

Review in Mutated Strains of Corona Virus

Dr. Nagham Mahmood Aljamali¹, Zahraa Abdul Kareem makki², Enas Raheem Al_kidsawey³

¹Professor, Ph. D, Department of Chemistry, Organic Synthetic Chemistry, Iraq.,

²Assist. Lecturer, Medical laboratory techniques Department, Al_Hilla University College, Iraq.

³Assist. Lecturer, Medical laboratory techniques Department, Al_Hilla University College, Iraq.

Received Date: 02 August 2021

Revised Date: 04 September 2021

Accepted Date: 16 September 2021

Abstract - The recent review conversed about mutated strain., The new mutated strains of the Corona virus are the mutated strain of Covid 19, the strain - also known as "variant" - is a version of the virus that includes a group of mutations, which means that each mutated strain includes a group of mutations. A mutation is a change in the arrangement of the genetic material in the virus, and some of these mutations may not leave a trace in the virus, but some of them may affect its ability to transmit and infection. There have been previous mutations recorded for the Corona virus, including the English, Brazilian and South African strains., Pfizer has designed a suitcase-sized container that "keeps doses at minus 70 for 10 days, holding 1,000 to 5,000 doses, and needs to be filled with fresh, dry ice within 24 hours, then tracked via GPS until it reaches the desired location, with Not to open it more than twice a day, and for one minute each time," according to what was quoted today by leaked documents from Pfizer yesterday, and its information indicates that vaccination will not be an easy process, but rather difficult for obstacles, especially since the effectiveness of the vaccine begins 28 days after vaccination.

Keywords - mutation ,Covide.19 ,Corona Virus, infection.

I. Introduction

This mutation may be able to spread more easily than previous forms of the virus. This is due to a mutation they carry called (L452R) that affects the virus's "spike" protein, the "key" that the virus uses to enter the body's cells. The mutation discovered in California called (B1427) contains the same mutation as (L452R) and is estimated to be about (20%) more transmissible than the previous form of the coronavirus that was circulating during the first wave. Mutations such as L452R that help in the link do not necessarily cause more severe disease or make the coronavirus more deadly. For example, the California mutation B1427 (B1427) appears to spread more easily, and preliminary research has not found it to be associated with more severe infections or higher viral loads. The same could be true of the mutation in India (B1617) although this remains to be investigated. But a particular concern is the effect the mutation might have on the effectiveness of the

vaccine. The vast majority of vaccines developed against the Corona virus rely on targeting the spike protein. Because the protein is on the outside of the virus, this is what your immune system often "sees" during infection, and thus makes effective antibodies against it. If mutations change the shape of the spike protein, these antibodies may become less effective. In fact, preliminary studies suggest that the (L452R) mutation can help the virus evade the immune system. Furthermore, (B1617) carries a second mutation, called (E484Q), which also alters the spike protein. Research suggests that similar mutations (affecting the same region of the skeletal protein) may make the virus less susceptible to pre-existing antibodies.

II. The danger of mutation and mutation of the virus

According to officials in India, the high number of cases in the country is not linked to these mutations, as the "B1617" mutations have not been detected in large enough numbers to determine whether they are directly responsible. However, this may be due to a lack of data, and many experts have stressed the importance of sequencing the virus to get a better picture. And India recorded more than two thousand deaths due to Covid-19 and about 300 thousand new infections within 24 hours in one, which is one of the largest daily numbers in the world since the beginning of the epidemic, according to official data reported by Agence France-Presse. Ministry of Health figures indicate that the number of new infections recorded reached (295,000) in the last (24 hours) , which brings the total number of infections to (15.6 million) in India. As for the number of deaths, it reached 2023, bringing the total number of those who died from the epidemic to (182,553 people). And the World Health Organization has confirmed since the sharp rise in infections that India - with a population of 1.3 billion people - is fighting a "big battle again." "The situation was under control a few weeks ago, and the second wave came like a hurricane," .

III. Mutations and mutations in viral strains

Like all viruses, the Corona virus (SARS-CoV-2) is constantly mutating, and some random mutations allow it to



spread further and resist acquired immune systems and vaccines. Scientifically speaking, a virus is a genetic material protected by a lipid membrane. With regard to the Corona virus, this membrane is covered with spicules consisting of 3 identical proteins that enable it to cling to human cells, and then fuse the membranes so that the viral genetic material can penetrate the cell. Then, the virus transforms the cell's machinery to produce its own protein and reproduce its cells. But this "reproduction" process is not perfect, as an error regularly slips into the different copies, and most of the time the "variable" virus disappears as quickly as it first appeared, but it succeeds in reproducing and spreading between humans sometimes.

IV. How do dangerous strains develop?

The authors show that this natural process allows the virus to evolve over time. Bruno Canard, director of research at the National Center for Scientific Research, which specializes in corona viruses, explains that "if the virus does not mutate, it is easy to eliminate it very quickly. Just likewise, if it mutates a lot, it produces a very large number of incomplete and incomplete copies." capable of multiplying and spreading. Researchers estimate that the SARS-CoV-2 virus records about two new mutations per month. Based on the original strain that was discovered in China, the virus formed during the last period an evolutionary tree that now contains thousands of branches, but only some of them pose a clear danger. Among the rest, the English, Brazilian and South African strains have gained worldwide attention. "These strains have gone beyond the evolutionary framework of the virus that has been observed so far," explains Etienne Simon Laurier, a specialist in RNA viruses at the Pasteur Institute. These strains are accompanied by dozens of new mutations, and although it is difficult to prove this, the hypothesis that the virus multiplies every time and for a long time is put forward in people with weak immunity to the point of accumulating all these mutations, before spreading throughout the world. In addition, some of these mutations seem to give the virus the advantage of spreading very quickly, and taking precedence over other strains, which is what happened with the English, Brazilian and South African strains.

