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Antibody-Dependent Complement Responses toward SARS-CoV-2 Receptor-Binding Domain Immobilized on "Pseudovirus-like" Nanoparticles

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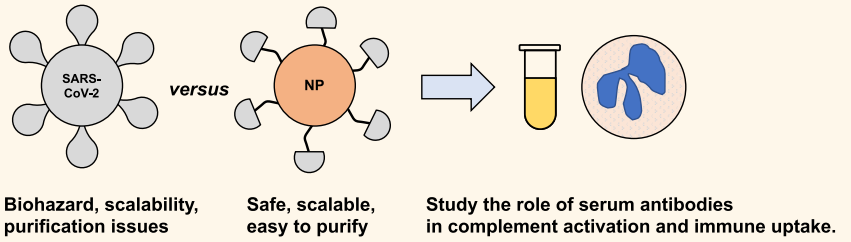

ABSTRACT: **Many aspects of innate immune responses to SARS viruses remain unclear. Of particular interest is the role of emerging neutralizing antibodies against the receptor-binding domain (RBD) of SARS-CoV-2 in complement activation and opsonization. To overcome challenges with purified virions, here we introduce "pseudovirus-like" nanoparticles with ∼70 copies of functional recombinant RBD to map complement responses. Nanoparticles fix complement in an RBD-dependent manner in sera of all vaccinated, convalescent, and naïve donors, but vaccinated and convalescent donors with the highest levels of anti-RBD antibodies show significantly higher IgG binding and higher deposition of the third complement protein (C3). The opsonization *via* anti-RBD antibodies is not an efficient process: on average, each bound antibody promotes binding of less than one C3 molecule. C3 deposition is exclusively through the alternative pathway. C3 molecules bind to protein deposits, but not IgG, on the nanoparticle surface. Lastly, "pseudovirus-like" nanoparticles promote complement-dependent uptake by granulocytes and monocytes in the blood of vaccinated donors with high anti-RBD titers. Using nanoparticles displaying SARS-CoV-2 proteins, we demonstrate subject-dependent differences in complement opsonization and immune recognition.**

KEYWORDS: *iron oxide nanoparticle, SARS-CoV-2, receptor-binding domain, antibody, complement, opsonization*

Complement is the critical arm of the innate immunity responsible for neutralization of pathogens and a plethora of foreign particulates.[1] The exposure of foreign surfaces to the blood results in a rapid surface assembly of complement convertases that promote opsonization through covalent attachment of C3b (a fragment of the third complement protein) to nucleophilic surface groups.[2] Complement activation also results in the liberation of anaphylatoxins (*e.g.*, C3a and C5a).[2] C3b and its cleavage products iC3b, C3d, and C3c promote recognition by a range of complement receptors on neutrophils, monocytes, eosinophils, lymphocytes, erythrocytes, and resident tissue macrophages.[1] The contribution of the complement system to SARS-CoV-2 infection and the pathology of COVID-19 is still actively debated,[3] but some aspects of complement activation are associated with worsening of the clinical outcome. Thus, C5a can cause inflammatory responses in virus-infected lungs,[4,5] and pathological findings implicate the involvement of complement in microvascular

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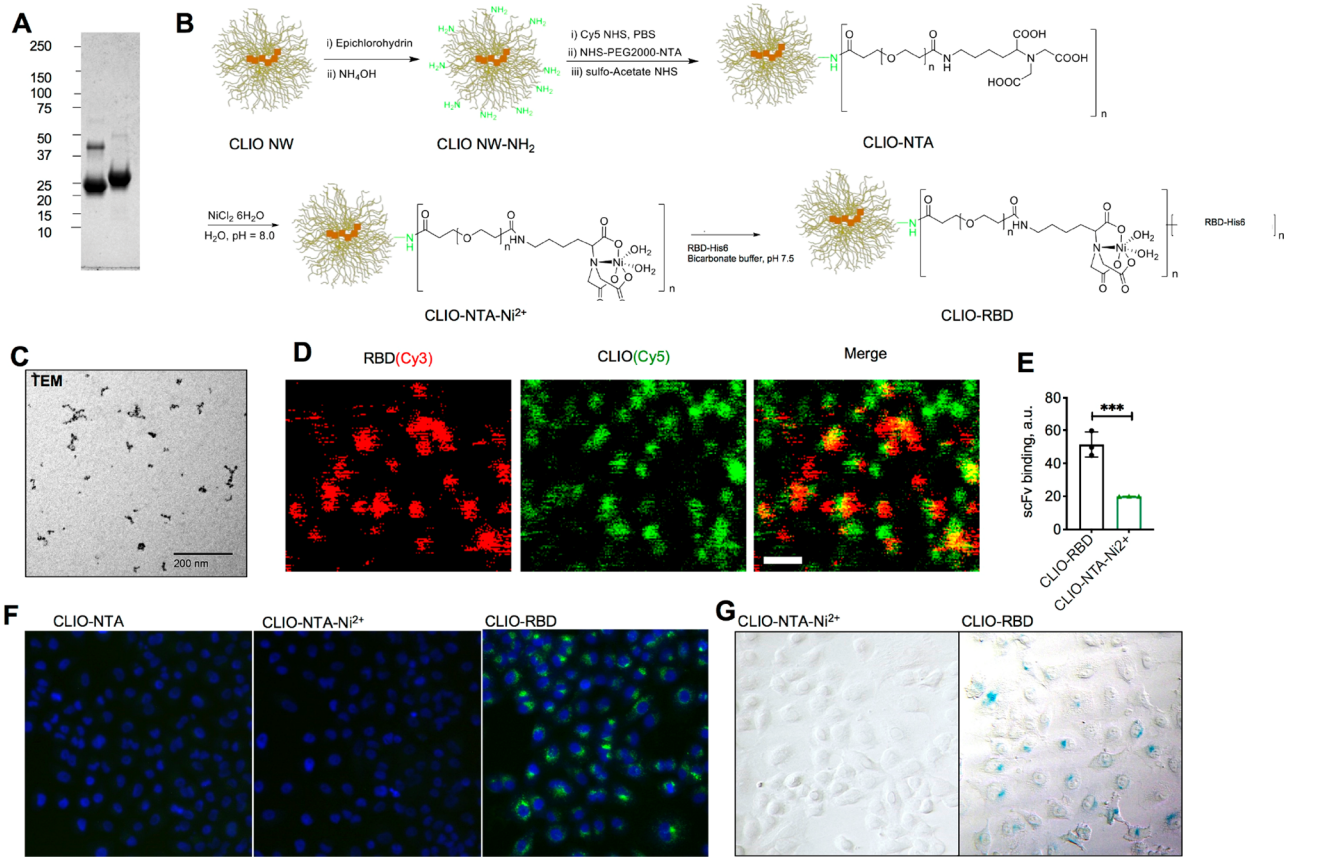

Figure 1. Synthesis and characterization of "pseudovirus-like" nanoparticles. (A) Purified His-tagged RBD (from left to right: nonreduced and reduced forms). (B) Synthesis of CLIO-RBD starting from cross-linked dextran iron oxide nanoworms (CLIO NWs). (C) Transmission electron microscopy of CLIO-RBD showing electron-dense iron oxide cores (the shell and the ligand are not visible). (D) High-magnification confocal microscopy of CLIO(Cy5)-RBD(Cy3). Scale bar, 0.5 μm. Nanoparticles appear larger than the optical resolution limit due to the fluorescence halo. (E) Binding of anti-RBD single-chain antibody to nanoparticles in full serum (prepandemic). ***$p < 0.001$. (F) Uptake of control and RBD-modified particles (Cy5 labeled) by human ACE2-expressing A549 cells by fluorescence microscopy and (G) Prussian blue staining. Incubation conditions are described in Methods. The experiment was repeated twice.

