

Research Article

Level of Knowledge of the Omicron Variant of the Sars-Cov2 Virus of Medical Students at Muhammadiyah Malang University

Diah Hermayanti^{1*}, Alifia Salsabila Teka², Vania Nabila Putri², and Yosiene Dhea Elfita²

¹Lecturer of Medical Faculty, University of Muhammadiyah Malang

²Students of Medical Faculty, University of Muhammadiyah Malang

ORCID

Diah Hermayanti: <https://orcid.org/0000-0002-4275-8296>

Abstract.

The second wave of the COVID-19 pandemic in Indonesia has subsided. However, it has begun to spread in several countries with an increase in COVID-19 cases with a new variant, the Omicron variant (B.1.1.529), and its presence has been detected in Indonesia. This variant is suspected of having a greater transmission power than other virus variants. This condition affects education in Indonesia. Learning activities using blended methods began in the 2021-2022 academic year at the Medical Faculty at the University of Muhammadiyah Malang. It is necessary to know the level of knowledge of students about the Omicron variant as one of the basics for preventing and controlling this virus on campus. To determine the level of knowledge of students in the Academic Stage of the Faculty of Medicine, the University of Muhammadiyah Malang, on the characteristics of the Omicron variant SARS-CoV2 virus, this study uses a descriptive type of research with a cross-sectional study approach. The results of the study of 300 respondents showed that the average level of knowledge was 77.13%. This average is included in the good criteria. The level of knowledge of students at the academic stage of the Faculty of Medicine, University of Muhammadiyah Malang, on the characteristics of the Omicron variant SARS-CoV-2 virus is included in good criteria.

Keywords: knowledge level, SARS-Cov2, Omicron

1. INTRODUCTION

The Covid-19 disease became known in 2020 in Wuhan, China, in December 2019. The World Health Organization (WHO) announced this disease under the new Coronavirus, COVID 19, on February 11, 2020. This disease spread throughout the world and was designated a pandemic by Public Health Emergency Concern on January 30, 2020(1).

Indonesia also cannot escape from this pandemic attack and the first reported emergence of Covid-19 in March 2020(2). The pandemic explosion in 2020 started to slow down at the end of 2020; however, it began to increase again in early 2021, reaching its peak in July-August 2021. The cause of this second wave of explosions is

Corresponding Author: Diah Hermayanti; email: diahhermayanti-umm@yahoo.com

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thought to be due to the effects of long holidays, public awareness of implementing health protocols at low levels, the entire population has not been vaccinated, and the emergence of several variants of the SARS-Cov2 virus.

In early to late 2021, several variants of the SARS-Cov2 virus were reported and identified in Indonesia, including alpha, beta, and delta variants. The delta variant dominates its distribution in Indonesia (3). The wave of the Covid-19 pandemic began to subside in the last three months of 2021; however, a worrying new variant of Omicron emerged. The Indonesian Ministry of Health, as of December 25, 2021, reported that 46 cases of Omicron variants had been identified in Indonesia based on the examination of whole-genome sequencing specimens by the Balitbangkes. This case is an imported case from patients undergoing quarantine from abroad (4).

The omicron variant is said to have the characteristics of being more easily spread, and the degree of severity caused is still unclear (5). All parties are expected to participate in the prevention and control of Covid-19 with the cause of this new variant, including in educational institutions, especially the Faculty of Medicine, University of Muhammadiyah Malang. It is necessary to know the level of knowledge of students at the academic stage of the Faculty of Medicine so that this data can be used as primary data in efforts to prevent and overcome it in the campus environment.