V. Most Contagious Mutations

Scientists' concerns today focus in particular on the mutations that can occur in the spike, which is centered on the surface of the virus. The spike is the virus's weapon that enables it to penetrate human cells, and it is at the same time its weak point that scientists have exploited to make vaccines, as antibodies in the immune system rush to stick to these spicules and prevent them from entering cells. The researchers fear two things, firstly, the emergence of a mutation at the level of the spike that makes the virus more dangerous and more contagious, and secondly, that the immune system - which has already received the vaccine -

does not recognize this mutation, so it becomes unable to provide the necessary protection for the body and the vaccination becomes ineffective. For his part, French researcher Etienne Simon Laurier explains that the more intense the spread of the virus, the more mutations will continue to appear, and the great risk is that vaccines will not be effective in addressing new random mutations, which means the epidemic will continue.

VI. Mechanism of Mutation in Covid

All viruses mutate naturally over time, and SARS-CoV-2 is no exception. Since the virus was first identified in early 2020, thousands of mutations have appeared. The mutated viruses are called strains, and most changes have little or no effect on the characteristics of the virus, according to the World Health Organization (WHO), and many of them disappear over time. But every now and then the virus gets lucky by mutating in a way that helps it survive and spread. Experts around the world are watching the way the SARS-CoV-2 virus (coronavirus) has developed so that governments can respond to important changes in the virus.

VII. Delta strain

Much attention has recently been focused on the Delta breed, which has proven to be a greater threat to public health than previous breeds. First, the infection rate of this strain is about 60 percent higher than the infection rate of the alpha strain, which actually has a 50 percent higher infection rate compared to the original strain of the Corona virus. The Delta strain already caused a second deadly wave of infections in India in April and May, and it has also become the dominant strain in Britain. This strain has been monitored in more than 90 countries around the world, with confirmed outbreaks in the United States, China, Africa, Scandinavia and the Pacific region. UK data shows that people infected with the delta strain who did not receive the vaccine are twice as likely to be hospitalized than those who have had the alpha strain.

VIII. Studies have also shown that the Delta strain is associated with different symptoms compared to previous strains of the Corona virus

The classic symptoms of Covid-19 approved by the National Health Service in Britain are persistent cough, fever and loss of sense of smell or taste. Professor Tim Spector, who studies Covid symptoms through the Zoe Covid app, says that although fever is still very common in the Delta strain, loss of smell is no longer among its top ten symptoms. Headaches, sore throat and runny nose are among the most common symptoms associated with infection with this strain in Britain. Prof Spector explains that this makes the virus look like a "severe cold" for young people, which increases the risk of them carrying the virus without realizing and continuing to infect other people.

IX. Delta Plus and Lambda strains

India is recovering from a second wave of Covid infection that swept the country in April and May and on June 23 India listed the Delta Plus mutation, a form of the current Delta strain, among the strains of concern. It was first described by Public Health England as being similar to delta but with an additional mutation (K417N) vesbic protein that enables the virus to attach itself to infected cells. Delta Plus is found in 9 other countries which are the USA, Britain, Portugal, Switzerland, Japan, Poland, Nepal, Russia and China. The Indian Ministry of Health says the Delta Plus strain spreads more easily, binds more easily to lung cells, and is potentially resistant to a type of treatment called monoclonal antibody therapy. But leading virologists say there is not enough data to support these conclusions and the World Health Organization has not classified it as a concern or concern. The World Health Organization says the lambda strain is responsible for a significant increase in transmission in Peru, Chile, Argentina and Ecuador. The World Health Organization says the lambda strain is responsible for a significant increase in transmission in Peru, Chile, Argentina and Ecuador. However, the World Health Organization has recently added the lambda strain to the list of strains of interest. This strain has been associated with cases of Covid in many countries, especially in South America and the Andean region (Peru, Chile, Argentina and Ecuador). This strain has been found in 29 countries, according to the Global Bird Flu Data Sharing Initiative, which also shares data on the coronavirus. "It is likely that the lambda strain is more infectious, so this is the only way to explain its rapid growth," Pablo Tsukayama, a bacteriologist from Cayetano Heredia University in Peru and one of the researchers behind the identification of the new strain, told the BBC.

