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1 **A monoclonal antibody collection for *C. difficile* typing ?**

2

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ABSTRACT

Clostridioides difficile is the leading cause of antibiotic-associated diarrhea and pseudomembranous colitis in adults. Various *C. difficile* strains circulate currently, associated with different outcomes and antibiotic resistance profiles. However, most studies still focus on the reference strain 630 that does not circulate anymore, partly due to the lack of immunological tools to study current clinically important *C. difficile* PCR ribotypes. The goal of this study was to generate monoclonal antibodies recognizing various epidemic ribotypes of *C. difficile*. To do so, we immunized mice expressing human variable antibody genes with the Low Molecular Weight (LMW) subunit of the surface layer protein SlpA from various *C. difficile* strains. Monoclonal antibodies purified from hybridomas bound LMW with high-affinity and whole bacteria from current *C. difficile* ribotypes with different cross-specificities. This first collection of anti-*C. difficile* mAbs represent valuable tools for basic and clinical research.

KEYWORDS (5-10 WORDS)

Clostridioides difficile, monoclonal antibodies, S-layer, hybridomas, ribotypes

INTRODUCTION

Clostridioides difficile is an anaerobic, gram-positive, and spore-forming bacterium that is the main agent responsible for antibiotic-associated diarrhea and pseudomembranous colitis in adults¹. In the past decades, there was a drastic increase in the incidence of both healthcare-associated *C. difficile* infection (CDI) and community-acquired CDI². There is a large phylogenetic diversity of *C. difficile* with more than 300 distinct PCR-ribotypes (RT) reported worldwide, including epidemic lineages associated with increased transmission and mortality³⁻⁶. The latest epidemiology data worldwide reported that 5 ribotypes i.e., RT001, RT002, RT014, RT027 and RT078, account for approximately 50% of the infections⁷.

Whereas several advances such as fluorescent mutants and novel fingerprinting techniques have contributed to a better understanding of *C. difficile* diversity and physiology⁸⁻¹⁰, basic research still relies on one single strain i.e., *C. difficile* 630 that belong to RT012. An increasing number of studies has been performed on the epidemic ribotype 027, which caused major outbreaks in the United States and Europe at the end of the 2010s^{11,12}. Other ribotypes remain largely unexplored even though some are associated with antibiotic resistance and increased severity³, which can be partly explained by the lack of genetic and immunological tools to study these strains.

C. difficile surface is composed of adhesins e.g., the flagellar cap protein FliD, the flagellin FliC, the cell wall protein Cwp66, the surface layer protein SlpA, and the protease Cwp84¹³. SlpA is expressed on the bacterial surface of all ribotypes and plays a crucial role in the pathogenesis and virulence of *C. difficile* by mediating interactions with the host cells and the surrounding environment¹⁴⁻¹⁷. SlpA contains two biologically distinct entities, the high-molecular weight (HMW) and the low molecular weight (LMW) subunits that assemble on the bacterial surface into a paracrystalline lattice¹⁸. Sequence variations of SlpA have been reported for the LMW that correlate with the diversity of clinical isolates, whereas the HMW is less variable^{19,20}. SlpA is highly immunogenic, meaning it can trigger an immune response in the host²¹. Indeed, antibodies against SlpA have been detected in the sera of patients infected with *C. difficile*, indicating its potential as a target for vaccine development^{21,22}.

In this work, we generated the first collection of mAbs that bind and discriminate predominant clinical ribotypes of *C. difficile*. Knock-in mice expressing human antibody variable genes for the heavy (V_H) and light chain (V_L)^{23,24} were immunized with a collection of recombinantly expressed LMW from five clinically relevant *C. difficile* ribotypes i.e., RT001, RT002, RT014, RT027 and RT078. Hybridomas were generated and their corresponding IgG

78 mAbs bound both recombinant LMW *in vitro* and LMW naturally expressed on the bacterial
79 surface. At least one mAb was identified against each of the five ribotypes used for
80 immunization, with 6 mAbs being cross-reactive between LMW subunits of two different *C.*
81 *difficile* ribotypes. The reduced sequence identity of LMW between different *C. difficile*
82 ribotypes²⁵ allows for specific identification of bacterial ribotypes by this anti-LMW mAb
83 collection that represents a novel toolkit for *C. difficile* research.

