ABSTRACT

BACKGROUND
In Goodpasture’s disease, circulating autoantibodies bind to the noncollagenous-1 (NC1) domain of type IV collagen in the glomerular basement membrane (GBM). The specificity and molecular architecture of epitopes of tissue-bound autoantibodies are unknown. Alport’s post-transplantation nephritis, which is mediated by alloantibodies against the GBM, occurs after kidney transplantation in some patients with Alport’s syndrome. We compared the conformations of the antibody epitopes in Goodpasture’s disease and Alport’s post-transplantation nephritis with the intention of finding clues to the pathogenesis of anti-GBM glomerulonephritis.

METHODS
We used an enzyme-linked immunosorbent assay to determine the specificity of circulating autoantibodies and kidney-bound antibodies to NC1 domains. Circulating antibodies were analyzed in 57 patients with Goodpasture’s disease, and kidney-bound antibodies were analyzed in 14 patients with Goodpasture’s disease and 2 patients with Alport’s post-transplantation nephritis. The molecular architecture of key epitope regions was deduced with the use of chimeric molecules and a three-dimensional model of the α345NC1 hexamer.

RESULTS
In patients with Goodpasture’s disease, both autoantibodies to the α3NC1 monomer and antibodies to the α5NC1 monomer (and fewer to the α4NC1 monomer) were bound in the kidneys and lungs, indicating roles for the α3NC1 and α5NC1 monomers as autoantigens. High antibody titers at diagnosis of anti-GBM disease were associated with ultimate loss of renal function. The antibodies bound to distinct epitopes encompassing region E_a in the α5NC1 monomer and regions E_a and E_b in the α3NC1 monomer, but they did not bind to the native cross-linked α345NC1 hexamer. In contrast, in patients with Alport’s post-transplantation nephritis, alloantibodies bound to the E_a region of the α5NC1 subunit in the intact hexamer, and binding decreased on dissociation.

CONCLUSIONS
The development of Goodpasture’s disease may be considered an autoimmune “conformeropathy” that involves perturbation of the quaternary structure of the α345NC1 hexamer, inducing a pathogenic conformational change in the α3NC1 and α5NC1 subunits, which in turn elicits an autoimmune response. (Fundied by the National Institute of Diabetes and Digestive and Kidney Diseases.)
Goodpasture's disease is an organ-specific autoimmune disorder characterized by rapidly progressive glomerulonephritis, pulmonary hemorrhage, and glomerular pathological findings that include linear deposits of antibodies along the glomerular basement membrane (GBM) (Fig. 1A).1-2 (For this article we have studied Goodpasture's disease, which describes the specific entity in which the cause of organ dysfunction is proven to be anti-GBM antibodies, in contrast with Goodpasture's syndrome, which is a clinical term used to describe rapidly progressive glomerulonephritis and pulmonary hemorrhage.) Lerner and colleagues3 passively transferred Goodpasture anti-GBM antibodies in a primate model, inducing glomerulonephritis and thereby showing that an autoantibody itself can cause disease. The target GBM antigen for circulating antibodies was subsequently identified as the noncollagenous-1 (NC1) domain of the α3 chain of collagen IVαє; further studies revealed that collagen IV is a family of six α-chains (α1 through α6).7 Immunization of laboratory animals indicated that the α3NC1 specifically induced severe proteinuria and glomerulonephritis, causally linking the self-antigen and antibody in Goodpasture's disease.8-10

The α3NC1 monomer is assembled into the collagen IV network through the association of the α3, α4, and α5 chains to form a triple helical protomer and through the oligomerization of α345 protomers by means of end-to-end associations and intertwining of triple helices.7 Two protomers associate through C-terminal NC1 domains, forming an NC1 hexamer.11 The major cross-linked hexamer is reinforced by novel sulfilimine bonds that fasten two protomers12 and must be dissociated in order for autoantibody binding to occur.11,13 In contrast, the hexamer that is not cross-linked can be dissociated by the antibodies themselves, after which they bind to subunits.11

The α345 network is also a target for anti-GBM alloantibodies in Alport’s post-transplantation glomerulonephritis, which occurs in 3 to 5% of patients with Alport’s syndrome who receive kidney transplants; in most such patients, the development of Alport’s post-transplantation nephritis results in allograft loss.14 Alport’s post-transplantation nephritis is mediated by the deposition of alloantibodies to the α3NC1 and α5NC1 domains in response to the “foreign” α345 collagen network that is absent in the kidneys of patients with Alport’s syndrome but present in the renal allograft.15,16

Thus, the α345NC1 hexamer is targeted by antibodies that arise in both Goodpasture’s disease and Alport’s post-transplantation nephritis, but these antibodies have different binding properties. Alloantibodies bind epitopes exposed on the native hexamer, whereas in Goodpasture’s disease the autoantibodies require hexamer dissociation to unmask hidden epitopes.7,17 Our retrospective study investigated the molecular basis for these differences in antibody binding to provide insight into the pathogenic mechanisms of autoimmunity in Goodpasture’s disease.

