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**Programa de Pós-Graduação em Doenças Infecciosas e Parasitárias – PPGDIP/UFMS**

**PROVA DE LÍNGUA INGLESA** – 11 de fevereiro de 2020 (Edital N° 06/2019 - PPGDIP/UFMS)

**Número da INSCRIÇÃO: GABARITO**

Considerando os textos (artigos científicos) abaixo, **responda em PORTUGUÊS ou INGLÊS as questões de 1 a 9 apresentadas após o texto**. A questão 10 deve ser respondida em português.

Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, et al. (2017) Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. **PLoS Pathogens** 13(11): e1006698.

<https://doi.org/10.1371/journal.ppat.1006698>

1            Severe Acute Respiratory Syndrome (SARS) is a severe emerging viral disease  
2 with high fatality characterized by fever, headache and severe respiratory symptoms  
3 including cough, dyspnea and pneumonia. Due to its high transmissibility among humans,  
4 after its first emergence in southern China in late 2002, it rapidly led to a global pandemic  
5 in 2003 and was marked as one of the most significant public health threats in the 21<sup>st</sup>  
6 century. The causative agent, SARS coronavirus (SARS-CoV), has been previously  
7 assigned to group 2b CoV and is now a member of the lineage B of genus Betacoronavirus  
8 in the family Coronaviridae. It shares similar genome organization with other  
9 coronaviruses, but exhibits a unique genomic structure which includes a number of  
10 specific accessory genes.

11            The feline known as masked palm civets (*Paguma larvata*) were initially  
12 hypothesized to be the animal origin of SARS-CoV. However, since a large number of  
13 genetically diverse SARS-related coronaviruses (SARSr-CoV) have been detected in  
14 multiple species of horseshoe bats (genus *Rhinolophus*) from different areas of China and  
15 Europe in the aftermath of SARS, it is prevailingly considered that SARS-CoV originated  
16 in horseshoe bats with civets acting as the intermediate amplifying and transmitting host.

17           Recently we have reported four novel SARSr-CoVs from Chinese horseshoe bats  
18 that shared much higher genomic sequence similarity to the epidemic strains, particularly  
19 in their S gene, of which two strains (termed WIV1 and WIV16) have been successfully  
20 cultured in vitro.

21           Genetically diverse SARSr-CoVs have been detected in various horseshoe bat  
22 species across a wide geographic range in China in the past decade.

23           SARS human case first emerged in Guangdong province in late 2002. However,  
24 SARSr-CoVs discovered in bats from neighboring areas of Guangdong to date have  
25 shown phylogenetic disparity from SARS-CoV especially in the S gene, suggesting SARS-  
26 CoV may have originated from another region.

27           Some authors have shown that frequent recombination events have happened  
28 among those SARSr-CoVs in the bat caves. While we cannot rule out the possibility that  
29 similar gene pools of SARSr-CoVs exist elsewhere, we have provided sufficient evidence  
30 to conclude that SARS-CoV most likely originated from horseshoe bats via recombination  
31 events among existing SARSr-CoVs. In addition, we have also revealed that various  
32 SARSr-CoVs capable of using human ACE2 (which is a receptor of SARS-CoV in humans  
33 for cell entry) are still circulating among bats in this region. Thus, the risk of spillover into  
34 people and emergence of a disease similar to SARS is possible. This is particularly  
35 important given that the nearest village to the bat cave we surveyed is only 1.1 km away,  
36 which indicates a potential risk of exposure to bats for the local residents. Thus, we  
37 propose that monitoring of SARSr-CoV evolution at this and other sites should continue,  
38 as well as examination of human behavioral risk for infection and serological surveys of  
39 people, to determine if spillover is already occurring at these sites and to design  
40 intervention strategies to avoid future disease emergence.

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42 Perlman, S. (2020). Another decade, another coronavirus. **The New England Journal of**  
43 **Medicine**. January 24, 2020. doi: 10.1056/NEJMe2001126

44           For the third time in as many decades, a zoonotic coronavirus has crossed species  
45 to infect human populations. This virus, provisionally called 2019-nCoV, was first identified  
46 in Wuhan, China, in persons exposed to a seafood or wet market in December 2019. The  
47 rapid response of the Chinese public health, clinical, and scientific communities facilitated  
48 recognition of the clinical disease and initial understanding of the epidemiology of the

49 infection. First reports indicated that human-to-human transmission was limited or  
50 nonexistent, but we now know that such transmission occurs, although to what extent  
51 remains unknown. Like outbreaks caused by two other pathogenic human respiratory  
52 coronaviruses (severe acute respiratory syndrome coronavirus [SARS-CoV] and Middle  
53 East respiratory syndrome coronavirus [MERS-CoV]), 2019-nCoV causes respiratory  
54 disease that is often severe. As of January 24, 2020, there were more than 800 reported  
55 cases, with a mortality rate of 3%.

56 As now reported in the Journal, Zhu et al. have identified and characterized 2019-  
57 nCoV. The viral genome has been sequenced, and these results in conjunction with other  
58 reports show that it is 75 to 80% identical to the SARS-CoV and even more closely related  
59 to several bat coronaviruses. It can be propagated in the same cells that are useful for  
60 growing SARS-CoV and MERS-CoV, but notably, 2019-nCoV grows better in primary  
61 human airway epithelial cells than in standard tissue-culture cells, unlike SARS-CoV or  
62 MERS-CoV. Identification of the virus will allow the development of reagents to address  
63 key unknowns about this new coronavirus infection and guide the development of antiviral  
64 therapies. First, knowing the sequence of the genome facilitates the development of  
65 sensitive quantitative reverse-transcriptase–polymerase-chain-reaction assays to rapidly  
66 detect the virus. Second, the development of serologic assays will allow assessment of  
67 the prevalence of the infection in humans and in potential zoonotic sources of the virus in  
68 wet markets and other settings. These reagents will also be useful for assessing whether  
69 the human infection is more widespread than originally thought, since wet markets are  
70 present throughout China. Third, having the virus in hand will spur efforts to develop  
71 antiviral therapies and vaccines, as well as experimental animal models.