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RESULTS

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87 LMW SlpA subunits from 5 predominant ribotypes of *C. difficile* i.e., RT001, RT002,
88 RT014, RT078 and RT027 (Fig. 1a), were recombinantly produced from transformed
89 *Escherichia coli* as his-tagged soluble proteins and affinity-purified. As anti-LMW antibodies
90 may potentially be of therapeutic interest for the treatment of CDIs, we used knock-in mice in
91 which the endogenous genes encoding the heavy chain variable domain (VH) and the kappa
92 light chain variable domain (Vκ) were replaced by their human counterparts
93 (Velocimmune)^{23,24} with one modification, i.e., only one allele of the endogenous Vκ locus was
94 replaced by human Vκ segments, and the second allele of the endogenous Vκ locus was
95 replaced by human Vλ segments (Fig. 1b). As the Vκ locus expresses 95% of the light chains
96 in mice²⁶, placing human Vλ segments at the Vκ locus increases the variability of light chain
97 expression. Thus, after hybridoma identification, cloning of these VH and VL into vectors
98 containing human heavy and light chain constant domains, allows for direct development - *in*
99 *fine* – of fully human anti-LMW mAbs. To generate hybridomas, mice were immunized at D0,
100 D21 and D42 with 50 µg/mouse of each LMW (Fig. 1c). High anti-LMW IgG serum titers were
101 obtained in all mice at day 42 (Fig. 1d). Mice were boosted with all five LMW at equimolar
102 ratio (Fig. 1c), and their spleen harvested 4 days later. Two different protocols were tested and
103 gave similar results; one based on the similarity between the LMW – grouping two highly
104 similar LMW in a single immunization; one based on their frequency in current CDI – grouping
105 LMW corresponding to current clinical ribotypes in a single immunization (Supp. Fig. 1). More
106 than 700 hybridomas were generated and among them 100 hybridoma were found to secrete
107 anti-LMW antibodies.

108 Among these 100 hybridomas, the 14 clones displaying the highest ratio of LMW
109 binding by ELISA compared to IgG concentration in their culture supernatant were expanded
110 and their antibodies purified. Their binding profiles towards the five recombinant LMW
111 proteins were assessed by ELISA (Fig. 2). 12 out of 14 (86%) significantly bound LMW-RT001
112 with variable profiles, 1 out of 14 (7%) bound LMW-RT002, 1 out of 14 (7%) bound LMW-
113 RT014, 6 out of 14 (43%) bound LMW-RT078 and 11 out of 14 (78%) bound LMW-RT027.
114 Among the eleven LMW-RT027-binding mAbs, four (36%) cross-reacted strongly with LMW-
115 RT001 (mAb SG8, TF1, TH4 and VA10) and one with both LMW-RT001 and LMW-RT078
116 (mAb RF12). mAb QE2 cross-reacted with four LMWs: LMW-RT001, LMW-RT014, LMW-
117 RT027 and LMW-RT078. Among the three mAbs that did not recognize LMW-RT027, mAb

118 RA11 was specific for LMW-RT078, mAb UA5 cross-reacted with LMW-RT001 and LMW-
119 RT002, and mAb SC6 cross-reacted with LMW-RT001 and LMW-RT078.

120 We next evaluated the affinity of the mAbs displaying the strongest interactions with
121 their respective targets i.e., LMW-RT001, LMW-RT002, LMW-RT014, LMW-RT078 and
122 LMW-RT027, by Bio Layer Interferometry (BLI), coupling IgGs to the sensors and keeping
123 LMW antigens in solution. mAbs displayed dissociation constant (K_D) values ranging more
124 than 3 logs from 0.08 nM to 200 nM, which corresponds to low to very high-affinity antibodies
125 (Fig. 3). We identified mAbs with a 1nM affinity or better for all ribotypes, except for RT014
126 that was only bound by mAb QE2 with a 9nM affinity. Noticeably, cross-specific mAbs
127 displayed different affinities for their targets, with systematically one ribotype bound with at
128 least a 10-fold better affinity, except for mAb VA10 that bound LMW-RT001 and LMW-
129 RT027 with comparable affinities.

130 As SlpA is the main component of the *C. difficile* surface, we investigated if this series
131 of mAbs could also bind LMW when exposed naturally at the bacterial surface. Fixed *C.*
132 *difficile* from the different ribotypes were used for bacterial flow cytometry (Fig. 4a). Each
133 ribotype could be significantly bound by at least one mAb. Consistent with the ELISA results
134 (Fig. 2), monospecific anti-LMW mAbs, the LMW-RT027-specific mAbs (PH4, QD8, QH5,
135 RD11 and TE8) and anti-LMW-RT078-specific mAbs (RA11), bound to *C. difficile* RT027 and
136 RT078 whole bacteria, respectively. However, cross-specific mAbs bound a restricted number
137 of ribotypes by bacterial flow cytometry (Fig. 4a) compared to ELISA (Fig. 2), indicating that
138 their epitopes are hidden or inaccessible, or that their affinity is not sufficient for flow cytometry
139 detection. Indeed, 3 out of 8 cross-specific mAbs showed restricted binding profile using flow
140 cytometry, e.g., QE2 mAb bound 4 distinct recombinant LMW ribotypes by ELISA but only 2
141 *C. difficile* ribotypes using flow cytometry. Table 1 summarizes the binding profiles of these
142 mAbs to the LMW recombinant proteins and the LMW exposed at the bacterial surface for the
143 five clinical ribotypes RT001, RT002, RT014, RT078, RT027.

