

FEATURED NEW INVESTIGATOR

Glomerular basement membrane and related glomerular disease

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The glomerular basement membrane (GBM) is lined by fenestrated endothelium from the capillary-lumen side and by interdigitating foot processes of the podocytes from the urinary-space side. These three layers of the glomerular capillary wall constitute the functional unit of the glomerular filtration barrier. The GBM is assembled through an interweaving of type IV collagen with laminins, nidogen, and sulfated proteoglycans. Mutations in genes encoding *LAMB2*, *COL4A3*, *COL4A4*, and *COL4A5* cause glomerular disease in humans as well as in mice. In addition, laminin $\alpha 5$ mutation in podocytes leads to proteinuria and renal failure in mice. Moreover, more neoepitopes in Goodpasture's disease and for the first time alloepitopes in Alport post-transplantation nephritis have been located in the collagen $\alpha 5(IV)$ NC1 domain. These discoveries underscore the importance of the GBM in establishing and maintaining the integrity of the glomerular filtration barrier. (Translational Research 2012;160:291-297)

Abbreviations: APTN = Alport post-transplantation nephritis; AS = Alport syndrome; BM = basement membrane; CCR2 = CC chemokine receptor 2; EA = epitope A; EB = epitope B; GAG = glycosaminoglycan; GBM = glomerular basement membrane; GFB = glomerular filtration barrier; HSPG = heparan sulfate proteoglycan; LAMB2 = laminin b2; LG domain = laminin globular domain; LN = laminin NH2-terminal; MCP-1 = monocyte chemoattractant protein -1; MM = mesangial matrix; MMP-12 = matrix metalloproteinase-12; NC1 = noncollagenous domain 1; SD = slit diaphragm; TBMN = thin basement membrane nephropathy

The kidney glomerular basement membrane (GBM) is an unusually thick basement membrane (BM) formed *via* fusion of distinct BMs assembled by podocytes and glomerular endothelial cells.¹ BMs are sheets of specialized extracellular matrix that underlie

all endothelial and epithelial cells and surround all muscle cells, fat cells, and peripheral nerves. They influence cell proliferation, differentiation, migration, and survival. BMs are also involved in filtration, in tissue compartmentalization, and in maintenance of epithelial

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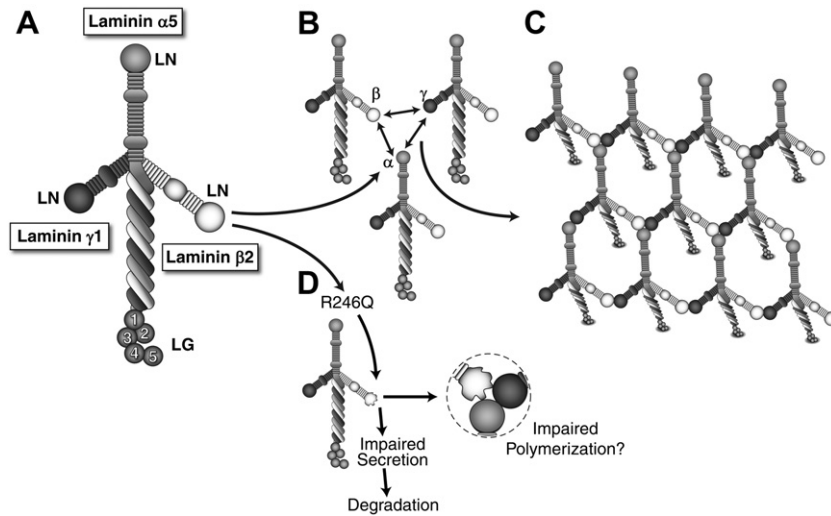


