




# The Runaway Evolution of SARS-CoV-2 Leading to the Highly Evolved Delta Strain

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## Abstract

In new epidemics after the host shift, the pathogens may experience accelerated evolution driven by novel selective pressures. When the accelerated evolution enters a positive feedback loop with the expanding epidemics, the pathogen's runaway evolution may be triggered. To test this possibility in coronavirus disease 2019 (COVID-19), we analyze the extensive databases and identify five major waves of strains, one replacing the previous one in 2020–2021. The mutations differ entirely between waves and the number of mutations continues to increase, from 3–4 to 21–31. The latest wave in the fall of 2021 is the Delta strain which accrues 31 new mutations to become highly prevalent. Interestingly, these new mutations in Delta strain emerge in multiple stages with each stage driven by 6–12 coding mutations that form a fitness group. In short, the evolution of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from the oldest to the youngest wave, and from the earlier to the later stages of the Delta wave, is a process of acceleration with more and more mutations. The global increase in the viral population size ( $M(t)$ , at time  $t$ ) and the mutation accumulation ( $R(t)$ ) may have indeed triggered the runaway evolution in late 2020, leading to the highly evolved Alpha and then Delta strain. To suppress the pandemic, it is crucial to break the positive feedback loop between  $M(t)$  and  $R(t)$ , neither of which has yet to be effectively dampened by late 2021. New waves after Delta, hence, should not be surprising.

**Key words:** SARS-CoV-2, Delta strain, runaway evolution, positive feedback.

## Introduction

Pathogens that made the jump from animal hosts may immediately experience novel selective pressures and rapid evolution in the human hosts (Parrish et al. 2008; Plowright et al. 2017; Cui et al. 2019; Andersen et al. 2020; Wei et al. 2020; Lytras et al. 2021; Ruan, Wen, He, et al. 2021; Wu et al. 2021; Deng et al. 2022). We now test the hypothesis that severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has experienced accelerated adaptive evolution in 2020–2021. The extensive genomic sequences of SARS-CoV-2 afford evolutionists an unprecedented opportunity to track the evolution in ways unimaginable in the study of any other living organisms. In particular, the data collection covers in real time the entire span of evolution across most geographical regions (Elbe and Buckland-Merrett 2017).

In addition to the host shift, there may be additional forces that could drive the accelerated evolution of SARS-CoV-2. First, the evolution of herd immunity may elicit an arms

race between host and pathogen (Peschel and Sahl 2006; Guo et al. 2020; Kajan et al. 2020; Ruan, Wen, He, et al. 2021). Second, new strains may evolve and compete in the infection of human hosts (Choi et al. 2020; Sashittal et al. 2020; Kemp et al. 2021). Third, with “mutations-begetting-mutations” (Ruan, Wang, Chen, et al. 2020), the mutation rate may increase dramatically, as documented in cancers. Fourth, viral adaptive evolution and viral population size may mutually reinforce each other. For example, the emergence of SARS-CoV-2 variants of concern may be driven by acceleration of evolutionary rate as the spread of infection increases (Tay et al. 2022). There is some evidence for each of these forces. Importantly, in each case, there is a positive feedback loop that would lead to the escalation of the rate of adaptive evolution. We will refer to the escalated adaptive evolution in such a loop “runaway evolution.” In particular, the feedback loop between the viral population size and the rate of adaptive evolution may be most easily tracked.

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In analyzing the very large number (>3 million) of sequenced genomes of modest size (~30 Kb for SARS-CoV-2), we take two complementary approaches, referred to as the infinite-allele and infinite-site model, respectively (Kimura and Crow 1964; Kimura 1969). In the former, one treats each sequence as an allele (i.e., haplotype) and compare the alleles by, for example, constructing their genealogical relationships (Forster et al. 2020; Rambaut et al. 2020; Tang et al. 2020; Ruan, Luo, et al. 2021; Kumar et al. 2021; Tang et al. 2021). This infinite-allele approach, commonly used in studying viral evolution, will be used here in a preliminary probe. For the in-depth analyses, we will use the infinite-site model whereby one examines each variable site across all sequences. The two models, equivalent in dynamics, reveal different aspects of the same evolutionary phenomena. In Part I, we outline the hypothesis of runaway viral evolution in a positive feedback loop. In the Results section (Part II), the genomic data of SARS-CoV-2 are analyzed to test the hypothesis.