damage in COVID-19 patients.[6,7] SARS-CoV-2 nucleocapsid (N)-protein has been shown to trigger the lectin pathway, which could induce tissue damage and thrombosis.[8,9] Spike (S)-protein of SARS-CoV-2 can interact with heparan sulfate on a cell surface, potentially blocking the binding of the complement regulator factor H, thereby enhancing the turnover of the complement alternative pathway.[10] These findings justified the development of clinical trials on the use of complement inhibitors against mild to moderate acute respiratory distress syndrome in COVID-19 patients (www.clinicaltrials.gov: NCT04402060). As opposed to the collateral damage, the complement system is the first line of immune defense that works in tandem with antibodies and phagocytes to recognize a wide range of viruses and virus-infected cells, resulting in neutralization of viruses and killing of the infected cells.[11,12]

High-titer, high-affinity antibodies against the receptor binding domain (RBD) of S-protein emerge during the disease and in immunized subjects and represent an important subset of antibodies that mediate virus neutralization and protection.[13−15] There is clinical evidence of the association between antiviral antibodies and fluid phase complement activation products in the plasma of COVID-19 patients with respiratory failure.[16] At the same time, the mechanistic link between anti-SAR-CoV-2 antibodies and complement activation has not been conclusively established. Antibodies can activate complement *via* the classical pathway (CP) through C1q binding to the Fc portions of adjacent IgG[17] and the lectin pathway (LP) through binding of mannan-binding lectin, collectins, and ficolins to glycosylated IgG residues.[18,19] In addition to these, IgG can enhance C3 deposition by acting as a scaffold for initial C3b binding and subsequently amplify C3b deposition through the assembly of the alternative pathway (AP) convertase.[20,21] We recently demonstrated that preclinical and clinical nanoparticles trigger complement *via* binding of natural antibodies.[22] We and others previously observed that complement activation pathways and processes depend on the nanoparticle size/curvature, ligand spacing, and density[23,24] and are modulated by a dynamic "protein corona".[25−27] A recent all-atom molecular dynamics simulation concluded strong interactions between SARS-CoV-2 RBD and albumin as well as apolipoprotein E.[28,29] Such modes of interaction may mask the binding of neutralizing antibodies and limit complement activation. Thus, by considering the dynamics of the protein corona, it would be essential to map out the role of neutralizing anti-SARS-CoV-2 antibodies in complement activation and C3 opsonization in full sera as well as complement-mediated leukocyte responses in whole human blood. Engineered virus pseudotypes are relatively safe and have been used in neutralization and cell uptake studies,[30,31] but they are difficult to produce in a purified form needed in precise immunological assays. Furthermore, while the neutralization

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Table 1. Characterization of Nanoparticles (Average of Three Measurements)

particle name	full name	Cy5/NP used	NHS-PEG2000-NTA/NP used	RBD/NP used	RBD/NP conjugated	zeta (mV)	size (nm)	PDI[a]
CLIO-NH_2	CLIO NW-NH_2					10.0 ± 0.658	67.34 ± 25.88	0.2
CLIO-NTA	CLIO NW-PEG2000-NTA	100	2000			1.39 ± 0.320	102.4 ± 68.43	0.273
CLIO-NTA-Ni^{2+}	CLIO NW- PEG2000-NTA-Ni^{2+}	100	2000			4.84 ± 0.142	82.39 ± 47.86	0.220
CLIO-RBD	CLIO NW- PEG2000-NTA-Ni^{2+}-RBD	100	2000	100	72	−6.27 ± 0.816	104.9 ± 59.19	0.358

[a]PDI, polydispersity index.

assays are normally performed in diluted sera to identify high-affinity/high-titer antibodies,[32] these conditions do not represent near-physiological environments (*e.g.*, nondiluted plasma or whole blood), which makes the studies of immune responses using virions extremely challenging.

In view of the above challenges, here we introduce synthetic nanoparticles displaying SARS-CoV-2 RBD as a simpler, safer, and more scalable alternative to virions and study complement activation, C3 opsonization, and immune recognition in full human serum/blood. These "pseudovirus-like" particles display 70 copies of the RBD protein in a functional orientation solely to denote the purpose of modeling aspects of the outer surface of SARS-CoV-2 and to stress the difference from common pseudoviruses. These "pseudovirus-like" particles improve our understanding of how SARS-CoV-2 surface proteins are recognized by the surveillance network of the innate immunity in a relevant biological milieu.

RESULTS AND DISCUSSION

1. Nanoparticle Synthesis and Characterization. To prepare synthetic nanoparticles that emulate SARS-CoV-2 complement activation properties, we first made sure that the virus does not contain complement regulators/inhibitors, as was found for many viruses.[11] Searching against the published NCBI Reference Sequence NC_045512.2 for sequences of CD46, CD55, CD59, CFH, VCP, SPICE, gC-1, FcγR, and C1q binding proteins did not result in any hits. Next, we prepared His6-tagged RBD (original Wuhan variant) in a baculovirus system.[33] The resulting protein was partially in a dimeric form (Figure 1A), likely due to free cysteines in the sequence.[33] To conjugate RBD to nanoparticles, we used 60 nm aminated cross-linked iron oxide nanoworms (CLIO NWs) that show excellent stability, are amenable to ligand and fluorophore modification, and can be easily purified from serum or blood for subsequent biological assays.[34] The particles were first reacted with ∼100 molecules of Cy5 and ∼2000 molecules of NHS-PEG2000-nitrilotriacetic acid (NTA) and then with $NiCl_2$ to produce CLIO NW-NTA-Ni^{2+} (Figure 1B, hereafter CLIO-NTA-Ni^{2+}). Residual amines were capped with acetyl groups. Lastly, His6-RBD (either nonlabeled or Cy3-labeled) was added to create CLIO NW-RBD particles (Figure 1B, hereafter CLIO-RBD) of ∼105 nm (Table 1), *vs* the reported ∼90 nm of SARS-CoV-2.[35] The net CLIO-RBD surface charge was slightly negative (Table 1). The conjugation resulted in ∼70 RBD copies per particle, which is close to the reported number on SARS-CoV-2 virions, which have ∼24 trimers of S-protein or ∼72 copies of RBD.[36] Transmission electron microscopy (TEM) of CLIO-RBD showed chain-like crystalline cores, which are typical for nanoworms[37] (the cross-linked dextran shell and the ligand are not visible in TEM) (Figure 1C). High-magnification confocal microscopy of double-labeled CLIO(Cy5)-RBD(Cy3) showed that approximately 60% of Cy5-labeled nanoparticles were colocalized with RBD(Cy3) (Figure 1D). To make sure that nanoparticle-immobilized RBD is recognized by antibodies in full serum, we used the single-chain scFv fragment of P2B-2F6 anti-RBD, class II antibody isolated from a convalescent patient (K_d 81.4 nM).[38] IRDye800-labeled scFv spiked in nondiluted naïve serum (10 μg/mL) bound to CLIO-RBD significantly better than to CLIO-NTA-Ni^{2+} (Figure 1E). To determine if RBD is in a functional orientation, CLIO(Cy5)-RBD were incubated with human ACE2 expressing A549 lung carcinoma cells, and the uptake was visualized with fluorescence microscopy and Prussian blue staining. The results showed that CLIO-RBD, but not control CLIO-NTA-Ni^{2+} or CLIO-NTA nanoparticles, were taken up by the cells (Figure 1F,G).

