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SARS-CoV-2 RBD219-N1C1: A Yeast-Expressed SARS-CoV-2 Recombinant Receptor-Binding Domain Candidate Vaccine Stimulates Virus Neutralizing Antibodies and T-cell Immunity in Mice

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17 Abstract

18	There is an urgent need for an accessible and low-cost COVID-19 vaccine suitable for low- and
19	middle-income countries. Here we report on the development of a SARS-CoV-2 receptor-binding
20	domain (RBD) protein, expressed at high levels in yeast (Pichia pastoris), as a suitable vaccine
21	candidate against COVID-19. After introducing two modifications into the wild-type RBD gene to
22	reduce yeast-derived hyperglycosylation and improve stability during protein expression, we show
23	that the recombinant protein, RBD219-N1C1, is equivalent to the wild-type RBD recombinant
24	protein (RBD219-WT) in an in vitro ACE-2 binding assay. Immunogenicity studies of RBD219-
25	N1C1 and RBD219-WT proteins formulated with Alhydrogel® were conducted in mice, and, after
26	two doses, both the RBD219-WT and RBD219-N1C1 vaccines induced high levels of binding IgG
27	antibodies. Using a SARS-CoV-2 pseudovirus, we further showed that sera obtained after a two-dose
28	immunization schedule of the vaccines were sufficient to elicit strong neutralizing antibody titers in
29	the 1:1,000 to 1:10,000 range, for both antigens tested. The vaccines induced IFN- γ , IL-6, and IL-10
30	secretion, among other cytokines. Overall, these data suggest that the RBD219-N1C1 recombinant
31	protein, produced in yeast, is suitable for further evaluation as a human COVID-19 vaccine, in
32	particular, in an Alhydrogel [®] containing formulation and possibly in combination with other
33	immunostimulants.

34 1 Introduction

35	The number of coronavirus disease 19 (COVID-19) cases globally is readily approaching the 50-
36	million-person mark, with over 1.2 million deaths. In response to the pandemic, an international
37	enterprise to develop effective and safe vaccines is underway. There are many ways to categorize the
38	more than 100 potential COVID-19 vaccine candidates ¹ , but one approach is to divide them as those
39	employing new technologies for production, but that have not yet been licensed for use, versus
40	traditional vaccine production approaches with prior experience in licensed vaccines ² . The Operation
41	Warp Speed (OWS) initiative in the United States ³ and other similar efforts in other parts of the
42	world ⁴ initially seemed to focus on approaches employing new platforms, including several
43	messenger RNA (mRNA)-based vaccines as well as non-replicating adenovirus vector vaccines ³ .
44	Among the more established or traditional approaches, whole-inactivated virus vaccines on
45	aluminum oxy-hydroxide have been developed in China ⁵ , as have several recombinant protein
46	vaccine candidates ⁶⁻⁸ . Each of these approaches offers both distinct advantages and disadvantages in
47	terms of production, scale-up, potential efficacy and safety, and delivery.
48	We have previously reported on recombinant protein-based coronavirus vaccine candidates,
49	formulated with Alhydrogel [®] to prevent severe acute respiratory syndrome (SARS) ⁹⁻¹¹ and Middle
50	East Respiratory Syndrome (MERS) ¹² . In both cases, the receptor-binding domain (RBD) of the
51	SARS or MERS spike proteins was used as the target vaccine antigen. In a mouse model, the SARS-
52	CoV RBD219-N1/Alhydrogel® vaccine induced high titers of virus-neutralizing antibodies and
53	protective immunity against a mouse-adapted SARS-CoV virus challenge. It was also found to
54	minimize or prevent eosinophilic immune enhancement compared to the full spike protein ⁹ .
55	The RBD of SARS-CoV-2 has likewise attracted interest from several groups now entering
56	clinical trials with RBD-based vaccines ^{7,13-17} . Our approach was to apply the lessons learned from the
57	development of the SARS-CoV vaccine candidate and accelerate the COVID-19 vaccine
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58	development efforts using microbial fermentation in the yeast Pichia pastoris; a technology that is
59	widely available and used to produce recombinant hepatitis B vaccines in several middle-income
60	countries (LMICs) ¹⁸ , including Bangladesh, Brazil, Cuba, India, and Indonesia. As COVID-19
61	spreads across the globe, especially among urban populations living in extreme poverty ¹⁹ , there will
62	be greater urgency to produce safe, effective, highly scalable, and affordable COVID-19 vaccines
63	locally or regionally. Therefore, the development of a yeast-expressed recombinant protein-based
64	COVID-19 vaccine allows developing it for global health and populations vulnerable to poverty-
65	related diseases ²⁰ .
66	Here, we present the first preclinical data of a COVID-19 recombinant protein-based vaccine
67	candidate, SARS-CoV2 RBD219-N1C1, formulated with Alhydrogel [®] . We demonstrate that
68	modifications made to the SARS-CoV2 RBD gene to improve production and stability preserve the
69	protein antigen functionality and its immunogenicity after Alhydrogel [®] adsorption.