## PART I—The Hypothesis of Runaway Viral Evolution

As stated in the Introduction, there are multiple factors that can accelerate the adaptive evolution of SARS-CoV-2. One of the factors that can be most easily formulated is the viral population size at time  $t$ ,  $M(t)$ . Other factors may be no less important, but the  $M(t)$  data are readily available. We shall follow the convention of using only one prevalent strain to represent the virions in each infected host. Hence,  $M(t)$  is assumed to be equivalent to the number of infections at that time. According to the standard theory (Crow and Kimura 1970; Eyre-Walker 2006; Ruan, Wang, Zhang, et al. 2020), the rate of adaptive evolution can be expressed as

$$R(t) = M(t)uf, \quad (1)$$

where  $u$  is the mutation rate and  $f$  is the fate of the mutation (expressed in probability). The rate of adaptive evolution,  $R(t)$ , is the number of advantageous mutations produced at time  $t$  that will become fixed, or at least become prevalent, in the population.

If all mutations are equal in fitness,  $f = 1/M(t)$ . Thus, the rate of neutral evolution would be  $R(t) = u$  and the rate is independent of the population size. For adaptive mutations,  $f$  is a function of the selective advantage that is often independent of  $M(t)$  (Crow and Kimura 1970; Eyre-Walker 2006; Ruan, Wang, Zhang, et al. 2020). Interestingly, a higher  $R(t)$  means more advantageous mutations that promote infections and increase  $M(t)$ . Therefore,  $R(t)$  and  $M(t)$  would form a positive feedback loop as indicated by arrows of acceleration:

$$R(t) \rightarrow M(t) \text{ and } M(t) \rightarrow R(t). \quad (2)$$

When such feedbacks are in operation,  $M(t)$  would grow like a snowball, leading to out-of-control epidemics.  $M(t) \rightarrow R(t)$  should not be in dispute but the other half, that is,  $R(t) \rightarrow M(t)$ , may not be true for most species. In general, adaptive evolution is not manifested as large population sizes, which are usually environmentally limited. In viral evolution,

however, an increase in  $R(t)$  may be directly translated into a larger population size, given that viral populations can rapidly expand or contract by orders of magnitude.

In this backdrop, we wish to assess the possibility of coronavirus disease 2019 (COVID-19) experiencing accelerated evolution in 2021. Although SARS-CoV-2 seemed to evolve slowly in the early part of 2020, there have been several waves of SARS-CoV-2 strains, including the latest Delta strain. We shall determine the genomic bases of the strains driving these waves.

## PART II—Results

In PART II, we analyze the mutants one site at a time across sequences to reveal the increasing number of new mutations as the epidemics progress. In the last subsection, we return to the haplotype analysis, one sequence a time across sites, to provide an overview of the evolutionary dynamics.

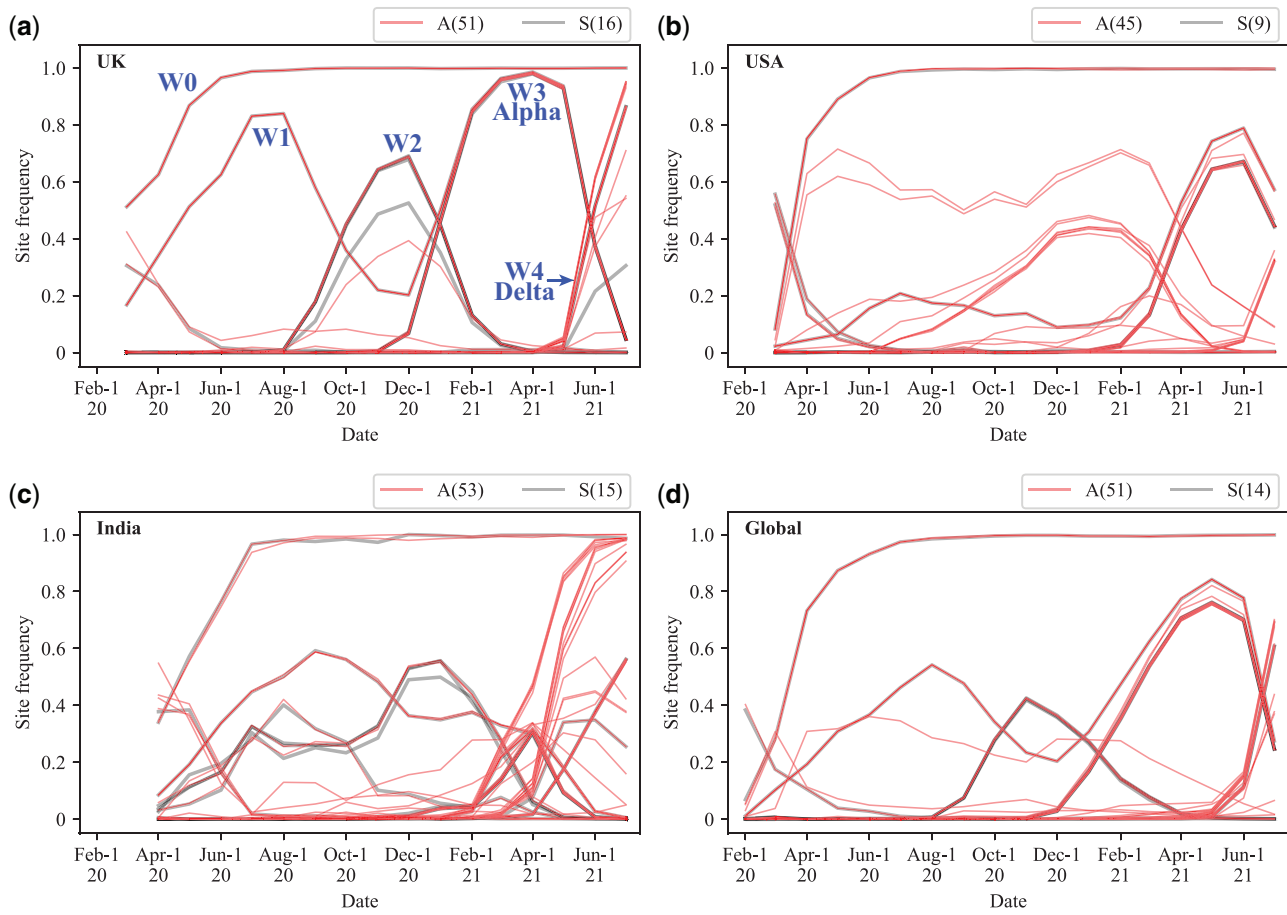
### The Five Waves of SARS-CoV-2 Evolution