2. Donor Characteristics. We collected blood from 10 anonymous post-COVID-19 convalescent patients (7 males, 3 females, age 33−69 years, collected during convalescent plasma treatment campaign in the summer of 2020 at the University of Colorado Hospital), 11 prepandemic naïve donors (4 males, 7 females, age 23−63 years, collected during routine blood donation), and 10 donors fully vaccinated prior to blood donation (4 males, 6 females, age 29−66 years, collected in the summer of 2021 during routine blood donation). Vaccination date and vaccination status (single, double, booster, *etc.*) were not disclosed to the investigators. A high-sensitivity microbead flow cytometry assay[39,40] performed in diluted sera (1:2000) found elevated concentrations of anti-RBD IgG and anti-N-protein IgG in 8/10 of the convalescent donors and elevated concentrations of anti-RBD IgG, but no anti-N-protein IgG in 10/10 vaccinated donors (Figure 2A). Mean anti-RBD IgG levels (Figure 2B) in sera of vaccinated and post-COVID19 convalescent donors were not significantly different, and both were significantly higher than in sera of naïve donors

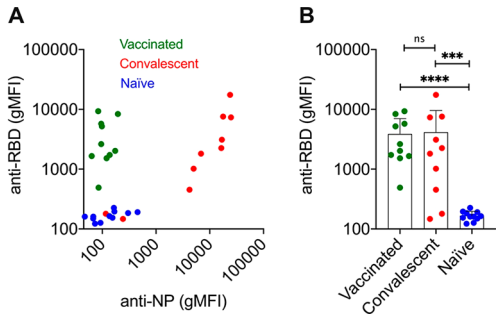

Figure 2. Anti-RBD and anti-N-protein levels in donors' sera. (A) Anti-RBD and anti-N-protein antibody (IgG) levels (geometric mean fluorescence intensity (gMFI), average of 3 technical replicates) by flow cytometry-based immunoassay (Methods). (B) Comparison of anti-RBD IgG levels in 3 donor groups (full statistical analysis in Supplemental Table 1; n = 10 vaccinated, 10 convalescent, and 11 naïve donors; ***p < 0.001; ****p < 0.0001).

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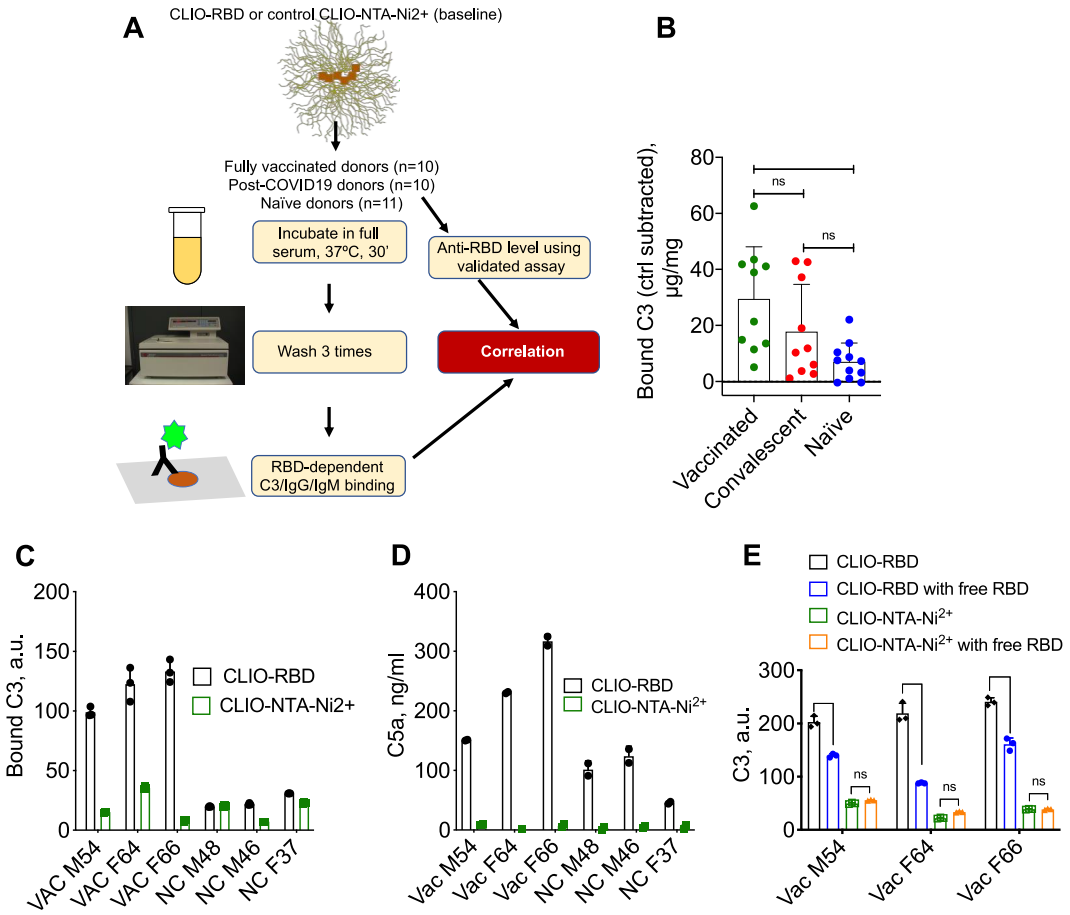

Figure 3. RBD-dependent C3 deposition on nanoparticles. (A) Study design. C3, IgG, and IgM binding were quantified by dot-blot assay. (B) Levels of bound C3 (μg C3/mg Fe, each dot is the mean value of 3 technical replicates) were calculated after subtracting C3 deposition on control CLIO-NTA-Ni^{2+} particles. Full raw data are in Supplementary Figure S1. On average, the deposition was increased in vaccinated sera compared to naïve sera (p-value = 0.0047, statistical analysis in Supplementary Table 2). Only some of the vaccinated and convalescent samples had higher RBD-dependent C3 deposition. (C, D) Deposition of C3 (C) and release of fluid phase marker C5a (D) after incubation of CLIO-RBD and CLIO-NTA-Ni^{2+} in vaccinated (VAC) and naïve (NC) sera (means of 3 technical replicates). Both assays demonstrate RBD-dependent complement activation, enhanced in vaccinated sera. (E) C3 deposition on CLIO-RBD is decreased in the presence of 0.2 mg/mL soluble RBD protein (means of 3 technical replicates, ****$p < 0.0001$).