**METHODS**

**PROTEINS**

We purified recombinant human monomers α1NC1 through α6NC1 and chimeras from the culture medium of stably transfected human embryonic kidney (HEK) 293 cells with the use of anti-FLAG agarose.10 To construct α5/α1 chime-
ras corresponding to the E_a and E_b regions of the α3NC1 domain, we used polymerase-chain-reaction mutagenesis (for details see the Supplementary Appendix, available with the full text of this article at NEJM.org). Collagen IV NC1 hexamers were isolated from bovine GBM with the use of collagenase digestion.13

**SERUM AND TISSUE SAMPLES**

Approval from local institutional ethics committees and written informed consent from patients were obtained before the collection of samples. Serum samples from 35 patients with anti-GBM glomerulonephritis were obtained from the serum bank of the Department of Nephrology at
Lund University Hospital as a representative subgroup of samples from a larger cohort that were used in our previous study. An additional 22 serum samples were collected at the Scripps Research Institute, Kansas University, and the Vanderbilt University Medical Center from 1985 through 2008. Samples were collected before plasma exchange or immunosuppressive drug treatment was initiated. Serum samples from 18 healthy adult volunteers were used as normal controls. Tissue eluates were isolated from the kidneys of 13 patients with Goodpasture’s disease after they underwent nephrectomy at the Scripps Research Institute, as previously described. Serum and tissue samples obtained at the time of autopsy from one patient with anti-GBM glomerulonephritis who had undergone hemodialysis and immunosuppressive therapy for 3 months were snap-frozen, stored at −80°C, and processed later for elution of kidney- and lung-bound antibodies.

Alloantibodies were purified from the rejected kidney allografts of two previously described patients with X-linked Alport’s post-transplantation nephritis. Patient 1 was a 23-year-old man with renal insufficiency, proteinuria, and microscopic hematuria. Nephrectomy was performed on a second transplant after linear IgG staining of GBM and crescentic glomerulonephritis were revealed on renal biopsy. In Patient 2, end-stage kidney disease developed at 20 years of age; alloantibodies were eluted from the fourth allograft. Kidneys and lungs from normal donors were obtained from the National Disease Research Interchange in Philadelphia.

Tissue-bound antibodies were eluted with the use of 0.1 M glycine, pH 2.8 and 2.2, after homogenization in TRIS-buffered saline (pH 7.4) with protease inhibitors.

**AFFINITY PURIFICATION OF GOODPASTURE AUTOANTIBODIES**

The recombinant domain α3NC1 or α5NC1 was coupled with Affi-Gel 10 (Bio-Rad Laboratories) at a concentration of 1 mg per milliliter. Plasmapheresis fluid from patients with Goodpasture’s disease was fractionated by means of sequential passing through α3NC1 and α5NC1 columns. Bound antibodies were eluted with 6 M urea in 50 mM sodium citrate (pH 4.0) diluted with TRIS-buffered saline (pH 7.4) and concentrated with the use of ultrafiltration.

**IMMUNOASSAYS**

Immunoassays of NC1 domains or chimeras were performed with the use of indirect and inhibition enzyme-linked immunosorbent assays.

**STATISTICAL ANALYSIS**

All data sets were analyzed for normality with the use of the Kolmogorov–Smirnov test. To determine differences between groups, we used the Mann–Whitney U test or the Kruskal–Wallis analysis of variance on ranks for continuous variables and Fisher’s exact test for categorical variables. A P value of less than 0.05 was considered to indicate statistical significance.