144 Finally, we studied the impact of LMW binding by the anti-LMW-RT027 mAbs in an
145 *in vitro* growth assay on *C. difficile* strain 027. Two monospecific mAbs for LMW-RT027
146 (QD8 and QH5) and two cross-specific mAbs (VA10 and TH4) were tested for their impact on
147 growth. Growth was followed over 24 hours with an isotype control IgG and showed an
148 exponential phase followed by a plateau (Fig. 4b). Anti-LMW-RT027 did not significantly alter
149 growth, even though mAb VA10 tended to delay growth, and mAb QD8 and, to a lesser extent,
150 mAb QH5, tended to increase growth.

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DISCUSSION

Herein, we report the first monoclonal antibody collection that targets a surface protein of *C. difficile*. Due to sequence variability in the low-molecular weight subunit of surface layer protein A, this mAb collection allows the detection of 5 different ribotypes of clinical interest. More than half the mAbs bound selectively to the bacterial surface of one of these ribotypes, whereas the cross-reactive mAbs bound to two different ribotypes. The relatively high affinity of the interaction (nanomolar range) allows to envision using these mAbs for various assays such as ELISA, flow cytometry, microscopy, or histology assays.

In this study we chose to immunize mice with the low-molecular weight subunit of surface layer protein A as it represents a major antigen of the *C. difficile* surface²⁷. Although we found by alignment stretches of conserved residues between the five ribotype sequences we used¹⁸, we could not identify any antibody cross-binding all five strains. The most cross-reactive anti-LMW mAbs recognized by bacterial flow cytometry only two different ribotypes. This suggests that conserved epitopes between LMW of different strains may not be dominant epitopes in terms of immunogenicity or may be hidden or poorly accessible to antibodies. Indeed, conserved amino acids have been implicated in the interaction between the LMW and the High Molecular Weight subunits which face inward toward the bacterial cell wall²⁸ and are therefore probably inaccessible to antibodies.

Mice were immunized sequentially with five different LMWs and boosted with a mix of all of them, leading to identification of mAbs to each of them. Varying the order of different LMWs in the immunization scheme did not significantly alter antibody titers for the various LMWs, except for LMW-RT001 when injected with a farther ribotype. Antibodies binding SlpA have also been detected in the sera of patients infected with *C. difficile*, suggesting that, indeed, SlpA or its LMW subunit are immunogenic. Even though the knock-in mice we used produce antibodies with human variable domains^{23,24}, thus potentially resembling those found in infected patients, we did not identify antibodies that significantly alter bacterial growth in our *in vitro* assays. It remains unclear whether such antibodies exist in patients in remission or if other mechanisms are at play. Interestingly, 30% of relapsing *C. difficile* infections are not due to the initial infecting strain but to a different strain, acquired from an exogenous source²⁹. Whether the sequence variability of LMW among *C. difficile* ribotypes is involved in this recurrence and escape from the host immune response remains to be investigated.

This novel series of anti-*C. difficile* mAbs contains three anti-LMW mAbs specifically recognizing epidemic ribotypes RT027, bound by mAb TE8, RT078 bound by mAb RA11, and

186 RT002 bound by mAb U5A. These three ribotypes have been associated with poor outcomes
187 after infection^{6,30,31}. Beyond *C. difficile* 630, the most studied *C. difficile* ribotype, this set of
188 mAbs could help to study ribotypes RT027, RT078 and RT002 by resorting to various assays
189 (ELISA, flow cytometry, microscopy, histology, blotting). One could even propose targeted
190 treatments, by coupling antibiotics to these mAbs (aka Antibody-Drug Conjugates, ADC) to
191 reduce antibiotic doses.

192 Our study however has limitations. While it has recently been reported, using whole-
193 genome sequencing, that diversity exists within a given ribotype³², we only tested five ribotypes
194 of *C. difficile*, each derived from a single clinical isolate. Therefore, more clinical isolates now
195 remain to be tested to determine whether mAb specificity encompasses all known strains in
196 each ribotype. Moreover, we only tested cross-specificity towards a limited panel of ribotypes.
197 It remains to be deciphered if these mAbs cross-react with other *C. difficile* ribotypes or even
198 to other closely related microbial pathogens that we did not include herein and that may prevent
199 using this mAb series to conduct detection or ribotyping in clinical samples.

200 To our knowledge, these mAbs represent the first collection of antibodies against *C.*
201 *difficile* surface protein SlpA. These mAbs bind LMW from different clinically relevant strains
202 *i.e.*, LMW-RT001, LMW-RT002, LMW-RT014, LMW-RT027 and LMW-RT078. These
203 mAbs represent interesting probes to better understand *C. difficile* infection, pathogenesis, and
204 epidemiology.