To study the rise of new strains, we track variant frequencies site-by-site since such sites can often be connected to functionality (Hou et al. 2020; Korber et al. 2020; Li et al. 2020; Dejnirattisai et al. 2021; Deng et al. 2021; Planas et al. 2021; Plante et al. 2021; Tao et al. 2021; Volz et al. 2021; Zhang et al. 2021). Furthermore, by using the site model, one only needs to track <100 variants sites, instead of more than 1 million sequences. Figure 1 tracks the variants that have reached 0.3 or above in frequency at its peak. In the UK samples (supplementary table 1, Supplementary Material online), 51 nonsynonymous, 16 synonymous, and 5 noncoding variants meet the criteria with an A:S:NC ratio of 51:16:5 (A for amino acid (AA) changes, S for synonymous ones, and NC for noncoding ones). These variants emerged in five waves in the UK data, labeled W0 to W4 in figure 1a. The decline of an earlier wave as the next wave ascends is in relative abundance as well as in absolute number, the latter obtained from the total number of infections.

The patterns from the four geographical regions (see supplementary tables 1–4, Supplementary Material online) are comparable but the waves appear more sharply defined in the UK. The mutations associated with each wave are given in Table 1 with each wave having 2, 4, 15, or 26 nonsynonymous changes. Mutations of the same wave may exhibit nearly identical trajectories (as seen in the overlapped darker line in fig. 1) yielding a single haplotype. In a slightly different manner, W2 and W4 are represented by multiple groups of mutations of varying frequencies, and they all rise and fall in concert.

Figure 2a portrays how mutations appear to evolve in concert even though each emerged sequentially. As shown, the abundance of the four mutations, A–D, differs by at most 11% in the end (5,000–5,555). Therefore, the four curves, if displayed as figure 1 does, would overlap almost completely. In the case of W2 and W4, the mutations do differ somewhat in their abundance but all mutations in the same wave still exhibit similar temporal dynamics (see figure 1).

The mutations of W0, which include D614G, are fixed by May of 2020 such that subsequent waves are all built on the



**Fig. 1.** Evolution of SARS-CoV-2 between February 1, 2020 and July 1, 2021 depicted by waves (i.e., successions of “mutation groups”) in UK (a), USA (b), India (c), and Global (d). Sequencing data were obtained from the GISAID database. The frequencies of nonsynonymous mutations (A) and synonymous mutations (S) reaching the frequency cutoff of 0.3 at their peaks are presented. The number of mutations is shown in the parentheses. Although a curve represents the rise and fall of a variant, each observed curve usually represents multiple curves that overlap completely. In COVID-19, there are five waves (W0 to W4). Note that the decline in each wave as the next one rises (between W1 and W2, W2 and W3, or W3 and W4) is true in both relative and absolute abundance.

**Table 1.** Number of Variant Sites Associated with Each of the Five Waves in UK.

Waves	Nonsynonymous (A)	Synonymous (S)	Noncoding (NC)	A:S:NC
W0	2 (C14408T, A23403G)	1 (C3037T)	1 (C241T)	2:1:1
W1	2 (G28881A, G28883C)	1 (G28882A)	0	2:1:0
W2	4 (C21614T, C22227T, C28932T, G29645T)	5 (T445C, C6286T, G21255C, C26801G, C27944T)	1 (G204T)	4:5:1
W3 (Alpha)	15 (see legends) <sup>a</sup>	5 (C913T, C5986T, C14676T, C15279T, T16176C)	1 (C27972T)	15:5:1
W4 (Delta)	26 (see legends) <sup>b</sup>	3 (C8986T, A11332G, T17040C)	2 (G210T, G29742T)	26:3:2