71 2 Methods

72 2.1 Cloning and expression of the genes encoding RBD219-WT and RBD219-N1C1:

The RBD219-WT recombinant subunit protein contains amino acid residues 331-549 of the SARS-73 74 CoV-2 spike protein (GenBank No.: QHD43416.1). It contains a hexahistidine tag at its C-terminus. In the tag-free RBD219-N1C1 antigen candidate, N331 is not present, and C538 has been mutant to 75 76 an alanine residue to prevent aggregation due to intermolecular disulfide bonding. The DNAs for 77 both antigen candidates were individually synthesized with their codon use optimized for translation 78 in *Pichia pastoris* and ligated into pPICZaA using the EcoRI and XbaI restriction sites (GenScript, 79 Piscataway, NJ, USA). The recombinant plasmids were electroporated into *P. pastoris* X33 following the EasySelectTM Pichia Expression Kit Manual (Invitrogen, Carlsbad, CA, USA). Transformants 80 81 were selected on YPD plates containing different concentrations of Zeocin (100-2000 µg/mL) and 82 incubated at 30°C for 72 hours. Individual colonies were screened for expression under induction 83 with methanol (0.5-2%) at the 10 mL culture level (MMGY medium) as described¹⁰. The expression 84 level of select colonies was identified by SDS-PAGE and Western Blotting using anti-SARS-CoV-2 85 antibodies (anti-SARS-CoV-2 spike rabbit monoclonal antibody, Sino Biological, Wayne, PA, USA, 86 Cat # 40150-R007), and research seed stocks of the highest expressing clones were frozen at -80 °C. 87 RBD219-WT and RBD219-N1C1 were expressed at the 5 L scale using a Celligen 310 88 benchtop fermentation system (Eppendorf, Enfield, CT, USA). For the RBD-WT, 2.5 L of basal salt 89 medium were inoculated with a seed culture to an initial OD₆₀₀ of 0.05 and grown at 30 °C, pH 5.0 90 with 30% dissolved oxygen until glycerol depletion. During the first hour of methanol induction, the 91 temperature was reduced from 30 °C to 26 °C and the pH was increased from 5.0 to 6.0. After 92 approximately 70 hours of induction (methanol feed at 1-11 mL/L/hr), the culture was harvested 93 from the fermenter, and cells were removed by centrifugation for 30 min at 12,227 x g at 4 °C. For

94 RBD219-N1C1, the fermentation process was slightly different in that low salt medium was used, the

95	induction temperature was set to 25 °C and the pH to 6.5 and, the methanol feed rate was between 1-
96	15 ml/L/hr. The fermentation supernatant (FS) was filtered (0.45 μm PES filter) and stored at -80 $^\circ C$
97	before purification.

98	A hexahistidine-tagged SARS-CoV-2 RBD219-WT was purified from fermentation
99	supernatant (FS) by immobilized metal affinity chromatography followed by size exclusion
100	chromatography (SEC). The FS was concentrated and buffer exchanged to buffer A (20 mM Tris-
101	HCl pH 7.5 and 0.5 M NaCl) using a Pellicon 2 cassette with a 10 kDa MWCO membrane
102	(MilliporeSigma, Burlington, MA, USA) before being applied to a Ni-Sepharose column (Cytiva,
103	Marlborough, MA, USA). The column was washed with buffer A plus 30 mM imidazole and elution
104	was undertaken in buffer A containing 250 mM imidazole. The RBD219-WT protein was further
105	purified using a Superdex 75 prep grade column (Cytiva, Marlborough, MA, USA) pre-equilibrated
106	in buffer B (20 mM Tris-HCl pH 7.5 and 150 mM NaCl) after concentrating eluates from the Ni
107	column using an Amicon Ultra-15 concentrator with a 10 kDa MWCO membrane (MilliporeSigma,
108	Burlington, MA, USA). Monomeric RBD219-WT was pooled, as eptically filtered using a 0.22 μm
109	filter, and stored at -80 °C.

110 For the purification of the tag-less RBD219-N1C1, ammonium sulfate salt was added to the

111 FS to a final concentration of 1 M (w/v) before the sample was applied to a Butyl Sepharose HP

112 column (Cytiva, Marlborough, MA, USA). The column was washed with buffer C (30 mM Tris-HCl

113 pH 8.0) with 1 M ammonium sulfate and protein was eluted with buffer C containing 0.4 M

ammonium sulfate. A polishing step using a Superdex 75 prep grade column (Cytiva, Marlborough,

115 MA, USA) pre-equilibrated in buffer B followed.

116

117 **2.2 SDS-PAGE**

118	To evaluate the size of RBD219-WT and RBD219-N1C1, 2 μ g of these two proteins were loaded								
119	onto a 4-20% tris-glycine gel under non-reduced and reduced conditions. These two proteins were								
120	also treated with PNGase-F (NEB, Ipswitch, MA, USA) under the reduced condition to remove N-								
121	glycans and loaded on the gel to assess the impact of the glycans on the protein size. Gels were								
122	stained using Coomassie Blue and analyzed using a Bio-Rad G900 densitometer with Image Lab								
123	software.								
124									
125	2.3 Vaccine formulation and Alhydrogel [®] -protein binding study								
126	SARS-CoV-2 RBD219-N1C1 was diluted in 20 mM Tris, 150 mM NaCl, pH 7.5 (TBS buffer) before								
127	mixing with Alhydrogel® (aluminum oxy-hydroxide; Catalog # 250-843261 EP, Brenntag, Ballerup,								
128	Denmark). To calculate the Langmuir binding isotherm of RBD219-N1C1 to Alhydrogel [®] , RBD219-								
129	N1C1 and Alhydrogel® were mixed at different ratios (from 1:2 to 1:20). The RBD219-								
130	N1C1/Alhydrogel [®] mixture was stored for one hour at RT, to reach an equilibrium state. The								
131	Alhydrogel® formulations were centrifuged at 13,000 x g for 5 min, and the supernatant was								
132	removed. The protein in the supernatant fraction and the pellet fraction were quantified using a micro								
133	BCA assay (ThermoFisher, Waltham, MA, USA).								
134									
135	2.4 ACE-2 binding assay								

