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Original Article

Estimated change of COVID-19 vaccine efficacy due to omicron variant SARS CoV2

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Abstract: COVID-19, an infection caused by SARS CoV2, is a worldwide public health problem at present. Pandemic of this respiratory viral infection has occurred since 2020. Recently, in late 2021, the new variant of SARS CoV2, omicron, was reported from Africa and already cause problems in many countries. Regarding omicron variant, there are many mutations within the molecule of SARS CoV2. The effect of molecular change is unknown and the study on its clinical impact is interesting. An important possible clinical impact of the mutation in omicron is a change of COVID-19 vaccine efficacy. Herein, we used a clinical mathematical model to assess the effect of mutations in omicron variants on vaccine efficacy. Compared to classical SARS CoV2, the omicron form has a large estimated decrease, believed to be roughly 12 times normal. Therefore, it is necessary to find out a new effective vaccine for controlling of the new omicron variant.

Keywords: Omicron, variant, COVID-19, vaccine, efficacy

Introduction

COVID-19, an infection caused by SARS CoV2, is a worldwide public health problem at present. Since its first appearance in China in 2019, the disease has spread to other regions in Asia and finally caused worldwide pandemic [1]. Until present, December 2021, the outbreak is still not resolved and there is still no effective antiviral therapy for COVID-19 [2]. For disease prevention, COVID-19 vaccine is currently available, but it cannot completely prevent the infection and vaccine ineffectiveness is still possible.

An important possible cause of unsuccessful control of COVID-19 by vaccine is the emergence of a variant of SARS CoV2 [3]. The new SARS CoV2 variant, omicron, was reported from Africa in late 2021 and is already causing problems in many countries [4]. A rapid spreading of the omicron is observed and it is expected that omicron variant will be the next main type of COVID-19 in year 2022 [5]. Regarding omicron variant, there are many mutations within the molecule of SARS CoV2. Reported mutations include "A67V, T95I, G142D, L212I, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K and L981F". The effect of molecular change is unknown and the study on its clinical impact is interesting. An important possible clinical impact of the mutation in omicron is a change of COVID-19 vaccine efficacy. Here, we performed a study to assess the effect of mutations in omicron variants on vaccine efficacy using a clinical mathematical model.

Materials and methods

Bioinformatics mathematical model study

The present study is a bioinformatics mathematical model study. For model development, the primary concept is a mutation in viral molecule can cause a change of molecular weight and the molecular weight can affect molecular reaction with the vaccine. The data for clinical mathematical modeling are based on a recent report that showed a reduction rate of vaccine efficacy resulted from mutation. According to that referencing report [6], a L452R mutation leads to a reduced 43 kDa molecular change which corresponds to 41% decreased vaccine efficacy [6]. Therefore, reduction rate per Kda decrease of molecular weight is equal to 1.04%. Hence, estimated change of vaccine efficacy for omicron variant can be estimated by on the mentioned reduction rate. First, the basic quantum calculation was used to determine the molecular weight of the naïve and omicron variant SARS CoV2. The magnitude of change of the molecular weight was calculated based on this equation change of molecular weight = derived molecular weight for omicron variant SARS CoV2 - derived molecular weight of naïve SARS CoV2. By applying direct variation assumption and the rule of three, the final change of efficacy of vaccine was calculated. Regarding change of molecular weight, the change was calculated by quantum calculation according to the method described in previous studies [7, 8].

Statistical analysis

The basic arithmetical calculation was used in the clinical mathematical model this study. A direct comparison of calculated molecular weight between omicron variant and classical SARS CoV2 was done. The degree of change was calculated by direct mathematical subtraction. The main observation outcome of this step is the magnitude of change of molecular weight. Then the estimation of change of efficacy of vaccine was performed based on the rule of three arithmetic model. Then the final change of efficacy of vaccine was derived.

Results

Considering L452R mutation, the derived change of molecular weight change was equal to and corresponding change of COVID-19 vaccine efficacy was equal to -41%. Compared to the naïve molecule, the derived molecular weight of L452R mutation was about 1.55 times higher. Regarding omicron variant, the calculated magnitude of molecular weight change was equal to 3500 kDa. Compared to the naïve molecule, the derived molecular weight of omicron variant was about 45.71 times higher.