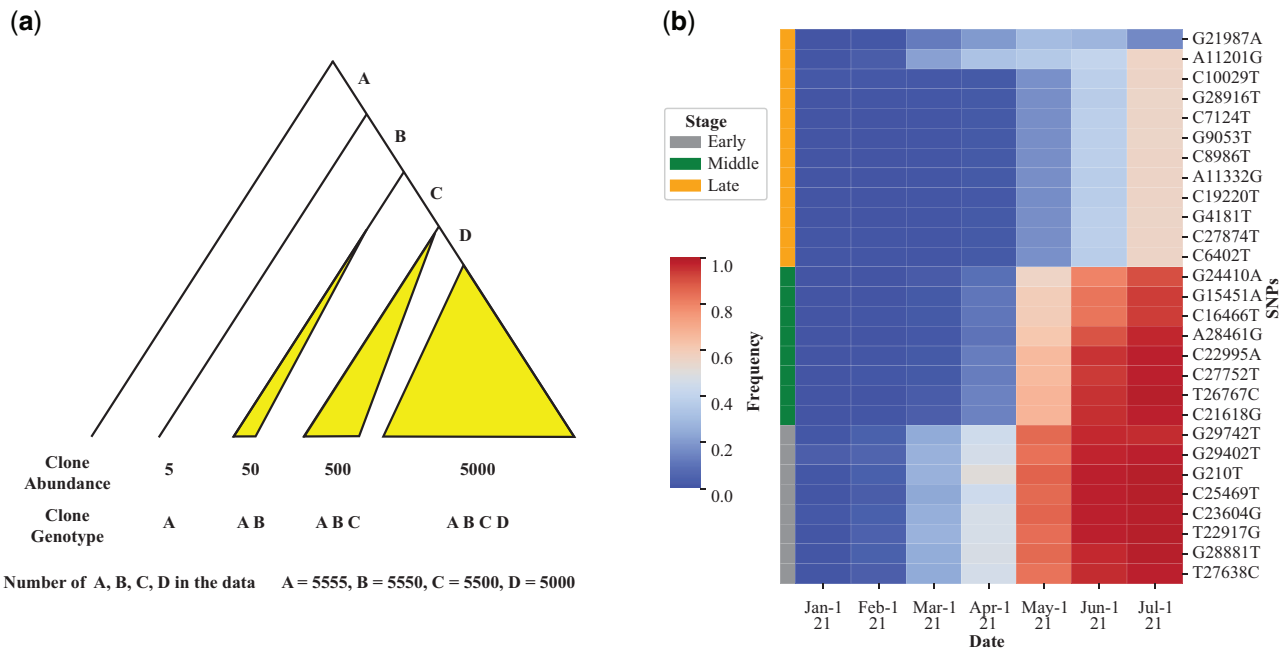
<sup>a</sup>C3267T, C5388A, T6954C, A23063T, C23271A, C23604A, C23709T, T24506G, G24914C, G28048T, A28111G, G28280C, A28281T, T28282A, and C28977T.

<sup>b</sup>G4181T, C6402T, C7124T, C7851T, G9053T, C10029T, A11201G, G15451A, C16466T, C19220T, C21618G, C21846T, G21987A, T22917G, C22995A, C23604G, G24410A, C25469T, T26767C, T27638C, C27752T, C27874T, A28461G, G28881T, G28916T, and G29402T.

strain of W0. The dynamics of the four W0 mutations (A:S:NC = 2:1:1; see Table 1) illuminates the twin-beginnings of COVID-19 as detailed in Ruan, Wen, Hou, et al. (2021). The W0 wave, however, is exceptional. All other strains appear to be driven out by another strain in the next wave. The decline and disappearance of the prevalent strain in later waves can be seen in both the relative and absolute abundance. The continual replacement of one strain by the next one in a series of waves has many implications. An obvious one is that SARS-CoV-2 has become ever more adapted

to human conditions, perhaps in response to humans’ social, behavioral, and immunological changes.

The most significant observation is the genetic changes of the strains. We note in Table 1 that each new wave is associated with more and more mutations. In the first two waves, there are only two AA replacements whereas the number increases to 15 and then 26 replacements in the later Alpha and Delta strains of W3 and W4. In Table 1, the number of AA replacements, a proxy of adaptive evolution rate,  $R(t)$ , has been increasing as the pandemic progresses. In the



**Fig. 2.** The process of mutation accumulation in clusters. (a) An illustration of the principle of mutation accumulation. Each of the four mutations, A–D, is acquired step-by-step but a large fitness gain is realized only when all of them are present. As the four mutations would become highly prevalent nearly concurrently, the trajectories of these mutations in [figure 1](#) would appear to overlap strongly. (b) The actual process of mutation accumulation in the evolution of the Delta strain in India. Each row represents a particular nucleotide site and these mutations fall into three groups, labeled E, M, and L (early, middle, and late, respectively).

remainder of this study, we will focus on the latest Delta strain.