136 For the ACE-2 binding study, the Alhydrogel[®]-RBD vaccine formulations were blocked overnight

137 with 0.1% BSA. After hACE-2-Fc (LakePharma, San Carlos, CA, USA) was added, the samples

138 were incubated for 2 hours at RT. After incubation, the Alhydrogel[®] was spun down at 13,000 x g for

139 5 min. The hACE-2-Fc which did not bind to the RBD on the Alhydrogel[®] remained in the

140 supernatant. The hACE-2-Fc content in the supernatant was quantified by ELISA using 96-Well

141	MaxiSorp Immuno plates (ThermoFisher, Waltham, MA, USA) coated overnight with 200 ng/well of
142	RBD219-WT protein. After blocking with 0.1% BSA, 100 μ L supernatant sample were added to
143	each well. Plates were washed 4 times with an automated plate washer using PBS with Tween
144	(PBST). A secondary antibody against human Fc was used to detect hACE-2-Fc bound the proteins
145	on the plate. Plates were washed 5 times with an automated plate washer using PBST before 100 μL
146	TMB solution were added. The enzymatic reaction was stopped with HCl and absorption readings
147	were made at 450 nm. The final concentration of the hACE-2 bound on the Alhydrogel® was
148	determined as [hACE-2-Fc on Alhydrogel [®]] = [Total hACE-2-Fc] – [hACE-2-Fc in supernatant].
149	

150 **2.5 Immunogenicity testing**

151 To examine RBD-specific antibodies in mouse sera, indirect ELISAs were conducted. 96-well 152 NUNC ELISA plates were coated with 2 µg/mL RBD219-WT in 100 µL 1x coating buffer per well 153 and incubated overnight at 4 °C. The next day the coating buffer was discarded, and plates were 154 blocked with 200 µL/well 0.1% BSA in PBST for 2 hours at room temperature. Mouse serum 155 samples were diluted from 1:200 to 1: 437,400 in 0.1% BSA in PBST. Blocked ELISA plates were 156 washed once with 300 µL PBST using a Biotek 405TS plate washer and diluted mouse serum 157 samples were added to the plate in duplicate, 100 μ L/well. As negative controls, pooled naïve mouse 158 serum (1:200 diluted) and blanks (0.1% BSA PBST) were added as well. Plates were incubated for 2 159 hours at room temperature, before being were washed four times with PBST. Subsequently, 1:6,000 160 diluted goat anti-mouse IgG HRP antibody (100 μ L/well) was added in 0.1% BSA in PBST. Plates 161 were incubated 1 hour at room temperature, before washing five times with PBST, followed by the 162 addition of 100 µL/well TMB substrate. Plates were incubated for 15 min at room temperature while 163 protected from light. After incubation, the reaction was stopped by adding 100 μ L/well 1 M HCl. The

164	absorbance at a wavelength of 450 nm was measured using a BioTek Epoch 2 spectrophotometer.								
165	Duplicate values of raw data from the OD ₄₅₀ were averaged. The titer cutoff value was calculated								
166	using the following formula: Titer cutoff = $3 \times average$ of negative control + $3 \times average$ deviation								
167	of the negative control. For each sample, the titer was determined as the lowest dilution of each								
168	mouse sample with an average OD450 value above the titer cutoff. When a serum sample did not								
169	show any signal at all and a titer could not be calculated, an arbitrary baseline titer value of 67 was								
170	assigned to that sample (baseline).								
171									
172	2.6 Pseudovirus assay:								
173	Pseudovirus was prepared in HEK-293T cells by previously reported methods ²¹ . Cells were								
174	transfected with 2.5 μg of the plasmid encoding the SARS-CoV-2 spike protein (p278-1) and 3.7 μg								
175	of luciferase-encoding reporter plasmid (pNL4-3.lucR-E) and Gag/Pol-encoding packaging construct								
176	(p Δ 8.9). Pseudovirus containing supernatant was recovered after 48 h and passed through a 0.45 μ M								
177	filter before use.								
178	For each serum sample, 30 μ L pseudovirus were incubated with serial dilutions of heat-								
179	inactivated serum (eight dilutions in a 4-fold step-wise manner) for 1 h at 37 °C. Next, 100 μ L of								
180	these sera-pseudovirus mixtures were added to 293T-hACE2 cells in 96-well poly-D-lysine coated								
181	culture plates. Following 48 h incubation in a 5% CO2 environment at 37 °C, the cells were lysed								

182 with 100 µL Promega Glo Lysis buffer, 15 min RT. Finally, 20 µL lysate was added to 100 µL luc

183 substrate (Promega Luciferase Assay System, Madison, WI, USA). The amount of luciferase was

- 184 quantified by luminescence (relative luminescence units (RLU)), using a Promega GloMax
- 185 luminometer (Steady-Glo program). The percent virus inhibition was calculated as (1- RLU of
- 186 sample/ RLU of negative control) x 100. Serum from vaccinated mice was also characterized by the

