Large-scale analysis of SARS-CoV-2 synonymous mutations reveals the adaptation to the human codon usage during the virus evolution

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Abstract

Many large national and transnational studies have been dedicated to the analysis of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) genome, most of which focused on missense and nonsense mutations. However, approximately 30 per cent of the SARS-CoV-2 variants are synonymous, therefore changing the target codon without affecting the corresponding protein sequence. By performing a large-scale analysis of sequencing data generated from almost 400,000 SARS-CoV-2 samples, we show that silent mutations increasing the similarity of viral codons to the human ones tend to fixate in the viral genome overtime. This indicates that SARS-CoV-2 codon usage is adapting to the human host, likely improving its effectiveness in using the human aminoacyl-tRNA set through the accumulation of deceitfully neutral silent mutations.

One-Sentence Summary. Synonymous SARS-CoV-2 mutations related to the activity of different mutational processes may positively impact viral evolution by increasing its adaptation to the human codon usage.

Key words: viral adaptation; intra-host variants; codon usage; SARS-CoV-2; viral genomics.
This bulk set of mutations is usually discarded during variant analyses, as they are considered functionally irrelevant. However, it is known from decades (Ikemura 1981; Ikemura 1982; Sharp, Tuohy, and Mosurski 1986; Yang and Nielsen 1998; McCarthy, Carrea, and Diambra 2017; Dhindsa et al. 2020) that silent mutations may have a profound impact on protein expression by, i.e. changing the aminoacyl-tRNA molecule responsible for translating the mutated codon into the corresponding amino acid, a well-known process coordinated by the ribosomal machinery. A silent substitution causing a switch to a more abundant aminoacyl-tRNA is prone to increase the overall protein translating efficiency, while the opposite may occur if the tRNA pairing with the mutated codon is less abundant than the original one (Alonso and Diambra 2020; Duret 2020; Kanaya et al. 2001; Comeron 2004; Lavner and Kotlar 2005). Therefore, we hypothesize that synonymous SARS-CoV-2 variants may play a functional role by adapting the sequence of the virus to the codon usage (CU) of the human host, thus improving its effectiveness in using the human aminoacyl-tRNA set, ultimately making the translation of viral particles more efficient (Chen et al. 2020).

Notice that SARS-CoV-2 variants might be classified into minor variants, i.e. detected with a low variant frequency (VF) within a host (i.e. VF < 90 per cent) and fixed variants, i.e. detected with high VF (i.e. VF > 90 per cent). VF profiles can be derived via variant calling from raw sequencing data of viral samples, as proposed, in (Graudenzi et al. 2021; Ramazzotti et al. 2021).

Owing to the complex viral transmission dynamics involving bottlenecks and founder effects (Graudenzi et al. 2021; Ramazzotti et al. 2021), mutations, originating in a small fraction of the virion pool, are fixed overtime only in the presence of positive selection, otherwise, they tend not to fixate in the population.

To investigate the impact of CU adaptation to the SARS-CoV-2 virus evolution, we analyzed a total of 390,899 viral samples and 3,178,178 silent viral mutations identified in almost 200 different studies (see Materials and Methods), showing that:

1. The viral adaptation to the human CU is showing an increasing trend overtime during the pandemic.
2. Mutations with high codon adaptation are preferred and have a higher chance of fixating in the (intra-host) population.

To analyze a possible trend leading to the adaptation of the viral codons to the human CU during the COVID-19 pandemic, we initially analyzed a subset of high-quality samples from North America (Dataset 1, see Materials and Methods). This dataset comprises a total of 213,737 COVID-19 cases, where viral SARS-CoV-2 RNA was sequenced using an Amplicon strategy with high coverage. After alignment of the raw viral data to the SARS-CoV-2-ANC reference genome (Ramazzotti et al. 2021) and variant calling (see Materials and Methods for further details), silent variants were annotated in terms of reference and mutated codon, VF, and sampling time (Supplementary Table S1), with ‘reference codon’ indicating the codon found in the SARS-CoV-2-ANC reference genome and ‘mutated codon’ the one generated by the presence of a single nucleotide variant. The relative codon usage (RCU) adaptation was calculated as the ratio between the human CU of the mutated codon and the human CU of the wild-type counterpart, with values > 1 indicating positive adaptation.

