Analysis of Amino Acid Sequence of SARS-CoV, SARS-CoV-2, and MERS-CoV Spike Glycoproteins: Preliminary Study for Obtaining Universal Peptide Vaccine Candidates

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ABSTRACT. In the manufacture of universal peptide vaccines, it is necessary to analyze the amino acids of the various candidates. Therefore, this study aims to examine the amino acids of the spike glycoproteins of SARS-CoV, SARS-CoV-2, and MERS-CoV. The method used is the alignment of the amino acid spike glycoprotein between SARS-CoV with SARS-CoV-2, MERS-CoV with SARS-CoV-2, and SARS-CoV with MERS-CoV using web-based software water emboss. The analysis result showed that SARS and SARS-CoV-2 were very similar with 87% similarity and 76.4% identity values. In contrast, SARS-CoV-2 with MERS and SARS with MERS were very different, having similarity and identity values less than 70%. Therefore, it is reasonable to conclude that spike glycoprotein's peptide is only useful from attacks by the SARS-CoV and SARS-CoV-2 viruses.

Keywords: Coronavirus; COVID-19; MERS, peptide vaccine; SARS

INTRODUCTION
Coronavirus is 65 to 125 nm in size and as a single-stranded RNA virus, it has the length of 26-32 kbp. Furthermore, it consists of four subfamilies of alpha (α), beta (β), gamma (γ), and delta (δ) (Shereen et al., 2020). Before now, the virus only infected animals, however, in the 2000s, there were known cases of SARS (Severe Acute Respiratory Syndrome), MERS (Middle East Respiratory Syndrome), and COVID-19 (Coronavirus Disease-2019) (Wang et al., 2013; Shereen et al., 2020). The Coronavirus that cause SARS, MERS and COVID-19 are known as SARS-CoV (SARS coronavirus), MERS CoV (MERS coronavirus) and SARS CoV 2 (COVID-19) respectively.

SARS-CoV is an etiologic agent of acute respiratory syndrome (Liu et al., 2014), and was endemic in 2002-2003 (Peiris et al., 2003). MERS (Middle East Respiratory Syndrome) is an infectious disease caused by the MERS virus (MERS-CoV), and it has similar symptoms with SARS, that cause flut-like illnesses which is respiratory tract disruption (da Costa et al., 2020; Li et al., 2020). Both belong to the genus Betacoronavirus (Schoeman & Fielding, 2019; ICTV, 2020). Initially, MERS-CoV case was first identified in Saudi Arabia in September 2012 by camel-to-human transmission, and then by human-to-human transmission (Jeong et al., 2017) and spread to countries in the Middle East (Zumla et al., 2015), precisely in the Arabian Peninsula and its surroundings such as the United Arab Emirates, Qatar, Oman, Jordan, Kuwait, Yemen, Iran, Egypt, and Lebanon (Rampengan, 2016; Shapiro et al., 2016; WHO, 2016). Importations of MERS had been reported in France (Mailles et al., 2013; Puzelli et al., 2013), Italy (Puzelli et al., 2013), Spain (Rashid et al., 2013), United Kingdom (Thomas et al., 2014), Tunisia (Abroug et al., 2014), Malaysia (Cunha & Opal, 2014), Philippines (Racelis et al., 2015), and Korea (Jeong et al., 2017) in the following years. The SARS-CoV-2 attack resurfaced at the end of 2019 in Wuhan, China, and has spread to almost all countries worldwide, and this condition was given the term COVID-19 (Corona Virus Disease-2019) (ICTV, 2020).

Vaccines for MERS, SARS and COVID-19 are yet to be discovered (Slamet et al., 2013) but...
the process continues to experience development. In addition, it consists of several amino acid residues (small proteins) (Subroto et al., 2013) and with the existence, it is possible to make a universal vaccine. This can serve a protective function against various types of antigens, which is primarily used for making peptide vaccines. Therefore, a strong similarity protein is needed to make a universal vaccine against coronaviruses (SARS, MERS and COVID-19) (Alouane et al., 2020; Khalaj-Hedayati, 2020; Wu et al., 2020).

