

1 mRNA bivalent booster enhances neutralization against  
2 BA.2.75.2 and BQ.1.1

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20 **Abstract**

21 The emergence of the highly divergent SARS-CoV-2 Omicron variant has jeopardized the  
22 efficacy of vaccines based on the ancestral spike. The bivalent COVID-19 mRNA booster  
23 vaccine within the United States is comprised of the ancestral and the Omicron BA.5 spike.  
24 Since its approval and distribution, additional Omicron subvariants have been identified with key  
25 mutations within the spike protein receptor binding domain that are predicted to escape vaccine  
26 sera. Of particular concern is the R346T mutation which has arisen in multiple subvariants,  
27 including BA.2.75.2 and BQ.1.1. Using a live virus neutralization assay, we evaluated serum  
28 samples from individuals who had received either one or two monovalent boosters or the  
29 bivalent booster to determine neutralizing activity against wild-type (WA1/2020) virus and  
30 Omicron subvariants BA.1, BA.5, BA.2.75.2, and BQ.1.1. In the one monovalent booster cohort,  
31 relative to WA1/2020, we observed a reduction in neutralization titers of 9-15-fold against BA.1  
32 and BA.5 and 28-39-fold against BA.2.75.2 and BQ.1.1. In the BA.5-containing bivalent booster  
33 cohort, the neutralizing activity improved against all the Omicron subvariants. Relative to  
34 WA1/2020, we observed a reduction in neutralization titers of 3.7- and 4-fold against BA.1 and  
35 BA.5, respectively, and 11.5- and 21-fold against BA.2.75.2 and BQ.1.1, respectively. These  
36 data suggest that the bivalent mRNA booster vaccine broadens humoral immunity against the  
37 Omicron subvariants.

## 38 Results

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40 The emergence of the highly divergent Omicron variant of SARS-CoV-2 led to concerns about  
41 the efficacy of vaccines based on the ancestral spike, and the approval of bivalent COVID-19  
42 vaccines within the United States (the ancestral spike and the Omicron subvariant BA.5 spike  
43 proteins)<sup>1-4</sup>. Since its approval and distribution, additional subvariants have been identified with  
44 key mutations that further escape vaccine-elicited antibodies and approved monoclonal  
45 antibodies<sup>5</sup>. Of particular concern is the R346T mutation which has arisen in multiple variants of  
46 different lineages, including BA.2.75.2 and BQ.1.1 (**Supplementary Fig. 1**). We tested serum  
47 samples from individuals who had received either one or two monovalent boosters or the  
48 bivalent booster to determine neutralization efficiency against wild-type (WA1/2020) virus and  
49 Omicron subvariants BA.1, BA.5, BA.2.75.2, and BQ.1.1 using a live virus neutralization assay.

50 We used an *in vitro*, live-virus focus neutralization test (FRNT) assay in a VeroE6-TMPRSS2  
51 cell line<sup>1</sup> to compare the neutralizing activity of serum from individuals who received one  
52 monovalent booster (7-28 days after vaccination), two monovalent boosters (70-100 days after  
53 vaccination), or the bivalent booster (16-42 days after vaccination). The fold change in  
54 neutralizing antibody response among these three cohorts were quantitated by comparing the  
55 FRNT<sub>50</sub> GMT (geometric mean titer) values of Omicron against the ancestral SARS-CoV-2  
56 virus. Samples that fell below the limit of detection (1:20) were given an arbitrary FRNT<sub>50</sub> of 10.

57 In all groups, a decrease in neutralization activity was observed against all omicron subvariants  
58 compared to WA1/2020, with the greatest decrease seen against BQ.1.1 (**Fig. 1**). In the one  
59 monovalent booster cohort, the FRNT<sub>50</sub> GMTs were 758 for WA1/2020, 60 for BA.1, 50 for  
60 BA.5, 23 for BA.2.75.2 and 19 for BQ.1.1. In the two monovalent booster cohort, the FRNT<sub>50</sub>  
61 GMTs were 1812 for WA1/2020, 205 for BA.1, 142 for BA.5, 65 for BA.2.75.2 and 53 for BQ.1.1.  
62 In both cohorts, relative to WA1/2020, this corresponded to a reduction in neutralization titers of  
63 9-15 fold against BA.1 and BA.5 and 28-39 fold against BA.2.75.2 and BQ.1.1. BA.2.75 showed  
64 comparable neutralization titers as BA.1 and BA.5 in these cohorts (**Supplemental Fig. 2**).