1.1. Coronavirus

The Corona virus that causes Covid 19 by WHO is named the 2019-nCoV virus.(6). This virus is a single-stranded positive-stranded RNA virus. This virus belongs to the Orthocoronavirinae subfamily, the family of the order Nidovirales, which is divided into subfamilies, namely α , β , γ genus and according to serotype and genomic characteristics.(7)(6)

Corona viruses are 50-100 nm in diameter, have an envelope, have spherical or elliptical particles, and are often pleomorphic. The surface of this virus is covered with protein S which is the main antigenic protein. (7)(6)

Coronavirus is a virus that causes zoonotic diseases. In humans, 6 Coronaviruses can infect, namely 229E, NL63 from the Polyomavirus genus, OC43 and HKU1 from the beta genus, Middle east respiratory syndrome-associated coronavirus (MERS-Cov), and severe acute respiratory syndrome-associated coronavirus (SARS-Cov). Coronavirus isolated from the lower respiratory tract of pneumonia patients in Wuhan is a new variant of the coronavirus.

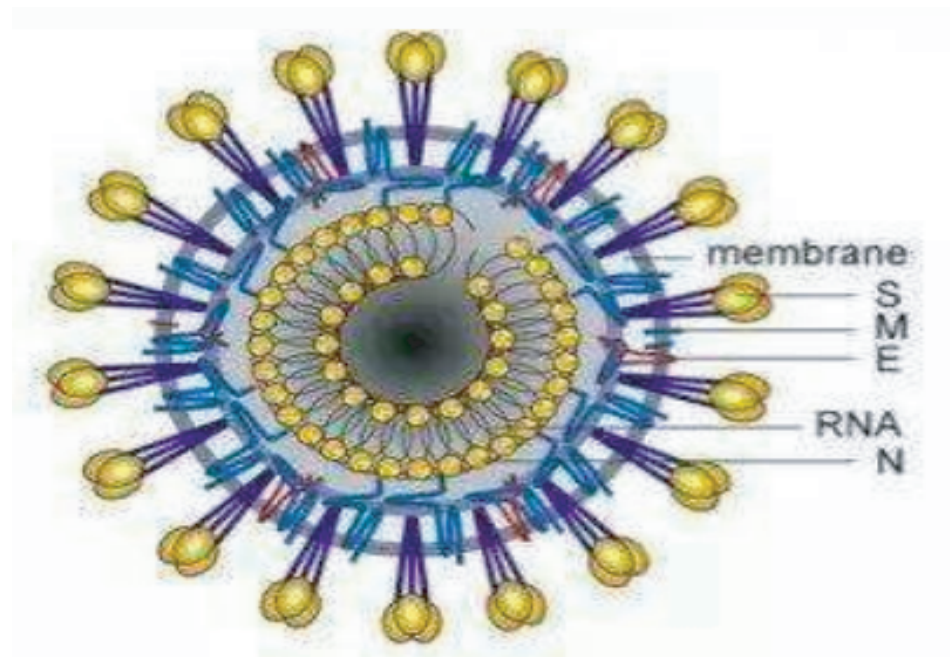


Figure 1: Corona Virus.(6).

The trans-membrane glycoprotein (spike protein) in the Corona virus causes the virus to attach to and enter the target cell through the Angiotensin Converting Enzymes 2 (ACE2) receptor (7)(8). The ACE2 receptor is expressed primarily by type II pneumocytes, but upper respiratory tract epithelial cells and small intestinal enterocytes also express this receptor. After entering the cell, the next viral RNA replication will occur in the target cell using RNA-dependent RNA polymerase (rdRp) (9). Viruses may have the ability to inhibit IFN's anti-viral response so that it can cause uncontrolled viral replication. The cytokines produced to drive the recruitment of neutrophil cells and macrophages, resulting in the hyperproduction of pro-inflammatory cytokines as the basis for the emergence of a cytokine storm.(10).

These innate cytokine responses can be predictive of the next clinical course. (11) B cells will then produce specific SARS-Cov-2 antibodies that can help neutralize the virus. (10)

1.2. Genomic surveillance Virus SARS-Cov2

The SARS-CoV2 genome is a viral gene that encodes instructions for viral growth and is organized into several parts. Genome sequencing is used to decode genes and learn more about viruses. Sequencing this genome makes the SARS-Cov2 virus identifiable, and its changes can be monitored over time, where these changes can lead to changes

in the characteristics of the virus. Viruses are constantly changing, and so is the SARS-Cov2 virus. These changes give rise to new virus variants from time to time, which may have different characteristics. Genomic surveillance of the SARS-Cov2 virus is also carried out continuously to monitor the emergence of new variants that have an impact on human health (12).