X. Do vaccines provide protection against strains?

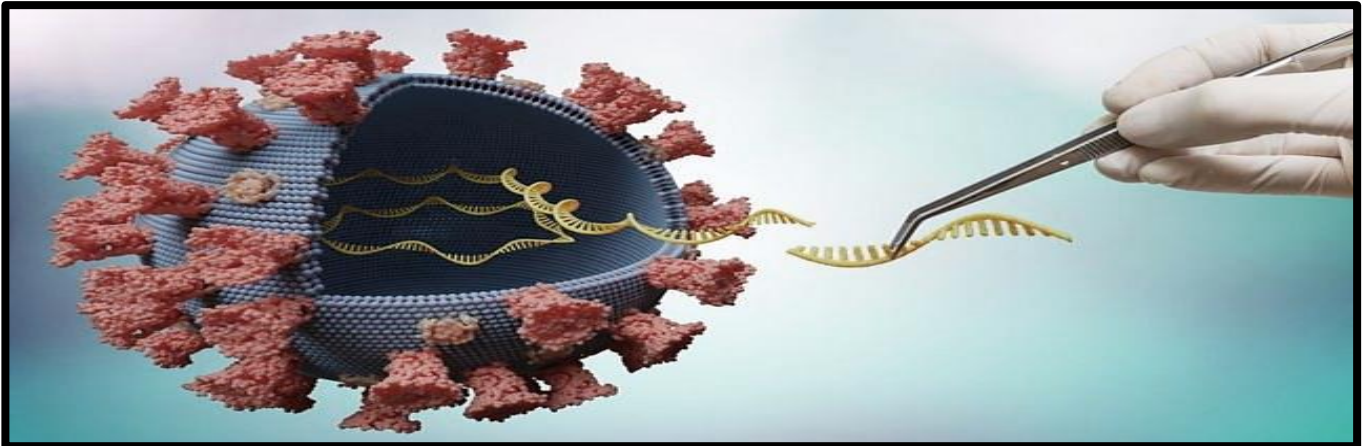
Studies show that available Covid vaccines are still effective against new strains. Fortunately, studies have shown that the available vaccines are still effective against the new strains of SARS-CoV-2, but they are less effective against the newer strains compared to the original strain of the Corona virus, especially after only one dose of the vaccine. In a study by Public Health England, a single dose of Pfizer or AstraZeneca provided only 33% of protection against a delta strain, compared to 50% against an alpha strain. However, after the second dose, these rates rose to 88 percent for the Pfizer vaccine, and 60 percent for the AstraZeneca vaccine. A separate study by Oxford University confirmed that the Pfizer and AstraZeneca vaccines were effective against the delta and kappa strains detected in India. In the journal Cell, the researchers referred to the two strains with their common ancestry code, saying: "There is no evidence of widespread infection, which indicates that the current generation of vaccines will provide protection against the B.1.617 strain." But because the vaccines are not 100 percent effective, the strains will also lead to hospitalizations and even deaths

among the people who have been vaccinated, says the US Centers for Disease Control and Prevention (CDC), especially among people who took only one dose of the vaccine. the vaccine. According to the Centers for Disease Control and Prevention, more than 144 million people were fully vaccinated in the United States as of June 14, and the same period saw 3,729 infections and 671 deaths.

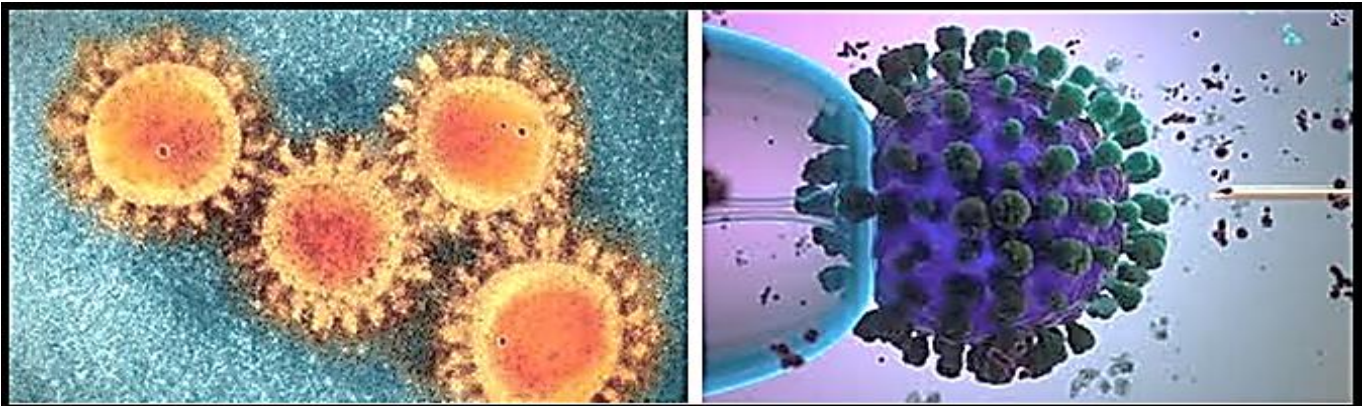
XI. How can we combat new strains?

Increasing the frequency of vaccination is a challenge in low to middle income countries. Increasing the frequency of vaccination is a challenge in low to middle income countries. In response to the rapid spread of the Delta strain in Britain, governments in England, Scotland and Northern Ireland are working to reduce the time gap between the first and second doses of the vaccine for older groups. Those over 40 can now book appointments after 8 weeks, a shorter time gap than the previous 12 weeks, with vaccinations also taking place on the weekends:

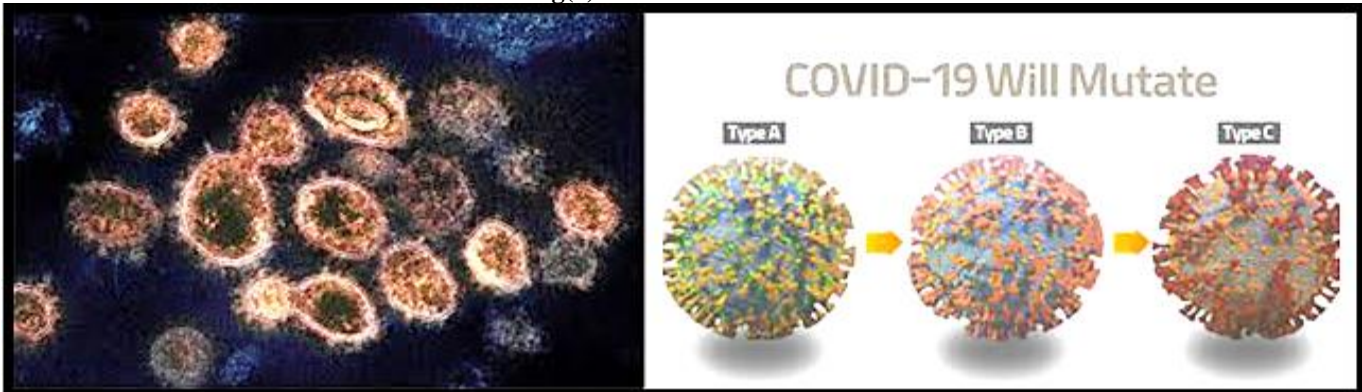
- a) Viruses tend to mutate, which is why new vaccines are required to be developed each year.
- b) Scientists have detected about 300,000 strains of corona so far, but the latter is the fastest in spreading.
- c) The novel coronavirus has a "self-correcting" mechanism to preserve its DNA.
- d) The new strain may have appeared in mid-September in London or was, according to what the British government adviser, Patrick Vallance, revealed.
- e) The new strain is responsible for 60% of Corona infections in Britain during the past week.
- f) The new Corona strain spreads faster than the first strain, and is 70 percent more transmissible.
- g) Until now, scientists do not know whether the new strain is associated with higher mortality rates or not.
- h) Epidemiologists do not know whether the new strain is affected by corona vaccines or not.
- i) The German government announced that approved vaccines are effective with the new strain.
- j) Epidemiologists hope that the new vaccines will be effective in stopping the spread of the virus in all its strains.
- k) The new strain carries a mutation called "N501Y" in the "spicule" protein of the Corona virus, which is present on its surface and allows it to attach to human cells to penetrate.
- l) The new strain was spotted intermittently around the world in Australia last June, the United States last July, and in Brazil in April.
- m) The new strain has the ability to spread in the blood circulation rapidly.
- n) Epidemiologists are beginning to analyze the behavior of the new strain, and to study the effect of its antibody response. Epidemiologists do not know if this strain is related to the transmission of the virus to minks, which appeared on farms in Spain and Denmark., figures(1,2).



Fig(1): Mutation in Virus



Fig(2): Corona Delta strain



Fig(3): Development of Corona strain

XII. Conclusion

Variant of interest or variant under investigation; A term under which a group of SARS-CoV-2 mutations are categorized. This classification is the third and last in the scale of classifications for Corona mutations in the United States, and second and penultimate in the same scale in the United Kingdom and the European Union, topped by the worrying degree Then the classification of mutations with

severe consequences (in the United States), followed by the classification of mutations under control in the United Kingdom and the European Union, the latter classification is not used in the United States. According to the Centers for Disease Control and Prevention, there are currently a number of interesting tagged mutations: B.1.617.