(Supplementary Table 1). At the same time, the levels of anti-RBD IgG were highly variable in vaccinated and convalescent cohorts, with up to 120-fold difference between high and low IgG titers. Notably, two of the convalescent donors had anti-RBD levels close to those of naïve donors, which could be due to the dynamic decrease in the titer following postdisease recovery or lower immune response.[41]

3. C3 Opsonization and Complement Activation by "Pseudovirus-like" Nanoparticles in Full Serum. We used the immuno dot-blot assay, with confirmed reproducibility across samples and species,[22,25] to measure RBD-dependent C3 and antibody deposition on nanoparticles (Figure 2A). CLIO-RBD and CLIO-NTA-Ni^{2+} particles were incubated in vaccinated, convalescent, and naïve sera for 30 min at 37 °C and washed in phosphate-buffered saline (PBS), and the amount of bound C3 (C3b and downstream cleavage fragments[42]) was measured. The results (Supplementary Figure 1) show highly variable C3 deposition on CLIO-RBD and CLIO-NTA-Ni^{2+} in vaccinated, convalescent, and naïve cohorts and no deposition in the presence of total complement inhibitor 10 mM EDTA. Since control particles also showed some C3 deposition (Supplementary Figure 1), we calculated for each donor the RBD-dependent C3 deposition (μg bound C3/mg Fe) after subtracting the deposition on CLIO-NTA-Ni^{2+} particles. Mean RBD-dependent C3 deposition was significantly higher in vaccinated (29.4 μg/mg) than in naïve donors (7 μg/mg), whereas the difference between convalescent and naïve donors, while noticeable, was not statistically significant (Figure 3B and Supplementary Table 2 for statistical analysis). At the same time, only 50% of vaccinated (5/5) and 37% of convalescent (3/10) sera demonstrated enhanced RBD-dependent C3 deposition compared to naïve donors (Figure 3B). Measurement of complement activation marker C5a in sera of vaccinated donors with high C3 deposition and in three naïve donors (Figure 3C,D) revealed RBD-dependent activation that was enhanced in vaccinated donors. To further confirm that C3 deposition is RBD-dependent, we measured C3 deposition in three vaccinated donors with and without addition of 0.2 mg/mL of soluble RBD. According to Figure 3E, addition of free RBD caused a significant decrease in C3 deposition on CLIO-RBD, but not on CLIO-NTA-Ni^{2+} in all three donors. The levels of total serum C3 and main complement regulator factor H in vaccinated (two high activators and two low activators) and naïve (two high activators and two low activators) donors were similar (Supplementary Figure 2), thereby ruling out the effect

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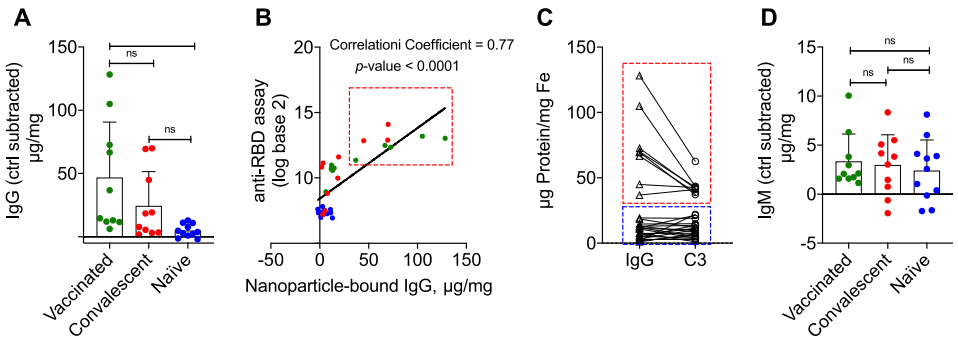

Figure 4. RBD-dependent immunoglobulin deposition on nanoparticles and association with anti-RBD levels and C3 deposition. (A) RBD-dependent IgG deposition (*µ*g IgG/mg Fe, each dot is the mean value of 3 technical replicates) is significantly higher in vaccinated and in post-COVID19 sera than in naïve sera. The baseline (control particle) values were subtracted from CLIO-RBD values. **$p < 0.01$. Raw data are in Supplementary Figure S3 and statistical analysis is in Supplementary Table 3. (B) Association between anti-RBD IgG levels measured with the immunoassay and RBD-dependent IgG binding in full serum. Since values for anti-RBD IgG were right skewed, a log base 2 transformation was used prior to correlation analysis. Parametric Pearson correlation coefficients were used for determining association. The cluster of subjects with higher IgG deposition (red rectangle) can be identified. (C) Subjects with higher RBD-dependent IgG deposition (red rectangle) have higher C3 deposition, and *vice versa* (blue rectangle). (D) RBD-dependent IgM deposition (*µ*g IgM/mg Fe, each dot is the mean value of three technical replicates) did not show significant differences between groups. The baseline (control particle) values were subtracted from CLIO-RBD values. Note a much greater deposition of IgG *vs* IgM (*µ*g/mg) in vaccinated and post-COVID19 sera. Full statistical analysis is shown in Supplementary Table 3.

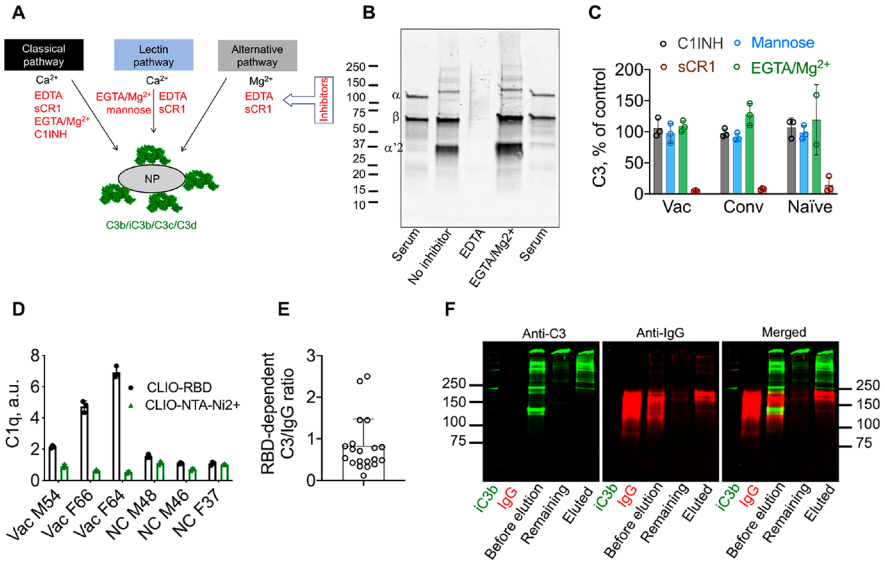

Figure 5. C3 deposition *via* IgG is alternative pathway-driven. (A) Three complement pathways converge into C3 cleavage and nanoparticle opsonization by C3 fragments (C3b/iC3b/C3c/C3d). Inhibitors for each pathway are shown in red. (B) Western blot analysis of nanoparticle-deposited C3 in vaccinated serum. Lane 1: serum 1:200 dilution shows native C3; lane 2: CLIO-RBD after incubation in serum; lane 3; after incubation in serum/EDTA; lane 4: SPIO NW after incubation in serum/EGTA/Mg^{2+}. Intact *α*-chain (115 kDa) and *β*-chain (75 kDa) are detectable in serum; *β*-chain and *α*′2 (43 kDa) are detectable on the particles. Some other *α*-chain fragments (*e.g.*, *α*′1-chain) are likely to be in the high molecular weight fraction bound to other proteins *via* amide or ester bonds and therefore could not be identified by their molecular weight. (C) Complement inhibition results (% of serum control) in donors with the highest RBD-dependent C3 deposition (means of 3 donors per group, 3 technical replicates per donor) showing that CP and LP are not involved in C3 opsonization. C1INH, 100 *µ*M; sCR1, 1 *µ*M; mannose, 250 *µ*M. (D) Dot-blot analysis of binding of C1q showing increased binding to CLIO-RBD in vaccinated sera, but the binding was extremely low and did not lead to activation of the classical pathway. (E) Molar ratio of RBD-dependent C3 over RBD-dependent IgG deposition for vaccinated and convalescent donors showing a relatively inefficient enhancement of complement opsonization. (F) Analysis of association between C3 and IgG on particles in vaccinated serum (VAC M54). Proteins were eluted with 5% SDS, and the eluted fraction and the nanoparticle-bound fraction were run in nonreducing SDS-PAGE and analyzed by anti-IgG/anti-C3 Western blot. C3 in the eluted fraction is mostly not associated with IgG but appears to be bound to other proteins (high molecular weight bands above 250 kDa). Repeated twice.

of serum C3 and factor H variability in the observed differences in C3 deposition.