Fig 1. Laminin trimers and assembly. **A**, Structure of a typical cruciform laminin $\alpha\beta\gamma$ heterotrimer, with some domain names indicated. **B** and **C**, Mechanism for polymerization of laminin trimers. **D**, The proposed mechanisms of the R246Q missense mutation causing congenital nephrotic syndrome. It may inhibit laminin secretion from podocytes, eventually leading to degradation intracellularly. In addition, the affected R246Q in the LN domain of laminin $\beta 2$ may impair the polymerization of laminin trimers to form the GBM. (Permission granted by Journal of the American Society of Nephrology.)

integrity. The GBM, like all BMs, contains members of 4 classes of proteins: laminin, type IV collagen, nidogen, and sulfated proteoglycans.²

Of the 9 known matrix proteins present in the mature GBM (laminins $\alpha 5$, $\beta 2$, $\gamma 1$; collagen IV $\alpha 3$, $\alpha 4$, $\alpha 5$; nidogen-1 and nidogen-2; and agrin), mutations in 4 of them (laminin $\beta 2$, collagen $\alpha 3$ (IV), collagen $\alpha 4$ [IV], and collagen $\alpha 5$ [IV]) have been identified to cause glomerular disease in human. Furthermore, the new identification of collagen $\alpha 5$ (IV) noncollagenous domain 1 (NC1) epitopes targeted by Goodpasture autoantibodies or Alport post-transplantation nephritis alloantibodies has provided novel insights into the molecular basis of these 2 forms of anti-GBM nephritis.

LAMININ AND PIERSON SYNDROME

Laminins are heterotrimeric glycoproteins containing 1 α , 1 β , and 1 γ chain. Figure 1, A shows a typical laminin heterotrimer. The major laminin heterotrimer in the mature GBM is laminin $\alpha 5\beta 2\gamma 1$, or LM-521.³ LM-521 is secreted by both podocytes and endothelial cells.⁴ During glomerulogenesis, there is a transition in laminin gene expression, such that the $\alpha 1\beta 1\gamma 1$ (LM-111) and $\alpha 5\beta 1\gamma 1$ (LM-511) trimers are present in the nascent GBM, but are replaced by LM-521 as maturation progresses.^{5,6} Laminin trimerization occurs in the endoplasmic reticulum and involves association of the three chains along their α -helical laminin coiled-coil domains to form the long arm.⁷ Once trimers are secreted into the extracellular space, they polymerize to

form a supramolecular network *via* interactions among the α , β , and γ short arm NH₂-termini (called LN domains)⁸ (Fig 1, B and C). The large COOH-terminal laminin globular (LG) domain of α chains mediates laminin and BM interactions with cellular receptors. Therefore, laminin polymerization both initiates basement membrane formation and provides signals to the adjacent cells.⁹

Laminin $\beta 2$ (LAMB2) is a component of laminin-521. Truncating or severe missense mutations in *LAMB2* cause Pierson syndrome.¹⁰ Also called microcoria-congenital nephrosis syndrome, Pierson syndrome is a rare autosomal recessive disease characterized by congenital nephrotic syndrome/diffuse mesangial sclerosis, distinct ocular abnormalities including microcoria (small pupils), muscular hypotonia, and impairment of vision and neurodevelopment.¹¹⁻¹³ Children affected by Pierson syndrome usually die within days or weeks after birth from renal failure. However, with dialysis and therapeutic nephrectomy, a few have lived for up to 2 years. *Lamb2*^{-/-} mice recapitulate the features of Pierson syndrome.¹⁴⁻¹⁹ In contrast, patients with some less severe missense *LAMB2* mutations, such as R246Q and C321R, exhibit nephrotic syndrome with significantly milder extrarenal defects.^{20,21}

To begin to investigate how specific missense mutations in *LAMB2* cause proteinuria, we generated 3 lines of transgenic mice, each with differing podocyte expression levels of R246Q-mutant rat laminin $\beta 2$ (Tg^{Lo}, Tg^{Med}, and Tg^{Hi}). The transgene-derived R246Q-mutant

