RBD mutations from circulating SARS-CoV-2 strains enhance the structure stability and infectivity of the spike protein

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Running title: RBD mutations enhance the stability and infectivity of SARS-CoV-2

Abstract

A novel zoonotic coronavirus SARS-CoV-2 is associated with the current global pandemic of Coronavirus Disease 2019 (COVID-19). Bats and pangolins are suspected as the reservoir and the intermediate host. The receptor binding domain (RBD) of the SARS-CoV-2 S protein plays the key role in the tight binding to human ACE2 for viral entry. In this study, we analyzed the worldwide RBD mutations and found 10 mutants under high positive selection pressure during the spread. The equilibrium dissociation constant (K_D) of three RBD mutants emerging in Wuhan, Shenzhen, Hong Kong and France were two orders of magnitude lower than the prototype Wuhan-Hu-1 strain due to the stabilization of the beta-sheet scaffold of the RBD. This indicated that the mutated viruses have evolved to acquire remarkably increased infectivity. Five France isolates and one Hong Kong isolate shared the same RBD mutation enhancing the binding affinity, which suggested that they may have originated as a novel sub-lineage. The K_D values for the bat and the pangolin SARS-like CoV RBDs indicated that it would be difficult and unlikely for this bat SARS-like CoV to infect humans; however, the pangolin CoV is potentially infectious to humans with respect to its RBD. These analyses of critical mutations of the RBD provide further insights into the molecular evolution of SARS-CoV-2, presumably while under selection pressure. This enhancement of the SARS-CoV-2 binding affinity to its host receptor ACE2 reveals a higher risk of more severe infections during a sustained pandemic of COVID-19 if no effective precautions are implemented.

Keywords: SARS-CoV-2, ACE2, RBD, spike glycoprotein protein, mutations, infectivity, receptor binding dynamics

Introduction

A novel coronavirus SARS-CoV-2 has caused the outbreaks of Coronavirus Disease 2019 (COVID-19) all over the world since the first appearance in mid-December 2019 in Wuhan, Central China[1–4]. Up to March 11, 2020, SARS-CoV-2 has infected more than 120,000 people world-wide, causing more than 4,600 deaths with the mortality rate of 3.69%[5].

The origin of SARS-CoV-2 remains elusive. However, the initial cases were largely associated with the seafood market, which indicated this were potential zoonotic infections[2]. Although bats and pangolins are most likely the reservoir hosts and the intermediate hosts in the wild, more evidences are in need to support the zoonotic infections and track the origin of this new coronavirus[6–8].

The angiotensin-converting enzyme 2 (ACE2) has been proven to the cellular receptor of SARS-CoV-2, which is the same receptor of SARS-CoV. The spike glycoprotein protein (S) of SARS-CoV-2 recognizes and attaches ACE2 when the viruses infect the cells. S protein consists of a receptor-binding subunit S1 and a membrane-fusion subunit S2. Previous studies revealed that the S1 binds to a receptor on the host cell surface for viral attachment, and S2 fuses the host and viral membranes, allowing viral genomes enter host cells[9–12].

The receptor binding domain (RBD) of the subunit S1 directly interact with ACE2 , while the other part of the S protein do not. This RBD alone is sufficient for tight binding to the peptidase domain of ACE2. Therefore, RBD is the critical determinant of virus-receptor interaction and thus of viral host range, tropism and infectivity[9,13,14].

Meanwhile, S protein participates in antigen recognition expressed on its protein surface, likely to be immunogenic as for carrying both T-cell and B-cell epitopes. The potential antibody binding sites that have been identified indicates RBD has important B-cell epitopes. The main antibody binding site substantially overlaps with RBD, and the antibody binding to this surface is likely to block viral entry into cells[15,16].

The amino acid mutations and recombination in the RBD of different host origin coronaviruses are deemed to be associated with the host adaption and across species infection. Recently research indicates that the recombination and a cleavage site insertion in the RBD may increase the virus infectivity and replication capacity[7]. The RBD sequences of different SARS-CoV-2 viruses spreading in the world are conserved. However, mutations in RBD still appeared, which might relate to the progression of the infectivity of this virus.

To invest whether these mutations in RBD have enhanced or weakened the receptor binding activity and if the viruses is becoming more aggressive and spreading more quickly, we investigated and compared the exact receptor binding dynamics between the SARS-CoV-2 RBDs of all the newly mutated strains and ACE2 of humans as well as their potential hosts such as bats and pangolins.

