The Dominant Humoral Epitope in Phospholipase A2 Receptor-1: Presentation Matters When Serving Up a Slice of $\pi$

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Phospholipase A2 receptor-1 (PLA2R), the major autoimmune target in primary membranous nephropathy,1 is one of four mammalian members of the mannose receptor (MR) family, which consists of the MR (encoded by the MRC1 gene), Endo180 (MRC2), DEC205 (LY75), and PLA2R itself.2 An additional member, the FcY receptor, is present in avian species and most closely related to PLA2R.3 All are transmembrane glycoproteins with extracellular regions that consist of an N-terminal cysteine-rich (CysR) domain, a fibronectin II-type (FnII) domain, and 8–10 C-type lectin-like domains (CTLDs).

Early studies characterizing the autoantibody–antigen interaction noted that reactivity to PLA2R was abolished if the Western blot (WB) was performed under reducing conditions,1 which suggested that disulfide bonds were crucial for stabilizing the conformation of the humoral epitope(s). The fact that other MR family members underwent conformational shifts in response to changes in pH2,4 also gave credence to a potential conformational epitope in PLA2R. Finally, the identification of several disease-associated single nucleotide polymorphisms within the PLA2R1 gene5–7 raised the possibility that a variant sequence might confer an altered configuration to PLA2R that might be recognized as foreign by the immune system. However, this speculation has since fallen out of favor, because additional sequence analysis has not identified any nonsynonymous single nucleotide polymorphisms unique to PLA2R-associated membranous nephropathy.8

In this issue of JASN, two groups hone in on the location of the major humoral epitope in PLA2R. Kao et al.9 elegantly show that the epitope is within the three most N-terminal domains of the protein and shares the reduction-sensitive properties initially noted for the entire molecule. Fresquet et al.10 go one step farther to localize the epitope to within the CysR domain. Before these reports, there was limited evidence about the position or number of relevant epitopes within PLA2R. It had been shown that preincubation of PLA2R with human autoantibodies did not interfere with binding of a well used commercial antibody generated against an epitope in the CTLD2–3 region.11 Behnert et al.12 identified several linear peptides within PLA2R that were reactive with anti-PLA2R-positive sera in an SPOT assay; several of these peptides were also able to partially inhibit autoantibody binding to the nondenatured molecule.

The core consensus domain of CysR is the ricin B domain, which was first identified as a repeated sugar-binding region in the B chain of the plant-derived toxin ricin. This evolutionarily conserved domain is thought to have arisen from gene triplication of an ancient galactoside-binding peptide, resulting in its current three-lobed (β-trefoil) structure.13 The ricin B domain exists in several contexts in mammalian proteins—most notably the N-terminal CysR domains of the MR family members and the C-terminal ricin B domains of the numerous polypeptide N-acetylgalactosaminyltransferases present in the Golgi. Both groups exhibit six conserved cysteine residues as opposed to the four residues in ricin B. The crystal structure of the MR CysR reveals three disulfide bonds, two of which are involved in internally stabilizing the individual lobes and the third links the final lobe to the extended structure of the molecule.14

Because of differences in nomenclature between the two works9,10 and for the purpose of describing the various PLA2R constructs used in these articles, I will abbreviate the CysR (or Ricin B) domain as R, the FnII domain as F, and the CTLD repeats as Cx–y. The full extracellular domain would, therefore, be designated as RFC1–x.