$\beta 2$ replaced the wild-type mouse laminin $\beta 2$ in the GBM. These transgenic mice developed much less severe proteinuria than their nontransgenic *Lamb2*-deficient littermates; the level of proteinuria correlated inversely with the level of R246Q-LAMB2 expression. *In vitro*, we tried to synthesize NH₂-terminal fragments of rat laminin $\beta 2$ containing the R246Q, R246W and C321R mutations (respectively) in transfected HEK 293 cells using a system in which the LN and LEa domains were fused to a human Ig Fc domain. Although the wild-type fusion protein was secreted into the medium, the mutant fusion proteins were not. Analysis of cell lysates showed that the mutant proteins were synthesized, but they remained inside the cells. These biochemical studies demonstrated that the missense mutations result in impaired secretion of laminin. Together with our transgenic mouse studies, our results suggest that the R246Q mutation causes nephrotic syndrome by impairing secretion of laminin-521 from podocytes into the GBM, resulting in subnormal GBM laminin levels, leading to a more porous GBM and a leaky glomerular filtration barrier (GFB). However, high-level expression of the R246Q mutant in Tg^{Hi} mutants mostly overcomes the effects of the secretion defect²² (Fig 1D). Our findings highlight the importance of *LAMB2* mutations in the pathogenesis of congenital nephrotic syndrome and suggest that therapies that can increase either expression or secretion of the mutant form should improve selectivity of the defective GFB.

While no mutations affecting human laminin $\alpha 5$ or laminin $\gamma 1$ have been reported, podocyte-specific ablation of *Lama5* resulted in varying degrees of proteinuria and progression to renal failure, though the overall renal phenotype was never as severe as observed in *Lamb2*-/- mice.²³ This is likely due to the inefficiency of Cre vs the germ-line deletion of *Lamb2*.

COLLAGEN IV AND HEREDITARY GBM DISEASE -ALPORT SYNDROME AND THIN BASEMENT MEMBRANE DISEASE

There are 6 chains of type IV collagen, $\alpha 1$ to $\alpha 6$, encoded by 3 pairs of genes on chromosomes 2, 13, and X. Each chain has 3 domains: a short 7S domain at the N-terminus, a long, interrupted collagenous domain in the middle, and a noncollagenous domain (NC1) at the C-terminus. The 6 distinct α chains are arranged into 3 different triple helical heterotrimeric protomers: $(\alpha 1)_2\alpha 2$, $\alpha 3\alpha 4\alpha 5$, and $(\alpha 5)_2\alpha 6$. Protomers polymerize to create collagen networks by uniting 2 trimeric NC1 domains to form NC1 hexamers, and by uniting 4 trimeric 7S domains to form 7S dodecamers.²⁴ At early stages of glomerulogenesis, the $(\alpha 1)_2\alpha 2$ network is a component of GBM, Bowman's capsule and mesangial matrix (MM). During normal glomerulogenesis,

most of the $(\alpha 1)_2\alpha 2$ network is replaced by $\alpha 3\alpha 4\alpha 5$ in the GBM and by $(\alpha 5)_2\alpha 6$ in Bowman's capsule, with $(\alpha 1)_2\alpha 2$ remaining in the subendothelial region of the GBM and in the MM.²⁵ Experiments in mice showed that podocytes, but not endothelial cells, synthesize the $\alpha 3\alpha 4\alpha 5$ network.²⁶

Alport syndrome (AS) and thin basement membrane nephropathy (TBMN) are genetically heterogeneous conditions characterized by structural abnormalities in the GBM. Although both conditions typically present with hematuria, AS is associated with proteinuria, progressive renal failure, and extrarenal syndromes. In contrast, TBMN is characterized by isolated persistent or recurrent hematuria, and generally never progresses toward end stage renal disease. The hall mark of TBMN is diffuse attenuation of the GBM, which also resembles the ultrastructural changes of early AS patients or Alport carriers.