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MATERIALS AND METHODS

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Bacterial strains and culture conditions. Clinical isolates of *C. difficile* RT001, RT002, RT014, RT027, RT078 were provided by The French National Reference Laboratory for *C. difficile*. Strains were grown anaerobically (5% H₂, 5% CO₂, 90% N₂) in TY medium (30 g/L tryptone, 20 g/L yeast extract). All media were purchased from Sigma-Aldrich.

Mice. Knock-in mice expressing human antibody variable genes for the heavy (V_H) and light chain (V_L) (VelocImmune) were described previously^{23,24} and provided by Regeneron Pharmaceuticals to be bred at Institut Pasteur. All animal care and experimentation were conducted in compliance with the guidelines. The study, registered under #210111 was approved by the Animal Ethics committee CETEA (Institut Pasteur, Paris, France) and by the French Ministry of Research.

Production of recombinant LMW proteins. Recombinant *C. difficile* LMW-SLPs (LMW-RT001, LMW-RT002, LMW-RT014, LMW-RT078, LMW-RT027, LMW630²⁵) were produced as N-terminal 6xHis-tagged proteins from plasmid pET-28a(+) (TwistBiosciences, #69864). Plasmids were transformed into *E. coli* strain DE3 and grown in NZY auto-induction lysogeny broth (LB) medium (NZYtech, #MB180). Bacteria were harvested by centrifugation and lysed using Cell Disruptor (Constant System) at 1.3 kbar. Recombinant LMW-SLP proteins from the soluble fraction were purified by affinity chromatography on Histrap FF crude 1mL columns (Cytiva life science, #29048631) followed by size exclusion chromatography on HiLoad 16/600 Superdex 75 pg (Cytiva life science, #28989333) using an AKTA pure (Cytiva life science). All proteins were stored in 50 mM sodium phosphate buffer pH 7.8, 300mM NaCl prior to analysis or long-term storage.

Production of LMW-specific monoclonal antibodies. VelocImmune mice were injected i.p. at day 0, 21 and 42 with 50 µg of each of five recombinant LMWs in alum mixed with 200 ng/mouse pertussis toxin (Sigma-Aldrich, #70323-44-3). ELISA was performed to measure serum responses to antigen (see methods below) and the 3 best immunized animals were boosted with the same antigen mix. Four days later, splenocytes were fused with myeloma cells P3X63Ag8 (ATCC, #TIB-9) using ClonaCell-HY Hybridoma Kit according to manufacturer's instructions (StemCell Technologies, #03800). Culture supernatants were screened using ELISA (see below) and antigen-reactive clones were expanded in RPMI-1640 complemented

242 with 10% IgG-free Fetal Calf Serum (Sigma-Aldrich, #F1283) into roller bottles (Sigma-
243 Aldrich, #CLS431344) at 37°C. After 14 days, supernatants were harvested by centrifugation
244 at 2500 rpm for 30 min and filtered (0.2 µm). Antibodies were purified by protein A affinity
245 chromatography (AKTA pure) as described previously³³.

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247 **ELISA assays.** Maxisorp microtiter plates (Dutscher, #055260) were coated with a total of 0.3
248 µg per well of LMW recombinant proteins in carbonate-bicarbonate buffer (pH 9.6) for 2 hours
249 at room temperature (RT). Free sites were blocked by a 2-hour incubation at RT with PBS 1%
250 BSA. Plates were washed three times with PBS 0.05% Tween 20 (PBS-T) before being
251 coincubated with serum, supernatants, or monoclonal antibodies at different concentrations
252 (from 10⁻⁶ µg/mL to 10 µg/mL) for 1h at RT. After five washes, goat anti-mouse IgG-Fc
253 fragment HRP conjugated antibody (Bethyl, dilution 1:20,000, #A90-131P) was added for 1h
254 at RT followed by incubation with OPD (o-phenylenediamine dihydrochloride) revelation
255 substrate for 10 min (Sigma-Aldrich, #P8287). Absorbances were analyzed at 492 vs 620 nm
256 on an ELISA plate reader (Berthold).

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258 **Bio-layer interferometry.** Biolayer interferometry assays were performed using Anti-Mouse
259 Fc Capture biosensors on an Octet Red384 instrument (ForteBio, #18-5088). Monoclonal
260 antibodies (10 µg/mL) were captured on the sensors at 25°C for 1,800 seconds. Biosensors were
261 equilibrated for 10 minutes in PBS, 0,05% Tween 20, 0.1% BSA (PBS-BT) prior to
262 measurement. Association was monitored for 1,200s in PBS-BT with LMW at a range of
263 concentrations from 0.01 nM to 500 nM followed by dissociation for 1,200s in PBS-BT. Traces
264 were reference sensor (sensors loaded with an unspecific mAb) subtracted and curve fitting was
265 performed using a global 1:1 binding model in the HT Data analysis software 11.1 (ForteBio),
266 allowing to determine K_D values.