187 IC50-value, defined as the serum dilution at which the virus infection was reduced to 50% compared

188	with the negative control (virus + cells). When a serum sample did not neutralize 50% of the virus									
189	when added at a 1:10 dilution, the IC50 titer could not be calculated and an arbitrary baseline titer									
190	value of 10 was assigned to that sample (baseline). As a control, human convalescent sera for SARS-									
191	CoV-2 (NIBSC 20/130) was used (National Institute for Biological Standards and Control, South									
192	Mimms, UK).									
193										
194	2.7 Statistical analysis									
195	To test for significant differences between groups in ELISA, Luminex, and flow cytometry results,									
196	Kruskal-Wallis tests in combination with Dunn's multiple comparison tests were performed. ns (not									
197	significant): p>0.05, *: p < 0.05 and **: p < 0.01.									
198										
199	2.8 Cytokine analysis									
200	2.8.1 Preparation of splenocytes for restimulation									
201	Single-cell suspensions from mouse splenocytes were prepared using a cell dissociator									
202	(GentleMACS Octo Dissociator, Miltenyi Biotec, Waltham, MA, USA) based on a previously									
203	optimized protocol ²² . The concentration and the viability of the splenocyte suspensions were									
204	measured after mixing with AOPI dye and counted using the Nexcelom Cellometer Auto 2000									
205	(Lawrence, MA, USA).									
206	For the re-stimulation assays, splenocyte suspensions were diluted to 8x10 ⁶ live cells/mL in a									
207	2-mL deep-well dilution plate and 125 μ L of each sample was seeded in two 96-well tissue culture									
208	treated culture plates. Splenocytes were re-stimulated with 10 μ g/mL RBD219-WT, 20 ng/mL PMA									
209	1 ug/mL Ionomycin or just modia (unstimulated). For the flow sytematry plate, the DMA/L was not									
	+ 1 µg/mL following in or just media (unstimulated). For the now cytometry plate, the PMA/1 was not									

210	added until the next day. 125 μL (2x concentration) of each stimulant was mixed with the 125 μL									
211	splenocytes suspension in the designated wells. After all the wells were prepared, the plates were									
212	incubated at 37 °C 5% CO ₂ . One plate was used for the cytokine release assay, while the other plate									
213	was used for flow cytometry. For flow cytometry, another plate was prepared with splenocytes,									
214	which would be later used as fluorescence minus one – controls (FMOs).									
215	2.8.2 In vitro cytokine release assay									
216	After 48 hours in the incubator, splenocytes were briefly mixed by pipetting. Then plates were									
217	centrifuged for 5 min at 400 x g at RT. Without disturbing the pellet 50 μ L supernatant was									
218	transferred to two skirted PCR plates and frozen at -20 °C until use.									
219	For the <i>in vitro</i> cytokine release assay, splenocytes were seeded in a 96-well culture plate at									
220	$1x10^{6}$ live cells in 250 µL cRPMI. Splenocytes were then (re-)stimulated with either 10 µg/mL									
221	RBD219-WT protein, 10 µg/mL RBD219-N1C1 protein, PMA/Iomycin (positive control), or nothing									
222	(negative control) for 48 hours at 37 °C 5% CO ₂ . After incubation, 96-well plates were centrifuged to									
223	pellet the splenocytes down and supernatant was transferred to a new 96-well plate. The supernatant									
224	was stored at -20°C until assayed. A Milliplex Mouse Th17 Luminex kit (MD MilliPore) with									
225	analytes IL-1 β , IL-2, IL-4, IL-6, IL-10, IL-12(p70), IL-13, IL-17A, IL-23, IFN- γ , and TNF- α was									
226	used to quantify the cytokines secreted in the supernatant by the re-stimulated splenocytes. An									
227	adjusted protocol based on the manufacturers' recommendations was used with adjustments to use									
228	less sample and kit materials ²³ . The readout was performed using a MagPix Luminex instrument.									
229	Raw data was analyzed using Bio-Plex Manager software, and further analysis was done with Excel									
230	and Prism.									

231 **2.8.3** Cytokine production of activated CD4+ and CD8+ T cells

- Surface staining and intracellular cytokine staining followed by flow cytometry was performed to measure the amount of activated (CD44=) CD4+ and CD8+ T cells producing IFN- γ , IL-2, TNF- α , and IL-4 upon re-stimulation with S2RBD219 WT.
- 235 Five hours before the 24-hour re-stimulation incubation, Brefeldin A was added to block
- 236 cytokines from secretion. PMA/I was also added to designated wells as a positive control. After the
- 237 incubation, splenocytes were stained for the relevant markers. A viability dye and an Fc Block were
- also used to remove dead cells in the analysis and to minimize non-specific staining, respectively.
- After staining, splenocytes were analyzed using an Attune NxT flow cytometer instrument at
- 240 the Baylor College of Medicine Cytometry and Cell Sorting Core. Raw data was analyzed in
- 241 VenturiOne software and gating results were copied in Excel. The %-gating values from the non-
- stimulated controls were subtracted from the re-stimulated controls to observe the difference in %-
- 243 gating induced by the re-stimulation.

The gating strategy from the analysis of the results is shown in **Supplemental Figure 1.** From all events collected the doublets are removed to obtain only single-cell events. Then events are selected on size and granularity to obtain splenocytes only. Following the removal of dead splenocytes, a gate is set to only select Activated (CD44+) T cells (CD3+)²⁴. T cells are then separated into CD4+ T helper cells and CD8+ cytotoxic T cells. For T helper cells the events positive for IFN-g, TNF-a, IL-2, and IL-4 were selected, while for cytotoxic T cells only IFN- γ , TNF- α , and IL-2 positive events were gated.