### The Evolution of Delta in the UK

W4 of [figure 1](#) is the Delta strain. The variants associated with W2 in UK and India are listed in [supplementary table 5, Supplementary Material online](#) which reports the monthly trend of variants that exceed 0.3 in their peak frequency. The UK has the most extensive sequences and is geographically confined whereas India is chosen for being the first to report a Delta case ([Cherian et al. 2021](#); [Planas et al. 2021](#); [Singh et al. 2021](#); [Zhang et al. 2021](#)). The Delta strain is defined by the three adjacent AA variants in the Spike protein, L452R, T478K, and P681R ([Singh et al. 2021](#); [Tao et al. 2021](#)). Of course, the Delta strain is far more complicated in its adaptation than the three AAs. The A:S:NC (noncoding) numbers shared between UK and India are 24:2:2 whereas the numbers unique to UK and India are, respectively, 2:1:0 and 4:1:0 ([supplementary table 5, Supplementary Material online](#)). Delta in the UK thus has the 26:3:2 ratio reported in [Table 1](#). Since the neutral A:S ratio is generally about 2.5:1 ([Li et al. 1985](#)), there is a large excess of nonsynonymous changes in the Delta strain, indicating its strong adaptive evolution.

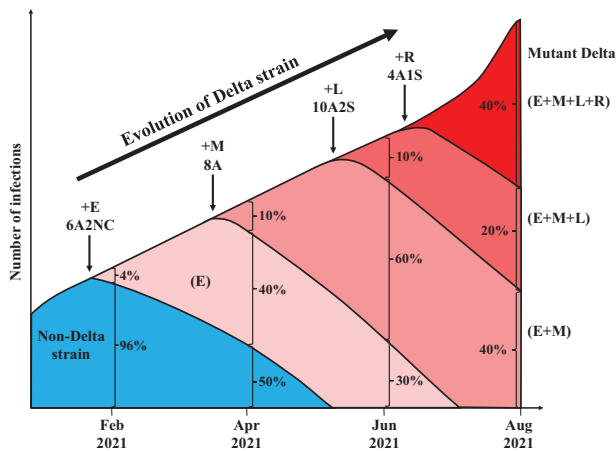
By December of 2020, 20 of the 24 AA mutations can be detected in the UK population, albeit in low frequency ( $\ll 1\%$ ). They remain in low frequency through April of 2021 ([fig. 1a](#)), during the time the Alpha type was the dominant strain. However, by March, all Delta mutations are seen in UK, suggesting that a complete Delta haplotype has been assembled. Very quickly, the complete haplotype reaches  $>1\%$  in May and  $>50\%$  by June and  $>90\%$  in July in UK

([supplementary table 5, Supplementary Material online](#)). In short, partial Delta haplotypes spread slowly but exploded out of the gate as soon as the full set of mutations has been in place, as illustrated in [figure 2a](#). This pattern would give the impression of simultaneous assembly of all mutations in one strain.

### The Multistage Evolution of Delta in India

To know how, where, and when all the Delta mutations are assembled into the mature product, we analyze the viral sequences from India where the first Delta case was reported ([Cherian et al. 2021](#); [Planas et al. 2021](#); [Singh et al. 2021](#); [Tao et al. 2021](#)). In [supplementary table 5, Supplementary Material online](#), the mutations are classified into four groups, E, M, L, and R (for early, middle, late, and recent) with each mutation's frequency in each month listed. The pattern in India is graphically presented by the heatmap of [figure 2b](#) that echoes the hypothetical dynamics of [figure 2a](#).

Mutations of each group share the same evolutionary dynamics as illustrated in [figure 2a and b](#). The E, M, and L groups are the main variants shared between India and UK, whereas the R groups are very recent mutations found only in India or UK. Among the E, M, and L groups, the first detection of variants  $>1\%$  happened in February, March, and April of 2021, respectively. The first time the variants reach 50% is in April, May, and July for the same groups ([fig. 2b](#)). The dynamics of the evolution of Delta in India is portrayed in [figure 3](#). Each of the E, M, and L groups confers a substantial fitness advantage over the previous group. Crucially, each group has six to ten AA changes. In the M group, for example, the A:S ratio is 8:0.