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268 **Flow cytometry assays.** mAb binding to whole bacteria was assessed by bacterial flow
269 cytometry, as previously described³⁴. Bacteria were fixed in 4% paraformaldehyde (PFA) for
270 30 min and resuspended in PBS and stained (10⁶ bacteria/condition) using 5 µM Syto9 (Thermo
271 Fisher Scientific, #S34854) in 0.9% NaCl for 30 min at RT. Bacteria were washed (10 min,
272 4,000g, 4°C) and resuspended in PBS, 2% BSA and 0.02% Sodium Azide (PBA). Monoclonal
273 antibodies were pre-diluted in PBA at 20 µg/mL and incubated with bacteria for 30 min at 4°C.
274 Bacteria were washed, and incubated with AF647 AffiniPure goat anti-mouse IgG (H+L)

275 antibody or isotype control (Jackson ImmunoResearch, #115-605-003) for 30 min at 4°C. After
276 washing, bacteria were resuspended in sterile PBS. Flow cytometry acquisition was performed
277 on a MacsQuant cytometer (Miltenyi) and analyzed on FlowJo software (BD Biosciences).
278 Staining index was calculated by subtracting the Mean Fluorescence Intensity (MFI) of the
279 isotype from the MFI of each condition with the anti-LMW mAbs, then divided by the MFI of
280 the isotype.

281

282 **Growth assays.** Overnight *C. difficile* cultures were grown in TY broth and sub-cultured to an
283 Optical Density at 600 nm (OD_{600nm}) of 0.05 in 200 µL of BHISG in 96-well flat bottom
284 plates (Merck, #Z707902) containing mAbs at 0.2mg/mL. Bacterial growth was followed for
285 24h or 18h with OD_{600nm} measurements every 30 min using GloMax Plate Reader (Promega).
286 Anaerobia was maintained with a O₂ less sealing film (Sigma-Aldrich, #Z380059).

287

288 **Sequence alignments.** Sequence alignments of the LMW of five clinical ribotypes (LMW-
289 RT001, LMW-RT002, LMW-RT014, LMW-RT027, LMW-RT078) have been performed
290 using by ClustalOmega software. Fully conserved residues are indicated by *, groups of strongly
291 similar properties by † and groups of weakly similar properties by *, . or †.

292

293 **Statistical analysis.** Growth and ELISA assays values were analyzed in Prism 8.0 (GraphPad,
294 San Diego, CA). Statistical analysis was performed using two-way ANOVA test. A p value
295 <0.05 was considered significant.

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301

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318

AUTHORSHIP CONTRIBUTIONS

319 Experimental design, LH, DS and PB; Conducting experiments, LH, BI, OG; Data analyses and
320 discussions: LH, PE, FB, BD, LM, GG, DS and PB. Writing (original draft), LH, DS and PB;
321 Writing (review and editing), all authors.

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323

COMPETING INTERESTS

324 Unrelated to the submitted work, P.B. received consulting fees from Regeneron

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LEGENDS

414 **Figure 1: Generation of anti-LMW-specific hybridomas from immunized mice.** (a)
415 Sequence alignments of the LMW of five clinical ribotypes (LMW-RT001, LMW-RT002,
416 LMW-RT014, LMW-RT027, LMW-RT078) by ClustalOmega software. Fully conserved
417 residues are indicated by *, groups of strongly similar properties by : and groups of weakly
418 similar properties by *, . or :. Signal peptide, domain 1 and 2 and the domain that interacts with
419 the HMW are indicated. (b) Schematic of the generation of mice knock-in for the human
420 variable VDJ segments in the endogenous variable heavy chain locus, and for the human
421 variable VJ segments in the endogenous variable light chain kappa locus. (c) Protocol outline.
422 Mice were immunized with LMW proteins according to the represented scheme combined to
423 alum and *Bordetella pertussis* toxin. Four days after the last boost, spleens were collected and
424 hybridoma generated. (d) Sera titers at day 42 of immunized mice for recombinant LMW-
425 RT001, LMW-RT002, LMW-RT014, LMW-RT078, LMW-RT027 measured by ELISA. OD
426 values for several dilutions for mice #1 to #5 are represented. Black curves (-) represent sera
427 titers of a naive mouse.

428

429 **Figure 2: Specificities of anti-LMW mAbs.** ELISA results (OD values 492 nm versus 620
430 nm) against recombinant LMW-RT001, LMW-RT002, LMW-RT014, LMW-RT078 and
431 LMW-RT027 of IgG mAbs at indicated concentrations. Black curves represent isotype
432 controls.

433

434 **Figure 3: Affinities of mAbs for the LMW of five clinical ribotypes.** Dissociation constant
435 (K_D) values measured by BLI. Each dot represents the K_D value of one mAb (mAb name
436 indicated) interacting with one LMW among LMW-RT001, LMW-RT002, LMW-RT014,
437 LMW-RT078 and LMW-RT027. Black bars represent median K_D values of the group of mAbs
438 binding one ribotype.

