, Price A, Taylor MV, Bate M: Drosophila dumbfounded: A myoblast attractant essential for fusion. *Cell* 102: 189–198, 2000

76. Bour BA, Chakravarti M, West JM, Abmayr SM: Drosophila SNS, a member of the immunoglobulin superfamily that is essential for myoblast fusion. *Genes Dev* 14: 1498–1511, 2000

77. Artero RD, Castanon I, Baylies MK: The immunoglobulin-like protein Hibris functions as a dose-dependent regulator of myoblast fusion and is differentially controlled by Ras and Notch signaling. *Development* 128: 4251–4264, 2001

78. Shen K, Bargmann CI: The immunoglobulin superfamily protein SYG-1 determines the location of specific synapses in C. elegans. *Cell* 112: 619–630, 2003

79. Yuan H, Takeuchi E, Salant DJ: Podocyte slit-diaphragm protein nephrin is linked to the actin cytoskeleton. *Am J Physiol Renal Physiol* 282: F585–F591, 2002

80. Saleem MA, Ni L, Witherden I, Tryggvason K, Ruotsalainen V, Mundel P, Mathieson PW: Co-localization of nephrin, podocin, and the actin cytoskeleton: Evidence for a role in podocyte foot process formation. *Am J Pathol* 161: 1459–1466, 2002

81. Welsch T, Endlich N, Kriz W, Endlich K: CD2AP and p130Cas localize to different F-actin structures in podocytes. *Am J Physiol Renal Physiol* 281: F769–F777, 2001

82. Lehtonen S, Zhao F, Lehtonen E: CD2-associated protein directly interacts with the actin cytoskeleton. *Am J Physiol Renal Physiol* 283: F734–F743, 2002

83. Ichimura K, Kurihara H, Sakai T: Actin filament organization of foot processes in rat podocytes. *J Histochem Cytochem* 51: 1589–1600, 2003

84. Kobayashi N: Mechanism of the process formation; podocytes vs. neurons. *Microsc Res Tech* 57: 217–223, 2002

85. Drenckhahn D, Franke RP: Ultrastructural organization of contractile and cytoskeletal proteins in glomerular podocytes of chicken, rat, and man. *Lab Invest* 59: 673–682, 1988

86. Hutchings NJ, Clarkson N, Chalkley R, Barclay AN, Brown MH: Linking the T cell surface protein CD2 to the actin-capping protein CAPZ via CMS and CIN85. *J Biol Chem* 278: 22396–22403, 2003

87. Lynch DK, Winata SC, Lyons RJ, Hughes WE, Lehrbach GM, Wasinger V, Corthals G, Cordwell S, Daly RJ: A Cortactin-CD2-associated protein (CD2AP) complex provides a novel link between epidermal growth factor receptor endocytosis and the actin cytoskeleton. *J Biol Chem* 278: 21805–21813, 2003

88. Badour K, Zhang J, Shi F, McGavin MK, Rampersad V, Hardy LA, Field D, Siminovitch KA: The Wiskott-Aldrich syndrome protein acts downstream of CD2 and the CD2AP and PSTPIP1 adaptors to promote formation of the immunological synapse. *Immunity* 18: 141–154, 2003

89. Narisawa M, Kawachi H, Oite T, Shimizu F: Divalency of the monoclonal antibody 5-1-6 is required for induction of proteinuria in rats. *Clin Exp Immunol* 92: 522–526, 1993

90. Topham PS, Kawachi H, Haydar SA, Chugh S, Addona TA, Charron KB, Holzman LB, Shia M, Shimizu F, Salant DJ: Nephritogenic mAb 5-1-6 is directed at the extracellular domain of rat nephrin. *J Clin Invest* 104: 1559–1566, 1999

91. Kawachi H, Abrahamson DR, St John PL, Goldstein DJ, Shia MA, Matsui K, Shimizu F, Salant DJ: Developmental expression of the nephritogenic antigen of monoclonal antibody 5-1-6. *Am J Pathol* 147: 823–833, 1995

92. Kaplan JM, Kim SH, North KN, Rennke H, Correia LA, Tong HQ, Mathis BJ, Rodriguez-Perez JC, Allen PG, Beggs AH, Pollak MR: Mutations in ACTN4, encoding alpha-actinin-4, cause familial focal segmental glomerulosclerosis. *Nat Genet* 24: 251–256, 2000

93. Michaud JL, Lemieux LI, Dube M, Vanderhyden BC, Robertson SJ, Kennedy CR: Focal and segmental glomerulosclerosis in mice with podocyte-specific expression of mutant alpha-actinin-4. *J Am Soc Nephrol* 14: 1200–1211, 2003

94. Kos CH, Le TC, Sinha S, Henderson JM, Kim SH, Sugimoto H, Kalluri R, Gerszten RE, Pollak MR: Mice deficient in alpha-actinin-4 have severe glomerular disease. *J Clin Invest* 111: 1683–1690, 2003

95. Yuan H, Takeuchi E, Taylor GA, McLaughlin M, Brown D, Salant DJ: Nephrin dissociates from actin, and its expression is reduced in early experimental membranous nephropathy. *J Am Soc Nephrol* 13: 946–956, 2002

96. Saran AM, Yuan H, Takeuchi E, McLaughlin M, Salant DJ: Complement mediates nephrin redistribution and actin dissociation in experimental membranous nephropathy. *Kidney Int* 64: 2072–2078, 2003