4. Correlation between C3 and Immunoglobulin Deposition. To determine the correlation between C3 deposition and anti-RBD antibodies, we first quantified RBD-dependent IgG and IgM binding (*µ*g protein/mg nanoparticle after subtracting the binding to control CLIO-NTA-Ni^{2+}). The IgG binding was significantly higher in vaccinated and convalescent donors than in naïve donors (mean values: 46.7, 24.4, and 4.9 *µ*g/mg, respectively; Figure 4A, Supplementary Figure 3 for raw data, and Supplementary Table 3 for statistical analysis). However, only 50% of vaccinated (5/5) and 37% of

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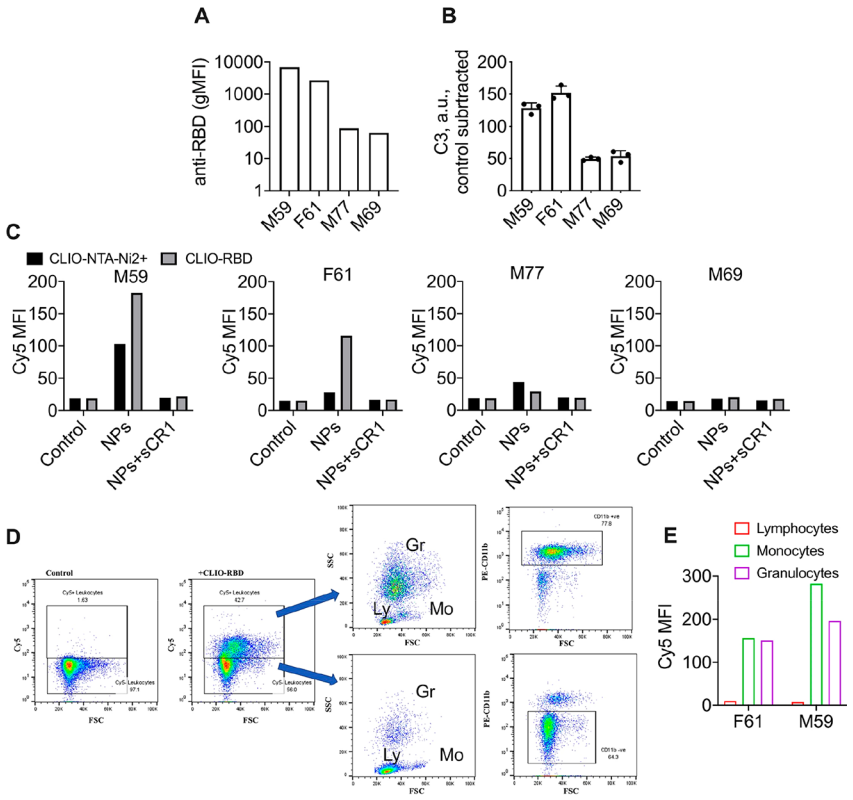

Figure 6. Variable uptake of "pseudovirus-like" nanoparticles by leukocytes in lepirudin blood. (A) Blood donors with high and low anti-RBD titers measured with the microbead assay (mean of triplicate run). (B) RBD-dependent C3 deposition in lepirudin plasma (mean and SD of triplicate). (C) Uptake of nanoparticles (mean fluorescence intensity) by total leukocytes and effect of sCR1 in 4 blood donors. (D) Flow analysis of uptake by leukocytes in blood from donor F61. Ly = lymphocytes; Mo = monocytes; Gr = granulocytes. (E) Uptake efficiency by different leukocyte types (determined from FSC/SSC plots) in 2 donors with high anti-RBD titers.

convalescent (3/10) donors showed higher RBD-dependent IgG binding than naïve donors (Figure 4A). Across all samples, binding of IgG positively correlated with the titer of anti-RBD IgG measured with the microbead immunoassay (Figure 3B, $R^2 = 0.77$, p-value $= 4.3 \times 10^{-7}$). However, seven donors with the highest RBD-dependent IgG deposition (three convalescent, four vaccinated) formed a separate cluster (red dotted boundary in Figure 4B). Notably, the same seven donors also had the highest RBD-dependent C3 deposition (Figure 4C, red dotted boundary). On the other hand, binding of IgM to nanoparticles was not statistically different between the cohorts (Figure 4D and Supplementary Table 2 for statistical analysis). Indeed, the amount of bound IgG was much higher than IgM (47 μg IgG/mg Fe *vs* 3.4 μg IgM/mg Fe in the vaccinated group and 24.4 μg IgG/mg Fe *vs* 2.95 μg IgM/mg Fe in the convalescent group).

5. C3 Opsonization of CLIO-RBD Is Mediated *via* the Alternative Pathway in All Sera. To understand the contribution of each pathway to RBD-dependent C3 opsonization, we used a panel of complement inhibitors (Figure 5A). To distinguish between pathways, we used 10 mM EGTA/10 mM Mg^{2+}, which is the universal inhibitor that blocks Ca^{2+}-sensitive classical pathway and lectin pathway in all species.[43,44] A representative Western blot of C3 eluted from CLIO-RBD that was incubated in the vaccinated serum with high C3 deposition confirmed the cleavage and appearance of the $\alpha'2$ chain, confirming the proteolytic processing of C3b into iC3b by factor H/I and the full inhibitory effect of 10 mM EDTA (Figure 5B). At the same time, there was no inhibitory effect of 10 mM EGTA/Mg^{2+}, suggesting no involvement of the calcium-sensitive lectin and C1q-mediated classical pathways. To verify these findings, we performed the inhibition studies in three "high activator" donors from vaccinated, convalescent, and naïve groups using more specific pathway inhibitors (Figure 5A): soluble complement receptor 1 (sCR1), which inhibits both alternative and classical C3 convertases; C1 inhibitor, which blocks CP and LP;[45] and mannose, which inhibits the mannan-binding lectin arm of the LP.[18] According to Figure 5C, the data demonstrate no inhibition by C1 inhibitor, EGTA/Mg^{2+}, and mannose, excluding the role of the CP and LP. The binding of C1q, the initial molecule of the CP, was significantly increased in sera with high complement activation (Figure 5D), but apparently its binding did not lead to appreciable CP activation. Indeed, the mean estimated amount of nanoparticle-deposited C1q in vaccinated sera was ~0.5 μg/mg Fe, or less than 1/300th of nanoparticle-deposited IgG on a molar basis.