251 3 Results

252 Here we report on the expression of a modified, recombinant RBD of the SARS-CoV-2 spike protein 253 using the yeast (P. pastoris) expression system. The candidate antigen selection, modifications, and 254 production processes were based on eight years of process development, manufacture, and preclinical 255 prior experience with a SARS-CoV recombinant protein-based receptor-binding domain (RBD)⁹⁻¹¹. 256 The RBDs of the SARS-CoV-2 and SARS-CoV share significant amino acid sequence similarity (>75% identity, >80% homology) and both use the human angiotensin-converting enzyme 2 (ACE2) 257 258 receptor for cell entry^{25,26}. Process development using the same procedures and strategies used for the 259 production, scale-up, and manufacture of the SARS-CoV recombinant protein allowed for a rapid 260 acceleration in the development of a scalable and reproducible production process for the 261 SARS-CoV-2 RBD219-N1C1 protein, suitable for its technological transfer to a manufacturer. 262 We found that the modifications used to minimize yeast-derived hyperglycosylation and 263 optimize the yield, purity, and stability of the SARS-CoV RBD219-N1 protein were also relevant to 264 the SARS-CoV-2 RBD expression and production process. The modified SARS-CoV-2 antigen, 265 RBD219-N1C1, when formulated on Alhydrogel[®], was shown to induce virus-neutralizing antibodies in mice, equivalent to those levels elicited by the wild-type (RBD219-WT) recombinant protein 266 267 counterpart.

268 3.1 Cloning and expression of the modified SARS-CoV-2 RBD

269 The wild-type SARS-CoV-2 RBD amino acid sequence comprises residues 331-549 of the spike (S)

protein (GenBank: QHD43416.1) of the Wuhan-Hu-1 isolate (GenBank: MN908947.3) (Figure 1).

271 In the RBD-219-WT construct, the gene fragment was expressed in *P. pastoris*. After fermentation at

the 5 L scale, the hexahistidine-tagged protein was purified by immobilized metal affinity

chromatography, followed by size-exclusion chromatography. We observed glycosylation and

aggregation during these initial expression and purification studies, and therefore, similar to our

275	previous strategy ¹⁰ , we generated a modified construct, the RBD219-N1C1, by deleting the N331
276	residue and mutating the C538 residue to alanine. The additional mutation of C538 to A538 was done
277	because we observed that in the wild-type sequence nine cysteine residues likely would form four
278	disulfide bonds. Therefore, the C538 residue was likely available for intermolecular cross-linking,
279	leading to aggregation. As a result, in the RBD219-N1C1 construct, and based on the modifications,
280	the Pichia-derived hyperglycosylation, as well as aggregation via intermolecular disulfide bridging,
281	were greatly reduced. We note that the deleted and mutated residues are structurally far from the
282	immunogenic epitopes and specifically the receptor-binding motif (RBM) of the RBD (Figure 1). On
283	SDS-PAGE tris-glycine gels, the RBD219-WT protein migrated at approximately 28 kDa under non-
284	reduced conditions and 33 kDa in the reduced condition, while the RBD219-N1C1 protein migrated
285	at approximately 24 kDa under non-reduced conditions and 29 kDa under reduced conditions.
286	However, after the N-glycans were removed enzymatically, these two proteins showed a similar
287	molecular weight of approximately 25 kDa (Supplemental Figure 2). The purity of both proteins
288	was analyzed by densitometry resulting in levels >95%.

A)								В)
S2-RBD S2-RBD-N1C1	331 331	NITNLCPFGE - ITNLCPFGE	VFNATRFASV VFNATRFASV	YAWNRKRISN YAWNRKRISN	CVADYSVLYN CVADYSVLYN	SASFSTFKCY SASFSTFKCY	380 380	RBM region
S2-RBD S2-RBD-N1C1	381 381	GVSPTKLNDL GVSPTKLNDL	CFTNVYADSF CFTNVYADSF	VIRGDEVRQI VIRGDEVRQI	APGQTGKIAD APGQTGKIAD	YNYKLPDDFT YNYKLPDDFT	430 430	Store S
S2-RBD S2-RBD-N1C1	431 431	GCVIAW <mark>NSNN</mark> GCVIAW <mark>NSNN</mark>	LDSKVGGNYN LDSKVGGNYN	YLYRLFRKSN YLYRLFRKSN	LKPFERDIST LKPFERDIST	EIYQAGSTPC EIYQAGSTPC	480 480	Cysteine
S2-RBD S2-RBD-N1C1	481 481	NGVEGFNCYF NGVEGFNCYF	PLQSYGFQPT PLQSYGFQPT	NGVGYQPYRV NGVGYQPY	VVLSFELLHA VVLSFELLHA	PATVCGPKKS PATVCGPKKS	530 530	(C538)
S2-RBD S2-RBD-N1C1	531 531	TNLVKNKCVN TNLVKNK <mark>A</mark> VN	FNFNGLTGT 5	549 549				Asparagine - (1) (N331)

- 290 Figure 1 A) Amino acid sequence alignment between SARS-CoV-2 RBD219-WT (S2-RBD) and
- 291 RBD219-N1C1 (S2-RBD-N1C1). In the N1C1-mutant, the N-terminal glutamine residue (N331, green) is
- removed and a C538A mutation (yellow) was introduced. Neither mutation is inside the receptor-
- 293 binding motif (RBM, purple). B) The structure model of RBD219-WT was extracted from the crystal
- structure of the SARS-CoV-2 spike protein (PDB ID 6VXX). The RBM (N436-Y508) is again shown in