Table 1. Reduction in vaccine efficacy due to omicron variant and other important variants of SARS CoV2

SARS CoV2 type	Reduction in vaccine efficacy (%)
Wild	0
L452R mutation [5]	-41
Omicron variant	-1209

Based on comparison with direct variation assumption, the reduction of vaccine efficacy in omicron variant is 29.49 times higher than that of L452R mutation. By applying the rule of three, estimated change of COVID-19 vaccine efficacy is equal to -1209%, as compared to vaccine efficacy of the wild type SARS CoV2 (**Table 1**).

Discussion

As a new emerging viral infection, knowledge of pathogenesis of the new omicron variant of COVID-19 is still unknown. When a new variant of SARS CoV2 emerges, there is an important question of its possible clinical impact. For omicron, it is the new variant firstly observe in Africa and it can cause a rapid disease spreading [2]. Its easy transmissibility leads to a global public health concern. Basically, there are more than 20 mutations in omicron variant. These mutations might result in change of clinical characteristics of infection including vaccine efficacy. In this study, a change of classical COVID-19 vaccine efficacy is studied.

Conceptually, it is believed that mutations in variant might result in change of new COVID-19 vaccine efficacy [6]. An assessment of change of vaccine efficacy due to the omicron variant can give useful data for planning for vaccination against COVID-19. According to this study, the significant change of vaccine efficacy, the estimated reduction about 12 times normal, was observed. In this work, the estimated change of COVID-19 vaccine efficacy was equal to -1209%, which means that there is still some protection, but the level is significantly reduced compared to the level corresponding to the wild type.

An observed reduction of vaccine efficacy might show that there is a possibility of vaccine ineffectiveness and escape phenomenon. This might imply that the vaccine might not help protect delta variant infection in the worst case. Finding for new effective COVID-19 vaccine against the new problematic delta variant is required. Indeed, partly resistance to classical COVID-19 vaccine due to omicron is already proposed [4]. Vaccine inefficacy in management of mutant SARS CoV2 is a new global public health issue. For the new variant, omicron, it is the current question on the effect of the genetic change in response to standard COVID-19 vaccines [9-13]. With a proof for possible effects on vaccine efficacy, a new development of new effective vaccine against new emerging variants of SARS CoV2 is necessary [14].

In the present investigation, the authors used a standard bioinformatic mathematical model approach for assessing change of vaccine efficacy due to variant. This technique is proven for tracking the effect of the variant. The technique has proven useful for detecting effects of genetic polymorphisms in several clinical disorders [7, 8]. For COVID-19, this technique was also used for evaluating change of transmissibility of the COVID-19 virus variant, VUI-202012/01 in a recent previous report [15]. Finally, it should note that this study is a bioinformatics-based study and there is still no in vitro or in vivo experimental data for confirmation. However, as a preliminary data, it can trigger the necessity for closed monitoring vaccine efficacy and concurrent searching for a new effective vaccine against the omicron variant.

In the authors' view, the change of molecular basic components due to mutations in the molecule of SARS CoV2 can bring the clinical implication. A variant with more mutation points is associated with a more magnitude of molecular change. This change can basically alter the molecular structure. The alteration of binding affinity can be expected. Additionally, the change can directly affect the total molecular weight. Since a molecular interaction between SARS CoV2 and other molecules (receptor protein, antibody, etc.) is a kind of biochemical reaction and follows basic principle of clinical biochemistry reaction, the molecular weight change can directly affect molecular binding energy. The alteration in the molecule omicron variant SARS CoV2 is much and there are many mutated positions, comparing to other previously reported variants of SARS CoV2. Hence, it can significantly alter the clinical response to the antibody. The reduction of vaccine efficacy can be expected. The present fundamental study can give evidence to support the worldwide concern on the observed reduction of COVID-19 vaccine efficacy against omicron variant of SARS CoV2. The result of the present study can give a concordant result with the recent observation that the omicron variant could result in reduced vaccine efficacy up to 16 times or 1600% decreasing [16].

Conclusion

The present preliminary study shows that there is a significant reduction in classical COVID-19 vaccine efficacy against the omicron variant of SARS CoV2. Hence, there will be a problem on using the classical COVID-19 vaccine for control of the new variant. Searching for new vaccine is needed.

Disclosure of conflict of interest

None.

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