Materials and methods

Genome sequence dataset in this study

Full-length protein sequences of S protein RBD were downloaded from the NCBI GenBank Database, China 2019 Novel Coronavirus Resource (https://bigd.big.ac.cn/ncov) and GISAID EpiFluTM Database (http://www.GISAID.org). We collected 254 SARS-CoV-2 and SARS-like CoV full genome sequences up to March 8, 2020, and filtered the sequence with mutations in S protein and RBD region. The genome sequences used in dynamics analyses are as follow: SARS-CoV-2 (NC_045512.2, EPI_ISL_407071, EPI_ISL_412028, EPI_ISL_411220, EPI_ISL_411219, EPI_ISL_410720, EPI_ISL_406597, EPI_ISL_406596, EPI_ISL_408511, EPI_ISL_406595, EPI_ISL_413522); Bat SARS-like CoV RaTG13: MN996532; pangolin SARS-like CoV GD 01: EPI_ISL_410721.

Sequences alignment and polymorphism analyses

Alignment of S protein sequences from different sources and comparison of ACE2 proteins among different species were accomplished by MAFFT version 7 online serve with default parameter （https://mafft.cbrc.jp/alignmeloadnt/server/）and Bioedit[17,18]. Polymorphism and divergence were analyzed by DnaSP6 (version 6.12.03)[19]. Analyses were conducted using the Nei-Gojobori model[20]. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in Mega X（version 10.0.2）[21].

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Molecular dynamics simulation

The complex structure of the SARS-CoV-2 S-protein RBD domain and human ACE2 was obtained from Nation Microbiology Data Center (ID: NMDCS0000001) (PDB ID: 6LZG)[9]. Mutated amino acids of the nCoV RBD mutants were directly replaced in the model, and the bat/pangolin CoV RBD domain was modelled using SWISS-MODEL[22]. Molecular dynamics simulation was performed using GROMACS 2019 with the following options and parameters: explicit solvent model, system temperature 37°C, OPLS/AA all-atoms force field, LINCS restraints. With 2fs steps, each simulation was performed 10ns, and each model was simulated 3 times to generate 3 independent trajectory replications. Binding free energy was calculated using MM-PBSA method (software downloaded from GitHub: https://github.com/Jerkwin/gmxtool) with the trajectories after structural equilibrium assessed using RMSD (Root Mean Square Deviation)[23].

Results

The profile of SARS-CoV-2 S protein RBD mapping the mutants

Among the 244 SARS-CoV-2 strains in the public databases with whole genome sequences, only 10 strains contained amino acid mutations in the RBD (details listed in Table S1). These mutants were isolated from multiple locations in the world, including Wuhan, Shenzhen, Hong Kong, England, France and India (Fig. 1A). Nine out of 10 mutants deviate from the firstly reported strain (SARS-COV-2 Wuhan-Hu-1) for only one amino acid, while the Shenzhen-SZTH-004 strain contain two amino acids substitutions (Fig. 1B). Mutation V367F was found in six individual isolates from four adult patients: three in France and one in Hong Kong, China, which suggested that these strains may have originated as a novel sub-lineage.

To be noted, none of the mutations in SARS-CoV-2 mutants were found in the Bat SARS-like

CoV-RaTG013 or in the Pangolin SARS-like CoV-GD-1. This demonstrated that these mutations were not recombinants from the animal-originated virus, at least in the RBD, but rather naturally selected during spreading and circulating among human beings.