Changes in the virus that occur from time to time, do not really affect the properties of the virus. However, these changes can affect the speed of spread, disease severity, vaccine performance, medical treatment, diagnostic tools, public health and social measures (5).



Figure 2: The SARS-Cov-2 genome(12).

In collaboration with partners, expert networks, national authorities, institutions, and researchers, WHO have been monitoring and assessing the evolution of SARS-CoV-2 since January 2020. In late 2020, the emergence of variants that increase global public health risks led to the characterization of Variants of Interest (VOI) and Variants of Concern (VOCs) to prioritize global monitoring and research and ultimately inform the ongoing response to the COVID-19 pandemic (5).

Classification of SARS-CoV-2 virus variants, as follows::

1.3. Variant of concern (VOC)

Variants of SARS-CoV-2 that fall into this group have one or more significant public health changes: increased transmission capability, adverse epidemiological changes for Covid-19, increased virulence or clinical changes in disease, or decreased effectiveness of public health and social measures. or availability of diagnostic tools, vaccines, and therapies (5).

1. *Variant of interest (VOI)*

2. The SARS-Cov-2 variant that falls within these criteria has genetic changes that are thought to or are known to affect viral characteristics such as transmission, disease severity, immune failure, diagnostic or therapeutic failure; and identified as a cause of significant community or multiple-cluster transmission of COVID-19, in

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Additional amino acid changes monitored*	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	+S:484K +S:452R	United Kingdom, Sep-2020	18-Dec-2020
Beta	B.1.351	GH/501Y.V2	20H (V2)	+S:L18F	South Africa, May-2020	18-Dec-2020
Gamma	P.1	GR/501Y.V3	20J (V3)	+S:681H	Brazil, Nov-2020	11-Jan-2021
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	+S:417N +S:484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GRA	21K, 21L 21M	+R346K	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

Figure 3: Variants of concern (VOCs) (5).

many countries with increasing relative prevalence concomitantly with increasing number of cases over time, or other significant epidemiological impact indicating an emerging risk to global public health (5).

WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	14-Jun-2021
Mu	B.1.621	GH	21H	Colombia, Jan-2021	30-Aug-2021

Figure 4: Variant of interest (VOI), (5).

1.4. Omicron Variant SARS-Cov2 Virus

The CDC has carried out genomic surveillance during the pandemic to track the SARS-Cov-2 virus variant, which causes the Covid-19 disease and inform it.

The variant of the Omicron virus, namely SARS-CoV-2 B.1.1.529, was first reported to WHO on November 24, 2021, from specimens taken on November 11, 2021, in Botswana, and November 14, 2021, in South Africa. On November 26, 2021, WHO gave the name of the SARS-CoV-2 virus, B.1.1.529, with the name Omicron and classified it as a Variant of

Concern (VOC). On December 1, 2021, the first confirmed case of Omicron was identified in America (13). In Indonesia, the Ministry of Health reported that one confirmed case of Omicron was first placed on December 16, 2021, and up to December 26, 2021, 46 cases had been confirmed. Most of them are imported cases. (4)

This variant has a large number of mutations, some of which are alarming. Preliminary evidence suggests an increased risk of reinfection with this variant compared with other VOCs. The number of cases of this variant appears to be increasing in almost all provinces in South Africa. The current SARS-CoV-2 PCR diagnostics continue to detect this variant. Several laboratories have indicated that for one widely used PCR assay, one of the three target genes is not seen (called S gene dropout or S gene target failure), and therefore this test can be used as a marker for this variant, pending sequencing confirmation. . Using this approach, this variant has been detected at a faster rate than the previous spike in infections (5).