**FIG. 3.** The evolution of the Delta strain in India. The rises (and falls) of five distinct strains are shown in different colors during the evolution of Delta. The light color indicates the non-Delta strains that eventually disappear. The four colors represent the pre-Delta strains (bearing E, E + M, and E + M + L mutations) as well as the latest Delta strain bearing E + M + L + R mutations. Note that each of the pre-Delta or Delta strains must start with a single haplotype bearing all the characteristic mutations; hence, the increase in frequency in the beginning must be very substantial. At each time point indicated, the portrayed strains add up to 100%. The size of the entire viral population increases with time, but the depiction of the total number corresponds only roughly with the trend. The sets of E, M, L, and R mutations are depicted in [figure 2b](#) shown in the figure as 10A2S for ten nonsynonymous and two synonymous mutations in the group. NC is for noncoding mutations.

The advantage of each group (E, M, L, or R) over the previous ones is substantial since the new group must start in one infected person, as shown in [figure 3](#). This single infection has to out-compete the earlier haplotype which could account for up to 60% of the total infections at that time. Within the Delta group in India, there have been four stages of adaptive shift within a period of 8 months. The A:S ratio suggests that at least 20 of the AA changes confer a fitness advantage and the adaptive mutations have been emerging in quicker successions in February to August of 2021. In every respect, the emergence of the Delta strain is a strong indication that COVID-19 has been experiencing accelerated evolution since early 2021.

### In the Very Beginning of the Delta Strain—The Distribution of Mutations among Haplotypes

We have so far shown the gradual assembly of the Delta strain in the population. In this subsection, we examine the individual haplotypes in the very beginning when even partial Delta haplotypes could not be detected in the population.

According to [supplementary table 5, Supplementary Material online](#), the Delta group variants only start to show signs of assembly on October 1, 2020. We now examine the polymorphism data of the 28 sites (E, M, and L group sites) before that day ([fig. 4a](#)). In a sample of 772 sequences collected in India from September 2 to October 1, 2020, 16 of 28 polymorphic sites are singletons (i.e., the variant occurring only once). In most polymorphism data, these rare variants would

be scattered among different sequences. In other words, the assembled haplotypes emerge only when the many needed mutations have become common in the population. However, [figure 4a](#) reveals that a particular haplotype (GISAID: EPI\_ISL\_2461258) has all of the 16 singleton sites. Furthermore, none of these singletons appear in the 657 sequences collected in the previous month ([supplementary table 5, Supplementary Material online](#)).

Patterns of [figure 4a](#) raise the following question. How could one haplotype (#2461258) accumulate so many mutants unique to itself? The peculiar phenomenon is plausible if we consider the sequence diversity within each infected individual. The explanation is illustrated in [figure 4b](#). The #2461258 haplotype is likely present in many individuals, but it is the prevalent haplotype (>50%) in only one individual among the 772 individuals sampled. In all others, the frequency is <50% and, hence, is not registered in the database.

[Figure 4a and b](#) shows that even the partial assembly of the haplotype #2461258 must have been in progress well before October of 2020. Importantly, the haplotype must first exist as a minor allele within infect hosts when it was being assembled. After October 2020, this haplotype would take several more months to become fully assembled. In short, the Delta strain could be as old as the pandemic itself if we consider the age of the first Delta mutation.

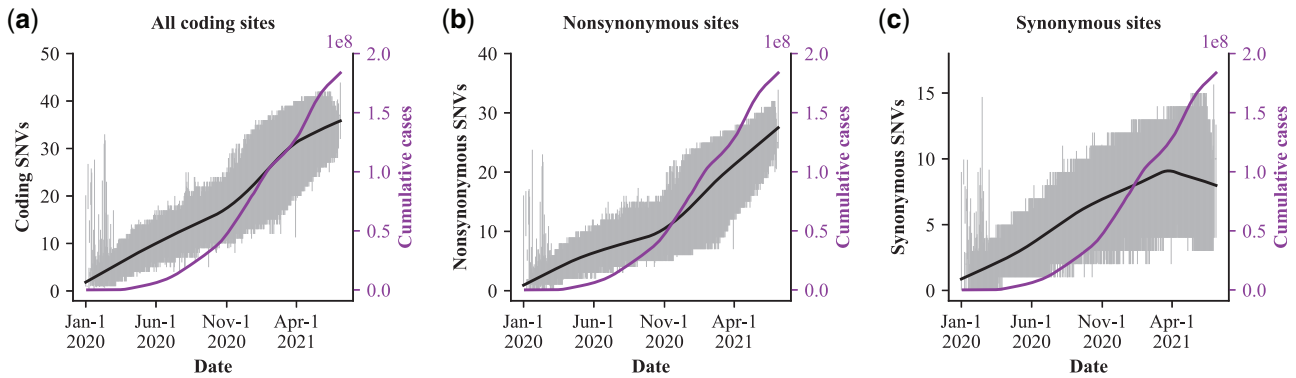
### The Accelerated Evolution of SARS-CoV-2 Corroborated by the Haplotype Analysis

The detailed analyses of [figures 1–4](#) and [table 1](#) show the trend of accelerated evolution in SARS-CoV-2. We compare the  $R(t)$  and  $M(t)$  values from the beginning of the COVID-19 ([fig. 5](#)).  $M(t)$ , the cumulative number of global infections reported by WHO, is shown by the right y-axis in each panel. For  $R(t)$ , we use the rate of nonsynonymous evolution, calibrated by the synonymous changes, as the proxy. The graphs present cumulative numbers; hence the focus should be on the rate of increase, that is, the slope of the curve.