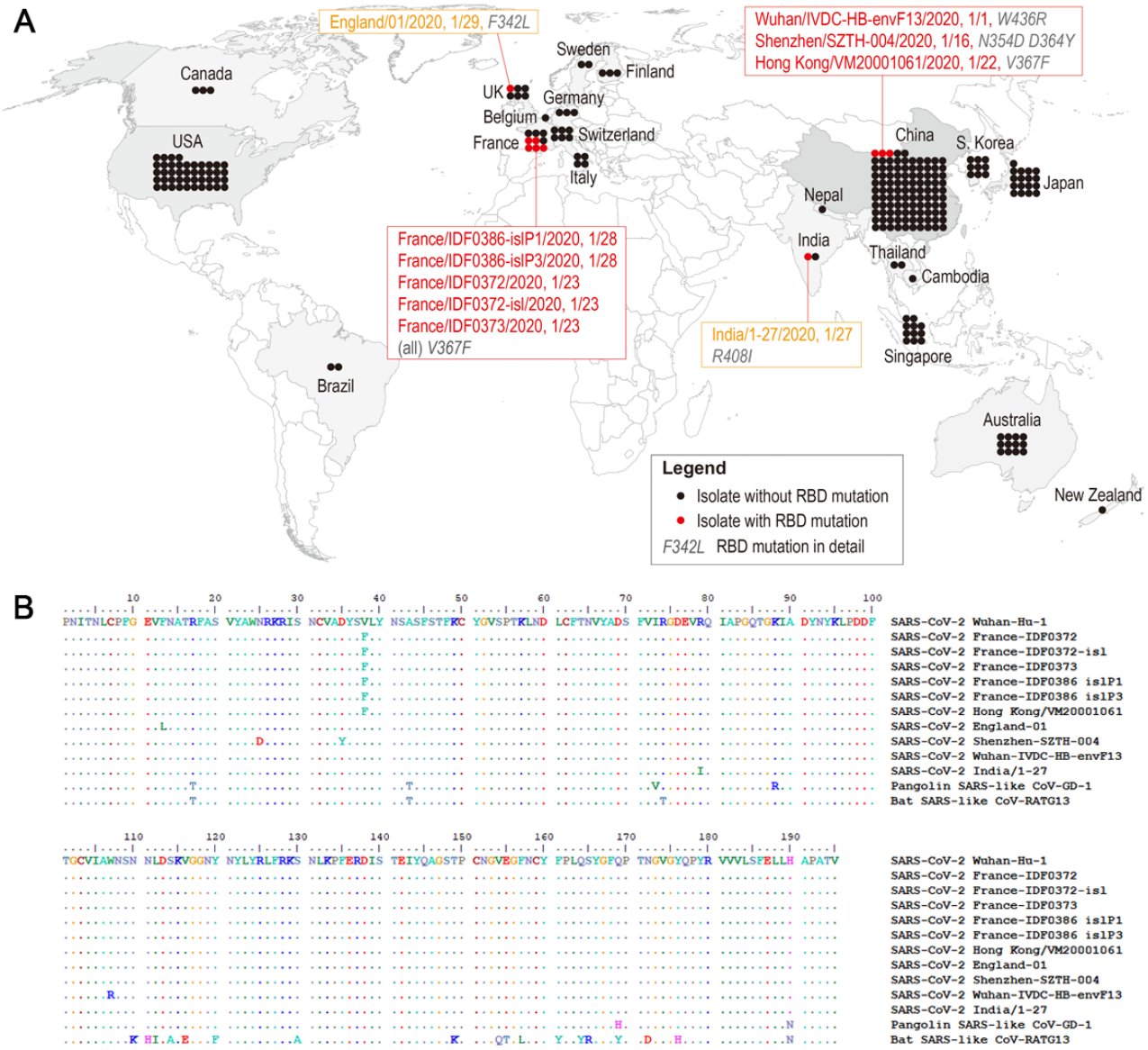

Fig. 1: The SARS-CoV-2 mutated strains in RBD of the S protein. (A) The geographic distribution of the RBD mutated isolates. The strains with names in red are mutants with the enhanced binding affinity. The strains with names in red are mutants with the enhanced binding affinity; The strains with names in yellow are mutants with similar binding affinity. (B) Multiple alignments of the RBD amino acid sequences. SARS-CoV-2 Wuhan-Hu-1, the first isolated strain, is used as reference. The bat and pangolin SARS-like virus are also included. Amino acid substitutions are marked.

Nucleotide diversity indicates strong positive selective pressure in RBD

The protein mutations are originated from the mutated RNA genome sequence, which is the nature of RNA virus. Since RBD is the only domain to bind human ACE2 to initiate the invasion, it is

thought that the RBD should be highly conserved. However, our nucleotide diversity analysis of the entire S gene showed that the RBD domain is as diverse as the other regions of the S protein (Fig. 2). The peak signals for diversity distribute in the entire S protein, and the peak in the RBD also reached the Pi value of ~0.01, higher than more than 90% of the peaks outside of RBD. Since the RBD function is essential for the virus, we hypothesize that the mutation-prone RBD should be selected to maintain or even improve the binding affinity against human ACE2.