The sequencing data found that there were 14 co-mutations (including three deletions and one insertion) that had been previously reported and 22 new mutations (including three deletions) in the spike gene. In addition, there are ten mutations (including four deletions) in ORF1a (K856R, S2083del, L2084I, A2710T, T3255I, P3395H, L3674del, S3675del, G3676del, and I3758V), four of these mutations occurring in NSP6.

New mutations in the spike protein are highlighted in yellow. The previously identified monoclonal antibody binding sites were counted, mutations corresponding to these sites were labeled. (B) Amino acid residues in the trimer or monomer structure of SARS-CoV-2 S1 (PDB:6CRZ) using bands and surface diagrams are labeled on the RBD according to the mutation site of the Omicron variant (highlighted in cyan). NTDs are shown in light blue; RBD is shown in light yellow; The S2 subunit is shown in gray. Mutations are highlighted in red; deletions are highlighted in orange; the insert is highlighted in pink. ACE2 binding sites are labeled using red brackets and antibody binding sites are labeled using arrows (14)

Two mutations were identified in ORF1b (P314L and I1566V). 26 accumulated mutations in other genes, including NSP9b (P10S, E27del, N28del, and A29del), E (T9I), M (D3G, Q19E, and A63T), and N (P13L, E31del, R32del, S33del, R203K, and G204R) gene. Previously identified anti-RBD monoclonal antibody binding residues¹¹ (B38, 80R, S230, F26G19, m396, CR3022, VHH-72, S309, E465, C144, C121, C135, P2B-2F6, REGN10987, BD23, C002 , Epitope-B antibodies 553-15, COV2-2130, COV2-2196, S1BCD-H014, H11-H4, and CB6) to check for possible antibody escape mutations. There were eight new overlapping mutations at the binding site. Notably, the Q493R mutation overlaps the seven mAbs binding sites. (14)