295 purple while the deleted asparagine (N331) and mutated cysteine (C538, mutated to alanine) in

296 **RBD219-N1C1** are highlighted in green and yellow, respectively

297

3.2 ACE-2 binds to recombinant SARS-CoV-2 RBD219-N1C1 protein formulated on Alhydrogel[®]

When mixing 25 μ g of either RBD219-WT or RBD219-N1C1 proteins to 500 μ g of Alhydrogel[®], we observed that >98% of the proteins bind to Alhydrogel[®] after 15 min of incubation. Only when the Alhydrogel[®] was reduced to less than 100 μ g (Alhydrogel[®]/RBD219 ratio <4), the Alhydrogel[®] surface was saturated, and protein started to be detected in the supernatant (**Figure 2A**). It is known that unbound protein may impact the immunogenicity of the vaccine formulation, therefore we proceeded to only evaluate formulations with Alhydrogel[®]/RBD219 ratios higher than 4.

Figure 2B shows that hACE-2-Fc, a recombinant version of the human receptor used by the
virus to enter the host cells, can bind with the RBD proteins that are adsorbed on the surface of the
Alhydrogel[®]. This demonstrates that bound RBD proteins are structurally and possibly functionally
active and that after adsorption the protein does not undergo any significant conformational changes
that could result in the loss of possible key epitopes around the receptor-binding motif (RBM).

311 We saw no statistical differences between the binding of hACE-2-Fc to RBD219-WT (red,

312 Figure 2B) or RBD219-N1C1 (green, Figure 2B) proteins, based on an unpaired t-test (P=0.670).

313 Likewise, we saw no relation between the amount of Alhydrogel[®] to which the RBD was bound and

314 the interaction with hACE-2-Fc, indicating that the surface density of the RBD proteins on the

315 Alhydrogel[®] plays no role in the presentation of ACE binding sites.



316

317 Figure 2 A) Langmuir binding isotherm of RBD219-N1C1 to Alhydrogel[®]. B) ELISA data, comparing

318 the binding interaction of hACE-2-Fc to RBD219-WT bound Alhydrogel[®] (red) and RBD219-N1C1

- bound on different amounts of Alhydrogel[®] (green, purple, orange, and black). Five hundred μg
- Alhydrogel[®] alone served as a negative control (blue). Data are shown as the geometric mean (n=3) with
 95% confidence intervals.
- 322

323 3.3 Recombinant RBD219-N1C1 protein, formulated with Alhydrogel[®], elicits a strong

324 neutralizing antibody response in mice

325 The recombinant RBD219-N1C1 protein (25 μ g) was formulated with various amounts (100 – 500

326 µg) of Alhydrogel[®]. Controls included a cohort receiving only Alhydrogel[®] and another receiving the

327 RBD219-WT antigen, also formulated with 500 µg Alhydrogel[®]. Six- to eight-week-old female

328 BALB/c mice were immunized 2-3 times subcutaneously at approximately 21-day intervals (Figure

329 **3A**). Blood samples were taken on day 35 from all study animals to assess total IgG antibody titers,

as well as neutralizing antibody titers (Dataset 1). Half of the mice, those with the highest IgG titers

- in their respective group, were euthanized on day 43 to allow the evaluation of the cellular immune
- 332 response after two immunizations. For this dataset (Dataset 2), we also measured IgG and

333	neutralizing antibody titers. The remaining mice received a third vaccination on day 43 and were
334	euthanized on day 57 for the assessment of humoral and cellular immune responses (Dataset 3).
335	Humoral immune response: On day 35 (Dataset 1), after receiving two vaccinations, all
336	groups that had received the recombinant protein formulated with at least 200 μ g Alhydrogel [®]
337	produced similar and robust IgG titers. The group receiving the protein with only 100 μ g
338	Alhydrogel [®] , produced a lower IgG response, albeit slightly higher than the negative control that had
339	been immunized with 500 µg Alhydrogel [®] alone (Figure 3B, Supplemental Table 1). Importantly,
340	based on a Mann-Whitney test, we determined that there was no statistical difference between the
341	groups vaccinated with the modified and the wild-type version of the RBD protein (p=0.3497). The
342	average neutralizing antibody titers observed on day 35 (IC50 range: 5.0×10^3 to 9.4×10^3 ,
343	Supplemental Table 2) matched with the total IgG titers, showing equally high IC50 values for all
344	vaccines that contained at least 200 μ g Alhydrogel [®] and lower IC50 values for the vaccine with only
345	100 μ g Alhydrogel [®] and no IC50 values for the adjuvant-only control (Figure 3C).
346	On day 43, 22 days after receiving the boost vaccination, half of the mice in each group
347	(N=4), those with the highest IgG titers, were sacrificed to determine the total IgG, the IgG subtypes,
348	and the neutralizing antibody titers. As we observed on day 35, all animals that had received the
349	vaccine produced strong antibody titers, with the groups receiving $\geq 200 \ \mu g \ Alhydrogel^{\mbox{\ensuremath{\$}}}$ eliciting a
350	higher titer than those that received only 100 μ g of Alhydrogel [®] , albeit no statistical significance was
351	detected (Figures 3B). For all animals, as typical for vaccine formulations containing aluminum, the
352	IgG2a:IgG1 titer ratio was <0.1 (Supplemental Figure 3). In the pseudovirus neutralization assay
353	for the day 43 samples (Figure 3C), all vaccines containing $\geq 200 \ \mu g \ Alhydrogel^{\ensuremath{\$}}$ elicited IC50 titers
354	that, on average, were several-fold higher than on day 35 (IC50 range: 1.1×10^4 to 1.2×10^5 ,
354 355	that, on average, were several-fold higher than on day 35 (IC50 range: 1.1×10^4 to 1.2×10^5 , Supplemental Table 2). There again was no difference between the RBD219-WT and RBD-N1C1