**RESULTS**

**CLINICAL DATA**

For this retrospective study, we included serum samples from 57 patients with Goodpasture’s disease. The median age of the patients at the time of diagnosis was 59 years (range, 19 to 87); 44% of all patients were women. There was no significant difference in age distribution between male and female patients. In 3 patients, no further clinical data were available. Among the remaining 54 patients, 22 (41%) had positive results for myeloperoxidase antineutrophil cytoplasmic antibodies (ANCA). Clinical data on lung involvement were available for 46 patients, and 12 of these patients (26%) had overt lung hemorrhage. Follow-up information was available for 50 of the 57 patients at 6 months; 17 patients (34%) remained alive, with stable kidney function; 21 (42%) were being treated with dialysis; and 12 (24%) had died.

**SPECIFICITY OF CIRCULATING AND KIDNEY-BOUND ANTIBODIES**

Serum samples from all 57 patients with Goodpasture’s disease reacted strongly with the α3NC1 domain. There were three categories of specificity: 12 samples reacted only with the α3NC1 monomer (Fig. 1B), 12 reacted with both the α3NC1 and α5NC1 monomers (Fig. 1C), and the remaining 33 samples were immunoreactive to α3NC1, α5NC1, α1NC1, and α4NC1, with occasional binding to α2NC1 and α6NC1 (Fig. 1D). Overall, 72% of the samples from these patients reacted with the α5NC1 monomer. The antibodies eluted from the kidneys of all 14 patients with Goodpasture’s disease showed binding to α3NC1 and α5NC1 monomers in the majority of samples (11 of 14,
Characterization of Circulating α3NC1 and α5NC1 Autoantibodies

We purified antibodies from seven patients with Goodpasture’s disease, using α3NC1 and α5NC1 affinity columns. All purified antibodies belonged to the IgG subclass (data not shown). Binding of the α3NC1 antibodies to immobilized α3NC1 was strongly inhibited with soluble α3NC1 but not with the α5NC1 monomer (Fig. 2A). Potent α3NC1 inhibition (half-maximal inhibitory concentration [IC50], 0.05 μg per milliliter) indi-
indicates high affinity of α3NC1 antibodies (apparent dissociation constant $[K_d]$, 2×10$^{-9}$ M). The α5NC1 IgG antibodies had lower affinity for the α5NC1 monomer (IC$_{50}$, 1.3 μg per milliliter; apparent $K_d$, 5×10$^{-8}$ M) (Fig. 2B). The absence of cross-inhibitory effects of α5NC1 and α3NC1 shows that α3NC1 antibodies and α5NC1 antibodies are two distinct populations of circulating autoantibodies in Goodpasture’s disease.

Reduction of the α5NC1 monomer completely inhibited binding of the purified α5NC1 antibodies (data not shown), indicating that the epitopes are conformational and dependent on a critical disulfide bond, analogous to that of α3NC1. Moreover, the α3NC1 and α5NC1 antibodies displayed negligible binding to native GBM NC1 hexamers, but the binding was greatly increased on dissociation of the hexamers into constituent subunits (Fig. 2C). We previously described this phenomenon for α3NC1 antibodies as cryptic (hidden) epitopes.

**EPI TOPE MAPPING FOR CIRCULATING α3NC1 GOODPASTURE ANTIBODIES**

We hypothesized that regions in the α5NC1 monomer that were homologous to the $E_A$ and $E_B$ regions of the α3NC1 monomer would harbor the epitopes for the α5NC1 antibodies. We created two α1/α5 chimeras by substituting unique amino acid residues in α1NC1, as a nonreactive scaffold, for those in α5NC1 (Fig. 2D). Preincubation with the $E_A$-α5 chimera, but not with the $E_B$-α5 chimera or a parental α1NC1 monomer, significantly inhibited binding of Goodpasture α5NC1 antibodies to α5NC1 in a dose-dependent manner (Fig. 2E). These results establish the $E_A$ region as a part of the epitope for circulating α5NC1 autoantibodies.

**EPI TOPE MAPPING FOR KIDNEY-BOUND AUTOANTIBODIES AND ALLOANTIBODIES**

Both the $E_A$ and $E_B$ regions of the α3NC1 monomer were targets for kidney-bound antibodies in 11 patients with Goodpasture’s disease (Fig. 3A). All kidney eluates also targeted the $E_A$ region of the α5NC1 monomer, whereas only 1 patient had antibodies that were reactive to the $E_B$ region (Fig. 3B). Moreover, comparison of samples from a single patient with Goodpasture’s disease revealed that circulating antibodies and lung-bound and kidney-bound antibodies shared the same specificity, affinity, and epitopes (Fig. 1 in the Supplementary Appendix). In contrast, the alloantibodies in kidney eluates from the two patients with Alport’s post-transplantation nephritis (Patients 1 and 2) targeted the α5NC1 monomer but not the homologous α1NC1 or α3NC1 monomer (Fig. 3C), and both strongly bound the $E_A$-α5 chimera, whereas the $E_B$-α5 chimera reacted with alloantibodies from Patient 2. These unexpected findings indicate that the $E_A$ region of the α5NC1 monomer is a critical part of the epitopes in both Goodpasture’s disease and Alport’s post-transplantation nephritis.

