

Brief communication

Computational characterization and design of SARS coronavirus receptor recognition and antibody neutralization

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Abstract

The sequential determination of crystal structures of the SARS coronavirus spike receptor-binding domain (RBD) in complex with its cellular receptor or neutralizing antibody opened a door for the design and development of antiviral competitive inhibitors. Based on those complex structures, we conduct computational characterization and design of RBD-mediated receptor recognition and antibody neutralization. The comparisons between computational predictions and experimental evidences validate our structural bioinformatics protocols. And the calculations predict a number of single substitutions on RBD, receptor or antibody that could remarkably elevate the binding affinities of those complexes. It is reasonable to anticipate our structure-based computation-derived hypotheses could be informative to the future biochemical and immunological tests.

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1. Introduction

As an envelope glycoprotein, the spike protein of severe acute respiratory syndrome coronavirus (SARS-CoV) plays a key role in the viral entry and neutralization (Bartlam et al., 2005; Denison, 2004; Lau and Peiris, 2005; Xu and Gao, 2004; Zhu, 2004). This structural protein consists of two functional regions: the outer globular S1 region responsible for the initial attachment to cellular receptor and the inner stalk S2 region contributing to the subsequent fusion between viral envelope and cellular membrane (Beniac et al., 2006; Hofmann and Pohlmann, 2004; Lin et al., 2005; Xiao and Dimitrov, 2004). A membrane-associated zinc metalloproteinase, angiotensin-converting enzyme 2 (ACE2), has been identified as the functional receptor for SARS-CoV (Li et al., 2003). And a soluble form of ACE2 could block the association of S1 region with the permissive Vero E6 cells (Li et al., 2003; Moore et al., 2004). In addition, a 193-amino acid fragment (residues 318–510), located within the S1 region, was demonstrated as an independently folded receptor-binding domain (RBD) capable of attaching ACE2 more efficiently ($IC_{50} < 10$ nM) compared with

the full S1 region ($IC_{50} \approx 50$ nM) (Wong et al., 2004). Besides, this RBD was able to elicit highly potent neutralizing antibodies in the immunized animals, which conferred those animals significant protection from the challenge of pathogenic SARS-CoV (Du et al., 2006; He et al., 2004, 2005a,b, 2006a,b,c,d; Zakhartchouk et al., 2006; Zhao et al., 2006). Moreover, a human monoclonal antibody 80R, isolated from a nonimmune human antibody library, was shown to potently neutralize SARS-CoV through targeting the RBD and blocking receptor recognition (Sui et al., 2004). The epitope mapping illustrated a 180-amino acid conformationally sensitive fragment (residues 324–503) within the RBD was the neutralizing epitope of 80R (Sui et al., 2005). Furthermore, another human monoclonal antibody m396 also exhibited potent neutralization of SARS-CoV by competition with ACE2 for binding to RBD (Prabakaran et al., 2006). Together those data suggest the receptor association process of SARS-CoV is an attractive opportunity for therapeutic intervention (De Clercq, 2006; He and Jiang, 2005; Hofmann and Pohlmann, 2004; Jiang et al., 2005; Kuhn et al., 2004; Yeung et al., 2006). The peptide or peptidomimetic antagonist leads, including the SARS-CoV spike RBD, the soluble form of ACE2 and the neutralizing antibodies 80R plus m396, should be able to potently abolish viral attachment to host cells. In this study, we conducted structural bioinformatics analyses on the crystal structures of the SARS-CoV RBD complexed with functional

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receptor or neutralizing antibody (Hwang et al., 2006; Li et al., 2005a,2006; Prabakaran et al., 2006) to predict single substitutions on spike RBD, receptor or antibodies possibly causing remarkable elevation in the binding affinities of complexes for the design and development of anti-SARS agents.

2. Materials and methods

Three coordinates files were retrieved from the Protein Data Bank (PDB) (Berman et al., 2000). One file is the ACE2-bound RBD (PDB code: 2AJF) (Li et al., 2005a), while the others are the RBD complexed with 80R (PDB code: 2GHW) (Hwang et al., 2006) or m396 (PDB code: 2DD8)(Prabakaran et al., 2006). Both the first and second files harbor a pair of sister complexes. And in the third file, either the heavy chain or the light chain of m396 makes its own contacts with the RBD. Thus, a total of six complex structures (AE/BF for ACE2-RBD, AB/CD for 80R-RBD and HS/LS for m396-RBD) are subject to computational simulations, respectively. Firstly, the program FoldX (Schymkowitz et al., 2005), based on an empirical effective energy function, was employed for calculation of the binding free energy values of wild type complexes. Then, a computational alanine scanning on the protein-protein interfaces was performed for evaluation of energetical contribution from single binding sites to the complex formation. Those positions yielding a calculated increase in association energy of more than 1 kcal/mol on alanine substitution were defined as energetic hot (important) spots according to previous criteria (Guerois et al., 2002; Guerois and Serrano, 2000; Kiel and Serrano, 2006; Kiel et al., 2004, 2005). The next step was to redesign the interactions between RBD and its binding partners through the software DeepView (Arnold et al., 2006; Guex and Peitsch, 1997). Each of the binding sites on the RBD, receptor or antibody was saturated with virtual substitutions, i.e., replaced with all the 20 natural amino acid residues except the original one. Finally, the reconstructed models were feed to the program FoldX to compute their binding energies. Here, only the variants rewarded a value of at least 1 kcal/mol lower than that of the wild type were taken into consideration.