65 In the BA.5-containing bivalent booster cohort, the neutralizing activity improved against all of  
66 the Omicron subvariants (**Fig 1C**). The FRNT<sub>50</sub> GMTs were 2312 for WA1/2020, 618 for BA.1,  
67 576 for BA.5, 201 for BA.2.75.2 and 112 for BQ.1.1. Relative to WA1/2020, this corresponded to  
68 a reduction in neutralization titers of 4-fold against BA.1 and BA.5 and 11- and 21- fold against  
69 BA.2.75.2 and BQ.1.1, respectively.

70 Individuals that received either one or two monovalent COVID-19 boosters had a dramatic  
71 decrease in neutralization activity against Omicron subvariants compared to WA1/2020. This  
72 decrease was especially profound for BA.2.75.2 and BQ.1.1, which contain the predicted  
73 escape mutation R346T. Individuals that received the BA.5-containing bivalent booster showed  
74 improved neutralizing activity against all Omicron subvariants. These responses are similar to  
75 recent observations in individuals with breakthrough Omicron infection showing broadened  
76 neutralizing activity against Omicron variants<sup>6</sup>. Limitations of this study include small cohort size,  
77 unknown impact of prior SARS-CoV-2 exposure, and examination of a single timepoint. These  
78 data demonstrate an overall serological benefit of bivalent booster immunizations.

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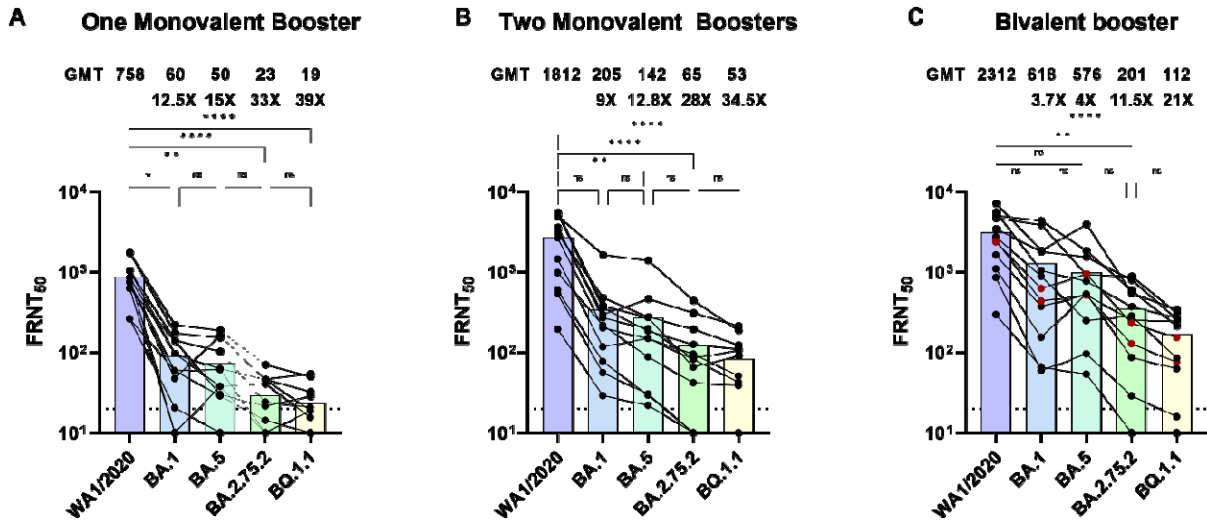
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93 **Figure Legend**

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97 **Figure 1. Neutralizing responses against WA1/2020, BA.1, BA.5, BA.2.75.2, and BQ.1.1.**

98 Shown is the neutralization activity against SARS-CoV-2 variants among 12 individuals who  
99 received one monovalent booster (Panel A), 12 individuals of received two monovalent boosters  
100 (Panel B), and 12 individuals who received the updated bivalent booster (Panel C). The focus  
101 reduction neutralization test (FRNT<sub>50</sub> [the reciprocal dilution of serum that neutralizes 50% of the  
102 input virus]) geometric mean titers for each variant are shown above each panel along with  
103 ratios of GMT compared to WA1/2020. The connecting lines between the variants represent  
104 matched serum samples. The horizontal lines represent the limit of detection of the assay  
105 (FRNT<sub>50</sub> GMT 20). Red symbols in panel C indicate two individuals self-reported prior SARS-  
106 CoV-2 infection. The differences between all groups were determined with the Kruskal–Wallis  
107 test with Dunn’s correction for multiple comparisons. \* p<0.05, \*\* p<0.01, \*\*\*p<0.001, \*\*\*\*  
108 p<0.0001, n.s not significant.

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