Furthermore, both the α3NC1 and α5NC1 autoantibodies were nonreactive to the normal α345NC1 hexamer until the hexamer was dissociated with protein denaturant. The induction of binding was observed for affinity-purified α3NC1 and α5NC1 antibodies from a single patient with Goodpasture’s disease (Fig. 3D), circulating antibodies from 27 patients with Good-
pasture’s disease, and kidney eluates from 14 other patients with Goodpasture’s disease (Fig. 3E). Collectively, these findings indicate that circulating and tissue-bound α3NC1 and α5NC1 antibodies in Goodpasture’s disease have identical properties — that is, their respective epitopes arise only after the dissociation of the NC1 hexamer. In sharp contrast, the alloantibodies associated with Alport’s post-transplantation nephritis have a strong reaction to the normal

Absorbance at 405 nm

α3 IgG α3 IgG Kidney Lung Patient 1 Patient 2 IgG

Patient with Goodpasture’s Disease APTN

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hexamer, and binding is greatly decreased on dissociation of the hexamer (Fig. 3D).

ASSOCIATION OF α3NC1 AND α5NC1 AUTOANTIBODIES WITH DISEASE ACTIVITY

A strong positive correlation was found between titers for α3NC1 and α5NC1 antibodies among all serum samples from patients with Goodpasture’s disease (Fig. 3F). The presence of the α3NC1 antibody in all samples and the gradual increase in α5NC1 reactivity suggest that α5NC1 autoantibodies may develop after α3NC1 autoantibodies.

Further analyses revealed no significant difference in age, sex, ANCA status, renal outcome, or serum reactivity to α3NC1 or α5NC1 monomers in patients with and those without lung hemorrhage. ANCA status was not associated with sex, presence or absence of lung involvement, renal outcome, or titers for α3NC1 and α5NC1 antibodies; however, patients with positive test results for ANCA were older than patients with negative test results (median age, 70 years vs. 58 years; P = 0.03). Patients with Goodpasture’s disease who were undergoing dialysis and those with preserved renal function at follow-up were of similar age (median, 45 years and 57 years, respectively), but patients who died were significantly older (median, 73 years; P < 0.001) and were excluded from further analyses. Patients undergoing dialysis had higher titers of α3NC1 antibodies at presentation than did patients with stable kidney function (Fig. 3G), and had much higher titers for α5NC1 antibodies (median, 0.922 vs. 0.262). A serum sample from 1 of 21 patients with progressive disease requiring dialysis had reactivity that was restricted to the α3NC1 monomer; the majority of samples (from 20 of 21 patients) were reactive with α3NC1 and α5NC1 monomers. In contrast, samples from 6 of 17 patients with preserved renal function had restricted α3NC1 reactivity (P = 0.03 by Fisher’s exact test). Thus, our results support the possibility that increased titers of circulating α3NC1 and α5NC1 autoantibodies are associated with a poor renal outcome.

THREE-DIMENSIONAL STRUCTURE OF THE α345NC1 HEXAMER

We analyzed the structure of the immunoreactive Eα and Eβ regions in the α345NC1 hexamer model (see the Supplementary Appendix). The Eα region of the α5NC1 subunit was not reactive to the Goodpasture autoantibodies in the α345NC1 hexamer cross-linked by sulfilimine bonds (Fig. 4A). This lack of reactivity is analogous to that of the Eα and Eβ regions of the α3NC1 subunit.11,25 However, disruption of the hexamer quaternary structure after treatment with guanidine or by lowering pH leads to dissociation into α35 and α44 dimers and antibody binding (Fig. 4B). The dissociation is concomitant with conformational changes that unlock domain-swapping interactions26.