1) De acordo com texto, quais são os sintomas ou qual é o quadro clínico da  
síndrome respiratória aguda grave causada pelo SARS coronavírus? (1,0 ponto)

**Resposta: A síndrome respiratória aguda grave (SARS) é caracterizada por febre, dor de  
cabeça e sintomas respiratórios graves, incluindo tosse, dispnéia e pneumonia.**

**Answer: Severe Acute Respiratory Syndrome (SARS) is characterized by fever, headache  
and severe respiratory symptoms including cough, dyspnea and pneumonia.**

- 2) Explique, de acordo com o texto, quais são as funções do gato de algália (*Paguma larvata*, também conhecida como civeta de palma mascarada) e do morcego-de-ferradura (morcego do gênero *Rhinolophus*) na dinâmica de transmissão do SARS coronavírus (SARS-CoV)? (1,0 ponto)

Resposta: o morcego-de-ferradura (morcego do gênero *Rhinolophus*) pode ter atuado como reservatório originário do SARS coronavírus (SARS-CoV) e a civeta de palma mascarada como hospedeiro intermediário de amplificação da transmissão do SARS-CoV.

Answer: it is prevailingly considered that SARS-CoV originated in horseshoe bats with civets acting as the intermediate amplifying and transmitting host.

- 3) De acordo com o texto, cite quando e onde (cidade e país) a doença causada pelo SARS-CoV foi identificada pela primeira vez. (1,0 ponto)

Resposta: o primeiro caso humano da síndrome respiratória aguda grave foi identificado na província de Guangdong, China, em 2002.

Answer: SARS human case first emerged in Guangdong province, China, in 2002.

- 4) Qual a provável hipótese para a origem do SARS coronavírus (SARS-CoV) apresentada pelos autores do primeiro texto? (1,0 ponto)

Resposta: os autores forneceram evidências suficientes para concluir que o SARS-CoV provavelmente se originou de morcegos-de-ferradura por meio de eventos de recombinação entre os SARSr-CoVs existentes.

Answer: the authors have provided sufficient evidence to conclude that SARS-CoV most likely originated from horseshoe bats via recombination events among existing SARSr-CoVs.

5) Além do SARS-CoV, quais outros dois vírus do grupo coronavírus causam infecções/doenças respiratórias agudas? (1,0 ponto)

Resposta: coronavírus da síndrome respiratória no Oriente Médio (MERS-CoV) e 2019-nCoV

Answer: Middle East respiratory syndrome coronavirus (MERS-CoV) and 2019-nCoV

6) Quando e onde ocorreram as exposições que originaram os primeiros casos da doença causada pelo coronavírus 2019-nCoV? (1,0 ponto)

Resposta: casos humanos de infecção causada por 2019-cCoV foram identificados pela primeira vez em Wuhan, China, em pessoas expostas a um mercado de frutos do mar ou mercado úmido em dezembro de 2019.

Answer: human cases of infection caused by 2019-cCoV were first identified in Wuhan, China, in persons exposed to a seafood or wet market in December 2019.

7) De acordo com o segundo texto, por que é importante a identificação e sequenciamento do 2019-nCoV? (1,0 ponto)

Resposta: a identificação e o sequenciamento do vírus permitirão o desenvolvimento de reagentes para tratar de questões importantes sobre essa nova infecção por coronavírus, irão orientar o desenvolvimento de terapias antivirais e facilitarão o desenvolvimento de testes quantitativos para detectar rapidamente o vírus, como a reação em cadeia da polimerase reversa.

Answer: identification and the sequence of the genome of the virus will allow the development of reagents to address key unknowns about this new coronavirus infection, guide the development of antiviral therapies and, facilitates the development of sensitive quantitative reverse-transcriptase–polymerase-chain-reaction assays to rapidly detect the virus.

8) De acordo com o segundo texto, qual método ou técnica favorecerá a estimativa da prevalência da infecção em humanos e a identificação de possíveis hospedeiros ou reservatórios zoonóticos? (1,0 ponto)

Resposta: ensaios ou testes sorológicos.

Answer: serologic assays.

9) Considerando os dois textos, qual é ou quais são as possíveis hipóteses para a ocorrência do surto causado pelo novo coronavírus 2019-nCoV? (1,0 ponto)

Resposta: pela terceira vez em tantas décadas, um coronavírus zoonótico cruzou espécies para infectar populações humanas. Eventos frequentes de recombinação entre SARSr-CoVs e o risco do evento de transbordamento (passagem da infecção que circulava em animais para seres humanos) para a população humana podem ter propiciado o surgimento de uma doença semelhante à SARS, como ocorreu em 2002.

Answer: For the third time in as many decades, a zoonotic coronavirus has crossed species to infect human populations. Frequent recombination events have happened among those SARSr-CoVs and the risk of spillover into people could be allowed the emergence of a disease similar to SARS in late 2002.

10) Considerando o contexto em que estão inseridas no texto, como você traduziria para o português as expressões abaixo? (1,0 ponto)

- epidemic strains (linha 18): **cepa epidêmica**
- spillover (linha 33): **infecção por transbordamento ou evento de transbordamento**
- outbreaks (linha 51): **surtos**
- reverse-transcriptase–polymerase-chain-reaction (linha 65): **reação em cadeia da polimerase por transcriptase reserva**