Calculation of molar binding stoichiometry (C3/IgG ratio) indicated that for each RBD-dependent IgG binding there was less than one added C3 (mean = 0.8; range = 0.11−2.43) in the convalescent and vaccinated groups (Figure 5D). Notably, even in the case of higher IgG deposition, the opsonization process was not efficient. Given that C3 can opsonize antigen−antibody complexes,[46,47] we questioned whether C3 is bound to IgG on the particles (*i.e.*, bound IgG is a scaffold for binding of C3 molecules). We eluted the nanoparticle-associated proteins with 5% SDS (without breaking the ester bonds that link C3b/iC3b/C3c to other proteins[46,47]) and analyzed the eluted C3 and IgG in nonreducing Western blot. SDS eluted the majority of IgG and about 50% of C3 (Figure 5E). Almost all of the eluted C3

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was not bound to the eluted IgG but rather to other proteins, except for a few weak high molecular weight bands >400 kDa, where both C3 and IgG appear to be colocalized (Figure 5E).

6. RBD Promotes Variable, Complement-Dependent Leukocyte Uptake in Vaccinated Donors. To study the effect of anti-RBD antibody and C3 opsonization on leukocyte uptake, we used the microbead assay to identify two vaccinated blood donors with high relative titers of anti-RBD IgG (gMFI 6904 and 2677) and two vaccinated blood donors with low relative titers of anti-RBD IgG (gMFI 86.5 and 63) (Figure 6A). RBD-dependent C3 deposition was higher in lepirudin plasma from donors with high anti-RBD IgG titer than in donors with low anti-RBD IgG titer (Figure 6B). We incubated 10 μg/mL of Cy5-labeled CLIO-RBD or control Cy5-labeled CLIO-NTA-Ni^{2+} in lepirudin blood (an anticoagulant that does not interfere with the complement system) from the above donors for 1 h at 37 °C, lysed red blood cells, and determined the uptake by leukocytes with flow cytometry. In the blood with low anti-RBD IgG, there was a minimally detectable leukocyte uptake of both particle types, and no difference between CLIO-RBD and CLIO-NTA-Ni^{2+} was observed (Figure 6C). At the same time, in the blood with high anti-RBD IgG titer, there was an increased uptake of CLIO-RBD compared to CLIO-NTA-Ni^{2+} (Figure 6C). To test the role of complement, we used 10 μg/mL sCR1, which potently and specifically inhibits complement-dependent uptake in whole blood.[34] The uptake of nanoparticles in all donors was almost completely inhibited by sCR1 (Figure 6C). According to the CD11b staining and forward-side scattering plots (Figure 6D,E), CD11b+ cells (mostly granulocytes and monocytes) were the predominant cell type positive for CLIO-RBD, whereas CD11b− cells (mostly lymphocytes) showed much less efficient binding/uptake in both donors with high anti-RBD titers (Figure 6D,E).

CONCLUSIONS

We synthesized "pseudovirus-like" CLIO-RBD nanoparticles with the ligand density and hydrodynamic size similar to that of the SARS-CoV-2 virus, to investigate the RBD-dependent immune responses in serum and blood. We focused on C3 opsonization as the direct measure of the complement activation, which is also relevant to the complement-dependent phagocytosis by blood leukocytes. Vaccinated and convalescent sera with the highest titers of anti-RBD IgG exhibited more efficient IgG binding to the "pseudovirus-like" nanoparticles and more C3 opsonization compared to sera with lower anti-RBD IgG titers. At the same time, some RBD-dependent binding of antibodies in naïve sera was also observed, and the difference in IgG binding between vaccinated/convalescent and naïve sera (Figure 4A) was not as dramatic as measured with the microbead assay (Figure 2B). Our binding and opsonization assays were performed in native full serum, which is different from the microbead assay[39,40] and neutralization assays[32] that are performed over several log dilutions to identify high affinity/high titer antibodies. Immunoglobulin is the important component of the protein corona of nanoparticles[22] and is also found in the protein corona of viruses.[28] Thus, nondiluted naïve sera have some neutralization properties,[48] probably due to binding of low-affinity natural antibodies. Accordingly, in some naïve donors we also observed an increased RBD-dependent C3 deposition, probably mediated by low-affinity natural antibodies in nondiluted serum.

RBD-dependent complement opsonization was exclusively *via* the AP, despite the binding of the CP mediator C1q. The AP can be triggered by initial C3b binding to antibody−antigen complexes *via* the thioester group,[27] forming high molecular weight adducts.[22,46,47] The majority of C3 that opsonized CLIO-RBD was not covalently bound to IgG, judging by the lack of colocalization in the nonreducing Western blot (Figure 5). While C3 is known to self-cleave from bound proteins,[49] the result suggests that C3 attacks other proteins of the nanoparticle surface, which was also observed for other types of nanoparticles,[22] whereas bound IgG serves as a "catalyst" for complement activation, in a rather inefficient manner (each bound IgG promotes opsonization with less than one C3 molecule).

While blood leukocytes took up CLIO-RBD nanoparticles exclusively *via* complement, the difference between blood donors with high anti-RBD and low anti-RBD titers cannot be explained entirely by differences in C3 opsonization, which were much smaller. C3 opsonization is not the single factor that controls the leukocyte uptake. For example, there is a cooperativity between complement receptor (CD11b/CD18) and Fc receptors on leukocytes, which would require both C3 and anti-RBD IgG for productive uptake.[50−52] Interestingly, a very recent report demonstrated antibody-dependent uptake of SARS-CoV-2 by circulating monocytes *via* Fcγ receptors.[53] Another option could be the donor-specific protein corona composition that might contain immune uptake-inhibiting factors (called dysopsonins[54]).

Studies with large patient cohorts with defined outcomes would be necessary to understand the role of the observed heterogeneity of complement opsonization and immune uptake in COVID-19 and other viral infections. Thus, complement opsonization and leukocyte uptake could affect the ability to clear viral infection, modulate the severity of the disease, and influence other health outcomes. It would be interesting to see if "high activators" have a different susceptibility to SARS-CoV-2 infection or have different outcomes.

While RBD-coated nanoparticles have been used for measurements of ACE2 binding and vaccination,[55,56] our data suggest that "pseudovirus-like" nanoparticles can be utilized to probe interactions between viral surface proteins and the immune system. Nanoparticles can be easily engineered to carry different ligand densities, as well as fluorescent labels. Other surface proteins, including S (spike)-, envelope (E)-, and membrane (M)-proteins, could be studied. Thus, S-protein, which is heavily glycosylated in the regions outside RBD,[57] has been demonstrated to trigger the LP.[3,58] Also, in view of the decreased affinity of anti-RBD antibodies to some of the COVID-19 variants,[59] it remains to be seen how the variants affect the opsonization pathway and efficiency. The very large total surface area of nanoparticles allows harvesting of a sufficient amount of surface-bound proteins for the analytical assays described in Figure 5 (the surface area of 10 μg of CLIO-RBD is equivalent to a surface of approximately 10 Petri dishes!). An additional advantage of iron oxide nanoparticles is the magnetic property, which can enable isolation of internalizing cells and/or binding proteins from complex cell suspensions or biological fluids, or after *in vivo* administration, for subsequent analysis. Finally, engineered nanoparticles can be decorated with other viral proteins, for example from the HIV or EBV envelope, to probe broader aspects of complement response.