Figure 4 (facing page). Topology of the Eα and Eβ Regions in the α345 Noncollagenous-1 Hexamer, Structural Determinants for the Binding of Alport Autoantibodies and Goodpasture Autoantibodies In Vitro, and Accessible Surface Area of the Eα-α3 and Eβ-α5 Regions of the Noncollagenous-1 Hexamer. The α345 noncollagenous-1 (NC1) hexamer is composed of two trimeric caps, each consisting of α3NC1 (red), α4NC1 (blue), and α5NC1 (green) subunits (Panel A). Two of the six sulfilimine bonds (S=N) that stabilize the trimer–trimer interface are shown (light yellow). The location and structure of the four homologous regions are also shown: Eα (yellow) and Eβ (orange) in the α3NC1 subunit, and Eα (pink) and Eβ (purple) in the α5NC1 subunit. Three regions, Eα and Eβ in α3NC1 and Eα in α5NC1, become critical parts of the neoepitopes for Goodpasture autoantibodies. The topology of the Eα regions in α3NC1 and α5NC1 is similar, as indicated in the ribbon diagrams (Panel A, bottom), with the characteristic folding pattern of a β-sheet stabilized with a disulfide bond. Ala19, Gin24, and Gin28 (pink) within the Eα region of α5NC1, exposed in the α345NC1 hexamer, are candidates for the binding of Alport autoantibodies (Panel B, bottom right). In contrast, Leu27 and Val28 (gray) are sequestered by their lateral interaction with the α4NC1 domain, and when exposed as a result of hexamer dissociation, they become critical to the binding of Goodpasture autoantibodies. Dissociation of the sulfilimine-cross-linked hexamer into α35 dimer subunits is concomitant with a conformational change that results in the formation of the neoepitopes encompassing the Eα regions of the α5NC1 and α3NC1 monomers and the binding of their respective autoantibodies (Panel B, bottom left). The accessible surface area of the Eα-α3 region (Panel C, top) and the Eβ-α5 region (Panel C, bottom) was calculated for a probe, which mimics the antibody molecule (radius, 9 Å); the area of individual residues in the α345NC1 hexamer (black bars) and the α3NC1/α5NC1 model monomers (gray bars) is shown. An increase in the surface area of the monomers indicates that residues are buried in the hexamer (Val27 and Leu28 in Eα-α3 and Leu27 and Val29 in Eβ-α5). In contrast, residues with similar areas within the hexamer and monomers are exposed in the hexamer (Ala19, Gin24, and Gin28 in Eα-α3).

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MOLECULAR ARCHITECTURE OF THE GOODPASTURE AUTOANTIGEN

B Goodpasture autoantibodies

Dissociation
Conformational change

Alport alloantibodies

Residues within α345NC1 hexamer
Residues within α3NC1 and α5NC1 monomers

Accessible Area, Å²

Eₐ-α₅

S₃₁

T₁₇

Gln24

Leu27

Gln28

Val29

Ala19

Sulfilimine bonds

α₃-IgG

α₅-IgG

α₅-IgG

Gln24

Leu27

Gln24

Eₐ-α₅

α₅ Allo-IgG

α₃ Auto-IgG

α₅ Auto-IgG

Motif magnified

Motif magnified

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and expose residues sequestered by neighboring subunits. The dissociation and conformational change are reversible, since Goodpasture antibodies do not bind the reassembled hexamer. Further evidence of conformational transition as a key step in neoepitope formation is provided by the differential effect of dissociating agents on the binding of Goodpasture and Alport post-transplantation nephritis antibodies to the E\textsubscript{\textalpha}-\textalpha region of the \alpha5NC1 subunit. Goodpasture autoantibodies react only with the subunits of a dissociated hexamer, whereas Alport post-transplantation nephritis alloantibodies bind to the intact hexamer and lose binding on dissociation. Analysis of the accessible surface area of the E\textsubscript{\textalpha}-\textalpha\textfive region of the \alpha5NC1 hexamer revealed that exposure of buried amino acid residues Leu\textsuperscript{27} and Val\textsuperscript{29} on hexamer dissociation transforms the E\textsubscript{\textalpha}-\textalpha\textfive region into a part of the Goodpasture neoepitope; likewise, homologous residues Val\textsuperscript{27} and Leu\textsuperscript{29} become exposed within the E\textsubscript{\textalpha}-\textalpha\textthree region (Fig. 4B and 4C). In contrast, Ala\textsuperscript{19}, Gln\textsuperscript{24}, and Gln\textsuperscript{28} are located on the hexamer surface and constitute a part of the alloepitope. The diminished binding of the alloantibodies indicates a conformational change in the E\textsubscript{\textalpha}-\textalpha\textfive region, which is concomitant with hexamer dissociation.