Eighty-five percent of AS patients have the X-linked form due to mutations in *COL4A5*. Although in most X-linked AS patients, the $\alpha 5$ chain of type IV collagen is missing from the GBM, in one study it was shown that the *COL4A5* transcript was clearly expressed in the podocytes of one of the three X-linked AS patients studied. Moreover, *COL4A3* and *COL4A4* transcripts were readily detected in the podocytes of all three patients despite the co-absence of these two chains from the GBM. These data suggest a post-transcriptional regulatory mechanism for type IV collagen chains and that transcription of the three genes is not co-regulated.²⁷ The *COL4A5* mutations also led to strong accumulation of $\alpha 1$ and $\alpha 2$ chains of type IV collagen across the entire width of the GBM, and the absence of the $(\alpha 5)_2\alpha 6$ network in Bowman's capsule. Concomitant mutations in the $\alpha 6$ gene, which is tightly lined to $\alpha 5$ on the X, are associated with diffuse leiomyomatosis, although the mechanism of pathogenesis remains unclear.

The *COL4A3/4* genes are involved in both autosomal AS and TBMN. Autosomal recessive AS accounts for about 15% of affected individuals and arises from either compound heterozygous or homozygous mutations in *COL4A3* or *COL4A4*. Autosomal dominant AS and 40% of TBMN are caused by heterozygous mutations in *COL4A3* or *COL4A4*. Heterozygous mutations in *COL4A3* or *COL4A4* typically cause the mild abnormalities seen in TBMN, although in rare cases, heterozygous mutations are associated with autosomal dominant AS.²⁸ However, although approximately 40% of patients with TBMN can be considered carriers for autosomal recessive AS,²⁹ linkage to *COL4A3* and *COL4A4* has been excluded in some families with TBMD, indicating that TBMD is a genetically heterogeneous condition.³⁰

The collagen $\alpha3\alpha4\alpha5(\text{IV})$ network is also present in cochlea and lens capsule. This explains why many AS patients can also present with sensorineural hearing loss and/or eye defects. Once the lens capsule becomes weak, the lens can herniate either anteriorly or posteriorly to cause lenticonus.

Immunohistologic analysis of the distribution of type IV collagen chains in renal and skin biopsies are crucial for the diagnosis of AS. In X-linked AS, no $\alpha3$, $\alpha4$, or $\alpha5$ deposition in the GBM is detectable in male patients because once $\alpha5$ is missing, the formation of the $\alpha3\alpha4\alpha5(\text{IV})$ protomer is disrupted. In contrast, the distribution of $\alpha3\alpha4\alpha5(\text{IV})$ trimers in the GBM is mosaic in a female carrier. In autosomal recessive AS, there is no $\alpha3$, $\alpha4$, or $\alpha5$ positive staining in the GBM. The $\alpha1$ and $\alpha2$ chains, which are normally confined to the mesangium and the subendothelial aspect of the GBM, are present throughout the entire width of the GBM in both forms of AS.

In X-linked AS, skin biopsy, which is much less invasive than kidney biopsy, can be highly informative because the $(\alpha5)_2\alpha6$ collagen IV network is normally present in the epidermal basement membrane. Thus, $\alpha5$ staining is absent from the epidermal basement membrane of male patients, whereas segmental staining of $\alpha5$ is seen in female carriers. In contrast, normal staining of the epidermal basement membrane is observed in patients with autosomal recessive or autosomal dominant AS.³¹ If the suspicion of X-linked AS is high based on family history, a skin biopsy should be performed first. Otherwise, a renal biopsy should be performed.³²