We downloaded 1,853,355 SARS-CoV-2 genome sequences with reliable information on the collection time from GISAID (<https://www.gisaid.org>, as of July 5, 2021). Among them, 97.8% belongs to the L lineage ([Tang et al. 2020, 2021](#)). Hence, almost all the comparisons are between the L strains and the reference genome (Wuhan-Hu-1, GenBank: NC\_045512), also of the L-type. In [figure 5a](#), we plotted the number of SNVs in the coding regions of each strain vis-a-vis the reference genome (y-axis) according to the isolation date of that strain (x-axis).

As pointed out by [Xia \(2021\)](#), the MRCA (most recent common ancestor) of the SARS-CoV-2 strains used in the analysis which would be a more appropriate reference genome ([Xia 2021](#)). This is because, in comparing the evolutionary rate, all sequences should be of equal distance to the reference genome. In particular, if one is interested in estimating the divergence time as in [Xia \(2021\)](#), the MRCA should be the focus. In our case, the focus is on rate comparison whereby the relative rate test (e.g., [Wu and Li 1985](#)) using an outgroup as the reference would be appropriate. According to a recent analysis ([Ruan, Wen, Hou, et al. 2021](#)), the Wuhan-Hu-1 strain is indeed an outgroup for the large number of sequences





**FIG. 5.** The number of Single-Nucleotide Variants (SNVs) accrued in the genomes of SARS-CoV-2 in the last 550 days. The number of SNVs relative to the reference genome of each strain (left y-axis) is plotted against collection date (x-axis). The SNVs are, respectively, from the coding regions (a), nonsynonymous sites (b), and synonymous sites (c). For each date, hundreds or thousands of strains were collected, and the left y-axis shows the average and 95% quantiles (shaded). The right y-axis shows the cumulative number of confirmed COVID-19 cases worldwide (downloaded from the WHO website).

## Discussion

In the mere 25 months, SARS-CoV-2 has been through a rather complex process of evolution with five waves of strains that rise, and often fall subsequently (fig. 1). The emergence of the new Omicron strain, likely the sixth wave, further strengthens the view of SARS-CoV-2 being in the runaway mode of evolution. In figure 1, the number of mutations in each wave increases from 3–4 in the first two, to 10 and then to 21 and 31 in the last two waves of Alpha and Delta strains (Table 1). Most significant is the A:S ratio that increases from approximately 1 in the first 3 waves to 3 and then to 8.7 in the last two. SARS-CoV-2 has indeed been experiencing adaptive evolution in an accelerated pace. This accelerated evolution can be even more clearly discerned in the evolution of the latest Delta strain, which proceeds in 4 stages accruing 6–12 coding mutations with a high A:S ratio in each stage (fig. 3). Although the assembly of mutations must proceed with one mutation at a time, a large fitness gain is realized only when all mutations are present, as illustrated in figure 2.

The main issues are, then, 1) how does the virus accumulate these many mutations, many of which conferring a fitness advantage? 2) Why does the proportion of advantageous mutations keep increasing? In Part I, we suggest runaway evolution via a positive feedback loop. There are indeed a number of forces that can be mutually reinforcing vis-a-vis the process of adaptive evolution. One of them is a growing  $M(t)$  since small fitness gains are much more likely to spread in large populations (see eq. 1). The positive feedback loop is expressed as  $R(t) \rightarrow M(t)$  and  $M(t) \rightarrow R(t)$ , which triggers the runaway evolution.

The indication is that the rate of SARS-CoV-2 evolution,  $R(t)$ , has been accelerating together with the growth of  $M(t)$ . Although  $M(t)$  has been through ups and downs due to human interventions, even highly vaccinated countries have not been able to contain it. We should note that the bidirectional influences of  $R(t) \rightarrow M(t)$  and  $M(t) \rightarrow R(t)$  can only be realized after a time lag. Hence, an exact correspondence between  $R(t)$  and  $M(t)$  is not expected. By permitting  $M(t)$  to become so large, human societies also permit SARS-CoV-2 to

accumulate many mutations. The global failure in minimizing  $M(t)$  in 2020 may be human societies' gravest error in dealing with COVID-19.