There have been many research related to the manufacture of vaccine candidates, one of which is the HPV (Human Papillomavirus). This study shows that the promising vaccine peptide candidate of the E1 protein obtained from HPV genome is LLITSNINA, from E5 is VLLCVCLLI and from E7 is LLMGTLGIV (Aprilyanto & Sembiring, 2017). Furthermore, they have been tested in vitro, and the results are useful in activating the immune response.

One of the conditions for making a peptide vaccine is that the protein antigen should be located at the outer part of the virus in order to ease the purification process. The spike glycoprotein is used as a peptide vaccine candidate since its position is in the outer part, and it is possessed by all types of Coronavirus. Therefore, this protein is used as a candidate source for peptide vaccines for all kinds of Coronavirus.

Initially, the research was conducted to obtain an overview of its potential as a vaccine candidate. In addition, an explanation of their potential will be obtained by testing the similarity and identity for the amino acid sequence of spike glycoproteins.

**MATERIALS AND METHODS**

This research used the following materials; amino acid sequence of SARS-CoV-2, SARS-CoV (SARS), and MERS-CoV (MERS) spike glycoprotein with NCBI having the Accession Number YP_009724390.1 (COVID-19), P59594, and A0A140AYZ5 respectively.

**Work Procedures.** This research was conducted in the following stages: SARS CoV-2 (COVID-19) spike glycoprotein downloaded at https://www.ncbi.nlm.nih.gov/; SARS CoV spike glycoprotein downloaded at http://www.uniprot.org; MERS spike glycoprotein download at http://www.uniprot.org; alignment process between spike glycoproteins of COVID-19 with SARS in the https://www.ebi.ac.uk/Tools/psa/emboss_water/program; alignment between spike glycoproteins of COVID-19 with MERS in the https://www.ebi.ac.uk/Tools/psa/emboss_water/program; alignment between spike glycoproteins of MERS with SARS in the program https://www.ebi.ac.uk/Tools/psa/emboss_water/program.

**RESULTS AND DISCUSSION**

Alignment result between COVID-19 with SARS.
Fig. 1. Alignment result between SARS CoV-2 with SARS-CoV spike glycoproteins.
Alignment result between COVID-19 with MERS

| Program: water | Aligned_sequences: 2 |
|----------------|----------------------|
| 1: YP_009724390.1 (Covid-19) | 2: A0A140AYZ5_9BETC (MERS) |
| Matrix: EBLOSUM62 | Gap_penalty: 10.0 |
| Extend_penalty: 0.5 | Length: 1440 |
| Identity: 433/1440 (30.1%) | Similarity: 654/1440 (45.4%) |
| Gaps: 276/1440 (19.2%) | Score: 1565.5 |

| YP_009724390. | 3 VFLVLLPL-------VSSQCVNLTTRTLQ------PPAYTNSFTR |
|----------------|--------------------------------------------------|
| A0A140AYZ5_9B | 5 VFLFLLTPTESYVDGFSVKSACIEVDIQQTFDDKTWPFPIDVS |
| YP_009724390. | 35 GVYYPDKVEHSVSLHSTQDLFLPF----FSNVWFAHIVSHTNGTКRF---- |
| A0A140AYZ5_9B | 55 GIIYPSGRTSNITYQGLF-PYQGDHDMYVYSSAGHATGTPQKFLVA |
| YP_009724390. | 80 ----DNVPVF--------NDGVYFSTEKSNIR--------GWIF |
| A0A140AYZ5_9B | 104 NYSQDKQVFANGVIRAAGANSTGVIIIPSTSATIRKIYPAMLGS |
| YP_009724390. | 107 GTTLDSK-----TQSLLIVNNTVKCEFQCNDFPFLGYY------- |
| A0A140AYZ5_9B | 154 GNSDGKMRFFNHTLVLFPDCGTLRA--FYMILEPRSNHCAGNSY |
| YP_009724390. | 145 ------YH--------KNNKSW ESEFRYSSANNCFEEY--------VSOQPLM |
| A0A140AYZ5_9B | 202 TSFATYHTFADCSGDNARRNASLNFKEYFNRENCTFTMYTIDEEL |
| YP_009724390. | 178 DLEGKQGNPFNLRERVFKNIDGYFIYKSYKHTPINLVRDLPGFSALEPLV |
| A0A140AYZ5_9B | 252 EWFGITQTAQVVHLFSSRVDY---