Kao et al.9 have masterfully engineered a full panel of PLA2R constructs and show that anti-PLA2R autoantibodies seem to exclusively recognize a reduction-sensitive epitope localized to the three most N-terminal domains, RFC1. Kao et al.9 could not further delimit the epitope-containing region because of the instability of the individual domains. However, deleting the first CTLD from the otherwise intact extracellular domain (i.e., RFC2–x) was sufficient to abolish all autoantibody binding by WB, suggesting an important role for this domain in stabilizing the structure of the humoral epitope. Of interest, introduction of the M292V or H300D risk alleles into CTLD1 did not, within the limits of the assay, affect binding. By artificially introducing proteolytic cleavage sites between the domains of RFC1, Kao et al.9 could selectively remove domains on either end (CysR or CTLD1); however, the smaller pieces did not retain antigenicity by WB. This line of experimentation also provided...
evidence that FnⅡ and CTLD1 might be linked by an interdomain disulfide bridge. Kao et al.⁹ conclude that the RFC1 structure is the smallest portion of PLA2R that allows accurate presentation of the epitope by WB because of an ill-defined interdependency of the three domains. This result was strengthened by the fact that soluble RFC1 could block autoantibody binding to the full extracellular domain.

The article by Fresquet et al.¹⁰ reveals that there are limitations to a comprehensive characterization of antibody–antigen interactions imposed by the typical WB protocol. Before SDS-PAGE, proteins are denatured with heat and detergents, disrupting tertiary structure. This is in contrast to other assay systems, such as ELISA, that allow detection of antigen in a more physiologic native state. Just as the routine performance of WB under reducing conditions may have delayed identification of PLA2R as the major antigen in membranous nephropathy, the reliance on WB alone to detect discrete epitopes in PLA2R may have resulted in an incomplete story.

Fresquet et al.¹⁰ use a variety of experimental systems to assess autoantibody binding to PLA2R and ultimately, define the major humoral epitope within the CysR domain proper. Like Kao et al.,⁹ they were unable to find reactivity by WB in small N-terminal constructs; in their hands, RFC1−3 was the smallest construct identified under denaturing WB conditions, because reactivity was lost with RFC1−2. However, when these same constructs were assayed under the non-denaturing conditions of a slot blot, anti-PLA2R autoantibodies detected RFC1−2 reactivity and more importantly, the isolated CysR domain. The larger constructs RFC1−3 and RFC1−8 were able to maintain the structure of the epitope, even in the face of denaturation or reduction, hinting at interdomain interactions within the context of the larger molecule. Experiments using surface plasmon resonance (SPR) reveal remarkably consistent binding affinities of purified anti-PLA2R to CysR and the larger constructs, strongly suggesting that, for the majority of sera tested by SPR, the autoantibody binds primarily to CysR and not to other locations within the extracellular domain.

In a parallel set of experiments, Fresquet et al.¹⁰ perform mass spectrometric analysis of the smallest common proteolytic fragments of PLA2R reactive with autoantibodies by WB. Fresquet et al.¹⁰ find that only two of the identified peptides, both from a similar region of CysR, can significantly inhibit anti-PLA2R binding to RFC1−3. When they add the intervening sequence of PLA2R to synthesize a 31-residue stretch roughly corresponding to the first lobe within the β-trefoil structure of CysR, Fresquet et al.¹⁰ discover that they have recreated the dominant epitope of PLA2R. It is remarkable that not only can this 31-mer inhibit anti-PLA2R binding to RFC1−3 by 85% but that it also exhibits a binding affinity identical to that of the larger constructs as determined by SPR and has reduction-sensitive properties because of an internal disulfide bond.

Fresquet et al.¹⁰ additionally use two techniques to show that, similar to its MR family counterparts, PLA2R has pH-dependent changes in configuration, behaving as a more compact structure at acidic pH. Although this change does not affect binding of anti-PLA2R, it is possible that such conformational change, possibly in conjunction with one or more disease-associated sequence variants, could influence processing of PLA2R within the acidic endosomes and lysosomes of an antigen-presenting cell. Finally, Fresquet et al.¹⁰ use transmission electron microscopy and single-particle averaging to generate low-resolution structural models of PLA2R. There is evidence that CysR and CTLD3 make contact to form a ring-like structure and that the overall PLA2R structure resembles the Greek character π.