97. Walikonis RS, Oguni A, Khorosheva EM, Jeng CJ, Asuncion FJ, Kennedy MB: Densin-180 forms a ternary complex with the (alpha)-subunit of Ca2+/calmodulin-dependent protein kinase II and (alpha)-actinin. *J Neurosci* 21: 423–433, 2001

98. Ahola H, Heikkila E, Astrom E, Inagaki M, Izawa I, Pavenstadt H, Kerjaschki D, Holthofer H: A novel protein, densin, expressed by glomerular podocytes. *J Am Soc Nephrol* 14: 1731–1737, 2003

99. Schnabel E, Anderson JM, Farquhar MG: The tight junction protein ZO-1 is concentrated along slit diaphragms of the glomerular epithelium. *J Cell Biol* 111: 1255–1263, 1990

100. Hung AY, Sheng M: PDZ domains: Structural modules for protein complex assembly. *J Biol Chem* 277: 5699–5702, 2002

101. Songyang Z, Fanning AS, Fu C, Xu J, Marfatia SM, Chishti AH, Crompton A, Chan AC, Anderson JM, Cantley LC: Recognition

of unique carboxyl-terminal motifs by distinct PDZ domains. *Science* 275: 73–77, 1997

102. Mitic LL, Van Itallie CM, Anderson JM: Molecular physiology and pathophysiology of tight junctions I. Tight junction structure and function: lessons from mutant animals and proteins. *Am J Physiol Gastrointest Liver Physiol* 279: G250–G254, 2000

103. Fanning AS, Anderson JM: PDZ domains: Fundamental building blocks in the organization of protein complexes at the plasma membrane. *J Clin Invest* 103: 767–772, 1999

104. Fanning AS, Ma TY, Anderson JM: Isolation and functional characterization of the actin binding region in the tight junction protein ZO-1. *FASEB J* 16: 1835–1837, 2002

105. Eremina V, Wong MA, Cui S, Schwartz L, Quaggin SE: Glomerular-specific gene excision in vivo. *J Am Soc Nephrol* 13: 788–793, 2002

106. Moeller MJ, Kovari IA, Holzman LB: Evaluation of a new tool for exploring podocyte biology: Mouse nphs1 5' flanking region drives LacZ expression in podocytes. *J Am Soc Nephrol* 11: 2306–2314, 2000

107. Moeller MJ, Sanden SK, Soofi A, Wiggins RC, Holzman LB: Two gene fragments that direct podocyte-specific expression in transgenic mice. *J Am Soc Nephrol* 13: 1561–1567, 2002

108. Mutai H, Heller S: Vertebrate and invertebrate TRPV-like mechanoreceptors. *Cell Calcium* 33: 471–478, 2003

109. Goodman MB, Schwarz EM: Transducing touch in Caenorhabditis elegans. *Annu Rev Physiol* 65: 429–452, 2003

110. Goodman MB, Ernstrom GG, Chelur DS, O'Hagan R, Yao CA, Chalfie M: MEC-2 regulates C. elegans DEG/ENaC channels needed for mechanosensation. *Nature* 415: 1039–1042, 2002

111. Kriz W, Kretzler M, Provoost AP, Shirato I: Stability and leakiness: Opposing challenges to the glomerulus. *Kidney Int* 49: 1570–1574, 1996

112. Smithies O: Why the kidney glomerulus does not clog: A gel permeation/diffusion hypothesis of renal function. *Proc Natl Acad Sci U S A* 100: 4108–4113, 2003

113. Kreidberg JA, Donovan MJ, Goldstein SL, Rennke H, Shepherd K, Jones RC, Jaenisch R: Alpha 3 beta 1 integrin has a crucial role in kidney and lung organogenesis. *Development* 122: 3537–3547, 1996

114. Eremina V, Sood M, Haigh J, Nagy A, Lajoie G, Ferrara N, Gerber HP, Kikkawa Y, Miner JH, Quaggin SE: Glomerular-specific alterations of VEGF-A expression lead to distinct congenital and acquired renal diseases. *J Clin Invest* 111: 707–716, 2003

115. Floege J, Kriz W, Schulze M, Susani M, Kerjaschki D, Mooney A, Couser WG, Koch KM: Basic fibroblast growth factor augments podocyte injury and induces glomerulosclerosis in rats with experimental membranous nephropathy. *J Clin Invest* 96: 2809–2819, 1995

116. Wharram BL, Goyal M, Gillespie PJ, Wiggins JE, Kershaw DB, Holzman LB, Dysko RC, Saunders TL, Samuelson LC, Wiggins RC: Altered podocyte structure in GLEPP1 (Ptpro)-deficient mice associated with hypertension and low glomerular filtration rate. *J Clin Invest* 106: 1281–1290, 2000

117. Banas B, Wornle M, Berger T, Nelson PJ, Cohen CD, Kretzler M, Pfirstinger J, Mack M, Lipp M, Grone HJ, Schlondorff D: Roles of SLC/CCL21 and CCR7 in human kidney for mesangial proliferation, migration, apoptosis, and tissue homeostasis. *J Immunol* 168: 4301–4307, 2002

118. Huber TB, Reinhardt HC, Exner M, Burger JA, Kerjaschki D, Saleem MA, Pavenstadt H: Expression of functional CCR and CXCR chemokine receptors in podocytes. *J Immunol* 168: 6244–6252, 2002