| YP_009724390. | 228 DLPIGINITRFQTL-------LALHRSYLFPSGSSSSTGWAGAAAAYVG |
|----------------|--------------------------------------------------|
| A0A140AYZ5_9B | 275 ----GGNMFQFATLPVYDITKSIYPHSIRSIQSDKAW----AAFYVY |
| YP_009724390. | 269 YLQPRTFLLKYNNENHTITDAVCAALDPLSETKCTLKSTVEKGIYQTSNF |
| A0A140AYZ5_9B | 317 KLOPLTFLLDPSVGYIIRRADCQFGNLDSQILHCYSEFDSVGEVS |
| YP_009724390. | 319 RVQPTESIVRFPNITNCLCFGEVFNFATRASVAYWNNKRISNCV |
| A0A140AYZ5_9B | 367 EAKPQGSVVEAQEGV--CDFSPLLGTG-FQVYNFKRLVFTNICYNLT |
| YP_009724390. | 369 YNSAFSTKCYGVSPTKNDCLCTNYYADSFVIRGDEVRQIAFGQTGKI |
| A0A140AYZ5_9B | 415 LSLFSVNDFTCSQPAAASNCYSSLILDFYSYPLSMKSDLSVSS |
| YP_009724390. | 419 ADFNYKLPPDFTGC-VIAWNSNDDSKVGG-NYNLYLRFKSNLKFGER |
| A0A140AYZ5_9B | 465 SQFNYKQSFSNPTCILATVIHYLNLTITKFLKYSINCKSRLLS----- |