Both articles provide evidence that, in the majority of cases, the epitopic region in the N-terminal portion of PLA2R explains all of the reactivity of anti-PLA2R–positive sera.⁹,¹⁰ In constructs lacking the three N-terminal domains, Kao et al.⁹ fail to detect reactivity to the residual domains of the molecule. In a cohort of serum samples from patients with primary membranous nephropathy, reactivity to RFC1 was almost entirely concordant with reactivity to the whole molecule. Although this analysis was performed by WB with the caveats above, it is reassuring that Fresquet et al.¹⁰ provide confirmatory data, with one exception: 10% of the subjects in the cohort described by Fresquet et al.¹⁰ do not exhibit inhibition by RFC1−3 of anti-PLA2R reactivity with the full molecule, suggesting that one or more epitopes may exist in the more C-terminal portion of the molecule. The location of these minor epitopes and the percentages of PLA2R-associated cases associated with antibodies to these minor epitopes will need to be better determined. For now, existing immunoassays containing the entire extracellular domain should be sufficient to detect all anti-PLA2R antibodies. Neither work shows any strong evidence for epitope spreading (i.e., additional subdominant epitopes that might appear later in the course of disease), although this has not been specifically investigated in either of the articles.⁹,¹⁰

The end result of these studies is that there is a dominant humoral epitope in the very N-terminal region of PLA2R with exposure that is clearly affected by experimental conditions and potentially, physiologic conditions as well. Such results move the field forward at a number of levels. By identifying a discrete region that seems to confer the majority of reactivity with anti-PLA2R autoantibodies, hypotheses about the initial events in the autoimmune process can better be proposed and studied. Fresquet et al.¹⁰ note that the nine-amino acid peptide within their 31-mer that itself is capable of inhibiting 47% of binding shares homology with a bacterial enzyme, thus invoking molecular mimicry as a potential initiator of autoimmunity. Although humoral (B cell) epitopes are not equivalent to T cell epitopes, Fresquet et al.¹⁰ propose a hypothetical model of how B cells, initially reactive with a specific bacterial antigen, might subsequently internalize and process a similar-appearing PLA2R, such that specific peptides are loaded into class II HLA molecules encoded by specific risk alleles (e.g., HLA-DQA1) in membranous nephropathy. In addition, if the identified region turns out to be the primary and dominant humoral epitope responsible for disease, a small molecular inhibitor of antigen binding might

be sufficient to neutralize anti-PLA₂R antibodies and render them unable to bind their target antigen.

Both groups are to be congratulated for their meaningful contributions to our evolving understanding of PLA₂R-associated membranous nephropathy, and we look forward to future studies that build on this exciting research.⁹,¹⁰

**DISCLOSURES**

None.

**REFERENCES**


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**A Breath of Fresh Air for Diabetic Nephropathy**

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Diabetic nephropathy (DN) is a leading cause of CKD and a common complication in patients with type 1 or type 2 diabetes mellitus. The disease, as it progresses through defined morphologic and clinical stages, frequently leads to ESRD. Despite certain therapeutic interventions that slow its progression (such as blockade of the renin-angiotensin axis and strict BP, lipid, and glycemic control), the risk of advancing to ESRD remains high. Innovative therapeutic interventions are urgently needed to halt the development and progression of this devastating disease, which is responsible for approximately 40% of all new ESRD cases in the United States.¹

In this issue of *JASN*, Nordquist and colleagues report that activation of the hypoxia-inducible factor (HIF) pathway with cobalt chloride (CoCl₂) protects kidneys from DN in a rat model of type 1 diabetes.² The investigators used streptozotocin to induce diabetes mellitus and began to treat animals with CoCl₂ at the time of streptozotocin administration for 4 weeks. Their study demonstrates that CoCl₂ treatment has strong bene-
cial effects on a functional and morphologic level. By the end of the study, diabetic rats had normal GFR and showed significant improvement in albuminuria compared to untreated control diabetic rats.³

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