**DISCUSSION**

The immunoreactivity of circulating Goodpasture autoantibodies to several NC1 domains of collagen IV was reported previously, but the specificity of tissue-bound autoantibodies is unknown, except in a single patient, in whom the antibodies were reactive to the \alpha3NC1 domain. We report here that \alpha5NC1 autoantibodies, in addition to \alpha3NC1 autoantibodies, are frequently present in the kidneys and lungs of patients with Goodpasture’s disease. The \alpha5NC1 Goodpasture antibodies bind to a conformation-dependent epitope encompassing the E\textsubscript{\textalpha} region in the \alpha5NC1 monomer. This region also encompasses the epitope for alloantibodies in patients with Alport’s disease.

In the \alpha345NC1 hexamer, quaternary interactions reinforced by sulfilimine cross-links present key structural constraints against the transition of E\textsubscript{\textalpha}-\textalpha\textthree and E\textsubscript{\textalpha}-\textalpha\textfive regions to pathogenic conformation in Goodpasture’s disease. Disruption of hexamer structure changes the conformation of the E\textsubscript{\textalpha} regions of \alpha3NC1 and \alpha5NC1 and the E\textsubscript{\textfive} region of \alpha3NC1, transforming them into neoepitopes for autoantibodies. In the GBM, an additional level of constraint is provided by the triple helical domain tethered to the hexamer (conformer 1) (Fig. 5). In the absence of cross-links, quaternary constraints against conformational transition are diminished (conformer 2), shifting the equilibrium toward the trimers (conformer 3). The presence of such trimers in basement membranes has been confirmed on electron microscopy. Moreover, Goodpasture antibodies can induce a conformational change, dissociate conformer 3, and form an antigen–antibody complex that is consistent with binding to a non–cross-linked hexamer in vitro and in passive-transfer experiments.

We postulate that an early pivotal step of Goodpasture’s disease involves conformational transitions in subunits of non–cross-linked hexamers or trimers (conformers 2 and 3), forming pathogenic neoepitopes that elicit both antibody production and binding (conformer 4). The triggering event may be an individual factor or a combination of factors — such as enzymatic or nonenzymatic post-translational modifications (oxidation, nitrosylation, and glycation), a rise in body temperature, or proteolytic cleavage — that perturbs the quaternary structure of the hexamer. Indeed, cleavage of a disulfide bond in \alpha3NC1 in a non–cross-linked hexamer (conformer 3) has been shown to enhance the binding of Goodpasture antibodies. Furthermore, environmental factors such as cigarette smoking or exposure to organic solvents could inhibit the putative enzyme that catalyzes formation of sulfilimine bonds and thereby increase the proportion of non–cross-linked hexamers (conformer 2).

Goodpasture’s disease may be considered an autoimmune “conformeropathy,” a designation that reflects the requirement for a conformational transition between two distinct NC1 conformers — a nonpathogenic conformer within the hexamer and a dissociated pathogenic conformer that elicits an autoimmune response. Grave’s disease and antiphospholipid autoimmune disease, which involve pathogenic conformational changes, and perhaps idiopathic membranous nephropathy may also be included in such a category. This conceptual framework re-
Reflects fundamental issues about the causes of autoimmune disease in molecular terms, answering questions about what triggers the conformational change.

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Disclosure forms provided by the authors are available with the full text of this article at NEJM.org.

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**Figure 5. Conformational Diversity and Differential Reactivity of α345 Noncollagenous-1 Hexamers of the Glomerular Basement Membrane.**

The diagram shows a portion of the collagen IV network with the α345 noncollagenous-1 (NC1) hexamer tethered to the triple-helical domain. The different possible NC1 conformers shown are the cross-linked form stabilized by sulfilimine bonds (conformer 1 [C-1]), the non-cross-linked form (C-2), and the form in which the NC1 hexamers are dissociated into trimers (C-3). In Goodpasture’s disease the latter may undergo a conformational change resulting in the formation of neoepitopes shown as white squares on the α3NC1 (red) and α5NC1 (green) subunits of C-4, eliciting antibody formation and subsequent binding to conformers C-3 and C-4. Conformers C-1 and C-2 have the potential to be transformed into the pathogenic conformer C-4.

**References**


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