

Highly Conserved Binding Region of ACE2 as Receptor for SARS-CoV-2 between Human and Mammals

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Keywords: ACE2, SARS-CoV-2, COVID-19, binding region

Abstract:

In Belgium, case of new coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection from owner to domestic cat was reported on March 27, 2020. So far, cases of SARS-CoV-2 infection from owners to their dogs have been reported. For the first time in the world, the case of SARS-CoV-2 transmission from the owner to a domestic cat has been confirmed. A tiger kept at a zoo in New York, USA, was reportedly infected with SRAS-CoV-2. It is believed that SRAS-CoV-2 has been transmitted to tiger from caretakers infected with SRAS-CoV-2. Therefore, we examined the homology of whole molecule and the 5 amino acids residues; KGDFR located in the binding region of the angiotensin converting enzyme-2 (ACE2) molecule, a receptor for the spike glycoprotein on the virion surface of SRAS-CoV-2, between humans, dogs, cats, tiger and other mammals. Although the transmission of human coronavirus to pets or animals is rare, the dangers of transmitting SARS-CoV-2 from animals or pets to humans have not been proven. Our findings with Shi's study provide important insights into the animal models for SARS-CoV-2 and animal management for COVID-19 control.

A novel human coronavirus that is now named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (formerly called 2019-nCoV) emerged in Wuhan, China, in late 2019 and is now causing a pandemic [1]. The genome of SARS-CoV-2 shares about 80% identity with that of SARS-CoV and is about 96% identical to the bat coronavirus BatCoV RaTG13 [2]. In the case of SARS-CoV, the spike glycoprotein on the virion surface mediates receptor recognition and membrane fusion [3,4,5]. During viral infection, the trimeric spike glycoprotein is cleaved into S1 and S2 subunits and S1 subunits are released in the transition to the post fusion conformation [4-7]. S1 contains the receptor binding domain (RBD), which directly binds to the binding region located in the peptidase domain (PD) of angiotensin-converting enzyme 2 (ACE2), whereas S2 subunit is responsible for membrane fusion [5,6].

In Belgium, case of new coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection from owner to domestic cat was reported on March 27, 2020. So far, cases of SARS-CoV-2 infection from owners to their dogs have been reported. For the first time in the world, the case of SARS-CoV-2 transmission from the owner to a domestic cat has been confirmed. A tiger kept at a zoo in New York, USA, was reportedly infected with SRAS-CoV-2. It is believed that SRAS-CoV-2 has been transmitted to tiger from caretakers who have been infected with SRAS-CoV-2. Jianzhong Shi et al. in Science 08 Apr 2020 report that cats are experimentally susceptible to airborne infection [7]. Therefore, we examined the whole molecule homology and the 5 amino acids residues; KGDFR located in the binding region of the angiotensin converting enzyme-2 (ACE2) molecule, a receptor for the spike glycoprotein on the virion surface of SRAS-CoV-2, between humans, dogs, cats, tiger and other mammals. As a result, the binding region with ACE2 molecule with SARS-CoV spike glycoprotein showed high homology and completely conserved the 5 amino acids residues: KGDFR between humans, dogs, cats, tiger, and other mammals. Although the transmission of human coronavirus to pets or animals is rare, the dangers of transmitting SARS-CoV-2 from animals or pets to humans have not been proven. The Belgian Health Service considers the zoonotic infection as a special case. However, the Belgian Health Service has called for individuals with SARS-CoV-2 to also avoid contact with pets or animals. Our findings with Shi's study provide important insights into the animal models for SARS-CoV-2 and animal management for COVID-19 control.

The Belgian Health Service reports that there is no medical evidence of SARS-CoV-2 transmission from pets to humans or other pets, the risk of SARS-CoV-2 transmission from pets to humans is much lower than in cases of SARS-CoV-2 transmission due to human contact. However, to prevent cross species transmitting SARS-CoV-2 from the owner to their pets, especially if the owner may be infected with SARS-

CoV-2, owners should avoid close contact with pets and refrain from licking their faces. The information from our examinations will support precision vaccine design and the discovery of antiviral therapeutics, accelerating medical countermeasure development.

Footnote

The materials (manuscript and figures) are original research, has not been previously published and has not been submitted for publication elsewhere while under consideration.