We analyzed the RCU profile of mutated vs wild-type codons in the North America subgroup. Interestingly, we noticed that the APOBEC variants (C > T and G > A mutations) are both consistently associated with a negative value of log2-transformed RCU (see Fig. 1 and Supplementary Figs S1 and S2, median value ~ −0.30), i.e. leading to a reduction in the adaptation to the human CU. As previously shown by our team and others (Woo et al. 2007; Stavrou and Ross 2015; Milewska et al. 2018; Graudenzi et al. 2021), a relevant subset of minor variants, linked to the C > T substitution type, are most likely generated by the activation of the human APOBEC machinery (despite other mutational processes cannot be excluded). APOBEC represents a family of cytidine deaminases playing a critical role in the intrinsic responses of the host to infections operated by a large set of viruses, among which retroviruses, herpesviruses, papillomaviruses, paroviruses, hepatitis B virus, and retrotransposons. APOBEC cytidine deaminases target the viral genome, eventually causing the functional inactivation of the pathogen. Therefore, APOBEC mutations globally represent a defense raised by the host cells to suppress viral infection (Chen et al. 2020).

In Fig. 1, we report the log2-transformed RCU for all the 12 possible mutation classes, i.e. all the possible mutations involving the four bases (Graudenzi et al. 2021). As one can notice, different mutation classes may constitutively show different trends in terms of RCU. As an example, let us consider the variants likely linked to mutations generated by the RNA-specific adenosine deaminase ADAR (even if other mutational processes cannot be excluded) (Graudenzi et al. 2021), which show an opposite behavior compared to the APOBEC ones. ADAR represent one of the other major observed sources of mutations in SARS-CoV-2 genomes and are associated with A > G and T > C mutations (Graudenzi et al. 2021); such variants show a positive trend of adaptation to the human CU with a median value of +0.58 log2-transformed RCU (see Fig. 1 and Supplementary Figs S1 and S2; APOBEC vs ADAR log2-transformed RCU t-test P-value < 0.001), indicating that synonymous mutations related to different mutational processes may lead to very different effects in terms of CU.

A similar pattern was detected in two additional datasets: the first one (Dataset 2, Supplementary Figs S1 and S2) comprising 118,386 samples from the United Kingdom and the second one (Dataset 3, Supplementary Figs S1 and S2) including 58,776 samples from the rest of the world (see Materials and Methods for details). All the analyses corroborated our hypothesis, confirming in these two additional datasets all the results and conclusions discussed above.

Furthermore, these results do not change significantly when the CoCoPUTs human CU reference dataset from the Hive Lab (https://hive.biochemistry.gwu.edu/cuts/about; Athey et al. 2017; Alexaki et al. 2019) is considered for the analyses in place of the classical Kazusa CU reference (https://www.kazusa.or.jp/codon/cgi-bin/showcodon.cgi?species=9606; Nakamura, Gojobori, and Ikemura 2000).

As different mutational processes may lead to different effects in terms of CU, we hypothesized that an RCU less fit to the human translational machinery could cause mutated SARS-CoV-2 genomes to reduce their translation efficiency, therefore undergoing purifying selection. As opposite, the variants leading to a better match with the human CU should undergo positive selection, overcome translational bottlenecks and outcompete wild-type viruses in protein synthesis, and ultimately improve the efficiency of viral packaging. Although a direct demonstration of this hypothesis is challenging, a greater RCU should correspond to increased viral fitness, therefore potentially translating into a greater VF at the global level. To shed light on this phenomenon,
we reasoned that the process of synonymous variants selection over time could be detected in very large time-series analyses. Accordingly, we binned all the silent variants based on their collection date in months intervals and we analyzed the trend of the VF for variants with positive or negative log2-transformed RCU, where positive values indicate an increase in the similarity to the human CU and negative values the opposite. In particular, we first divided the mutations into two groups, i.e. the ones with a negative RCU (among which we have the majority of the APOBEC-associated mutations) and the ones with a positive RCU. We then grouped variants by collection date (months) and analyzed for each of the two groups the presence of any statistical trend over-time of their RCU multiplied by VF, and finally log2-transformed. In line with the original hypothesis, silent variants in the positive CU group (Fig. 2 and Supplementary Figs S3–S7) showed an increase of the log2-transformed VF-weighted RCU over time, significant for all three datasets (one-sided Mann–Kendall test, P-value = 0.004, 0.006, and 0.004 for Dataset 1, Dataset 2, and Dataset 3, respectively), suggesting that CU adaptation might play a significant role in the evolution of SARS-CoV-2 virus. As expected, no increase could be detected for the variants in the negative CU group. In conclusion, the results provided here point to the evidence that CU adaptation may play a role in the dynamics of minor mutations transitioning to fixed, in addition to functional selection.

