

Abstract

Cross reactivity of neutralizing antibodies against SARS-CoV-2 patients by classification of clade

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Variant viruses or mutant viruses are neither new nor unexpected. It is the nature of RNA viruses, such as the SARS CoV-2 coronavirus, to evolve and change over time. In addition to the Coronavirus Disease-19 (COVID-19) virus that was first detected in China, Korea has recorded multiple variants.

The aim of this study was to analyze the characteristics of the neutralization antibody cross-reaction of various COVID-19 variant viruses through an analysis of the neutralization antibody cross-reaction of the COVID-19 non-variant virus. Furthermore, by examining the neutralizing ability of variant viruses, this study aimed to analyze whether the neutralizing ability also acts on different viruses.

Seven clades (S, L, V, GR, G, GH, GV) were isolated. The clades were confirmed through analysis of the sera (i.e., upper respiratory tract tissue samples) of 19 confirmed COVID-19 patients. The sera were analyzed using Real-time RT-PCR and full-length genomic analysis and the cross reactivity of neutralizing antibodies was confirmed using the non-variant viruses of the seven clades.

Among the sera samples, there were 10 cases of S clade, five cases of V clade, and four cases of GH clade identified through a full-length genomic analysis. A plaque reduction neutralization antibody test was performed using seven types of non-variant virus isolates. Results showed that neutralizing antibodies against the same clade virus in one case of V clade serum and one GH genotype serum exhibited more than four times the neutralizing ability against viruses of different clades (i.e., GR, G and GV). Although differences in the neutralizing ability of viruses of the same or different clades were found, this study confirmed that a similar level of neutralizing antibody cross-reactivity was observed in all 19 sera.

In this study, we confirmed the possibility of protecting existing infected people from exposure to the risk of re-infection because the existence of neutralizing antibody cross-reactivity against COVID-19. Nevertheless, we still can't rule out the risk of re-infection completely. Further study need to inform strategies for the development of effective immunotherapies and universal vaccines against emerging variant COVID-19 viruses because of antigenic cross-reactivity is a key scientific question that needs to be addressed.

Keywords: Coronavirus Disease-19 (COVID-19), Whole Genome Sequencing, Cross-reactions of neutralizing antibodies

Table 1. Classification of clade for SARS-CoV-2 (WHO)

Clade	Target genome for classification of clade	Target amino acid for classification of clade	
S clade	ORF8	L84S	
V clade	NS3	G251V	
G clade	S	D614G	
G group	S	D614G	
	GH clade	NS3	Q57H
	GR clade	S	D614G
	GR clade	N	G204R
GV clade	S	D614G, A222V	
L clade	Genetic correlation with WIV04 strain (Isolate of Wuhan)		

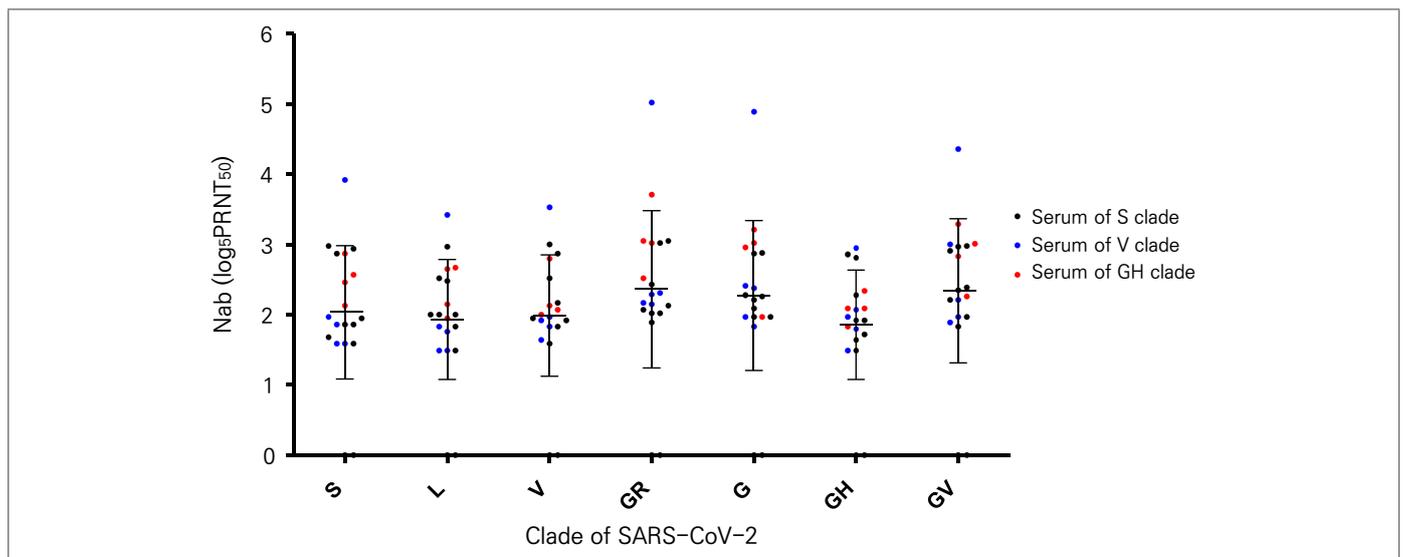


Figure 1. Scatter plot of neutralizing antibody for SARS-CoV-2 by clades