Disclosure

The authors declare no potential conflicts of interest. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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angiotensin-converting enzyme 2 precursor [Homo sapiens]

NCBI Reference Sequence: NP_001358344.1

353..357 kgdfr /region_name="Interaction with SARS-CoV spike glycoprotein" /note="propagated from UniProtKB/Swiss-Prot (Q9BYF1.2)"

Species Protein ID Whole Homology

Species	Protein ID	Whole Homology								
Homo.	NP_001358344.1		301	awdaqrifke	aefffvsvgl	pnmtqgfwen	smltdpgnvq	kavchptawd	lgkdfrilm	
Dog#1	NP_001158732.1	91.0%	301	wdarkifkea	ekfffvsvglp	nmtqefwgn	mltepsdsrk	vvchptawdl	gkdfrimkc	
Dog#2	XP_005641049.1	92.0%	301	wdarkifkea	ekfffvsvglp	nmtqefwens	mltepsdsrk	vvchptawdl	gkdfrimkc	
Dog#3	XP_013966804.1	92.0%	301	wdarkifkea	ekfffvsvglp	nmtqefwens	mltepsdsrk	vvchptawdl	gkdfrimkc	
Dog#4	XP_022271214.1	79.0%	181	darkifkeae	kfffvsvglpn	mtqefwensm	ltepsdsrkv	vchptawdlg	kdfrimct	
Cat#1	XP_023104564.1	91.0%	301	nqswdarrif	keaefffvsv	glpnmtqgf	ensmltepgd	srkvvchpta	wdlgkdfr	
Cat#2	NP_001034545.1	92.0%	301	swdarrifke	aefffvsvgl	pnmtqgfwen	smltepgdsr	kvvchptawd	lgkdfrimk	
Tiger#1	XP_007090142.1	92.0%	291	nqswdarrif	keaefffvsv	glpnmtqgf	ensmltepgn	sqkvvchpta	wdlgkdfr	
Bat#1	XP_014399780.1	88.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#2	XP_014399781.1	88.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#3	XP_014399782.1	89.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#4	XP_014399783.1	80.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#5	XP_024425698.1	88.0%	301	wdaqrifkea	ekffksvglf	smtqgfdwn	mltkpddgre	vvchptawdl	gnkdfrimkc	
Bat#6	XP_024425699.1	81.0%	231	dqswwaqrif	keaefffksv	glfsmtqgf	dnsmltkpdd	grevvchpta	wdlgnkdfr	
Bat#7	XP_008153150.1	88.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#8	XP_027986092.1	88.0%	301	wdaekifkea	ekfymsvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#9	XP_023609437.1	88.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#10	XP_023609438.1	88.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#11	XP_023609439.1	89.0%	301	wdaekifkea	ekfyisvglp	smtpgfwns	mltepgdgrk	vvchptawdl	gkdfrimkc	
Bat#12	XP_028378317.1	87.0%	301	aqrifkeae	ffvsvglf	tqgfdwnsm	tkpddgre	chptawdlg	kdfrimctk	
Bat#13	XP_019522936.1	89.0%	301	kwdakkifqe	aefffvsvgl	pnmtkgfwen	smltepgdgr	kvvchptawd	lgkdfrimk	
Bat#14	XP_019522943.1	89.0%	301	kwdakkifqe	aefffvsvgl	pnmtkgfwen	smltepgdgr	kvvchptawd	lgkdfrimk	
Bat#15	XP_019522954.1	89.0%	301	kwdakkifqe	aefffvsvgl	pnmtkgfwen	smltepgdgr	kvvchptawd	lgkdfrimk	
Pan#1	XP_017505746.1	91.0%	301	twdanrifke	aefffvsvgl	pkmtqtfwen	smltepgdgr	kvvchptawd	lgkdfrimk	
Pan#2	XP_017505752.1	91.0%	301	twdanrifke	aefffvsvgl	pkmtqtfwen	smltepgdgr	kvvchptawd	lgkdfrimk	
Sna#1	XP_026530754.1	75.0%	361	ekkwtdvsif	kaaefffisi	glfnmtesfw	knsmlleepkd	grkvvchpta	wdmgkedyri	
Sna#2	XP_032082934.1	74.0%	321	tkkwtdvsif	kaaeqfftsi	glfpmtdnfw	nnsmlleepkd	grkvvchpta	wdmgkdyri	

Whole molecule homology and Amino acid sequence alignment of the binding region of angiotensin converting enzyme 2 (ACE2) as receptor for SARS-CoV-2 spike glycoprotein and its phylogeny.

Whole molecule homology and the homologous binding region of Angiotensin Converting Enzyme 2 (ACE2) between human and other animal species including dogs, cats, tiger, bats, pangolins and snakes are indicated in figure. The key 5 amino acid residues KGDFR involved in the interaction with human SARS-CoV-2 spike glycoprotein are marked with the red bold words. Detailed information including protein accession numbers of ACE2 of other animal species can be found in the supplementary material.

