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1 **Influence of treatment with neutralizing monoclonal antibodies on the**  
2 **SARS-CoV-2 nasopharyngeal load and quasispecies**

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29 **Short running title:** SARS-CoV-2 evolution after mAbs therapy

30 **ABSTRACT (219 words)**

31 **TEXT (1198 words)**

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33 **Objectives:** We aimed to evaluate the impact of neutralizing monoclonal antibodies (mAbs)  
34 treatment and to determine whether the mAbs selective pressure could facilitate the  
35 proliferation of virus variants with spike protein mutations that might attenuate mAb  
36 effectiveness.

37 **Patients and methods:** We therefore evaluated the impact of mAbs on the nasopharyngeal  
38 (NP) viral load and virus quasispecies of mAb-treated patients using single molecule real time  
39 sequencing (Pacific Biosciences). The mAbs used were: Bamlanivimab alone (4 patients),  
40 Bamlanivimab/Etesevimab (23 patients), and Casirivimab/Imdevimab (5 patients).

41 **Results:** The NP SARS-CoV-2 viral load of mAb-treated patients decreased from 8.2 log<sub>10</sub>  
42 copies/ml before administration to 4.3 log<sub>10</sub> copies/ml 7 days after administration. Five  
43 immunocompromised patients given Bamlanivimab/Etesevimab were found to have mAbs  
44 activity-reducing spike mutations. Two patients harbored SARS-CoV-2 variants with a  
45 Q493R spike mutation 7 days after administration, as did a third patient 14 days after  
46 administration. The fourth patient harbored a variant with a Q493K spike mutation 7 days  
47 post-treatment, and the fifth patient had a variant with a E484K spike mutation on day 21.  
48 The emergence of the spike mutation was accompanied by stabilization or rebound of the NP  
49 viral load in 3/5 patients.

50 **Conclusion:** Two-mAb therapy can drive the selection of resistant SARS-CoV-2 variants in  
51 immunocompromised patients. Patients given mAbs should be closely monitored and  
52 measures to limit virus spread reinforced.

53

54 **Keywords:** SARS-CoV-2, neutralizing monoclonal antibodies, quasispecies, COVID-19,  
55 RBD, mutations, spike protein, SMRT sequencing

56 **TEXT (1198 words)**

57 **INTRODUCTION**

58

59 Neutralizing monoclonal antibodies (mAbs) are promising tools for protecting at-risk  
60 patients from a severe COVID-19 infection. They prevent the virus attaching to human ACE2  
61 receptors and entering cells by targeting the receptor-binding domain (RBD) of the virus  
62 spike-protein [1]. The mAbs available in France were Bamlanivimab (LY-CoV555) until  
63 March 2021, then combinations of Bamlanivimab/Etesevimab (LYCoV016), and  
64 Casirivimab/Imdevimab (REGEN-COV) [2,3]. New variants containing key changes in the  
65 RBD have recently appeared that can be more transmissible, more pathogenic, and resistant to  
66 endogenous or exogenous antibodies, than the original virus [4,5]. The full spectrum of key  
67 spike mutations associated with resistance to mAbs is not yet established, but mutations  
68 K417N, E484D/K/Q, Q493R/K and S494P seem to be involved in virus escape and resistance  
69 to mAbs [6–8]. It is not clear how frequently these mutations occur in mAbs-treated-patients  
70 or how they influence virus clearance.

71 We evaluated the impact of neutralizing mAb therapy on the nasopharyngeal viral  
72 load and the diversity of the virus genome encoding the spike protein by single-molecule real-  
73 time (SMRT) sequencing.

74

75 **METHODS**

76

77 Nasopharyngeal samples (NPs) were taken from infected SARS-CoV-2 patients not requiring  
78 oxygen who were treated with neutralizing mAbs at the Toulouse-University-Hospital. These  
79 patients were immunosuppressed, aged >80 years, or had a combination of risk-factors for  
80 severe COVID-19. Bamlanivimab (700mg) was used from 27 February to 15 March, 2021,  
81 and Bamlanivimab/Etesevimab (700mg/1400mg) or Casirivimab/Imdevimab  
82 (1200mg/1200mg) from 16 March to 20 May, 2021. NPs were collected before treatment  
83 (Day 0), 7 days after infusion (Day 7), and weekly until the viral load reached the 31 cycle-  
84 threshold (Ct). The controls for solid-organ-transplant (SOT) patients were an historical  
85 control group of untreated SARS-CoV-2-infected SOT patients.