REFERENCES

- [1] Alwan A ·Mahjour J ·Memish ZA, Novel coronavirus infection: time to stay ahead of the curve. *Eastern Mediterranean Health Journal*, 19 Suppl, 12(4)1 (2013) S3–4. PMID 23888787., Available at : http://www.xinhuanet.com/english/2021-02/02/c_139716241.htm
- [2] Laude H ·Rasschaert D ·Delmas B ·Godet M ·Gelfi J ·Charley B . Molecular biology of transmissible gastroenteritis virus. *Veterinary Microbiology*, 23 (1–4) (1999) 147–54. PMID 2169670 . doi:10.1016/0378-1135(90)90144-K., Available at : <https://www.voanews.com/covid-19-pandemic/malawi-sticks-astazeneca-despite-concerns-over-efficacy>
- [3] Nagham Mahmood Aljamali, Enas Raheem Al_kidsawey, Zahraa Abdul Kareem Makki. Review in Stages of Development of Corona Virus Vaccines. *International Journal of Analytical and Applied Chemistry*. 7(1) (2021) 17–25p.
- [4] Nagham Mahmood Aljamali, Farah Wadai El-Taei, Asaad H Enad ., Survey in Forms of Corona Vaccines Licensed by Global Health Organizations, *Journal of Pharma and Drug Regulatory Affairs.*, 3(2) (2021) 55-62.
- [5] Sola I ·Alonso S ·Zúñiga S ·Balasch M ·Plana-Durán J ·Enjuanes L, Engineering the transmissible gastroenteritis virus genome as an expression vector inducing lactogenic immunity. *Journal of Virology*, 77 (7) (2003) 4357–69. PMC 150661. PMID 12634392. doi:10.1128/JVI.77.7.4357-4369.2003.
- [6] Tajima M . Morphology of transmissible gastroenteritis virus of pigs. A possible member of coronaviruses. Brief report. *Archiv für die Gesamte Virusforschung.*, 29 (1) (1970) 105–8 . PMID 4195092 doi:10.1007/BF01253886.
- [7] Liu P ·Shi L ·Zhang W ·He J ·Liu C ·Zhao C ·Kong S ·Loo JF ·Gu D ·Hu L., Prevalence and genetic diversity analysis of human coronaviruses among cross-border children. *Virology Journal*, 14 (1) (2019) 230. PMC 5700739 PMID 29166910. doi:10.1186/s12985-017-0896-0.
- [8] Forgie S ·Marrie TJ, Healthcare-associated atypical pneumonia". *Seminars in Respiratory and Critical Care Medicine*, 30 (1) (2009) 67–85. PMID 19199189. doi:10.1055/s-0028-1119811.
- [9] Aseel Mahmood Jawad, Nagham Mahmood Aljamali, Saher Mahmood Jwad. Development and Preparation of ciprofloxacin Drug Derivatives for Treatment of Microbial Contamination in Hospitals and Environment, *Indian Journal of Forensic Medicine & Toxicology*, 14 (2020) (2) 1115-1122.
- [10] Imad Kareem Alwan Alsabri, Hasaneen Kudhair Abdullabass, Nagham Mahmood Aljamali., Invention of (Gluta.Sulfazane-Cefixime) Compounds as Inhibitors of Cancerous Tumors., *Journal of Cardiovascular Disease Research*, 11(2)(2020).
- [11] Nagham Mahmood Aljamali, Imad Kareem Alwan Alsabri, Aseel Mahmood Jawad, Muayad Baqer Mohammed Alfahham, Hanan Ali Hussein. Scientific Study:(Solutions and Recommendations to avoid the Spread of Corona Virus Covid 19 in Iraq) , *Forefront Journal of Engineering &Technology*, 2(4) (2020) 13-22.
- [12] Nagham Mahmood Aljamali ,Kawther Mejbel Hussein., Review on Benefits and Harms of Nutritional Supplements on Health ., *Journal of Pharma and Drug Regulatory Affairs.*, 3(1) (2021) 42-49.
- [13] Alexander E Gorbalenya ·Susan C. Baker ·Christian Drosten ·Bart L. Haagmans ·Benjamin W. Neuman ., The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2 , *Nature Microbiology*, 544(5) (2019) 536, <https://dx.doi.org/10.1038/S41564-020-0695-Z> — <https://pubmed.ncbi.nlm.nih.gov/32123347>
- [14] Nagham Mahmood Aljamali, Aseel Mahmood Jawad, Imad Kareem Alwan Alsabri., *Public Health in Hospitals*, 1 First Edition, (2020), Eliva Press ,ISBN: 9798636352129 .
- [15] Liu P, Shi L, Zhang W, He J, Liu C, Zhao C, et al. Prevalence and genetic diversity analysis of human coronaviruses among cross-border children. *Virology Journal*. 14 (1)(2017)230. doi:10.1186/s12985-017-0896-0. PMC 5700739. PMID 29166910.
- [16] Aseel Mahmood Jawad, Nagham Mahmood Aljamali., Innovation, Preparation of Cephalixin Drug Derivatives and Studying of (Toxicity & Resistance of Infection), *International Journal of Psychosocial Rehabilitation*, 24(04) (2020) 3754-3767 .