357	On day 57, all remaining animals were sacrificed. In contrast to the animals studied on days
358	35 and 43, these animals had received a second boost vaccination. A robust immune response in all
359	vaccinated mice, including those immunized with the protein adsorbed to 100 μ g Alhydrogel [®]
360	achieved high average IgG titers. The total IgG titers in the mice sacrificed on day 57, had increased
361	after the third vaccination, compared to the titers seen on day 35. Likewise, we observed a
362	corresponding increase in the average IC50 values (IC50 range: 3.8x10 ² to 1.1x10 ⁴ , Supplemental
363	Table 2) for all animals, including those immunized with the protein adsorbed to 100 μ g
364	Alhydrogel [®] . Interestingly, for this time point, the cohort receiving 25 μ g RBD219-N1C1 with 500
365	μ g Alhydrogel [®] appeared to show higher neutralizing antibody titers than the corresponding

366 RBD219-WT group, albeit that difference was not statistically significant.



Figure 3. A) Study design. B) Total IgG titers of Datasets 1, 2, and 3 measured respectively at days 35,
43, and 57 post the prime injection. IgG titers were determined against RBD219-WT protein. Closed

370 data points represent data from mice with the highest IgG titers (Dataset 2), open data points represent

data from mice with the lowest IgG titers (Dataset 3). C) IC50 values measured by a pseudovirus
 neutralization assay. Datasets 1, 2, and 3 are measured respectively at day 35, 43, and 57 after the first
 injection. Baselines indicate the lowest dilution measured. Lines on each group represent the geometric

- 374 mean and 95% confidence intervals.
- 375

376	Cellular immunity: For all animals sacrificed on day 43 (having received two vaccinations)
377	and day 57 (having received three vaccinations), the cellular immune response was characterized
378	through the restimulation of isolated mouse splenocytes with the recombinant RBD219-WT protein.
379	For all samples, we employed Flow Cytometry to quantify intracellular cytokines in CD4+ and CD8+
380	cells after restimulation (Figure 4A). On day 43, high percentages of CD4 ⁺ -IL-4 and, to a slightly
381	lesser extent CD4 ⁺ -TNF α producing cells were detected. Conversely, as expected for an
382	Alhydrogel [®] -adjuvanted vaccine, low levels of IL-2 producing CD4 ⁺ cells were seen. In a cytokine
383	release assay, strong IFN-7, IL-6, and IL-10 secretion was observed independent of whether the
384	animals had received two or three immunizations, whereas low amounts of secreted Th1-typical
385	cytokines such as IL-2 or IL-12 were seen (Figure 4B).

CD8 TMF⁴

CD811.2

A) Cytokines production by stimulated T-cells

Dataset 2: mice with high IgG titers after 1st boost (Day 35), (sacrificed on Day 43)



B) Cytokines secreted by stimulated splenocytes

Dataset 2: mice with high IgG titers after 1st boost (Day 35), (sacrificed on Day 43)







Dataset 3: mice with low IgG titers at 1st boost (Day 35), that received 2nd boost on Day 43 (sacrificed on Day 57)



387

388 Figure 4: A) Heatmap of the cytokine response of CD4+ and CD8+ T cells after restimulation with

389 SARS-CoV-2 RBD219-WT or RBD219-N1C1, re-stimulated splenocytes were surface and

390 intracellularly stained and subsequently analyzed by flow cytometry. Splenocytes were obtained from

391 mice who received two vaccinations (day 43) or three vaccinations (Day 57). Non-stimulated controls

392 were subtracted from re-stimulated samples. B) Heatmap of secreted cytokines in supernatant from re-

stimulated splenocytes from mice who received two vaccinations (day 43) or three vaccinations (Day 57). 393

394 Cytokine concentrations of non-stimulated controls were subtracted from re-stimulated samples.

396 4 Discussion

397	Here we report on a yeast-expressed SARS-CoV-2 RBD219-N1C1 protein and its potential as a
398	vaccine candidate antigen for preventing COVID-19. Building on extensive prior experience
399	developing vaccines against SARS-CoV and MERS-CoV ¹⁰⁻¹² , we initially selected and compared the
400	SARS-CoV-2 RBD219-WT and the SARS-CoV-2 RBD219-N1C1 proteins for their potential to
401	induce high titers of virus-neutralizing antibodies, T-cell responses, and protective immunity.
402	Previously we observed that the SARS-CoV RBD219-N1 antigen, formulation with
403	Alhydrogel [®] elicited high levels of neutralizing antibodies without evidence of eosinophilic immune
404	enhancement. That RBD-based vaccine was even superior to the full-length spike protein in inducing
405	specific antibodies and fully protected mice from SARS-CoV infection while preventing eosinophilic
406	pulmonary infiltrates in the lungs upon challenge ⁹ .
407	In this work, using the SARS-CoV-2 RBD219 protein analog, we observed that, just like in
408	the case of the SARS-CoV RBD antigen, the deletion of the N-terminal asparagine residue reduced
409	hyperglycosylation, thus allowing for easier purification of the antigen obtained from the yeast
410	expression system. Moreover, mutagenesis of a free cysteine residue further improved protein
411	production through the reduction of aggregation. Based on the predicted structure of the RBD, no
412	impact on the functionality of the RBD219-N1C1 antigen was expected, and using an ACE-2 in vitro
413	binding assay we indeed showed similarity to the RBD219-WT antigen. In addition, we showed that,
414	in mice, the modified RBD219-N1C1 antigen triggered an equivalent immune response to the
415	RBD219-WT protein when both proteins were adjuvanted with Alhydrogel [®] .
416	Similar to our previous findings with the SARS-CoV RBD antigen ⁹ , we show the RBD219-
417	N1C1 protein when formulated with Alhydrogel [®] elicits a robust neutralizing antibody response with
418	IC50 values up to 4.3x10 ⁵ in mice, as well as an expected T-cell immunological profile. Some of the