86 NP SARS-CoV-2 RNA was extracted with MGI Easy Nucleic Acid Extraction kits (MGI,  
87 Shenzhen, China) and quantified using the Ct values obtained with the TaqPath COVID-19  
88 RT-PCR assay (Thermo Fisher Scientific, Waltham, MA) and digital-droplet-RT-PCR  
89 (BioRad, Hercules, CA). SARS-CoV-2 RNA from NPs with N-gene values of <25Ct was  
90 amplified and sequenced (PacBio SMRT; Pacific BioSciences, Menlo Park, CA)  
91 (Supplementary material). Haplotypes were aligned on the reference genome (NC\_045512.2)  
92 to detect mutations associated with reduced mAb activity [6,7].

93 Changes in the NP viral load of treated patients were compared using the Wilcoxon matched-  
94 pairs signed rank test. Differences between the viral loads of patients and controls were  
95 compared using the Mann-Whitney U-test (GraphPad Prism 8.0; GraphPad Software, San  
96 Diego, CA). These analyses were part of the national SARS-CoV-2 surveillance. French law  
97 (CSP Art.L1121-1.1) does not require institutional review board approval for anonymous  
98 retrospective studies.

## 99 **RESULTS**

### 100 **Patient characteristics**

101 32 SARS-CoV-2-infected patients were treated with neutralizing mAbs at the  
102 Toulouse-University-Hospital (average age: 69 years; range: 23-95; 56% men). The 17/32  
103 who were immunocompromised including 11/17 SOT patients (Table S1). Most patients (31;  
104 97%) harbored the B.1.1.7 variant; one had the B.1, clade 20A. Four patients were given  
105 Bamlanivimab, 23 were given Bamlanivimab/Etesevimab, and 5 were given  
106 Casirivimab/Imdevimab.

107

### 108 **Changes in NP viral load after mAb administration**

109 The RT-PCR N-gene values became greater than 31Ct a median of 21 days after  
110 treatment (range: 7-28 days). The median SARS-CoV-2 viral load of mAb-treated patients  
111 decreased from 8.2 log<sub>10</sub>copies/ml [IQR: 7.1-9.0] on day 0 to 4.3 log<sub>10</sub>copies/ml [IQR: 3.4-  
112 5.2] on day 7 ( $p<0.001$ ) (Figure 1A). The viral loads of all three mAb groups decreased  
113 similarly: by 3.65 log<sub>10</sub>copies/ml [IQR: 1.53-6.30] for Bamlanivimab patients, 3.67  
114 log<sub>10</sub>copies/ml [IQR: 2.40-4.90] for Bamlanivimab/Etesevimab patients, and 3.60  
115 log<sub>10</sub>copies/ml [IQR: 2.95-5.15] for Casirivimab/Imdevimab patients (Figure 1B).

116 We compared the decreases in viral load of the 11 treated SOT-patients and 10 untreated  
117 SOT-patients to determine the antiviral effect of mAb therapy in a homogeneous group. The  
118 median decreases in the NP viral load were: 3.63 log<sub>10</sub>copies/ml [IQR: 2.85-4.91] for treated  
119 patients and 2.47 log<sub>10</sub>copies/ml [IQR: 2.14-3.31] for controls ( $p=0.03$ ) (Figure S1).

120

### 121 **SARS-CoV-2 quasispecies evolution after mAbs administration**

122 We followed-up with spike-sequencing 23 (78%) mAb-treated patients. We detected  
123 no key mutation associated with reduced mAb activity in treated patients on day 0 (Table S2).

124 However, several spike-haplotypes appeared over time in 2 (50%) Bamlanivimab-treated  
125 patients, 5 (31%) Bamlanivimab/Etesevimab-treated patients and one (33%)  
126 Casirivimab/Imdevimab-treated patient (Table S2). SARS-CoV-2 variants with mAb activity-  
127 reducing spike protein mutation appeared in five (31%) Bamlanivimab/Etesevimab-treated  
128 patients, all of whom were SOT-patients. A variant with the Q493R spike mutation was first  
129 detected in Patient#1 and Patient#2 on day 7 and in Patient#3 on day 14. The Q493K spike  
130 mutation was detected in Patient#4 on day 7 and a variant with the E484K spike mutation was  
131 detected in Patient#5 on day 21. The SARS-CoV-2 viral loads of these patients decreased  
132 over time, but the viral loads of Patient#3 and Patient#5 rebounded when the mutation was  
133 first detected; the load of Patient#1 first stabilized and then decreased (Figure 2).



134 **DISCUSSION**

135

136           The impact of neutralizing anti-SARS-CoV-2 mAbs on the development of resistant  
137 variants is still unclear. Our analysis of the SARS-CoV-2 spike protein evolution in infected  
138 patients treated with mAbs indicated that key mAb activity-reducing mutations (Q493R/K,  
139 E484K) appeared in 5 SOT-patients treated with Bamlanivimab/Etesevimab.