- [17] Gorbalenya AE. Severe acute respiratory syndrome-related coronavirus – The species and its viruses, a statement of the Coronavirus Study Group. *bioRxiv*, 02(07) (2020). 937862. doi:10.1101/2020.02.07.937862.
- [18] Huynh J, Li S, Yount B, Smith A, Sturges L, Olsen JC. Evidence supporting a zoonotic origin of human coronavirus strain NL63. *Journal of Virology*, 86 (23) (2012) 12816–25. doi:10.1128/JVI.00906-12 . PMC 3497669 . PMID 22993147.
- [19] Nagham Mahmood Aljamali., Abdullabass, H. K., Jawad, A. M., Alfatlawi, I. O., & Jawd, S. M. Review on Types of Automatic Sterilization Systems in Hospitals. *International Journal of Industrial Biotechnology and Biomaterials*, 6(1) (2020) 15-21.
- [20] Nagham Mahmood Aljamali., A M Jawad., Alfatlawi, I. O., Saher Mahmood Jawd. (2020). Review on Hospital Bacteria (Causes, Infections, Prevention). *Infection*, 11(2020) 16.
- [21] Vijaykrishna D, Smith GJ, Zhang JX, Peiris JS, Chen H, Guan Y. Evolutionary insights into the ecology of coronaviruses". *Journal of Virology*. 81(8) (2007) 4012–20. doi:10.1128/jvi.02605-06. PMC 1866124 . PMID 17267506.
- [22] Nagham Mahmood Aljamali , Hasaneen Kudhair Abdullabass, Imad Kareem Alwan Alsabri, Nemah Sahib Mohammed Husien, Ahmed Adnan Abdul Hussein, Wisam Hassan Ali Alfartosi., Review on Reasons for The Spread of Corona Virus., *International Journal of Cell Biology and Cellular Process*, 6(1)(2020).
- [23] Nagham Mahmood Aljamali .,Imad Kareem Alwan A., Hasaneen Kudhair Abdullabass., Aseel Mahmood Jawad .,Intisar O Alfatlawi ., Ahmed Adnan Abdul H .,Manar Ghayath Abd Almutalib A , Review in SARS-Corona Virus (Types, Infection, Diagnosis, Chemical Antiseptics for this Virus), *Journal of Science and Technology*, 05(3) (2020) 111-224.
- [24] Nagham Mahmood Aljamali ,Muhsin Mohammed Al Najim (2020). Review in Hospital-Acquired Infection. *International Journal of Advances in Engineering Research*. 20(3) (2020) 7-20.
- [25] Nagham Mahmood Aljamali., Aseel Mahmood Jawd.,Anaam Jawad Alabbasy, Layla Ali M S. A Literature Review on Types of Contamination (Biological, Chemical, Medical). *International Journal of International Journal of Green Chemistry* .; 5 (1) (2019) 7–14.
- [26] Gouilh MA, Puechmaille SJ, Gonzalez JP, Teeling E, Kittayapong P, Manuguerra JC. SARS-Coronavirus ancestor's foot-prints in South-East Asian bat colonies and the refuge theory. *Infection, Genetics and Evolution*. 11 (7) (2011) 1690–702. doi:10.1016/j.meegid.2011.06.021 PMID 21763784.
- [27] Cui J, Han N, Streicker D, Li G, Tang X, Shi Z, et al. Evolutionary relationships between bat coronaviruses and their hosts. *Emerging Infectious Diseases*. 13 (10) (2007) 1526–32. doi:10.3201/eid1310.070448 . PMC 2851503. PMID 18258002.
- [28] Crossley BM, Mock RE, Callison SA, Hietala SK, Identification and characterization of a novel alpaca respiratory coronavirus most closely related to the human coronavirus 229E. *Viruses*, 4 (12) (2012) 3689–700, doi:10.3390/v4123689. PMC 3528286. PMID 23235471.
- [29] Forgie S, Marrie TJ. Healthcare-associated atypical pneumonia. *Seminars in Respiratory and Critical Care Medicine*. 30 (1) (2009) 67–85. doi:10.1055/s-0028-1119811. PMID 19199189.
- [30] Corman VM, Muth D, Niemeyer D, Drosten C. Hosts and Sources of Endemic Human Coronaviruses. *Advances in Virus Research*. 100 (2018) 163–88. doi:10.1016/bs.aivir.2018.01.001. ISBN 978-0-12-815201-0 . PMID 29551135.
- [31] Wang C, Horby PW, Hayden FG, Gao GF. A novel coronavirus outbreak of global health concern. *Lancet*. 395 (10223) (2020) 470–473. doi:10.1016/S0140-6736(20)30185-9. PMID 31986257.
- [32] Lau EH, Hsiung CA, Cowling BJ, Chen CH, Ho LM, Tsang T, et al. A comparative epidemiologic analysis of SARS in Hong Kong, Beijing and Taiwan. *BMC Infectious Diseases*. 10(50) (2010). doi:10.1186/1471-2334-100. PMC 2846944. PMID 20205928.