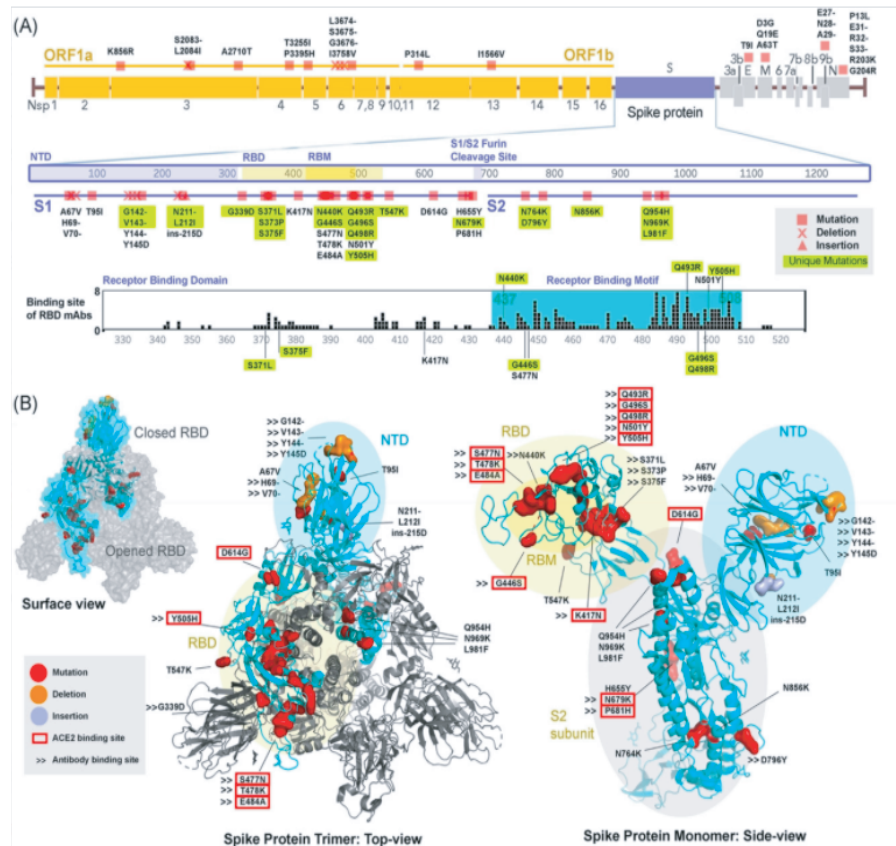


Figure 5: Mutation Changes in Omicron Variants. (A) Illustration of the mutation position of the Omicron variant.

1.5. Update of Omicron SARS-Cov-2 variant

Researchers in South Africa and worldwide are researching better to understand the Omicron variant virus from many aspects and will be informed once it becomes available.

The following are characteristics of the Covid-19 disease due to the Omicron variant (5):

a. Transmission:

It is not clear whether Omicron is more transmissible (e.g., more easily spread from person to person) than other variants, including Delta. There is an increasing number of people testing positive in the South African region affected by this variant, but epidemiological studies are underway to understand whether this is due to Omicron or other factors.

b. Severity:

The severity of Omicron infection is unclear whether it causes a more severe disease than infection with other variants, including Delta. Reports from South Africa suggest

an increase in hospitalization rates, but this may be due to an increase in the overall number of people infected, not to specific infections with Omicron. There is currently no information to suggest that the symptoms associated with Omicron differ from those of the other variants. The initial infections reported were among younger college students who tended to have milder disease, but understanding the severity of the Omicron variant would take days to weeks. All variants of COVID-19, including the Delta variant, which is dominant worldwide, can cause severe illness or death, particularly in the most vulnerable, so prevention is always the key.

c. Effectiveness of previous SARS-CoV-2 infection

Prior evidence suggests that there may be an increased risk of reinfection with Omicron (i.e., people who previously had COVID-19 may be reinfected more easily with Omicron), compared with other variants of concern, but information is limited. More information on this will be available in the coming days and weeks.

d. Vaccine effectiveness:

WHO is working with technical partners to understand the potential impact of this variant on prevention measures, including vaccines. Vaccines remain essential for reducing disease severity and mortality, including against the dominant circulating variant, Delta. Current vaccines remain effective against severe disease and death.

e. Current test effectiveness:

The most current test used to detect infections, including Omicron infections, is the PCR test, as with the other variants. Studies are ongoing to determine if there is an impact on other types of tests, including rapid antigen detection tests.

f. Effectiveness of current treatment:

Corticosteroids and IL6 Receptor Blockers will still be effective in treating patients with severe COVID-19. Other treatments will be assessed to see if they are still effective given the changes in viral moiety in the Omicron variant.

1.6. World Health Organization (WHO) Recommendation

WHO recommends the Omicron variant as a Variant of Concerns, as follows (5):

a. Recommendations for countries.

WHO recommends increasing surveillance and case sequencing; share genome sequences on available databases, such as GISAID; report initial cases or clusters to WHO; conduct field surveillance and laboratory assessments to better understand if Omicron has different transmission or disease characteristics, or impacts on the effectiveness of vaccines, therapeutics, diagnostics or public health and social measures.

Countries are advised to continue to implement effective public health measures to reduce the overall circulation of COVID-19, using risk analysis and a science-based approach. They must improve their public health and medical capacity to manage the increasing cases. WHO provides support and guidance to countries for preparedness and response. It is important to ensure that vulnerable groups, including health workers and the elderly, receive the first and second doses, as well as equitable access to treatment and diagnostics.

b. Recommendations for residents.

The most effective step that individuals can take to reduce the spread of the COVID-19 virus is to maintain a physical distance of at least 1 meter from other people; wear a suitable mask; open windows to increase ventilation; avoid poorly ventilated or crowded spaces; keep hands clean; coughing or sneezing into a bent elbow or tissue, and vaccinated.; menjaga tangan tetap bersih; batuk atau bersin ke siku atau tisu yang tertekuk; dan divaksinasi.

