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Introduction

Pathogens are the viruses, bacteria and parasites causing outbreaks around the world. Some infectious agents can cause global pandemics,

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people and killed nearly 800 between November, 2002 and September, 2003 [4,5]. SARS I spread to more than 29 countries and regions, with a death rate of 9.6% [5].

On 1 September, 2012, MERS was emerged leading by primary super antigen MERS D614: Ten years later, on 1 September, 2012, middle east respiratory syndrome broke out. e MERS coronavirus was rst recorded in the Kingdom of Saudi Arabia (KSA) in 2012 and later in 2014, 180 cases were detected in two years with a death rate of 43%. e sequence of protein QJX19948 contains the spike protein in wild MERS. is is the second coronavirus outbreak. Compared with the 8,000 cases of SARS I, MERS cases were scattered outbreaks in local areas.

On 12 December, 2019, rst wave of Corona Virus Disease 2019 (COVID-19) was caused pandemic leading by primary superantigen SARS II D614: On 12 December, 2019, 17 years a er the SARS I outbreak, the rst wave of COVID-19 was witnessed, caused by the SARS II D614 primary superantigen [6]. is strain was used as a reference strain. 12 December, 2019, is used as the reference date for the outbreak of the reference strain. SARS II D614 was used as the reference superantigen. e amino acid sequence of the spike protein QHD43416 is in wild SARS II D614, the third coronavirus outbreak.

COVID-19 is a devastating disease that, despite the availability of a vaccine, can still kill those infected. e disease is caused by the SARS II coronavirus, a RNA-positive virus that has been divided into four major pandemic waves (D614, D614G, Delta, and Omicron) [6].

e original strain contains 4 superantigens. ey are the primary superantigen D614, 37 amino acids; the second superantigen N148, 38 amino acids; the tertiary superantigen I358, 41 amino acids; and the quaternary superantigen F718,43 amino acids [7].

On 10 March, 2020, second wave of COVID-19 was caused pandemic leading by sub-primary super antigen SubD614G: However, on 10 March, 2020, during the epidemic, a er 2.9 months of stability, the D614 superantigen did mutate to D614G and became dominant [8], and caused the second wave of SARS II pandemic. e amino acid sequence of protein "7KDK_A" contains mutated SARS II D614G. is is the fourth coronavirus outbreak. e D614G mutation remains within the delta and omicron waves.

In October, 2020 third wave of COVID-19 was caused pandemic leading by secondary super antigen SARS II N148.ID-19 was cac

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23.4 months, and the stability is 23.4 months.

state is x2=0. e regression equation for the stability of super antigen MERS D614 is $y=7.3027x1^2-56.325x1+222.9195x2-139.1754=87.37$ months. On the same day, MERS D614 broke out on 1 September, 2012. X1 and x2 are both internal genetic factors that program MERS D614 to erupt on a speci c date.

e third outbreak corona virus SARS II D614, caused by

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e h outbreak corona virus SARS II N148, in Indian strain, led third wave of SARS II Delta pandemic

e third wave of SARS II was caused by a mutation of SARS II D614G to SARS II N148 or SARS II Delta subtype. Which superantigens will undergo mutations in the next step?.

e SD of SARS II N148 is 26.92, while the SD of SARS II I358 is 31.66. e length of SARS II N148 is 38 amino acids, while the length of SARS II I358 is 41 amino acids. e virus hopes to rst and later mutate the next secondary superantigen, SARS II N148, with the closest but slightly more 0.5((D)-5.9(e)4(l)12(t4 Tw 1.47"e(cien)19(t)-5(i)3(s)5(ts)5(t o)12(r)13(m)5)16(y)ligenengt [11].

e thirdave of SARS II was causd ble tho SARS II N148 or s pirummarypelrantig.5(II,)0.5(t)-6(h)0.6(s)-8(e)-5(co)12(n)4(d)-3(a)9(r)-s in superantigSARS I aaswe mutncatasw18(y 5)-9-3(w)8(e)-5(d t)-6(h)3(

Although the precision of antigens did not predict the prevalence of alpha, beta, and gamma subtypes, the failure of predictions did prove that this prediction was correct. Alpha, beta, and gamma subtypes have not formed the major waves in the world. ese three subtypes all appeared one month before the Delta type, in September 2020. If it is the main subtype, it is di cult to cause a global outbreak of another subtype within a month. ere are no cases of these three subtypes in China. is antigen precision can only predict major infectious disease epidemics and outbreaks.

Superantigens SARS II D614, SARS II D614G, SARS II N148, and SARS II I358 are factors that contribute to immune system escape and increase viral infectivity. e predicted outbreak date for SARS II I358 or SARS Omicron is 23 November, 2021, the same day as the actual outbreak.

e quaternary super antigen

e SD of the super antigen SARS II F718 is 20.69, even less than 25.23. Why hasn't this "rough" antigen mutated? e possible reason may be the distribution of amino acids, as it does not contain any of the largest amino acids, tryptophan (W). If any superantigen does not contain "W", it may not show a trend of rst order mutations.

Excluding potential epidemic candidate strains without "W" amino acids in superantigen is a statistical bias issue, as the absence of the amino acid with the highest molecular weight may interfere with SD calculations. Tryptophan does have its own biochemical functions, one of which is that it can be translated from the "stop codon". According to reports, ymine Guanine Adenine (TGA termination codon) in spirochetes is the termination codon for tryptophan, while in other species, the termination signal [11].

Tryptophan may play an important role in infectivity. is requires further research. At least four superantigens, D614, N148, I358, and F718, have been discovered from the coronavirus. e successive collaboration of these four superantigens has driven the spread of this disease through a precise program. e average prevalence time guided by one superantigen is 9 months, and the total prevalence time guided by four superantigens is 36 months. is is in line with the Chinese saying that the epidemic should not exceed 3 years.

In summary, just like how SARS II D614 mutated into SARS II D614G, then again mutated into SARS II N148 (Delta) subtype, and nally mutated into SARS II I358 (Omicron), it started with a "rough" state and ended with a "precise" state. e goal of evolution is a precise state. For SARS II, the correlation coe cient R between antigen precision and stability is 0.998.

If SARS I and MERS are added to the mathematical model, the correlation coe cient R between antigen precision and stability reaches 1. Some scientists may be skeptical about this based on empirical evidence that the correlation is close to 1 but cannot reach 1. If we ignore cases of epidemic diseases with a correlation coe cient of 1, we may miss a way to discover the truth. We have no reason to ignore it. For the sake of caution, we calculated more than 3 times, with a decimal point accurate to 7, and found that R is really 1. e R of SARS II has reached 0.998. A er adding the data of SARS I, the R reaches 1, and the tting is getting better and better. Logically, it can be inferred that this is correct.

Conclusion

ere are at least four superantigens acting as chain reactions in the epidemic population. In the cases of SARS I, MERS, and SARS

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