The characteristic electron microscopic findings of the GBM in AS are irregular thickening, thinning and basket weaving, which consists of irregular splitting of the lamina densa, giving rise to multiple thin interwoven lamellae separated by lucent space.³³ The molecular mechanisms underlying these ultrastructural changes are still obscure. It has been suggested that the thickened GBM may represent areas of matrix deposition.^{34,35} Furthermore, it has been shown that the anomalous persistence of the fetal $\alpha1(\text{IV})$ and $\alpha2(\text{IV})$ isoforms in AS confers an increased susceptibility to endoproteolytic cleavage as compared to the more cysteine-rich $\alpha3\alpha4\alpha5(\text{IV})$ network in the mature GBM of normal kidneys; this may explain the progressive GBM splitting and increased deterioration.³⁶ Recently, it has been demonstrated that the proteolytic degradation of the GBM in $\alpha3(\text{IV})$ knockout Alport mice may be mediated, in part, by induction of matrix metalloproteinase-12 (MMP-12) in podocytes. It has also been suggested that monocyte chemoattractant protein -1 (MCP-1) activation of CC chemokine receptor 2 (CCR2) on podocytes may underlie the elevated expression of MMP-12.³⁷

COLLAGEN IV AND ACQUIRED ANTI-GBM NEPHRITIS – GOODPASTURE’S DISEASE AND ALPORT POST-TRANSPLANTATION NEPHRITIS

There are two forms of anti-GBM nephritis: Goodpasture’s disease and Alport post-transplantation nephritis (APTn). Goodpasture’s disease is a disorder in which circulating autoantibodies attack the GBM and/or pulmonary alveolar BM, thereby causing rapidly progressive glomerulonephritis with crescent formation and/or pulmonary hemorrhage. Epitopes A and B (E_A and E_B), located in the $\alpha3$ chain NC1 domain, were identified as the Goodpasture autoantigen.³⁸⁻⁴⁰ APTn occurs in 3% to 5% of Alport patients who receive renal transplants. The recipient can sometimes mount an alloimmune response against the normal type IV collagen existing in the normal donor kidney. However, the target antigen in APTn had been elusive.

Recent work from Billy Hudson’s group has advanced our understanding of the pathogenesis of these two forms of antibody-mediated glomerulonephritis.⁴¹ Besides E_A and E_B identified in $\alpha3\text{NC1}$, they discovered a new E_A region in the $\alpha5$ NC1 domain as a Goodpasture autoantigen. In addition, these investigators identified the E_A region in $\alpha5$ NC1 as the alloantigen in APTn. It is more intriguing that their new work showed a clear difference between neopeptides in Goodpasture’s disease and alloepitopes in APTn. The amino acid residues in neopeptides are cryptic and sequestered in the quaternary structure of the hexamers. Disruption of the hexamer changes the conformation and exposes neopeptides to elicit the production of Goodpasture autoantibodies. In sharp contrast, the amino acid residues in alloepitopes are exposed on the surface of the hexamer, and binding with APTn alloantibodies decreases upon dissociation of the hexamer. In Goodpasture’s disease, they hypothesize that a variety of triggering events including post-translational modifications (oxidation, nitrosylation, and glycation), proteolytic cleavage and environmental factors such as cigarette smoking or exposure to organic solvents promote the conformational transition to a dissociated pathogenic conformer that elicits an autoimmune response.

HEPARAN SULFATE PROTEOGLYCAN

The charge selectivity of the GFB has been the subject of extensive investigations for decades. Heparan- and chondroitin-sulfate glycosaminoglycan (GAG) side chains of heparan sulfate proteoglycans (HSPGs) endow the GBM with its electronegative charge. Three distinct BM-HSPGs have been identified: perlecan, collagen XVIII, and agrin. Glomerular charge selectivity was attributed to the GBM’s anionic sites enriched with HSPGs.⁴²⁻⁴⁵ However, this concept has been challenged.