419	titers of virus-neutralizing antibodies exceed the titer, 2.4×10^4 , measured in-house with human
420	convalescent serum research reagent for SARS-CoV-2 (NIBSC 20/130, National Institute for Biological
421	Standards and Control, UK).

422 In a mouse virus challenge model for the SARS CoV RBD recombinant protein vaccine, we found that Alhydrogel[®] formulations induced high levels of protective immunity but did not 423 stimulate eosinophilic immune enhancement, suggesting that Alhydrogel[®] may even reduce immune 424 enhancement. This prior experience offers the potential for Alhydrogel[®] as a key adjuvant for 425 consideration during coronavirus vaccine development²⁷. Such findings have led to a reframing of the 426 basis for immune enhancement linked to coronavirus respiratory infections²⁸. A recent analysis and 427 428 review by the NIH ACTIV Vaccine Working Group confirms that aluminum or Th2 responses 429 remain viable options for vaccine development concluding that "it is not possible to clearly prioritize 430 or down-select vaccine antigens, adjuvants, biotechnology platforms, or delivery mechanisms based 431 on general immunological principles or the available preclinical data²⁹.

Therefore, the RBD219-N1C1 vaccine antigen on Alhydrogel[®] merits its evaluation as a 432 433 COVID-19 vaccine possibly with or without other immunostimulants. Looking at the landscape of 434 recombinant protein-based COVID-19 vaccines, the WHO lists several advanced COVID-19 candidates that are based on recombinant proteins³⁰, and at least seven COVID-19 vaccines include 435 aluminum as part of the adjuvant component^{7,13,15,16,31-37}, often in combination with other 436 437 immunostimulants, such as CpG, to achieve a balanced immune response. Furthermore, these 438 recombinant protein vaccines, including RBD219-N1C1, might find an additional important use as a 439 booster if one of the newer platform vaccines, e.g., mRNA or adenovirus-based vaccines induce 440 lower than expected immunogenicity or protection. Such prime-boost approaches have been used successfully with the chimp adenovirus vaccine for malaria and other systems, for example^{38,39}. 441

442 The selection of the *P. pastoris* expression platform for the production of the RBD antigen 443 was motivated by the intent to develop a low-cost production process that could easily be transferred 444 to manufacturers in LMICs. Currently, there are several types of COVID-19 vaccine candidates in 445 advanced clinical trials^{6,40-45}. The focus of some of the initiatives behind these vaccines is to provide 446 vaccines for the developed world that might struggle to be successful without advanced 447 infrastructure. Being able to match the existing experience in LMICs with the production of other 448 biologics in yeast increases the probability of successful technology transfer²⁰. For example, 449 currently, the recombinant hepatitis B vaccine is produced in yeast by several members of the 450 Development Country Vaccine Manufacturers Network (DCVMN), and we foresee that, given the 451 existing infrastructure and expertise, those facilities could be repurposed to produce a yeast-produced 452 COVID-19 vaccine⁴⁶. Recently, the research cell bank and production process for the RBD219-N1C1 453 antigen was technologically transferred to a vaccine manufacturer in India and produced under cGMP 454 conditions with the intent to enter into clinical development. In addition, preclinical studies using the 455 RBD219-WT and RBD219-N1C1 antigens are ongoing to further optimize and evaluate other novel 456 formulations, including a challenge study in a non-human primate model.

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468 Author Contributions

- 469 BZ and JW planned and executed all cloning and small-scale expression studies. ZL conducted the
- 470 fermentations. JL executed the protein purifications. WHC and RTK conducted the characterization
- 471 of the purified proteins. JP and BK conducted mouse studies. LV, RA, MJVM, ACAL, JAR ran
- 472 ELISAs. LV and CP executed the cellular assays. JP, CP, MJVM, and JAR conducted pseudovirus
- 473 studies. RA and JP executed the ACE-2 binding study. MEB, JP, PJH, US, and WHC drafted the
- 474 manuscript. All authors were involved in the experimental design and planning and reviewed and
- 475 edited the final submission.

476 Data availability

- 477 All data generated or analysed during this study are included in this published article (and its478 supplementary information files).
- 479

481 **Competing Interests Statement**

- 482 The authors declare that Baylor College of Medicine recently licensed the RBD219-N1C1
- 483 technology to an Indian manufacturer for further development. The research conducted in this paper
- 484 was performed in the absence of any commercial or financial relationships that could be construed as
- 485 a potential conflict of interest.

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