3. Results and discussion

The calculated binding energy values and hot spots of the wild type complexes are shown in Table 1. The

complexes ACE2-RBD (AE/BF) and 80R-RBD (AB/CD) show a close correlation between their interaction energies ($-15.78/-14.82$ kcal/mol versus $-18.36/-16.53$ kcal/mol) and buried surface area (1700 \AA^2 versus 2200 \AA^2), gap volume (7000 \AA^3 versus 4000 \AA^3), or binding affinity (1.70 nM versus 1.59 nM)(Hwang et al., 2006). Those obvious associations indicate that the higher geometric complementarity, corresponding to the larger buried surface area and the smaller gap volume, offers the complex 80R-RBD rather than the complex ACE2-RBD the lower interaction energy and consequently the stronger binding affinity. Similarly, the correlation of binding energy with buried surface area is also found for the complex m396-RBD in which the heavy chain and the light chain contribute 66% and 34% to the total buried surface (Prabakaran et al., 2006). And the RBD association energy of the former chain (-8.64 kcal/mol) is remarkably lower than that of the latter (-5.42 kcal/mol). The perfect agreements of computational predictions with structural observations or biochemical evidences strongly suggest the reliability of our protocols.

As to the hot spots of complexes, the consistency between computational predictions and experimental evidences is clearly detected for RBD and receptor. In ACE2-RBD complexes, three receptor residues (GLU37, ASP38 and TYR41 on the chain A of complex AE or GLU37, TYR41 and LYS353 on the chain B of complex BF) form one hot spot cluster interacting with another hot cluster formed by five or six RBD residues (ARG426, TYR436, TYR475, TYR484 and TYR491 on the chain E of complex AE and the chain F of complex BF, whereas ASN473 only on the chain F). The interactions between the two hot clusters make the major contribution to the binding free energy of ACE2-RBD complexes. Notably, our predictions are in agreement with previous experimental alanine mutagenesis, which identified two hot spots on RBD (ARG426 and ASN473) (Chakraborti et al., 2005) and another two on receptor (TYR41 and LYS353) (Li et al., 2005b). In addition, computational alanine scanning on the sister complexes AB and CD successfully identify a RBD hot spot (ASP480) revealed in mutational binding analyses (Sui et al., 2005). In sharp contrast to ACE2, the antibody 80R possesses four hot residues (TYR102, ASN164, ARG223 and TRP226) being scattered on the binding surface rather than centralized into a cluster. The difference in the number and distribution of hot spots might account for the large gap between the interaction energies of 80R-RBD (-18.3627 and -16.5309 kcal/mol) and those of ACE2-RBD (-15.7765 and

Table 1
Calculated binding free energies and hot spots of wild type complexes

Complex	Binding free energy (kcal/mol)	Hot spots
AE	-15.78	Chain A: GLU37, ASP38, TYR41; chain E: ARG426, TYR436, TYR475, TYR484, TYR491
BF	-14.82	Chain B: GLU37, TYR41, LYS353; chain F: ARG426, TYR436, ASN473, TYR475, TYR484, TYR491
AB	-18.36	Chain A: TYR436, PRO470, LEU472, ASP480, TYR484, TYR491; chain B: TYR102, ASN164, ARG223, TRP226
CD	-16.53	Chain C: TYR436, PRO470, ASP480, TYR484; chain D: TYR102, ASN164, ARG223, TRP226
HS	-8.64	Chain H: none; chain S: TYR491, GLN492
LS	-5.42	Chain L: TRP91, ASP92; chain S: ILE489

The complexes AE and BF with the chains A, B for ACE2 and the chains E, F for RBD; the complexes AB and CD with the chains A, C for RBD and the chains B, D for 80R; the complexes HS and LS with the chains H, L and S for heavy and light chains of m396 plus RBD.

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