Perlecan and collagen XVIII are localized primarily to the MM and Bowman's capsule and are only prominent in the GBM during development.^{46,47} Whereas perlecan mutant mice (*Hspg2*^{Δ3/Δ3}) lacking attachment sites for three heparan sulfate side chains exhibited no morphologic abnormalities in kidneys, they had a greater susceptibility to protein overload.^{48,49} Gene ablation studies of collagen XVIII in mice showed that the mutants have mild MM expansion and slightly elevated serum creatinine levels compared with the controls. However, the study did not reveal any change of the GBM in the knockout mice.⁵⁰ Agrin is the predominant GBM-HSPG at maturity, and it is derived primarily from podocytes. Podocyte-specific knockout of agrin demonstrated that despite a marked reduction in the number of anionic sites in the GBM, the GFB was not compromised, even when challenged with albumin overload. These findings, thus, indicate that agrin is dispensable for the establishment or maintenance of the integrity of the GFB.⁵¹ Moreover, in perlecan/agrin double mutants, the absence of perlecan-HS in combination with agrin did not cause proteinuria, and excretion of a negatively charged Ficoll tracer was unchanged as compared to that in wild type mice.⁵² In line with these findings, reduction of anionic sites in the GBM by heparanase by using mice overexpressing heparanase did not lead to proteinuria.⁵³

The charge selectivity of the GFB is highly controversial. In view of the recent *in vivo* studies, it appears that the GBM does not play a significant role in the charge-selective properties of the GFB. Recently, Axelsson et al.⁵⁴ has demonstrated that the diffusion of conformationally identical anionic Ficoll across the rat GFB was significantly reduced compared with that of neutral Ficoll. This finding is in contrast with their previous finding of increased glomerular permeability of negatively charged Ficoll relative to neutral Ficoll.⁵⁵ Their explanation is that the charge modification of Ficoll in their previous study had significantly increased the molecular radius for all molecular weights, making it more flexible and hyperpermeable across the GFB compared with neutral Ficoll. Based on this finding and other experimental evidence indicating that the GFB does retard anionic proteins compared with neutral or cationic proteins,⁵⁶⁻⁵⁸ they speculate that the charge selectivity of the GFB may reside in the endothelial glycocalyx.

NIDOGENS

Nidogens 1 and 2, also known as entactins 1 and 2, are BM glycoproteins expressed by distinct genes located on different chromosomes.⁵⁹⁻⁶¹ They bind tightly to the laminin $\gamma 1$ chain short arm and also bind to type IV collagen. Therefore, previously it was thought that nidogens are the major molecular link between the

laminin and collagen IV networks and should, therefore, be crucial for BM formation. However, this notion is not supported by the gene deletion studies. The loss of either isoform had no effect on BM formation and organ development.^{62,63} However, genetic ablation of both nidogens 1 and 2 in mice resulted in perinatal lethality, which was associated with impaired lung and cardiac development. But despite the ubiquitous presence of nidogens in basement membranes, most of the nidogen double-null mice had developed functioning kidneys with well-defined GBM, suggesting tissue-specific roles of nidogen in the formation and maintenance of certain basement membranes.⁶⁴

CONCLUSION

Various studies have been performed to delineate whether the GBM or the slit diaphragm (SD), a cell-cell junction spanning the spaces between the interdigitating foot processes, is the primary filtration barrier of kidney. In recent years, the composition and functions of the SD have been extensively investigated. However, the GBM should not be overlooked. To maintain the integrity of the GFB, it appears that the laminin and type IV collagen networks of the GBM are critical, while HSPG and nidogen are dispensable.

For several decades, the GBM has been envisioned as being a charge-selective barrier for glomerular filtration. However, the recent genetic studies including agrin deletion and compound agrin/perlecan deletion in the GBM have challenged the traditional concept. It seems that the GBM does not contribute much to the charge selectivity of the GFB. It has been postulated that the endothelial cell layer may exert more pronounced effect on the charge selectivity of the GFB. Further experimentation will be required to elucidate the exact mechanisms of the charge-selectivity of the GFB.

In conclusion, all strata of the glomerular capillary wall including GBM, podocytes and endothelial cells operate in a synchronic and integrated manner to maintain the permselectivity of the GFB.

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