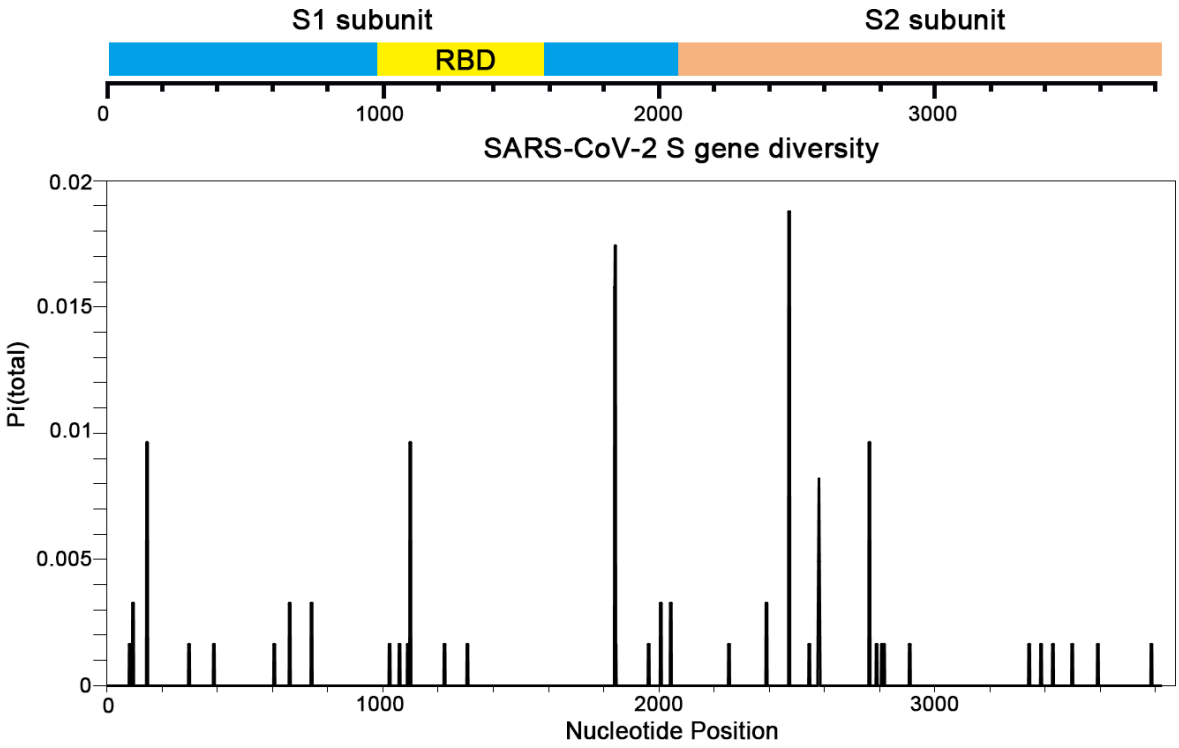

Fig. 2: Polymorphism and divergence graph of SARS-CoV-2 S gene. Structural domains are annotated. The Pi values are calculated with window size: 5 nt, step size: 1.

To further test this hypothesis, we investigated the selective pressures of the S gene by calculating nonsynonymous/synonymous rate ratio (dN/dS ratios) for various segments of the S gene in the 244 SARS-CoV-2 strains. In accordance to our hypothesis, the entire S gene exhibited a dN/dS of 1.9336, remarkably greater than 1, showing that the S gene is under positive selective pressure (Table 1). Surprisingly, the S1 subunit showed a much higher dN/dS value of 7.4971. More strikingly, inside the S1 subunit, no synonymous substitutions were observed in RBD, resulting in a practical infinite dN/dS ratio in this domain. Therefore, RBD is the major contributor of positive selective pressure to the S gene. The extremely high dN/dS value of RBD indicates that very high selective pressure is applied to this functionally essential domain. Therefore, the functional relevance of these mutations can be postulated.

Table.1 Estimates of Average Codon-based Evolutionary Divergence over S gene Pairs

The numbers of nonsynonymous and synonymous differences per sequence from averaging over all sequence pairs are shown. Analyses were conducted using the Nei-Gojobori model. The analysis involved 244 SARS-CoV-2 nucleotide sequences. All positions containing gaps and missing data

were discarded.

Segment	Length (bp)	Mean Non-synonymous substitutions/site	Mean Synonymous substitutions/site	dN/dS
Entire S	3822	0.4250	0.2198	1.9336
S1	2043	0.3062	0.0408	7.4971
S1-RBD	585	0.0892	0.0000	∞
S2	1779	0.1790	0.1188	1.5066

Most mutants bind ACE2 with higher affinity

To estimate the functional alteration caused by the RBD mutations, we performed molecular dynamics simulation for the original SARS-CoV-2 and the RBD mutants to assess their binding energy to human ACE2. Each model was simulated in triple replicates. All trajectories reached plateau of RMSD after 2~5ns (Fig. 3A), indicating that their structure reached an equilibrium. Therefore, all the subsequent computation on thermodynamics was based on the 5~10ns trajectories. Four out of five RBD mutants (except R408I) showed a decreased binding free energy compared to the prototype Wuhan-Hu-1 strain. Three of them (N354D and D364Y, V367F, W436R) exhibited statistical significance, suggesting their significantly increased affinity to human ACE2 (Fig. 3B). The ΔG of these three mutants were all around -200 kJ/mol, ~25% lower than the prototype WH-1 strain. Considering the K_D = 14.7 nM of the prototype RBD, the equilibrium dissociation constant (K_D) of these three mutants are calculated as 0.12 nM for N354D adn D364Y, 0.11 nM for V367F, and 0.13 nM for W436R (Fig. 3C), two orders of magnitude lower than the prototype strain, indicating a remarkably increased infectivity of the mutated viruses.