- [33] Karlberg J, Chong DS, Lai WY. Do men have a higher case fatality rate of severe acute respiratory syndrome than women do?. *American Journal of Epidemiology*. 159 (3) (2004) 229–31. doi:10.1093/aje/kwh056. PMID 14742282.
- [34] Oh MD, Park WB, Park SW, Choe PG, Bang JH, Song KH, et al. (March 2018). Middle East respiratory syndrome: what we learned from the 2015 outbreak in the Republic of Korea. *The Korean Journal of Internal Medicine*. 33 (2) (2018) 233–246. doi:10.3904/kjim.2018.031. PMC 5840604. PMID 29506344.
- [35] Namendys-Silva SA. Respiratory support for patients with COVID-19 infection. *The Lancet. Respiratory Medicine*. doi:10.1016/S2213-2600(20) 30110-7. PMID 32145829.
- [36] Douclef M, Scientists Go Deep On Genes Of SARS-Like Virus. Associated Press. Archived from the original on 2012-09-27. Retrieved 2012-09-27.
- [37] Falco M. New SARS-like virus poses medical mystery. *CNN Health*. Archived from the original on 2013-11-01. Retrieved 2013-03-16.
- [38] Kelland K. New virus not spreading easily between people: WHO. *Reuters*. Archived from the original on 2012-11-24. Retrieved 2013-03-16.
- [39] Sang-Hun C. MERS Virus's Path: One Man, Many South Korean Hospitals. *The New York Times*. Archived from the original on 2017-07-15. Retrieved 2017-03-01.
- [40] Cohen J. Wuhan seafood market may not be source of novel virus spreading globally. *Science Mag American Association for the Advancement of Science. (AAAS)*. Archived from the original on 2020-01-27. Retrieved 2020-01-29.
- [41] Eschner K. We're still not sure where the COVID-19 really came from. *Popular Science*. Archived from the original on 2020-01-30. Retrieved 2020-01-30.
- [42] Hui DS, I Azhar E, Madani TA, Ntoumi F, Kock R, Dar O. The continuing 2019-nCoV epidemic threat of novel coronaviruses to global health—The latest 2019 novel coronavirus outbreak in Wuhan, China. *International Journal of Infectious Diseases*. 91 (2020) 264–66. doi:10.1016/j.ijid.2020.01.009. PMID 31953166.
- [43] Eschner K. We're still not sure where the COVID-19 really came from. *Popular Science*. Archived from the original on 2020-01-30. Retrieved 2020, 1, 30.
- [44] Murphy FA, Gibbs EP, Horzinek MC, Studdart MJ. *Veterinary Virology*. Boston: Academic Press. (1999) 495–508. ISBN 978-0-12-511340-3.
- [45] Bande F, Arshad SS, Bejo MH, Moeini H, Omar AR, Progress and challenges toward the development of vaccines against avian infectious bronchitis. *Journal of Immunology Research*. 2015: 424860. doi:10.1155/2015/424860. PMC 4411447. PMID 25954763.
- [46] Murray J (2014-04-16). "What's New With Ferret FIP-like Disease?" (xls). Archived from the original on 2014-04-24. Retrieved 2014-04-24.
- [47] Weiss SR, Navas-Martin S. Coronavirus pathogenesis and the emerging pathogen severe acute respiratory syndrome coronavirus". *Microbiology and Molecular Biology Reviews*. 69 (4) (2005) 635–64. doi:10.1128/MMBR.69.4.635-664.2005. PMC 1306801. PMID 16339739.
- [48] Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, et al. Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. *Nature*. 556 (7700) (2018) 255–58. Bibcode:2018Natur.556.255Z. doi:10.1038/s41586-018-0010-9. PMID 29618817.
- [49] Tirota E, Carbajal KS, Schaumburg CS, Whitman L, Lane TE. Cell replacement therapies to promote remyelination in a viral model of demyelination. *Journal of Neuroimmunology*. 224 (1–2)(2010)101–07. doi:10.1016/j.jneuroim.2010.05.013. PMC 2919340. PMID 20627412.
- [50] Cruz JL, Sola I, Becares M, Alberca B, Plana J, Enjuanes L, Zúñiga S., Coronavirus gene 7 counteracts host defenses and modulates virus virulence. *PLoS Pathogens*. 7 (6) (2011) e1002090. doi:10.1371/journal.ppat.1002090. PMC 3111541. PMID 21695242.
- [51] Cruz JL, Becares M, Sola I, Oliveros JC, Enjuanes L, Zúñiga S. Alphacoronavirus protein 7 modulates host innate immune response. *Journal of Virology*. 87 (17) (2013) 9754–67. doi:10.1128/JVI.01032-13. PMC 3754097. PMID 23824792.
- [52] Wei X, She G, Wu T, Xue C, Cao Y. PEDV enters cells through clathrin-, caveolae-, and lipid raft-mediated endocytosis and traffics via the endo-/lysosome pathway. *Veterinary Research*. 51 (1) (2020) 10. doi:10.1186/s13567-020-0739-7. PMC 7011528. PMID 32041637.
- [53] Thiel V (editor), *Coronaviruses: Molecular and Cellular Biology* (1st ed.). Caister Academic Press(2007). ISBN 978-1-904455-16-5.
- [54] Fan Y, Zhao K, Shi ZL, Zhou P. Bat Coronaviruses in China. *Viruses*. 11 (3)(2019)210. doi:10.3390/v11030210. PMC 6466186. PMID 30832341.
- [55] De Groot RJ, Baker SC, Baric R, Enjuanes L, Gorbalenya AE, Holmes KV, Perlman S, Poon L, Rottier PJ, Talbot PJ, Woo PC, Ziebuhr J. Family Coronaviridae. In King AM, Lefkowitz E, Adams MJ, Carstens EB, International Committee on Taxonomy of Viruses, International Union of Microbiological Societies. *Virology Division* (eds.). Ninth Report of the International Committee on Taxonomy of Viruses. Oxford: Elsevier. (2011) 806–28. ISBN 978-0-12-384684-6.
- [56] Sexton NR, Smith EC, Blanc H, Vignuzzi M, Peersen OB, Denison MR. Homology-Based Identification of a Mutation in the Coronavirus RNA-Dependent RNA Polymerase That Confers Resistance to Multiple Mutagens. *Journal of Virology*. 90 (16) (2016) 7415–28. doi:10.1128/JVI.00080-16. PMC 4984655
- [57] McIntosh K, Arber W, Haas R, Henle W, Hofschneider PH, Jerne NK, Koldovský P, Koprowski H, Maaløe O, Rott R (eds.). *Coronaviruses: A Comparative Review*. Current Topics in Microbiology and Immunology / Ergebnisse der Mikrobiologie und Immunitäts for schung. Current Topics in Microbiology and Immunology / Ergebnisse der Mikrobiologie und Immunitäts for schung. Berlin, Heidelberg: Springer: 87(1974) doi:10.1007/978-3-642-65775-7_3. ISBN 978-3-642-65775-7.
- [58] Kahn JS, McIntosh K. History and recent advances in coronavirus discovery. *The Pediatric Infectious Disease Journal*. 24 (11Suppl) (2005) S223–27, discussion S226. doi:10.1097/01.inf.000188166.17324.60. PMID 16378050.
- [59] Geller C, Varbanov M, Duval RE. Human coronaviruses: insights into environmental resistance and its influence on the development of new antiseptic strategies. *Viruses*. 4 (11) (2012) 3044–68. doi:10.3390/v4113044. PMC 3509683. PMID 23202515.
- [60] Almeida JD, Berry DM, Cunningham CH, Hamre D, Hofstad MS, Mallucci L, McIntosh K, Tyrrell DA. *Virology: Coronaviruses*. *Nature*. 220(5168)(1968)650. doi:10.1038/220650b0. PMC 7086490. [T]here is also a characteristic "fringe" of projections 200 A long, which are rounded or petal shaped..This appearance, recalling
- [61] The solar corona, is shared by mouse hepatitis virus and several viruses recently recovered from man, namely strain B814, 229E and several others.
- [62] Sturman LS, Holmes KV. Lauffer MA, Maramorosch K (eds.). *The molecular biology of coronaviruses*. *Advances in Virus Research*. 1983, 28: 35–112. doi:10.1016/s0065-3527(08)60721-6. PMID 6362367. [T]hese viruses displayed a characteristic fringe of large, distinctive, petal-shaped peplomers or spikes which resembled a crown, like the corona spinarum in religious art; hence the name coronaviruses.
- [63] Goldsmith CS, Tatti KM, Ksiazek TG, Rollin PE, Comer JA, Lee WW. Ultrastructural characterization of SARS coronavirus. *Emerging Infectious Diseases*. 10 (2) (2004) 320–26. doi:10.3201/eid1002.030913. PMC 3322934. PMID 15030705.
- [64] Fehr AR, Perlman S. Maier HJ, Bickerton E, Britton P (eds.). *Coronaviruses: an overview of their replication and pathogenesis*. *Methods in Molecular Biology*. Springer. 2015, 1282: 1–23. doi:10.1007/978-1-4939-2438-7_1. ISBN 978-1-4939-2438-7. PMC 4369385. PMID 25720466. See section: Virion Structure.
- [65] Neuman BW, Adair BD, Yoshioka C, Quispe JD, Orca G, Kuhn P. Supramolecular architecture of severe acute respiratory syndrome