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440

441 **Figure 4: Binding of mAbs to LMWs expressed at the surface of *C. difficile* bacteria. (a)**
442 *Right:* Flow cytometry analysis of mAbs binding to LMW of indicated *C. difficile* ribotypes.
443 Results are displayed as staining index (*refer to methods section*). *Left:* representative
444 histograms for staining of strain RT078 by mAbs PH4, RA11, SC6 and QE2 are shown. **(b)**
445 Growth of *C. difficile* strain RT027 in BHISG medium incubated with indicated anti-LMW027
446 mAb or with an unspecific IgG (isotype). Growth was followed continuously over 24h. Each
447 dot represents the mean of three technical replicates, and the bars indicate standard deviations.
448 ns: non-significant.

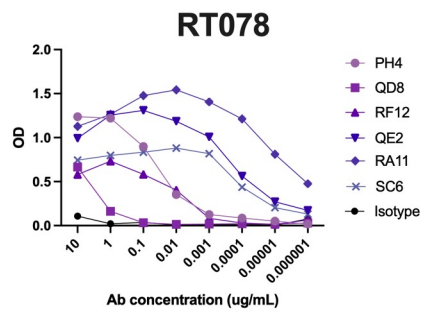
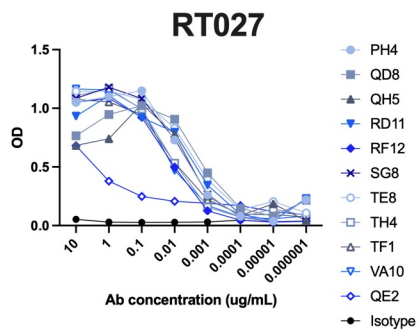
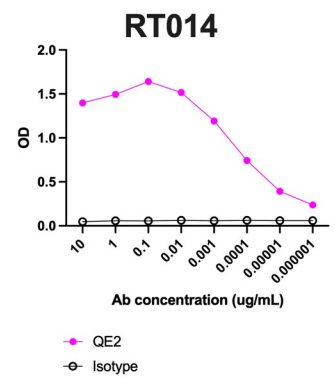
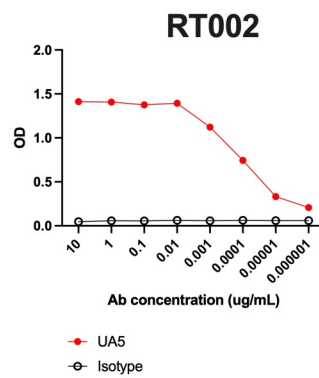
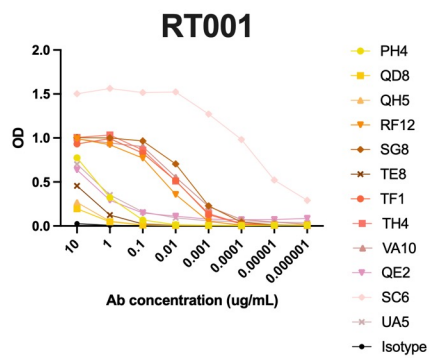
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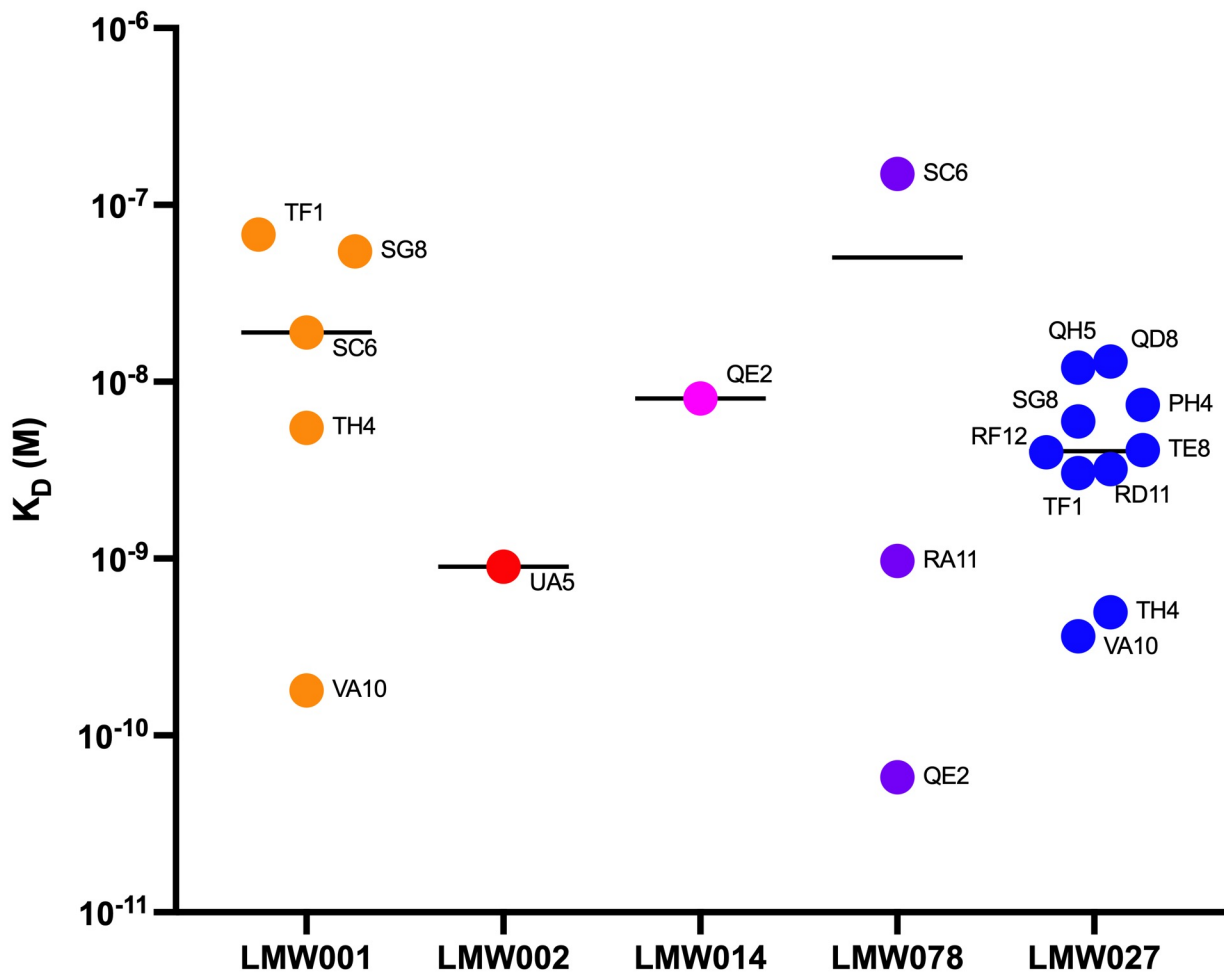
450 **Table 1: Summary table of mAbs binding profiles to LMW recombinant proteins and**
451 **LMW expressed at the bacterial surface of *C. difficile* bacteria for five clinical ribotypes.**
452 E indicates binding by ELISA and F binding by flow cytometry. Blanks indicate absence of
453 binding.