140           Previous in vitro studies showed that mAbs can induce the production of SARS-CoV-  
141 2 variants with mutation E484K and/or Q493R/K [9–11]. We have demonstrated that  
142 exposure to mAbs in vivo induces the emergence of variants harboring these mutations in the  
143 spike-RBD of immunocompromised-patients 7 to 21 days after Bamlanivimab/Etesevimab  
144 treatment. The Q493R mutation has also been reported in one patient with  
145 cholangiocarcinoma [12].

146           A clinical study of Bamlanivimab and Bamlanivimab/Etesevimab (2800mg/2800mg)  
147 treatment found that new spike variants emerged in 11% of Bamlanivimab/Etesevimab-  
148 treated patients [13]. However, this study only looked for mutations E484K/Q, F490S and  
149 S494P. We found that a spike mutation in position 493 was selected in four mAbs-treated  
150 patients. The high proportion of patients who developed key mutations could be due to the  
151 lower dose of Bamlanivimab/Etesevimab (700mg/1400mg) used or to patient characteristics.  
152 Key mutations emerged in five of our mAb-treated SOT patients, suggesting that  
153 immunosuppression could restrict virus elimination, enhancing the risk of virus mutation  
154 under mAbs. Published clinical studies of Casirivimab/Imdevimab treatment have not looked  
155 for new treatment-induced variants [14] and we found no new key mutations in our  
156 Casirivimab/Imdevimab patients.

157

158           The PacBio SMRT system has been invaluable for analyzing virus diversity, as it  
159 provides all the haplotypes, enabling us to detect all variants, even minor ones. This is the  
160 first time this approach has been used to evaluate the impact of neutralizing anti-SARS-CoV-  
161 2 mAbs on a patient's virus population. We tracked the changes in viral load in addition to  
162 monitoring the emergence of new variants. Although we found that mAbs reduced the viral  
163 load of treated patients, this change did not occur in all the patients who harbored key  
164 mutations.

165

166           The limitation of this study is the small number of patients in each group, all of whom  
167 were treated at a single center. However, we have shown that key mutations emerged in a  
168 substantial number of Bamlanivimab/Etesevimab-treated patients. Only five patients were  
169 treated with Casirivimab/Imdevimab and we detected no key mutation, in agreement with a  
170 recent study [15]. While we had no control for all the patient categories, we could compare  
171 the decreases in the viral loads of mAb-treated and untreated SOT-patients.

172           Our findings highlight the need for close virological monitoring of mAbs-treated  
173 patients to limit the spread of SARS-CoV-2 variants.

174 **Footnotes:**

175

176 **Contributions**

177 CV and JI designed the study. GMB, PD, NK; ADB, AD, ZS and LT provided medical care  
178 to the participants and collected NPs; CV and NR collected biological data; NJ processed the  
179 data, CV analyzed the results, prepared the figures and performed statistical analyses; CV and  
180 JI drafted the initial version of the paper. All the authors revised the manuscript and approved  
181 the final version.

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188 and ANRS-MIE (Emergen, Quasicov study)

189

190 **Conflict of interest**

191 The authors declare no conflict of interest.

192

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198 **References**

- 199 [1] Tuccori M, Ferraro S, Convertino I, Cappello E, Valdiserra G, Blandizzi C, et al. Anti-  
200 SARS-CoV-2 neutralizing monoclonal antibodies: clinical pipeline. *MAbs*  
201 2020;12:1854149. <https://doi.org/10.1080/19420862.2020.1854149>.
- 202 [2] US Food Drug and Administration. Fact Sheet For Health Care Providers Emergency  
203 Use Authorization (Eua) Of Bamlanivimab And Etesevimab n.d.:34.
- 204 [3] US Food Drug and Administration. Fact Sheet For Health Care Providers Emergency  
205 Use Authorization (Eua) Of REGEN-COV (Casirivimab and Imdevimab) n.d.
- 206 [4] Harvey WT, Carabelli AM, Jackson B, Gupta RK, Thomson EC, Harrison EM, et al.  
207 SARS-CoV-2 variants, spike mutations and immune escape. *Nat Rev Microbiol* 2021:1–  
208 16. <https://doi.org/10.1038/s41579-021-00573-0>.
- 209 [5] Ju B, Zhang Q, Ge J, Wang R, Sun J, Ge X, et al. Human neutralizing antibodies elicited  
210 by SARS-CoV-2 infection. *Nature* 2020;584:115–9. <https://doi.org/10.1038/s41586-020->  
211 2380-z.
- 212 [6] Wang P, Nair MS, Liu L, Iketani S, Luo Y, Guo Y, et al. Antibody resistance of SARS-  
213 CoV-2 variants B.1.351 and B.1.1.7. *Nature* 2021. <https://doi.org/10.1038/s41586-021->  
214 03398-2.
- 215 [7] Wang P, Casner RG, Nair MS, Wang M, Yu J, Cerutti G, et al. Increased resistance of  
216 SARS-CoV-2 variant P.1 to antibody neutralization. *Cell Host Microbe* 2021;29:747-  
217 751.e4. <https://doi.org/10.1016/j.chom.2021.04.007>.
- 218 [8] Starr TN, Greaney AJ, Dingens AS, Bloom JD. Complete map of SARS-CoV-2 RBD  
219 mutations that escape the monoclonal antibody LY-CoV555 and its cocktail with LY-  
220 CoV016. *Cell Reports Medicine* 2021;2:100255.  
221 <https://doi.org/10.1016/j.xcrm.2021.100255>.