Only one mutant isolated from Shenzhen possesses dual amino acids mutation (N354D, D364Y). We also made models of single amino acids respectively and performed molecular dynamics simulation to investigate their individual influence to the affinity. The N354D substitution decreased the affinity, while the D364Y single mutation reached even higher affinity than the dual mutant (Fig. 4B). This indicated that the D364Y is the major contributor to the affinity.

In comparison, the bat CoV RaTG13 showed only minor binding free energy to human ACE2, while the pangolin CoV discovered in Guangdong showed remarkable ΔG, but slightly higher than the prototype human SARS-CoV-2 Wuhan-Hu-1 strain. The K_D of the SARS-CoV RBD of bats and pangolins to human ACE2 are estimated as 1.17mM and 1.89μM, respectively (Fig. 3C). Considering that the SARS-CoV RBD binds to human ACE2 at an affinity of K_D = 0.326μM, these data indicated that bat SARS-like CoV RaTG13, which was the closest bat CoV to human SARS-CoV-2, may be hardly infectious to humans. However, the K_D of pangolin CoV is only 5.8 times higher than the SARS-CoV. This indicated that the pangolin CoV is potentially infectious for humans by unprotected close contact with the virus-rich media, such as body fluid of the infected animal. This was consistent with the situation in the seafood market.