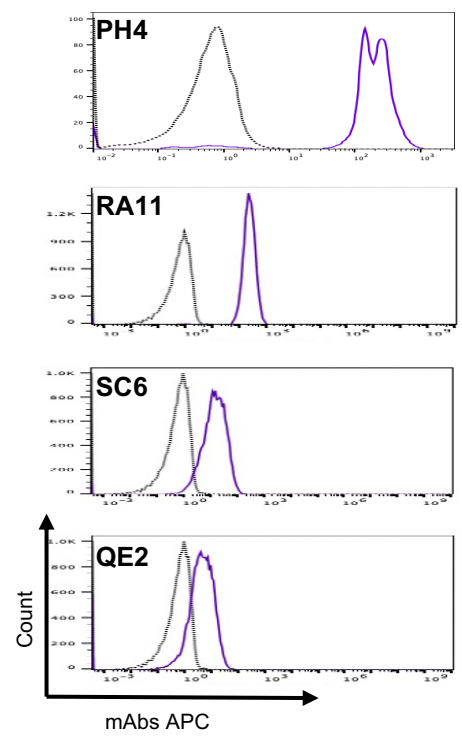
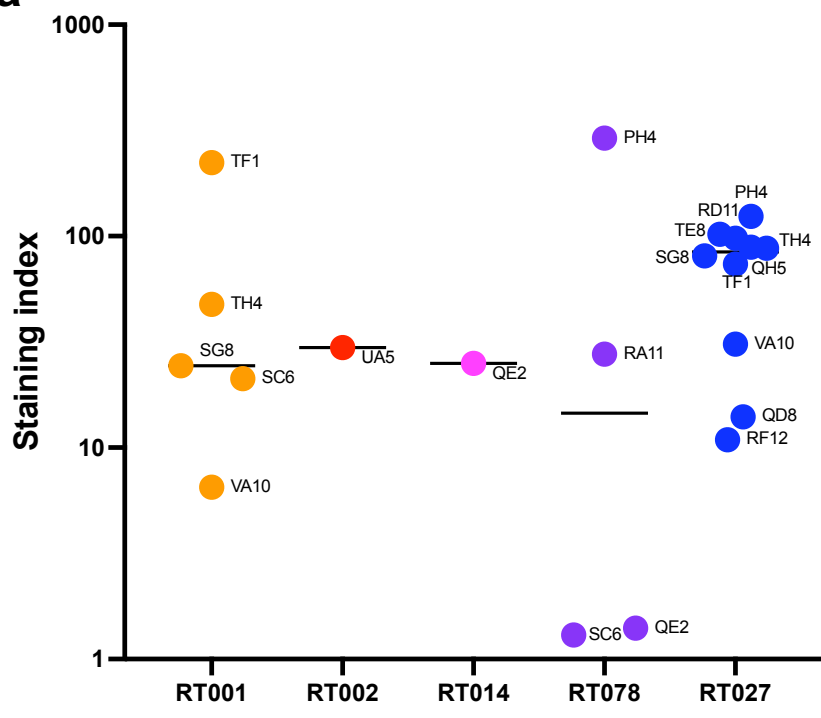
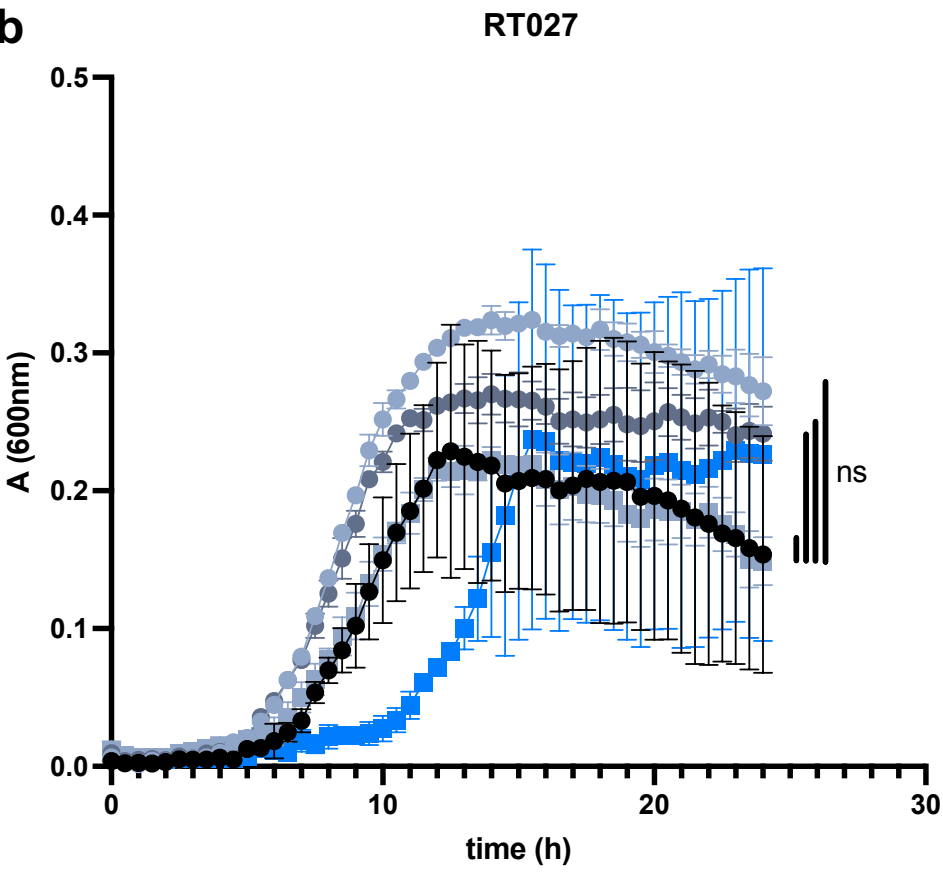
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455 **Figure S1. Comparison of two immunization protocols using recombinant LMWs.** Mice
456 were immunized following two different protocols termed “similarity” and “frequency”. **(a)** In
457 the “Frequency” protocol, mice are immunized with LMWs in the order of their frequency in
458 current CDI, and boosted with a mix of all five LMWs. In the “Similarity” protocol, mice are
459 immunized with two highly similar LMW the same day, and boosted with a mix of all five
460 LMWs. **(b)** Dose response of sera titers of immunized mice from the protocols depicted in (a)
461 are measured by ELISA against the indicated LMW ribotype. Data are presented as mean values
462 (\pm SD) for each group of mice (n=5). ns: non-significant; *: $p < 0.05$. Black curves represent sera
463 from naive mice prior immunization.

464





a**b**

| Antibody | RT | | | | |
|-----------------|------------|------------|------------|------------|------------|
| | 001 | 002 | 014 | 078 | 027 |
| PH4 | E | | | E/F | E/F |
| QD8 | E | | | E | E/F |
| QH5 | E | | | | E/F |
| RD11 | | | | | E/F |
| RF12 | E | | | E | E/F |
| SG8 | E/F | | | | E/F |
| TE8 | E | | | | E/F |
| TF1 | E/F | | | | E/F |
| TH4 | E/F | | | | E/F |
| VA10 | E/F | | | | E/F |
| QE2 | E | | E/F | E/F | E |
| RA11 | | | | E/F | |
| SC6 | E/F | | | E/F | |
| UA5 | E | E/F | | | |