YP_009724390. | 418 YNSAFSTKCYGVSPTKNDCLCTNYYADSFVIRGDEVRQIAFGQTGKI |
A0A140AYZ5_9B | 465 SQFNYKQSFSNPTCILATVIHYLNLTITKFLKYSINCKSRLLS----- |
**Alignment Result between SARS CoV-2 with MERS CoV Spike Glycoproteins.**

```
# Program: water
# Aligned_sequences: 2
# 1: SPIKE_CVHSA      (SARS)
# 2: A0A140AYZ5_9BETC (MERS)
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
# Length: 1400
# Identity:     443/1400 (31.6%)
# Similarity:   662/1400 (47.3%)
# Gaps:         214/1400 (15.3%)
# Score: 1561.0

SPIKE_CVHSA  3 IFLLFLTLTS-------GSD--------LDRCTTFDDQAPNYQTHTSSM  37
A0A140AYZ5_9B 5 VFLLMFLTPTESYVDGPDVSVKSAIEVIDIQQTFDFKTWPFPID-VSKA 53

SPIKE_CVHSA  38 RGVYYDEIFRSDTLYLTQDLFHPYESNVTGHINHTFGNPVIPFKDI
A0A140AYZ5_9B 54 DGIIPQGRYNITYQGLF-PRQDGHDGMYVSAGATGTPQ---

SPIKE_CVHSA  88 YFAATEKSNV---VRGW--FGSTMNKQSчувствивность к летальному
A0A140AYZ5_9B 100 LFVANYSQDVKQFANGFVWiragaan---STGTVIISPSTIRK----

SPIKE_CVHSA  133 CDNPPFAVSKEMGQTQ---------HTMIF--D-------NAFCNTFE--
A0A140AYZ5_9B 144 --YPAFLMGSSGVNFSDGKRFNFHHTLVLIPGCGTLLRAFYCILEPR

SPIKE_CVHSA  163 ----------YISDAF---SLDVSEKSGNFK-----LRELVFKKNKDFG
A0A140AYZ5_9B 192 GNHPAAGNLSFATYHTPATDCD--GNYNRRALSNSFKEYFNLNRCTF

SPIKE_CVHSA  194 LYYV--------KGYQPIDVVR-----DLPSG----------FNT
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Biogenesis: Jurnal Ilmiah Biologi 190

A0A140AYZ5_9B 240 MYTNITEDEILEWFGITQTAQGVHLFSRYVDLYGGNMFQFATLPVYDT 289
SPIKE_CVHSA 216 LKPIFKLPGINITNFRAILTAFSPQDIWGTSAAYAVGVLKPTTMLK 265
A0A140AYZ5_9B 290 IKYYSIIPSIR-------------SIQSDRKAN--------APFYVYKLQPLTFLD 326
SPIKE_CVHSA 266 YDENTITDADVCQSNPLAEKLCSVSFIEIDKGIYQTSNFRVVPSPGDVVR 315
A0A140AYZ5_9B 327 FSVDOYIERRAIDCGNDFLQQLHCYESFDVGEYSVSSFPEAKPSGSVVE 376
SPIKE_CVHSA 316 FPNIITNLCPFEVNFMATKFKPSVYAWERKKSINCVDAYSVLYNSTFTF--- 363
A0A140AYZ5_9B 377 QAEGVE-DFSPLLSTP---PVQYNFKRLVPTNC---NYNLTKLLLSFVSND 422
SPIKE_CVHSA 364 FKCYGVSAATKNLDCSFNFLCVLAWNTTRNIGHTSTGNYNKYKVR-LRHKLKPFFERDISNV 458
A0A140AYZ5_9B 423 FTCQSISPAAILASCNNYSSLLDDYFSYPLSMKSD----LSVSSAGPSQFN 468
SPIKE_CVHSA 350 YKLPPDFFMC-VCVLAWNTTRNIGHTSTGNYNKYKVR-LRHKLKPFFERDISNV 458
A0A140AYZ5_9B 469 YKQFSNPTCLILATVPHNL---TTITKPLKSYSINKCS-RRLLSSDREV 514
SPIKE_CVHSA 459 PFSFPG---KCPCTFPALNCYWPFLNDY-------------GFYTTTGGYQPY 494
A0A140AYZ5_9B 515 PQLVMNANQYPSVCSTVPSTWEDGDYRQLPSLEGGWLVASGTVMT 564
SPIKE_CVHSA 495 RVVVLSFELLNAPAT----VCGFKL---STDLIKNO---CVNFFNGLGTG 548
A0A140AYZ5_9B 565 EQLQMGFQTVQYGTDNSVC---PKLEFANDTKIASQNLGVEYSLYGVS 613
SPIKE_CVHSA 535 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 568 PVSVIY---DKETKTHATLFSGVACEHISTM---SQYSRSTRSMKLRRDST 703
SPIKE_CVHSA 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 573 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 593 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 593 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 593 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 593 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 593 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 593 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
A0A140AYZ5_9B 629 F---QTQAGCLIAGAEHTVSDT---ECDIPIGAGICASYHTVSLLRSTQK 672
A0A140AYZ5_9B 704 YGPLQTPVGVCLGL---VNSLFLVEEDCKLPLQLSGCALPDLTPSTLPVR 751
SPIKE_CVHSA 593 TGVL---TFSSKRFQPP---QFQGRDSVFDTSVREDPKTSEIDLIPSCFG 579
A0A140AYZ5_9B 614 RGVFQNCTAVGRVQRFVYDAYQNLVGYYSDD-----GNYYCLRACSV 657
SPIKE_CVHSA 580 GVSVITPTNASEAVLYQDVNTCDSTVSAIHADQTLPAWR-IYSTGNNV 628
Fig. 3. Alignment result between MERS CoV with SARS CoV spike glycoproteins.

Table 1 represents the results of the alignment shown by the value of identity and similarity. The Identity is the percentage of identical matches between the two sequences over the reported aligned region (including any gaps in the length). The following are the results of alignment among the three viruses.

Table 1. Conclusions on the alignment results of the coronavirus spike glycoprotein.

| No | Aligned Type         | Identity (%) | Similarity (%) |
|----|----------------------|--------------|----------------|
| 1  | Covid-19 x SARS      | 76.4         | 87.0           |
| 2  | Covid-19 x MERS      | 30.1         | 45.4           |
| 3  | SARS x MERS          | 31.6         | 47.3           |