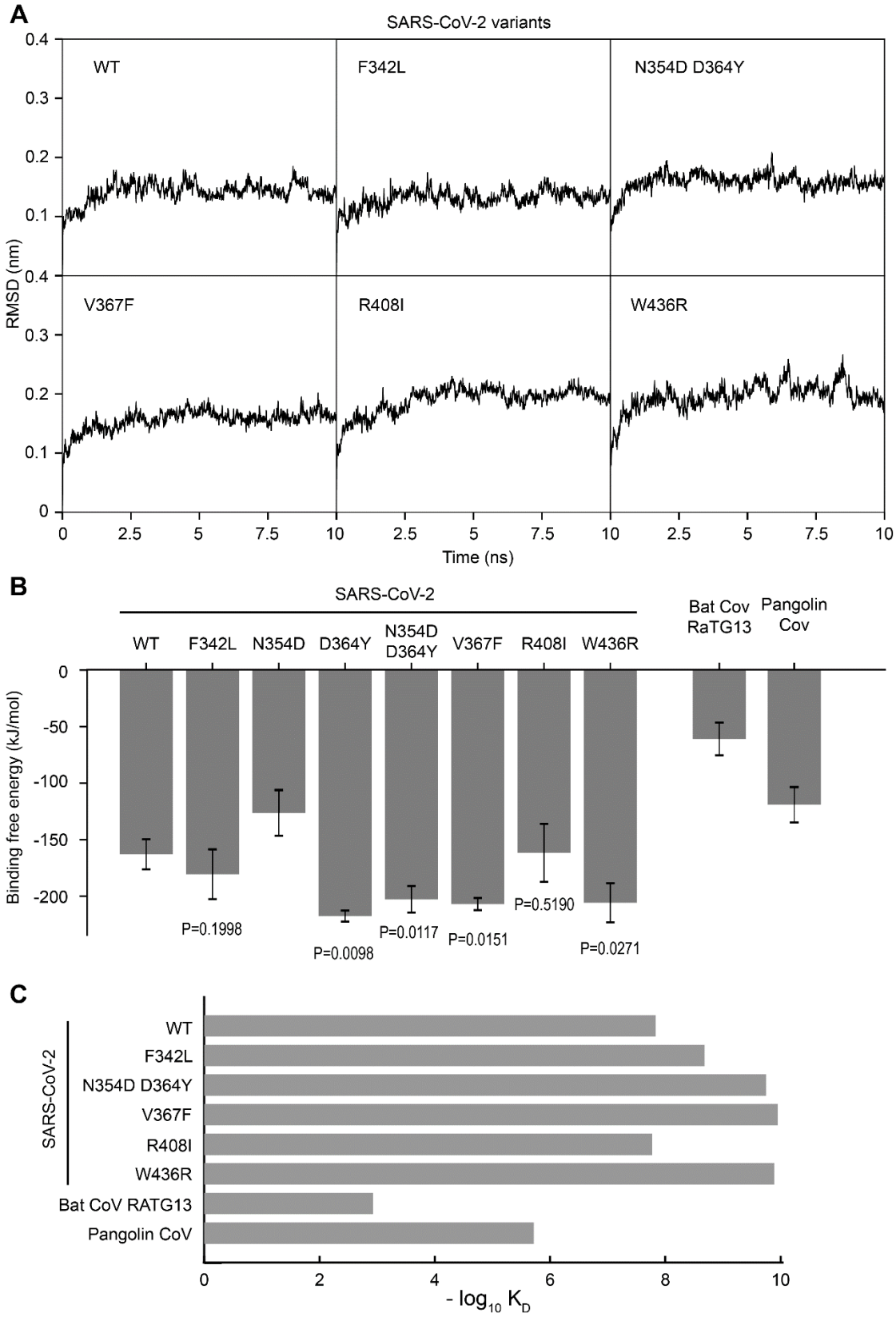

Fig. 3: Binding free energy of the SARS-CoV-2 S-RBD to human ACE2. (A) RMSD of typical MD trajectories of SARS-CoV-2 prototype and mutants. (B) Binding free energy (ΔG) of the RBDs and the human ACE2. Lower ΔG means higher affinity. Data are presented as mean±SD. P-values were calculated using single-tailed student t-test. (C) The equilibrium dissociation constant (K_D)

calculated according to the ΔG.

Structural basis of the increased affinity

To explain the structural basis of the increased affinity, we investigated deeper into the dynamics of the residues of these structures. The 6 mutants were divided into two groups: the “similar affinity” group (F342L, R408I), whose affinity is not significantly increased, and the “higher affinity” group (N354D D364Y, V367F, W436R), whose affinity is significantly increased. We compared the RMSF (Root Mean Square of Fluctuation) of the mutants to the prototype Wuhan-Hu-1 strain (Fig. 4A). The only feature which is exhibited by all three “higher affinity” mutants but not in the “similar affinity” mutants lays in the C-terminal of the RBD domain, namely the amino acids 510-524. The three “higher affinity” mutants showed considerable decrease of the RMSF at this region, but not in the “similar affinity” mutants. Coincidently, the mutated amino acids which caused the affinity increase (D364Y, V367F, W436R) are all located near this fragment, while the mutated amino acids which did not increase the affinity (F342L, N354D, R408I) are away from this fragment (Fig. 4B). This explains the structural influence. Lower fluctuation reflects more rigid structure. The fragment 510-524 is the center of the beta-sheet structure (Fig. 4B, marked as red), which is the center scaffold of the RBD domain. To be noted, the binding surface of the RBD to ACE2 is largely in random-coil conformation, which lacks structural rigidity. In this case, a firm scaffold should be necessary to maintain the conformation of the interaction surface and thus may facilitate the binding affinity.

To test this hypothesis, we analyzed the contribution of each amino acids to the binding free energy. In the binding site region, the insignificant mutant F342L did not show an obvious decrease in ΔG, while the other three mutants exhibited a general decrease of ΔG in this region (Fig. 4C). Although the R408I mutant showed also a general decrease of ΔG in the binding site, the substitution R408I itself caused a remarkable increase of ΔG (Fig. 4C) and thus weakened the affinity. This evidenced the above mentioned hypothesis that the firm scaffold facilitates the binding. In addition, the D364Y and W436R themselves directly contributed to the ΔG decrease. In contrast, the N354D mutation directly elevated the ΔG, which coincides its consequence (Fig. 4B).