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MATERIALS AND METHODS

Materials. Chemicals used for CLIO NW synthesis, including iron salts, epichlorohydrin, and 12−25 kDa dextran, were purchased from Sigma-Aldrich (Saint Louis, MO, USA). NTA-PEG2000-NHS was purchased from NANOCS (New York, NY, USA). Cy5 *N*-hydroxy succinimide (NHS) ester was from Lumiprobe Corporation (Hunt Valley, MD, USA), and sulfosuccinimidyl acetate was from ThermoFischer. Nickel chloride was from GFS Chemicals Inc. (Powell, OH, USA). Bovine serum albumin and D-mannose were from Sigma-Aldrich. Amicon Ultra centrifugal filters were purchased from Millipore Corporation, USA. Nitrocellulose membrane (0.45 μm pore) was from Bio-Rad. Primary monoclonal human IgG1k anti-SARS-CoV antibody against RBD was from BEI Resources (#NR-52481; Manassas, VA, USA). Anti-RBD scFv antibody (clone P2B-2F6) was cloned and purified as described.[38] Secondary goat anti-human IgG antibodies labeled with IRDye 800CW or IRDye 680 were from Li-COR Biosciences (926-32232; Lincoln, NE, USA). Goat IgG fraction against human C3 was from MP Biomedicals, LLC (cat. #55033; Solon, OH, USA). Secondary donkey anti-goat IgG labeled with IRDye 800CW was from Li-COR (#926-32214). ChromPure human IgG and IgM (whole molecule) and AffiniPure goat anti-human IgM (Fc5μ specific) were from Jackson Immuno Research (#926-32232, #009-000-003, and #109-005-043, respectively; West Grove, PA, USA). EGTA/Mg^{2+} and purified human C3 and C1 esterase inhibitor (C1INH) were from Complement Technology (#B106, #A113, and #A140, respectively; Tyler, TX, USA). Recombinant hirudin (lepirudin) was from Aniara Diagnostica, LLC (West Chester, OH, USA). FITC-labeled anti-human CD11b antibody (#101205) was from BioLegend (San Diego, CA, USA). Soluble sCR1 (short consensus repeats 1−10 of CD35) was provided by Alexion Pharmaceuticals, Inc. (New Haven, CT, USA) as described[60] and aliquoted at 6 mg/mL. All proteins were stored at −80 °C with less than three freeze−thaw cycles per aliquot. The 2× Laemmli sample buffer and precast Mini-PROTEAN TGX gels were from Bio-Rad.

Methods. *RBD Expression and Purification.* The recombinant SARS-CoV-2 RBD protein was expressed using the baculovirus-insect expression system. The encoding sequence (residues Arg319-Phe541)[61] was codon-optimized for the insect cell expression and fully synthesized. The sequence was cloned into a two-promoter *E. coli* baculovirus transfer vector behind baculovirus polyhedrin promoter using the *Eco*RI and *Bam*HI restrict enzyme sites.[62] The sequence encoding the signal peptide gp67 was inserted before the N terminus of the RBD protein for protein secretion, and a hexa-His tag was added to the C terminus to facilitate further purification. The final construction was sequenced and then incorporated into baculovirus in SF9 insect cells using standard homologous recombination with Baculogold (Pharmingen) as the recipient baculovirus DNA. The recombinant protein was expressed using High Five cells after five-day culture in serum-free IPL-41 medium. The soluble RBD protein was isolated from the supernatant by cOmplete His-Tag purification resin (Roche 5893682001). The 250 mM imidazole eluate from the column was concentrated and further purified by Superdex 200 size exclusion chromatography. The homogeneous peaks corresponding to MWs of ∼30 and ∼60 kDa were collected separately and concentrated in 1× PBS at pH 7.2. The ∼30 and ∼60 kDa peaks corresponded to the monomer and dimer of RBD protein as observed before.[61]

Synthesis of CLIO NWs-NH_2. CLIO NWs were prepared by the previously described method[23,63] with modifications. Briefly, SPIO NWs (60 nm, 10 mg Fe/mL in double-distilled water, DDW) were mixed with PEG10K (100 mg/mL), epichlorohydrin, and sodium hydroxide (10 N) at a volume ratio of 1:1:1:1. The mixture was stirred for 24 h at 37 °C and then stirred with ammonia (final concentration 2.5%) overnight at 4 °C. The samples were ultrafiltrated against DDW using a Pall reverse osmosis system (Pall Corporation, Port Washington, USA), filtered through a sterile 0.2 μm membrane disk filter, and stored at 4 °C.

Synthesis of CLIO-NTA. CLIO NW-NH_2 (400 μL, 5 mg Fe/mL) were combined with a 100-fold excess of Cy5-NHS (0.14 μg in 4 μL of DMSO) in PBS 1× (pH 7.4). The reaction mixture was incubated at room temperature for 2 h, and then NTA-PEG2000-NHS (0.8 mg, 2000 fold molar excess) was added to the mixture. The reaction was stirred at 4 °C for 12 h; then a 2000-fold excess of sulfosuccinimidyl acetate (0.52 mg) was added and the mixture was stirred for an additional 2 h at room temperature. The reaction mixture was purified with a 10 kDa Amicon Ultra centrifugal filter (Sigma) at 500*g* for 10 min, three times. The resulting CLIO-NTA particles were resuspended in nanopure water.

Synthesis of CLIO-NTA-Ni^{2+}. CLIO-NTA from the previous step (400 μL, 5 mg Fe/mL) were combined with a 40 000-fold molar excess of $NiCl_2$ (1.9 mg) in deionized water (pH 8.0, adjusted with 0.1 N NaOH). The reaction was stirred at 4 °C for 12 h. The reaction mixture was purified with a 10 kDa Amicon Ultra centrifugal filter (Sigma) at 500*g* for 10 min, three times. The resulting CLIO-NTA-Ni^{2+} particles were resuspended in nanopure water.

Synthesis of CLIO-RBD. A 100-fold molar excess of purified His-tagged RBD protein (248 μg) was combined with CLIO-NTA-Ni^{2+} (200 μL, 5 mg/mL) in bicarbonate buffer (pH = 9.4). The reaction mixture was incubated at 4 °C for 12 h and purified using 100 kDa Amicon Ultra centrifugal filters by washing three times with deionized water and once with PBS. The nanoparticle size distribution and zeta potential were measured in 10% PBS, pH 7.0, with a Malvern Zeta Sizer Nano ZS (Malvern Instruments, Malvern, UK). To determine the number of RBD molecules per nanoparticle, particles were loaded in 2 μL of triplicates on a 0.45 μm nitrocellulose membrane, and the membrane was blocked in 5% milk/0.1% Tween-20/PBS, then incubated with anti-RBD antibody and then with IRDye 800CW goat anti-human secondary antibody. The membrane was scanned at the 800 nm channel using a Li-COR Odyssey (Li-COR Biosciences, Lincoln, NE, USA). The integrated density of dots in 8-bit TIFF images was measured with ImageJ. The number of RBD/NP was calculated from standard dilutions of RBD applied on the same membrane.