The similarity is the percentage of matches between the two sequences over the reported aligned region (including any gaps in the length) (Taupiqurohman et al., 2016). In addition, Identity value indicates the identical equation of the compared amino acids, while the similarity value indicates the conformity on chemical properties (Hui et al., 2020). Table 1 also shows that Coronaviruses of SARS and COVID-19 have a high similarity with an identity value of 76.4% and 87%. On the contrary, the comparison of MERS and COVID-19 is relatively not similar because the alignment results are below 70%. The low result is also shown by the comparison between SARS with MERS having 31.6% identity, and 47.3% similarity. This is consistent with the explanation of Andriani (2016) and Li et al. (2020), where it was stated that the coronaviruses of SARS and COVID-19 are very close based on evolution tree. According to Rice et al. (2000), phylogenetic results (evolutionary kinship) cannot be concluded because of the type of protein being compared. Therefore, this research has illustrated the great potential of spike glycoprotein to be the source of peptide vaccine candidates for the SARS and COVID-19 diseases. Below is the structure of the spike glycoprotein of SARS-CoV, SARS-CoV-2, and MERS based on the database (pdb.org).
Work Principles of Universal Peptide Vaccine. The sequential analysis shows that spike glycoprotein can only be used as the source of peptide vaccine candidates for SARS and COVID-19. This should be properly conducted since the working principle of peptide vaccine is based on the immune system. The two common parts when a virus infects are the outside (specific body tissue) and the inside of an infected cell (body cell). When a part of the tissue is infected, the immune cells in the region begin to respond (Mothes et al., 2010; Mallapaty, 2020). This is evident in macrophages, which is one type of immune cell that is responsible for initiating the formation of antibodies through the activation of helper T cells. To activate these cells, macrophages will phagocytize the incoming antigen protein. Furthermore, the results of phagocytosis (small peptides) are raised to the surface of the body by major histocompatibility (MHC) class II protein to be recognized by helper T cell receptors (Li et al., 2020). Andriani (2016) stated the predicted part and made into a peptide vaccine.

During an internal cellular infection, the cell responds through a series of reactions (Fig. 4). An important part of this response in relation to the peptide vaccine is that the cell will attempt to bring the virus part to the surface. This is conducted by the MHC class I and recognized by cytotoxic T cells, which functions to reduce infection (Li et al., 2020). The part of the virus raised by MHC I and II is another peptide vaccine candidate that is predicted by using the spike glycoprotein (marked in the box in the picture). This protein is a potential candidate for peptide vaccine since it is found on the outer part of the virus spike glycoprotein is also in the outer part of the virus, thus it is a potential candidate for peptide vaccine. Initially, it is recognized or attached to the cell surface, and the location is given below.

Every disease has a cure. If the right medicine is found for a disease, the disease will be cured with the permission of Allah Azza wa Jalla (Sahih Muslim No. 4084). Based on this hadith, we can learn that there is no disease on this earth that was created by Allah without a cure. As at present, many kinds of research have been carried out by scientists to find the most appropriate vaccine candidates for use in the prevention of infectious diseases caused by the coronavirus. The success of finding a vaccine candidate with the highest level of effectiveness is also inseparable from the power of Allah Almighty, as His word in QS. Ash-Shu'ara verse 80 (Kementerian Agama RI, 2019). This verse explains that it is Allah who heals a man when he is sick. Allah has the power to heal any disease that a person has. But man, through the use of the mind by studying science, must also find out how to obtain this healing. Through science, humans can find out
the types of amino acids from the glycoprotein spike of various types of coronaviruses that are most appropriate to be used in the production of universal peptide vaccines for various types of infectious diseases caused by various types of coronaviruses. The lesson that can be taken from this verse is that diseases experienced by humans are the result of human actions themselves, including infection with diseases caused by the coronavirus, one of which is the lack of a clean lifestyle. Through the efforts made by humans and by the will of Allah swt, diseases suffered by humans can be cured. Diseases that occur in humans can also be a reminder to always be grateful for the various blessings from Allah swt. One of which is the favor of healing from an illness.

CONCLUSION

SARS CoV-2 (COVID-19) and SARS are very similar with 87% similarity and 76.4% identity values. In contrast, covid-19 with MERS and SARS with MERS are very different because of their reduced similarity and identity values below 70%. Therefore, the spike glycoprotein can only be used as the peptide vaccine candidate for COVID-19 and SARS.

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