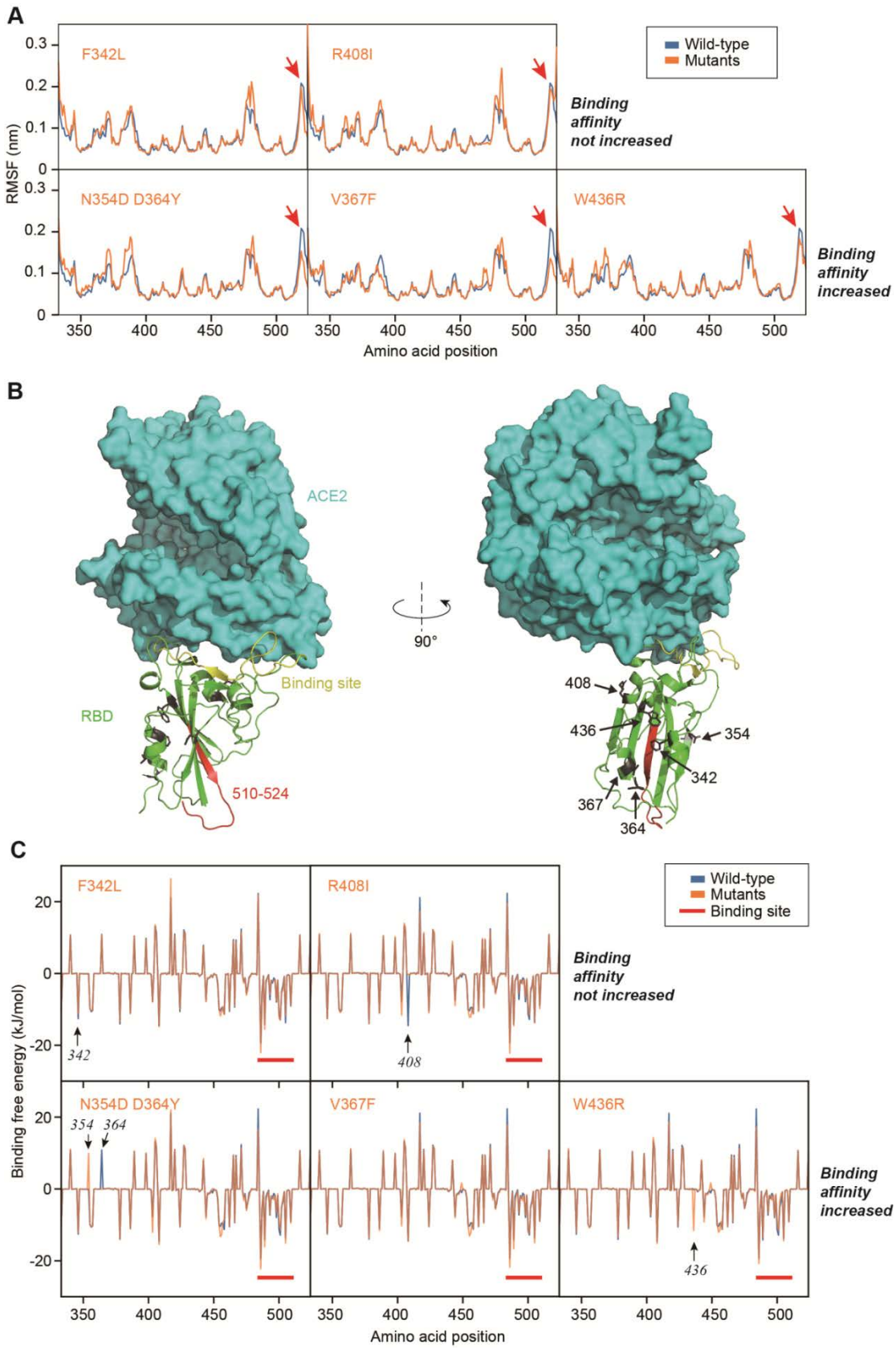

Fig. 4: Structural analysis of RBD mutants on their affinity. (A) RMSF of the 5 mutants compared to the prototype. Red arrows denote the fragment of residues 510-524. (B) Spatial location of the mutated amino acids and the fragment 510-524. (C) Contribution of each amino

acids to the binding free energy. Red bars denote the binding site.

Discussion

Due to the pandemic and constant mutations of the SARS-CoV-2 virus all over the world, the evolution of infectivity is one of the most interested questions by the public. Alterations of infectivity may severely influence the quarantine policies. Our work tried to unravel the functional aspect of the RBD mutants.

Firstly, we investigated the polymorphism and diversity among the available SARS-CoV-2 S gene sequences. Among them, several diversity hot spots in S protein have been found in the whole gene, i.e., in both S1 and S2 subunits, including RBD domain which was related to receptor binding and antigen cognition. The high non-synonymous and synonymous mutation rate ratio revealed the strong selective pressure of S gene, especially in S1 subunit gene.

By the detailed alignment of all the S gene sequences available in the databases, two groups of amino acid mutations in SARS-CoV-2 RBD domain were identified: the “similar affinity” group (F342L, R408I) and the “higher affinity” group (N354D D364Y, V367F, W436R). Mutations F342L, N354D, D364Y, and W436R were only discovered in single isolate. However, mutation V367F was discovered in six isolates. It was firstly discovered in one Hong Kong isolate, later appeared in five French isolates, across the continent. As RBD is conserved in SARS-CoV-2, the coincidence of six strains with the same mutation V367F in RBD in both France and Hong Kong is presumed significant for the virus transmission. It also indicates that these isolates may have originated as a novel sub-lineage, which has been circulating in the world, considering the close isolation dates (January 22 and 23, respectively). More epidemiological data are needed to confirm their potential relatedness.

The origination of the virus is a constant hot topic since the virus outbreak. Due to the high homology of the bat SARS-like CoV genome and pangolin CoV RBD to the SARS-CoV-2, these wild animals, especially the ones which were illegally on sale in the Wuhan Huanan Seafood Market, were thought to initiate the infection in human. Our results provided more clues on this postulation. In one aspect, the binding energy of the bat SARS-like CoV RBD is too high to directly bind human ACE2 (K_D in millimolar range). In contrast, the pangolin CoV showed a K_D to human ACE2 at micromolar range, just ~6x higher than that of the human SARS virus (Fig. 4), which indicates that the pangolin CoV can potentially infect human in close contact. The highly homologous pangolin CoV has been widely detected among the illegally transported Malayan pangolins in recent years in multiple provinces in China[7,8], which means that the wild pangolins are frequent carriers of the CoV in the nature. This indicates that the risk of zoonotic infection from wild animals to human constantly and widely exists. In another aspect, however, the sequence pattern suggested that this outbreak of SARS-CoV-2 was not directly originated from the pangolin CoV infection. The pangolin CoV deviate from human SARS-CoV-2 for 6 amino acids in RBD, but none of the 244 SARS-CoV-2 strains contain any of these 6 amino acids (Fig. 1B). Alignment of the genomic sequences of SARS-CoV-2 and pangolin CoV viruses indicated the evidence for recombination events in RBD domain between pangolin and bat viruses [6,8].