- coronavirus revealed by electron cryomicroscopy. *Journal of Virology*, 80 (16) (2006) 7918–28. doi:10.1128/JVI.00645-06. PMC 1563832. PMID 16873249. Particle diameters ranged from 50 to 150 nm, excluding the spikes, with mean particle diameters of 82 to 94 nm;
- [66] Chang CK, Hou MH, Chang CF, Hsiao CD, Huang TH. The SARS coronavirus nucleocapsid protein—forms and functions. *Antiviral Research*. 103 (2014) 39–50. doi:10.1016/j.antiviral. 2013.12.009 . PMID 24418573.
- [67] Neuman BW, Kiss G, Kunding AH, Bhella D, Baksh MF, Connelly S, et al. A structural analysis of M protein in coronavirus assembly and morphology. *Journal of Structural Biology*. 174 (1) (2011)11–22. doi:10.1016/j.jsb.2010.11.021. PMC 4486061. PMID 21130884.
- [68] Snijder EJ, Bredenbeek PJ, Dobbe JC, Thiel V, Ziebuhr J, Poon LL, et al. Unique and conserved features of genome and proteome of SARS-coronavirus, an early split-off from the coronavirus group 2 lineage. *Journal of Molecular Biology*. 331 (5) (2003) 991–1004. doi:10.1016/S0022-2836(03)00865-9. PMID 12927536.
- [69] Simmons G, Zmora P, Gierer S, Heurich A, Pöhlmann S. Proteolytic activation of the SARS-coronavirus spike protein: cutting enzymes at the cutting edge of antiviral research. *Antiviral Research*. 100 (3)(2013) 605–14. doi:10.1016/j.antiviral.2013.09.028. PMC 3889862. PMID 24121034.
- [70] Sexton NR, Smith EC, Blanc H, Vignuzzi M, Peersen OB, Denison MR. Homology-Based Identification of a Mutation in the Coronavirus RNA-Dependent RNA Polymerase That Confers Resistance to Multiple Mutagens. *Journal of Virology*. 90 (16) (2016) 7415–28. doi:10.1128/JVI.00080-16. PMC 4984655
- [71] Fehr AR, Perlman S. Coronaviruses: an overview of their replication and pathogenesis. In Maier HJ, Bickerton E, Britton P (eds.). *Coronaviruses. Methods in Molecular Biology*. 1282. Springer. (2010) 1–23. doi:10. 1007/978-1-4939-2438-7_1. ISBN 978-1-4939-2438-7. PMC 4369385. PMID 25720466.
- [72] Masters PS. The molecular biology of coronaviruses. *Advances in Virus Research*. Academic Press. 66(2006) 193–292. doi:10.1016/S0065-3527(06)66005-3. ISBN 978-0120398690. PMID 16877062 .
- [73] Cui J, Li F, Shi ZL, Origin and evolution of pathogenic coronaviruses. *Nature Reviews. Microbiology*. 17 (3) (2019) 181–92. doi:10.1038/s41579-018-0118-9. PMID 30531947. Different SARS-CoV strains isolated from several hosts vary in their binding affinities for human ACE2 and consequently in their infectivity of human cells 76, 78 .
- [74] Li F, Li W, Farzan M, Harrison SC. Structure of SARS coronavirus spike receptor-binding domain complexed with receptor. *Science*. 309 (5742) (2005) 1864–68. Bibcode:2005Sci.309.1864L. doi:10.1126/science.1116480. PMID 16166518.
- [75] Wertheim JO, Chu DK, Peiris JS, Kosakovsky Pond SL, Poon LL. A case for the ancient origin of coronaviruses. *Journal of Virology*. 87 (12) (2013) 7039–45. doi:10.1128/JVI.03273-12. PMC 367 6139. PMID 23596293.
- [76] Woo PC, Lau SK, Lam CS, Lau CC, Tsang AK, Lau JH, et al. Discovery of seven novel Mammalian and avian coronaviruses in the genus delta coronavirus supports bat coronaviruses as the gene source of alpha coronavirus and beta coronavirus and avian coronaviruses as the gene source of gamma coronavirus and delta coronavirus. *Journal of Virology*. 86 (7) (2012) 3995–4008. doi:10.1128/JVI.0 6540-11. PMC 3302495. PMID 22278237.
- [77] Bidokhti MR, Trávén M, Krishna NK, Munir M, Belák S, Alenius S, Cortey M. Evolutionary dynamics of bovine coronaviruses: natural selection pattern of the spike gene implies adaptive evolution of the strains. *The Journal of General Virology*. 94 (Pt 9) (2013) 2036–49. doi:10.1099/vir.0.054940-0. PMID 23804565.
- [78] Vijgen L, Keyaerts E, Moës E, Thoelen I, Wollants E, Lemey P. Complete genomic sequence of human coronavirus OC43: molecular clock analysis suggests a relatively recent zoonotic coronavirus transmission event. *Journal of Virology*. 79 (3)(2005) 1595–604. doi:10.1128/ jvi.79.3. 1595-1604.2005. PMC 544107 . PMID 15650185.
- [79] Lau SK, Lee P, Tsang AK, Yip CC, Tse H, Lee RA. Molecular epidemiology of human coronavirus OC43 reveals evolution of different genotypes over time and recent emergence of a novel genotype due to natural recombination. *Journal of Virology*. 85 (21) (2013) 11325–37. doi:10.1128/JVI.0 5512-11. PMC 3194943 . PMID 21849456.
- [80] Lau SK, Li KS, Tsang AK, Lam CS, Ahmed S, Chen H. Genetic characterization of Beta coronavirus lineage C viruses in bats reveals marked sequence divergence in the spike protein of pipistrellus bat coronavirus HKU5 in Japanese pipistrelle: implications for the origin of the novel Middle East respiratory syndrome coronavirus. *Journal of Virology*. 87 (15) (2013) 8638–50. doi:10.1128/JVI.01055-13. PMC 3719811. PMID 23720729.