2. MATERIALS AND METHODS

This study uses a descriptive type of research with a cross sectional study approach. The study was conducted in January 2022. The population in this study were students of the academic stage of the Faculty of Medicine, University of Muhammadiyah Malang. Samples were taken by simple random sampling. The sample size was calculated using the Slovin formula with an error rate of 5%.

3. RESULTS

3.1. Respondent's Descriptive Data

The research data was obtained from filling out google forms by student respondents from the Faculty of Medicine, University of Muhammadiyah Malang. Respondents are active academic students from Class 2018, 2019, 2020, and 2021. The total number of

respondents is 300 students, exceeding the minimum number of respondents calculated by the Slovin formula, which is 286. Most of the respondents are female (70%), aged in the range of 17 to 23 years.

Respondents have the behavior of implementing the Health protocol, namely wearing masks properly (97.3%), and diligently washing hands when they feel their hands are dirty and contaminated (94%). Respondents who had a history of contracting Covid-19 infection were 69 students (23%).

TABLE 1: Respondent's Gender

Gender	n	%
Male	90	30
Female	210	70

(Primary data sources)

TABLE 2: Respondent's Age.

Age (year)	n	%
17	3	1
18	23	7,7
19	64	21,3
20	72	24
21	89	29,7
22	40	13,3
23	9	3

(Primary data sources)

3.2. Knowledge Level About Characteristics of Variant Omicron SARS Cov2 Virus

The research questionnaire consists of 10 statements of knowledge about the characteristics of the Omicron variant of Covid-19 and its conditions in Indonesia. The average score of the overall knowledge level is 77.13. These criteria are included in the suitable criteria, namely 76-100% correct answers.

4. DISCUSSION

All respondents answered the questionnaire regarding the potential mutation of the SARS-CoV-2 virus and answered 100% correctly. The SARS-CoV-2 virus generally has the potential to mutate from time to time. These changes can affect the speed of

TABLE 3: Knowledge of the Characteristics of the Omicron Variant of the SARS Cov2 Virus.

No.	Characteristics	Answer			
		True		False	
		n	%	n	%
1	The SARS-Cov2 virus over time, has the potential to mutate	300	100	0	0
2	Omicron variant SARS-Cov2 virus found only in South Africa.	282	94	18	6
3	The Omicron variant of the SARS-Cov2 virus is less infectious than the other variants.	278	92,7	22	7,3
4	The Omicron variant of the SARS-Cov2 virus causes Covid-19 disease with more severe symptoms than other variants.	138	46	162	54
5	The Omicron variant of SARS-Cov2 cannot be prevented by vaccination.	208	69,3	92	30,7
6	People who have been infected with Covid-19 (survivors) cannot be infected again with the Omicron variant	290	96,7	10	3,3
7	Covid-19 PCR examination cannot detect Omicron variant	239	79,7	61	20,3
8	The government pays less attention to the spread of the Omicron variant, because the pandemic has been going on for a long time	79	26,3	221	73,7
9	Patients with the Omicron variant of Covid-19 do not need to isolate or quarantine, because the population has already obtained Herd immunity	293	97,7	7	2,3
10	Health protocols by keeping a distance, washing hands with soap, and wearing masks, are less able to prevent the spread of the Omicron variant	207	69	93	31

(Primary data source)

spread, disease severity, vaccine performance, medical treatment, diagnostic tools, public health, and social measures (5). WHO, in collaboration with partners, expert networks, national authorities, institutions, and researchers, has been monitoring and assessing the evolution of SARS-CoV-2 since January 2020 and characterizing Variants of Interest (VOI) and Variants of Concern (VOCs) to prioritize monitoring and global research, and ultimately to inform the ongoing response to the COVID-19 pandemic(5). Genomic sequence analysis of Omicron variants has revealed many non-synonymous mutations, including several mutations involved in the transmission, disease severity, and immune shedding. Overall, more than 60 substitutions/deletions/inserts have been identified in the Omicron variant,12 making Omicron the variant with the most significant number of mutation sites of all the SARS-CoV-2 variants characterized so far (15).