Nanoparticle Imaging. For TEM analysis, nonstained particles diluted in DDW were applied on a carbon grid (Electron Microscopy Sciences, Hatfield, PA, USA) and imaged with a FEI Tecnai Spirit BioTwin electron microscope at 100 keV. For confocal imaging of CLIO(Cy3)-RBD(Cy5), a Nikon Eclipse AR1HD inverted confocal microscope with 561 and 640 nm excitation lasers was used. For high-magnification imaging, nanoparticles were diluted 1:1000 in PBS and mixed with glycerol at a 1:1 ratio; ∼2 μL was placed on a slide and covered with a glass coverslip. After the droplets fully spread under the coverslip, they were imaged with an Apo100 oil objective at 2048 × 2048 line resolution.

scFv Binding. Anti-RBD scFv was labeled with IRDye800CW-NHS ester (Li-COR Biosciences) at ∼1 fluorophore per protein according to the manufacturer's instructions. The antibody was added to naïve serum with a low level of anti-RBD IgG at 10 μg/mL, and CLIO RBD and CLIO-NTA-Ni^{2+} were added at 0.25 mg/mL and incubated with serum for 1 h at RT. Particles were washed three times with PBS at 450000*g* for 10 min at 4 °C in a Beckman Optima TLX ultracentrifuge equipped with a TLA-100.3 rotor. The pellets were resuspended in PBS, and 2 μL of sample was dotted in triplicates on a 0.45 μm pore nitrocellulose membrane and scanned with Li-COR Odyssey scanner at 800 nm wavelength. The dot mean intensity in 8-bit images was quantified in Fiji and plotted with Prism v. 9.0 (GraphPad, San Diego, CA, USA).

A549 Cell Uptake. A549 breast carcinoma cells stably expressing human ACE2 were obtained from Dr. Thomas (Tem) Morrison (University of Colorado) and maintained in Dulbecco's modified Eagle medium (DMEM, Corning Life Sciences, Tewksbury, MA, USA) supplemented with 10% v/v fetal bovine serum (FBS) (Corning Life Sciences) and puromycin (0.5 μg/mL, ThermoFisher Scientific). No more than 20 passages were allowed, and cells were certified mycoplasma free. Cells were detached with trypsin and washed in 1% BSA/PBS, and 2×10^6 cells/mL PBS (1% BSA) were incubated with 10 μg Fe/mL of nanoparticles. After 1 h of incubation at 37 °C cells were washed three times in 1% BSA/PBS. Labeled cells were applied to a slide using Shandon Cytospin III (ThermoFisher), fixed for 30 min with 10% formalin, and mounted with DAPI/antifade mounting media

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(Vector Laboratories). Cells were imaged with a Nikon Eclipse AR1HD confocal microscope.

Serum and Blood Samples. Human whole blood (3−5 mL) was collected in Vacutainer Z (no additives, or 10 μg recombinant lepirudin/mL blood) from consenting donors at the University of Colorado Blood Donor Center under the Center's Institutional Review Board protocol for anonymous collection. Only age, gender, convalescence, and vaccination status were made available to the investigators. Sera were collected by separation from clotted blood according to the protocol described previously,[27] while adhering to strict precautions to preserve functional complement.[64,65] Serum aliquots were frozen and stored at −80 °C and were subject to no more than one freeze−thaw cycle before using in assays. Blood was used within 2 h postcollection.

Immuno Dot-Blot Assay of C3, IgG, and IgM Deposition. Control and RBD-functionalized nanoparticles were incubated with human serum with or without inhibitors. The immuno-dot assay was performed to measure complement component 3 (C3) according to our previous report.[22] Briefly, particles at 1 mg/mL (Fe) were added to freshly thawed serum at a 1:3 volume ratio and incubated on a water bath for 30 min at 37 °C. Particles were washed three times with PBS at 450000*g* for 10 min at 4 °C in a Beckman Optima TLX ultracentrifuge equipped with a TLA-100.3 rotor. The pellets were resuspended in PBS, and 2 μL of sample was applied in triplicates on a 0.45 μm pore nitrocellulose membrane. To calculate the amount of bound protein, standard dilutions of human C3, human IgG, and human IgM were dotted on the same membrane. For estimating C1q binding, serum dilutions (average concentration in adult serum: 113 ± 40 μg/mL) were dotted along with the samples. The membranes were blocked with 5% (w/v) milk, probed with anti-C3 antibody for 1 h at room temperature, washed, and then incubated with the IRDye 800CW-labeled secondary antibody. For IgG and IgM detection, the corresponding IRDye 800CW-labeled antibodies were directly used. The membrane was scanned using an Odyssey infrared imager (Li-COR Biosciences, Lincoln, NE, USA), and the integrated intensities of dots were determined from 8-bit grayscale images using ImageJ software. The quantification data were plotted using Prism software v. 9.0 (GraphPad, San Diego, CA, USA).

C3 and IgG Western Blot. Nanoparticles washed from serum (0.5 mg Fe/mL final concentration) were mixed with sample buffer including 5% β-mercaptoethanol (Sigma) as 1:1 ratio and boiled at 100 °C for 5 min. For the nonreducing gel, particles were incubated in 5% SDS for 1 h at room temperature prior to loading on the gel. In that case, sample buffer was without β-mercaptoethanol, and the samples were heated to 50 °C only for 5 min. Samples were loaded onto 4−20% polyacrylamide gel (reducing) or 7.5% polyacrylamide gel (non-reducing), run at 100 mV for 75 min (reducing) or 50 mV for 180 min (nonreducing), and transferred to a 0.45 μm nitrocellulose membrane at 4 °C at 100 mV for 80 min.

Leukocyte Uptake and Flow Cytometry. Fresh lepirudin anti-coagulated whole blood (plain or with complement inhibitors) was incubated with Cy5-labeled nanoparticles (10 μg Fe/mL) at 37 °C for 1 h under 300 rpm rotation. Erythrocytes were lysed with the RBC lysis buffer per manufacturer's instructions, cells were centrifuged at 200*g* for 10 min and resuspended in 1% BSA/PBS, cells were resuspended at ∼0.5 million/mL, and 20 000 events were detected with a Guava EasyCyte HT flow cytometer (Luminex). For CD11b staining, the cell pellet was preblocked with Ultra-LEAF purified anti-mouse CD16/32 antibody (BioLegend, San Diego, CA, USA) in PBS supplemented with 2% FBS 10 min at 4 °C before staining with FITC-labeled CD11b specific antibody. FITC fluorescence was detected in the Yellow-B fluorescence channel using the blue (488 nm) laser, and Cy5 fluorescence was detected in the Red-R fluorescence channel using the red (647 nm) laser. FSC/SSC threshold was set to exclude debris and to analyze leukocyte populations (granulocytes, lymphocytes, and monocytes). The data were analyzed using FlowJo software version V10 and plotted with Prism 8 (GraphPad, San Diego, CA, USA).

Statistical Analysis. A one-way ANOVA model with *post hoc* testing using the Tukey method for multiple comparisons was to compare bound IgG, IgM, and C3 levels among patient groups (vaccinated, convalescent, and naïve) and to compare log base 2 transformed values of anti-RBD among groups. Technical replicates were averaged prior to statistical analysis, and the differences of CLIO-RBD and control particles were calculated within subject. Correlation coefficients were calculated using a Pearson product−moment correlation. Analyses were done in R Statistical Software (version 4.0.4), and graphics were generated using Prism.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acsnano.2c02794.

Tables of statistical analysis of differences in levels of anti-RBD antibody; statistical analysis of differences in levels of C3 between groups of subjects; and statistical analysis of differences in IgG and IgM binding to CLIO-RBD between groups; supplemental figures of raw values of C3 bound to CLIO-RBD and CLIO-NTA-Ni^{2+}; levels of total C3 and factor H in serum; and raw values of IgG and IgM bound to CLIO-RBD and CLIO-Ni^{2+} (PDF)

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Notes

The authors declare no competing financial interest.

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