Furthermore, to provide additional evidence to confirm that codon adaptation is improving when acquiring mutations over the course of the pandemic, we performed two additional analyses for all the three considered datasets:

1) With the aim of evaluating whether, in general, variants leading to better codon adaptation are preferred with respect to the ones not improving CU, we performed the following analysis. We considered the genome position of 100,000 randomly selected mutations (both synonymous and non-synonymous) present in Dataset 1, Dataset 2, and Dataset 3 (e.g. position 150 for variant 150 C>T), tested all the alternative nucleotide substitutions for that position (i.e. 150 C>G and 150 C>A), and checked whether each of such substitutions would lead to the synthesis of the same
protein generated by the original variant (i.e. 150 C>T). This led us to a set of variants where different mutations lead to the synthesis of the same protein. Within this set, we compared the distribution of the CU values obtained with the original variants to the one that would be achieved with the alternative substitutions by performing a standard t-test, which led to a very significant P-value (<0.0001) for all three datasets. When repeating the same analysis with the CoCoPUT’s human CU, the results were confirmed.

2) We first split the timeline covered by the datasets in two subsequent time frames: (i) first half of the timeline (2020/01/01 to 2020/11/30 for Dataset 1; 2020/01/01 to 2020/10/31 for Dataset 2; 2020/01/01 to 2020/12/31 for Dataset 3), (ii) second half of the timeline (until 2021/09/30 for Dataset 1, 2021/07/31 for Dataset 2 and until 2021/11/30 for Dataset 3); we selected the variants displaying a VF >0.90 for the first time in either one of the two time frames (i.e. fixed variants), we finally compared the number of such variants belonging to the APOBEC group. Specifically, we reported: for Dataset 1 41.45 per cent of APOBEC variants in time frame (i) and 11.13 in time frame (ii); for Dataset 2 42.34 per cent of APOBEC variants in time frame (i) and 15.17 in time frame (ii); for Dataset 3 38.71 per cent of APOBEC variants in time frame (i) and 16.19 in time frame (ii). We finally performed a standard z-test to compare the proportions for each timeframe and obtained a highly significant P-value (<0.0001) for all the three datasets, confirming that APOBEC variants (with negative codon adaptation, on average) show a reduced trend of fixation in the population as the pandemic continues, hinting at the evidence that mutations showing negative CU have lower likelihood of transitioning from minor to fixed.

Taken globally, these results suggest that silent mutations may play a role in viral evolution, by increasing the adaptation of the viral genome to the human CU. To this end, it is tempting to speculate that the observed continuous adaptation of its CU overtime may underlie an increase in the overall efficiency of viral protein production and packaging, with viral genomes with a better adaptation being able to generate more viral particles over time, therefore outperforming other, less adapted, viruses. It is widely accepted that improvements in CU adaptation, by removing translation bottlenecks, may contribute to the overall protein synthesis efficiency (Plotkin and Kudla 2011). Indeed, proteins differing only at silent sites can have several orders of magnitude of difference in their expression level (Kudla et al. 2009). This finding has been widely exploited in both research and industry to adapt coding sequences to specific organisms to optimize protein synthesis. Recently, CU optimization was also proposed as an effective strategy to drive high levels of viral protein expression in human cells to stimulate a very robust immune response (Stachyra et al. 2016). Recent studies pointed also to more complex scenarios, where the use of different codons may allow to fine-tune the translation time of individual gene regions, to allow proper folding of complex domains as well as to maximize the occurrence of post-translational modifications (Fu et al. 2016) in this context a very fast translational process is not always an advantage, as in specific conditions pausing the translation machinery may be beneficial for the production of functional, properly folded proteins. Further analyses and very large datasets will be required to identify these specific events, if present.

As the number of available viral sequences is quickly increasing over time, it will be similarly interesting to isolate individual silent variants showing relevant changes in their VF over large time spans to study specific CU adaptation patterns in the context of individual viral genes/proteins. Notably, the effect of codon adaptation could be also directly assessed in terms of viral fitness. By using a reverse genetics approach, in vitro modified viral RNA genomes could be generated carrying progressively more human-adapted genomes. The functional effect of these modifications could be then assessed in terms of increased viral fitness or competition assays. Similarly, the overall level of protein expression could be tested in target cells by using conventional approaches such as western blot and confocal microscopy.

In conclusion, global as well as time-series analyses of silent mutations indicate that CU adaptation may play a relevant role in the evolution of SARS-CoV-2, suggesting that the evolution of the viral genome has been intense. Further studies will be required to thoroughly dissect the overall impact and clinical relevance of these findings. Soon, it will be important to assess if specific viral genomes with a high CU adaptation also show an increased infectiousness and/or clinical aggressiveness, which, at the time being, is very difficult, owing to the limited availability of clinical data in publicly available SARS-CoV-2 sequencing studies. In this regard and given the profound impact of the COVID-19 pandemic, every effort should be made to share clinical information together with sequencing data, which is unfortunately rarely done.

Data availability
All data are available in the main text or the supplementary materials or can be downloaded from the original SARS-CoV-2 sequence repositories.

Supplementary data
Supplementary data is available at Virus Evolution online.

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Author contributions
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