The questionnaire regarding the spread of the SARS-Cov-2 variant of the Omicron virus was answered correctly by 94% of respondents. This data shows that there are still 6% of respondents who have less knowledge about the spread of the Omicron variant. The variant of the Omicron virus, namely SARS-CoV-2 B.1.1.529, was first reported to WHO on November 24, 2021, from specimens taken on November 11, 2021, in Botswana, and November 14, 2021, in South Africa.

WHO on 26 November 2021 gave the name of the SARS-CoV-2 virus, B.1.1.529 with the name Omicron and classified it as a Variant of Concern (VOC) (16). On December 1, 2021, the first confirmed case of Omicron was identified in America(13). In Indonesia, the Ministry of Health reported that one confirmed case of Omicron was first identified on December 16, 2021(4). It was reported that until January 12, 2022, 572 patients were detected who were exposed to the Omicron variant (17)

The questionnaire regarding the transmission power of the SARS-Cov-2 virus, the Omicron variant, was answered correctly by 92.7% of the respondents. This data shows that 7.3% of respondents still have less knowledge about the transmission power of the Omicron variant. It is unclear whether Omicron is more transmissible (e.g., more easily spread from person to person) than other variants, including Delta. An increasing number of people testing positive in the South African region are affected by this variant. Still, epidemiological studies are underway to understand whether this is due to Omicron or other factors (5). Epidemiological data show that the percentage of infections associated with the Omicron variant is 90% of the 25 days of the outbreak in South Africa, which is very high compared to the Beta variant, which increased by 50%, the delta variant by 80% around 100 days from the outbreak. The initial doubling times of the BBeta, Delta, and omicron variants were calculated from about 1.7 each; 1.5; 1.2 days. The data suggest that the Omicron variant may be more infectious than the Delta and Beta variant (15).

Questionnaires regarding the severity or severity of illness due to the SARS-Cov-2 variant of the Omicron virus were answered correctly by 46% of the respondents. This data shows that 54% of respondents still have less knowledge about the severity of Covid-19 caused by the Omicron variant. The severity of Omicron infection is unclear whether it causes a more severe disease than infection with other variants, including Delta. Reports from South Africa suggest an increase in hospitalization rates, but this may be due to an increase in the overall number of people infected, not to specific infections with Omicron. There is currently no information to suggest that the symptoms associated with Omicron differ from those of the other variants. The initial conditions reported were among younger college students who tended to have milder disease, but

understanding the severity of the Omicron variant would take days to weeks. All variants of COVID-19, including the Delta variant, which is dominant worldwide, can cause severe illness or death, particularly in the most vulnerable, so prevention is always key (5).

The questionnaire regarding the effectiveness of prevention by vaccines against the attack of the SARS-Cov-2 virus variant Omicron was answered correctly by 69.3% of respondents. These data indicate that there are still 30.7% of respondents who have less knowledge about the vaccine's effectiveness against Omicron variant attacks. WHO is working with technical partners to understand the potential impact of this variant on preventive measures, including vaccines. Vaccines remain essential for reducing disease severity and mortality, including against the dominant circulating variant, Delta. The current vaccine remains effective against severe disease and death (5). However, despite this, spike RBD is a primary target of neutralizing antibodies, and Omicron has 15 available substitutions in this region. Several antigenic sites were identified in RBD, namely RBS-A, RBS-B, RBS-C, CR302, and S309. All 15 mutations identified in Omicron spike RBD could be found at one or more of these antigenic sites, indicating potential Omicron resistance to monoclonal antibodies targeting these sites. As for antibody treatment in clinical use, a cocktail consisting of LY-CoV555 (also known as Bamlanivimab) and LY-CoV016 (also known as Etesevimab) has been approved for emergency use. Previous studies have revealed that mutations at positions 484 and 417 of the spike are associated with immune evasion. Beta and Gamma variants can escape neutralization of LY-CoV555 (due to E484K) and LY-CoV016 (due to K417N/T). Since the Omicron variant also contains the E484A and K417N mutations, likely, Omicron will also fight these antibodies. (15)