The study has many implications. An obvious example pertains to the intense interest in and out of the academia in unraveling the origin of SARS-CoV-2 as if the origin happened suddenly (Ruan, Wen, He, et al. 2021; Wu et al. 2021). In contrast, Dawkins (1986) has famously promoted the Blind Watchmaker argument for the evolution of complex biological traits through a long process of step-by-step evolution (Dawkins 1986). By the same argument, it has been suggested that SARS-CoV-2 must have been through a long process of stepwise adaptive evolution (Wu et al. 2021) with features outlined in a previous model (Ruan, Wen, He, et al. 2021). Even between two strains of the same human host (Alpha vs. Delta), there have been 41 AA changes. Therefore, the host shift from animals to humans may likely require even more changes obtainable step by step and in nature only.

Perhaps, the most profound impacts of SARS-CoV-2 will be on our understanding of biological evolution itself. The study reveals very extensive epistasis, shown in figures 1 and 2 where the fitness effect is realized only when the whole group of mutations is in place. Such strong epistasis has been evident only in interspecific studies. For example, hybrid sterility is due to massive epistasis (Wu and Palopoli 1994; Perez and Wu 1995; Ting et al. 1998; Sun et al. 2004; Wu and Ting 2004). After all, interspecific hybrids carry the genomes from two species, neither of which being deleterious. It has been assumed that individual genic effect may still dominate the evolution within species and epistasis is only gradually built up during species divergence. The evolution shown in figures 1 and 2, however, suggests strong epistasis even within the same populations.

An observation no less surprising is the decline of waves shown in figure 1. (The decline is in absolute numbers as well as in relative abundance.) Advantageous mutations that rise to 80% in the population often decrease to a very low level when the next strain rises. The rises and falls of advantageous mutations would raise questions about the nature of selective

advantage. Theories in evolutionary genetics address this issue include clonal interference (McVean and Charlesworth 2000; Park and Krug 2007), Muller's Ratchet (Muller 1964; Felsenstein 1974), and frequency-dependent selection (Ayala and Campbell 1974). These concepts can be viewed as a subset of the more general Hill–Robertson effect (Hill and Robertson 1966; McVean and Charlesworth 2000; Lu et al. 2006), the essence of which being “the lower the recombination rate, the lower the efficacy of selection.” Since SARS-CoV-2 has been reported to recombine infrequently, Hill–Robertson effect could be an appropriate framework for studying its evolution.

In conclusion, the evolution of SARS-CoV-2 illuminated by the unprecedented amount of genomic data in both space and time will have a long-lasting impact on epidemiology, viral ecology, and molecular evolutionary biology. It may not be farfetched to suspect a conceptual “paradigm shift” (Kuhn 1962) after this pandemic.

## Materials and Methods

### Data Collection and Preprocessing

We download SARS-CoV-2 genomes from the GISAID database (Elbe and Buckland-Merrett 2017) as of July 5, 2021 with the following download options: 1) “complete”: genomes >29,000 nt; 2) “low coverage excel”: exclude viruses with >5% Ns (undefined base). All animal isolate strains were removed and 2,063,459 SARS-CoV-2 genomes were retained. In addition, we filtered out sequences without collection date or with an implausible collection date and retained 1,853,355 genomes for downstream analysis.

### Sequence Alignment, Single Nucleotide Polymorphism Calling and Annotation

We aligned these 1,853,355 genome sequences to the reference sequence (Wuhan-Hu-1 [Wu et al. 2020], GenBank: NC\_045512, GISAID: EPI\_ISL\_402125) using MAFFT (–auto –keeplength; Katoh and Standley 2013). We used snp-sites (–v; Page et al. 2016) to identify single nucleotide polymorphisms (SNPs) and BCFtools (merge –force-samples -O v; Li et al. 2009) to merge the vcf files. Interestingly, although the reference genome size is only 29,903 nt, we found 67,650 SNP sites from these 1,853,355 genome sequences, indicating multiple substitutions at the same sites. We annotated the 67,650 SNP sites by ANNOVAR (Yang and Wang 2015).

### Analysis of SNPs

In this study, we track the variant frequency at each variable site (e.g., C→T). If we set the cutoff by ignoring variants that fail to reach 0.3 in frequency, there are usually fewer than 100 variants to keep track of. To observe the changes in site frequencies in a geographic region, we group the data into bins each covering a 1-month period. Only variants reaching the frequency cutoff of 0.3 at their peaks are retained. For the retained variants, we grouped them by pairwise Pearson coefficients with the cutoff of 0.9 (i.e., if the Pearson coefficient across the time span between two variants is equal or greater

than 0.9, they would belong in the same group). With this cutoff, there are five major waves (fig. 1).

### The Counting of Multiple Hits

Some sites must have mutated independently multiple times among the approximately 1.9 million sequences, given the large number of SNPs (67,650) than the number of sites (29,903). Nevertheless, since each sequence is compared with the same reference genome in figure 5, such multiple hits would be counted multiple times, exactly as their occurrences.

## Supplementary Material

Supplementary data are available at *Molecular Biology and Evolution* online.

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## Data Availability

All genomic data in this study are available, on registration, from GISAID (<https://www.gisaid.org/>).

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