Our analysis of molecular dynamics simulation indicates the remarkable enhancement of the affinity efficiency of mutated S protein. Compared to the prototype virus Wuhan-Hu-1, the binding energy of mutants decreased ~25%. Mutants bind ACE2 more stably due to the enhancement of the base rigidity. Potential and recent animal-to-human transmission events of SARS-CoV-2, may explain the strong positive selection and enhancement of the affinity during the pandemic. The viruses have been adapting to transmission and replication in humans; mutation or recombination events in RBD may boost the affinity, causing the human to human transmission more easily.

The S protein is also important for antigen cognition. Fortunately, only a few amino acid mutations have been found in the RBD domain of the S protein, which showed the conservativeness of this domain. Judging from this point, the vaccines which focus on the RBD of S protein may still work for the SARS-CoV-2. However, the variation of S protein may change the antigen of virus and influence the vaccine immune efficiency. The biological outcomes of the mutations need further confirmation in the future.

In summary, our study identified two groups of amino acid mutations in SARS-CoV-2 RBD domain. The “higher affinity” group included the amino acids that were located at the firm scaffold, which facilitated the receptor binding. The four mutations of RBD under the positive selective pressure enhanced the infection efficiency of the SARS-CoV-2. Knowing the structural binding mechanism will support the vaccine development and facilitate prevention countermeasure development. The mutation of S protein RBD will provide the insights to the evolutional trend of SARS-CoV-2 under selection pressure. Combined with the epidemiology data, mutation surveillance is important and it can reveal more exact spreading routes of the epidemics and provide early warning for the possible outbreaks. Enhancement of SARS-CoV-2 binding affinity to human ACE2 reveals the higher risk of more severe epidemic and pandemic of COVID-19 in the world if no effective precautions are taken. The emergence of RBD mutations in Hong Kong, France and wherever in other countries, needs great attention.

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Conflict of interest

The authors declare that they have no conflicts of interest.

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Appendix:

Table.S1 Meta data of the isolates with mutations in spike glycoproteins RBD

Accession ID:	GISAID Virus name	Collection date	Location	Gender	Patient age	Specimen source	Additional location information	RBD mutation
EPI_ISL_412028	hCoV-19/Hong Kong/VM20001061/2020	2020/1/22	Asia / Hong Kong	Male	39	Nasopharyngeal aspirate & Throat swab		V367F
EPI_ISL_406596	hCoV-19/France/IDF0372/2020	2020/1/23	Europe / France / Ile-de-France / Paris	Female	31	Oro-Pharyngeal swab		V367F
EPI_ISL_410720	hCoV-19/France/IDF0372-isl/2020	2020/1/23	Europe / France / Ile-de-France / Paris	Female	31	Oro-Pharyngeal swab		V367F
EPI_ISL_406597	hCoV-19/France/IDF0373/2020	2020/1/23	Europe / France / Ile-de-France / Paris	Male	32	Orao-pharungeal swab		V367F
EPI_ISL_411219	hCoV-19/France/IDF0386-islP1/2020	2020/1/28	Europe / France / Ile-de-France / Paris	Female	30	Naso-pharyngeal swab	related to EPI_ISL_406596	V367F
EPI_ISL_411220	hCoV-19/France/IDF0386-islP3/2020	2020/1/28	Europe / France / Ile-de-France / Paris	Female	30	Naso-pharyngeal swab	related to EPI_ISL_406596	V367F
EPI_ISL_408511	hCoV-19/Wuhan/IVDC-HB-envF13/2020	2020/1/1	Asia / China / Hubei / Wuhan	not applicable		Environment	Huanan Seafood Market	W436R
EPI_ISL_406595	hCoV-19/Shenzhen/SZTH-004/2020	2020/1/16	Asia / China / Guandong / Shenzhen	Male	63	Alveolar lavage fluid		N354D,D364Y
EPI_ISL_413522	hCoV-19/India/1-27/2020	2020/1/27	Asia / India / Kerala	Female	20	Throat swab	Travel history to China	R408I
EPI_ISL_407071	hCoV-19/England/01/2020	2020/1/29	Europe / England	Female	50	swab	England cluster patient 1	F342L