The questionnaire regarding the knowledge of whether Covid survivors can still be infected with the SARS-Cov-2 variant of the Omicron virus was answered correctly by 96.7% of respondents. This data shows that there are still 3.3% of respondents who have less knowledge about the transmission power of the Omicron variant in Covid-19 survivors. Prior evidence suggests that there may be an increased risk of reinfection with Omicron (i.e., people who previously had COVID-19 may be reinfected more easily with Omicron) compared with other variants of concern, but the information is limited (5).

The questionnaire regarding the knowledge of the ability of PCR to detect the SARS-Cov-2 virus, the Omicron variant, was answered correctly by 79.7% of the respondents. This data shows that 20.3% of respondents still have less knowledge. The most current test used to detect infections, including Omicron infections, is the PCR test, as with the other variants. The current SARS-CoV-2 PCR diagnostics continue to witness this

variant. Several laboratories have indicated that for one widely used PCR assay, one of the three target genes is not seen (called S gene dropout or S gene target failure). Therefore this test can be used as a marker for this variant, pending confirmation of the whole gene sequencing. Using this approach, this variant has been detected at a faster rate than the previous spike in infections (5). Studies are ongoing to determine if there is an impact on other types of tests, including rapid antigen detection tests (5).

The questionnaire regarding the government's efforts to prevent the outbreak of SARS-Cov-2 virus cases, the Omicron variant, was only answered correctly by 26.3% of respondents. This data shows that most of the respondents (73.3%) are unaware of the government's efforts to prevent the emergence of the third wave of Covid-19 due to the Omicron variant in Indonesia. Indonesia is a member of WHO and implements all regulations recommended by WHO. WHO recommends increasing surveillance and case sequencing; sharing genome sequences on available databases, such as GISAID; reporting initial cases or clusters to WHO; conduct field surveillance and laboratory assessments to understand better if Omicron has different transmission or disease characteristics or impacts on the effectiveness of vaccines, therapeutics, diagnostics or public health and social measures. Countries are advised to continue implementing effective public health measures to reduce the overall circulation of COVID-19, using risk analysis and a science-based approach. They must improve their public health and medical capacity to manage the increasing cases. WHO provides support and guidance to countries for preparedness and response (5).

The questionnaire regarding the isolation or quarantine of Covid-19 sufferers due to the Omicron variant was answered correctly by 97.7% of respondents. This data shows that there are still 2.3% of respondents who have less knowledge about isolation or quarantine in cases of the Omicron variant. Isolation or quarantine of probable and confirmed COVID-19 patients with the Omicron variant is a crucial first step to breaking the chain of transmission. Based on the research mentioned above, this variant has a higher ability to spread or infect than other variants.

The questionnaire regarding the prevention of transmission of the SARS-Cov-2 variant of the Omicron virus by carrying out health protocols were answered correctly by 69% of respondents. These data indicate that 31% of respondents still have less knowledge about the effectiveness of health protocols in preventing the spread of Omicron variants. The most effective step that individuals can take to reduce the spread of the COVID-19 virus is to maintain a physical distance of at least 1 meter from other people; wear a suitable mask; open windows to increase ventilation; avoid poorly ventilated or crowded

spaces; keep hands clean; coughing or sneezing into a bent elbow or tissue, and vaccinated (5).

5. CONCLUSION

The level of knowledge of students at the academic stage of the Faculty of Medicine, University of Muhammadiyah Malang about the characteristics of the SARS-Cov-2 variant of the Omicron virus is included in good criteria.

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