- 222 [9] Baum A, Fulton BO, Wloga E, Copin R, Pascal KE, Russo V, et al. Antibody cocktail to  
223 SARS-CoV-2 spike protein prevents rapid mutational escape seen with individual  
224 antibodies. *Science* 2020;369:1014–8. <https://doi.org/10.1126/science.abd0831>.
- 225 [10] Weisblum Y, Schmidt F, Zhang F, DaSilva J, Poston D, Lorenzi JC, et al. Escape from  
226 neutralizing antibodies by SARS-CoV-2 spike protein variants. *ELife* 2020;9:e61312.  
227 <https://doi.org/10.7554/eLife.61312>.
- 228 [11] Li Q, Nie J, Wu J, Zhang L, Ding R, Wang H, et al. SARS-CoV-2 501Y.V2 variants  
229 lack higher infectivity but do have immune escape. *Cell* 2021;184:2362-2371.e9.  
230 <https://doi.org/10.1016/j.cell.2021.02.042>.
- 231 [12] Focosi D, Novazzi F, Genoni A, Dentali F, Gasperina DD, Baj A, et al. Emergence of  
232 SARS-COV-2 Spike Protein Escape Mutation Q493R after Treatment for COVID-19.  
233 *Emerg Infect Dis* 2021;27. <https://doi.org/10.3201/eid2710.211538>.
- 234 [13] Gottlieb RL, Nirula A, Chen P, Boscia J, Heller B, Morris J, et al. Effect of  
235 Bamlanivimab as Monotherapy or in Combination With Etesevimab on Viral Load in  
236 Patients With Mild to Moderate COVID-19: A Randomized Clinical Trial. *JAMA*  
237 2021;325:632–44. <https://doi.org/10.1001/jama.2021.0202>.
- 238 [14] Weinreich DM, Sivapalasingam S, Norton T, Ali S, Gao H, Bhore R, et al. REGN-  
239 COV2, a Neutralizing Antibody Cocktail, in Outpatients with Covid-19. *N Engl J Med*  
240 2021;384:238–51. <https://doi.org/10.1056/NEJMoa2035002>.
- 241 [15] Copin R, Baum A, Wloga E, Pascal KE, Giordano S, Fulton BO, et al. The monoclonal  
242 antibody combination REGEN-COV protects against SARS-CoV-2 mutational escape in  
243 preclinical and human studies. *Cell* 2021;184:3949-3961.e11.  
244 <https://doi.org/10.1016/j.cell.2021.06.002>.

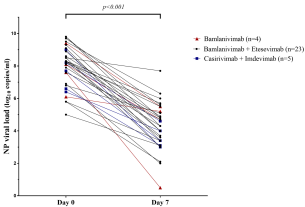
## Figure legends

### Figure 1:

**1.A** Evolution of the viral load in NPs from mAb-treated patients between days 0 and 7. The horizontal black line of the histogram indicates the median of difference (day 7 – day 0). Red: Bamlanivimab alone (n=4), dark grey: Bamlanivimab/Imdevimab (n=23) and blue: Casirivimab/Imdevimab (n=5).

**1.B** Differences in the viral load in NPs from mAb-treated patients between days 0 and 7. The horizontal black line of the histogram indicates the median of difference (day 7 – day 0). Red: Bamlanivimab alone (n=4), dark grey: Bamlanivimab/Etesevimab (n=23) and blue: Casirivimab/Imdevimab (n=5).

**Figure 2:** Changes in NP viral load, detection of spike protein mutations and SARS-CoV-2 genetic diversity in 5 Bamlanivimab/Etesevimab-treated patients. NP samples were analyzed for: clade, spike-protein mutations in the RBM, and percentage of haplotypes detected. Red stars indicate the appearance of key mAb activity-reducing mutations. Red: key mutation, blue: minor mutations.



**Delta NP viral load**  
(log<sub>10</sub> copies/ml)

