

# The global impact of SARS-CoV-2 variant BA.2.86: a comprehensive analysis with the latest developments and transmission trends – an epidemiological study

S.A. MEO<sup>1</sup>, A.S. MEO<sup>2</sup>, D.M. HALEPOTO<sup>3</sup>

<sup>1</sup>Department of Physiology, College of Medicine, King Saud University, Riyadh, Saudi Arabia

<sup>2</sup>The School of Medicine, Medical Sciences and Nutrition, University of Aberdeen, Scotland, United Kingdom

<sup>3</sup>Department of Physiology, College of Medicine, King Saud University, Riyadh, Saudi Arabia

**Abstract. – OBJECTIVE:** The variant BA.2.86 of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is causing concern globally. The virus contains a large number of mutations, and transmission trends are rapidly changing globally. This study investigates the global epidemiological and transmission trends of SARS-CoV-2 new variant BA.2.86 in various continents and countries.

**MATERIALS AND METHODS:** The data were recorded using key terms, including SARS-CoV-2, Omicron, BA.2.86, epidemiology, occurrence, incidence, prevalence, and transmission trends. The data on SARS-CoV-2 variant BA.2.86 were searched by the World Health Organization (WHO), Centers for Disease Control and Prevention (CDC), the Global Initiative on Sharing All Influenza Data (GSIAD), PubMed, and Web of Science. Initially, 40 documents were identified, and finally, 8 documents were included for the data analysis and discussion. The analysis of findings on transmission trends was based on the data from August 14, 2023, to February 28, 2024.

**RESULTS:** The SARS-CoV-2, novel variant BA.2.86, crossed the international borders of 6 continents and 89 countries and infected 19,532 people. In Europe, 32 countries are affected and involved 12,667 people (64.85%), North and South America 18 countries with 3,515 cases (17.99%), Asia 27 countries with 2,063 people (10.56%), Oceania 2 countries with 689 cases (3.52%), and Africa 10 countries with 598 (3.06%) cases. The BA.2.86 rapidly spread and mainly affected the people in the United Kingdom 3,228 (16.52%), Sweden 2,380 (12.18%), USA 1,929 (9.87%), Denmark 1,621 (8.29%), Canada 1,516 (7.67%), France 833 (4.26%), Japan 810 (4.14%), Netherlands 725 (3.71%), Germany 681 (3.48%), Spain 665 (3.40%), South Korea 556 (2.84%), and Australia 512 (2.62%).

**CONCLUSIONS:** The SARS-CoV-2, novel variant BA.2.86, spread over six continents and 89

countries and affected 19,532 people worldwide. The disease is more prevalent in the United Kingdom, United States of America, and European countries. The detection of the disease in multiple continents and countries suggests some degree of transmissibility. Global health authorities need to rethink their policies and implement strict strategies to eradicate emerging variants and minimize the global disease burden.

*Key Words:*

SARS-CoV, Omicron, BA.2.86, Incidence, Epidemiology, Transmission trends.

## Introduction

Since December 2019, in four years, there has been no end to the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2), COVID-19 pandemic. Still, the disease has been occurring in various shapes across the globe<sup>1</sup>. As of October 24, 2023, the pandemic has infected 771.40 million people and caused 6.97 million deaths, as the World Health Organization reported<sup>1,2</sup>. About 70.5% of the global population has received at least one dose of a COVID-19 vaccine worldwide, and 13.51 billion doses have been administered, with 32.62% of the population being from low-income countries<sup>3</sup>. Despite extensive efforts worldwide by health authorities, the COVID-19 pandemic persists, with recent occurrences of a newly emerging variant of the SARS-CoV-2 virus, specifically sublineage BA.2.86, causing concern globally<sup>4,5</sup>. This new sub-variant of omicron, BA.2.86, also known as “Pirola” was discovered on August 14, 2023, in Denmark and

Israel. This variant contains more mutations than the previous strains of the virus<sup>2</sup>. SARS-CoV-2 has persisted in changing its genetic code *via* mutations, resulting in the acquisition of unique characteristics, and altered nature of the spread and magnitude of the disease, thereby leading to higher rates of the spread of infection<sup>6,7</sup>.

The SARS-CoV-2, sublineage BA.2.86, possesses evolving pathogenic appearances that have also raised great public health concerns. The genetic sequence of BA.2.86 has more than 35 amino acid differences on its spike protein compared with Omicron BA.2, which was the dominant Omicron lineage in the year 2022, and also with more recently circulating Omicron subvariant XBB.1.5 (also known as “Kraken”), which was dominant during the year 2023. This set of genetic mutations is the same magnitude as seen between the initial Omicron variant and the Delta variant<sup>8,9</sup>.

The BA.2.86 subvariant is gaining the attention of health officials and policymakers for its highly mutated spike and transmission trends across the world. Although, there is no evidence that the BA.2.86 variant causes severe illness and death<sup>10</sup>. However, the spread of the BA.2.86 variant could lead to the accumulation of more mutations that evade immunity and increase transmission rates<sup>10</sup>. The COVID-19 pandemic-related public health emergency has ended, but the COVID-19 pandemic remains a public health challenge, as new variants are identified in various countries with various genetic makeup and epidemiological trends<sup>11</sup>. There is a need to understand the epidemiological and transmission trends of this new variant, BA.2.86; this study aims to explore the global emergence and transmission trends of the novel Omicron variant BA.2.86.

## Materials and Methods

### Research Methodology

This study was performed at the Department of Physiology, College of Medicine, King Saud University, Riyadh, Saudi Arabia. This study recorded the most updated data on the global prevalence of a novel variant of SARS-CoV-2, BA.2.86. For data collection, the literature was searched using the key terms, including SARS-CoV-2, Omicron, a new variant, BA.2.86, epidemiology, occurrence, incidence, prevalence, and transmission trends from August 14, 2023 to February 28, 2024. The information was searched and obtained from the World Health

Organization<sup>8</sup>, Centers for Disease Control and Prevention (CDC)<sup>9</sup>, the Global Initiative on Sharing All Influenza Data” (GISAID)<sup>11</sup>, PubMed, Web of Science, Google Scholar, and Scopus. Initially, 40 documents, including those from international health organizations and articles, were identified. Following a review of these materials, 8 documents were chosen for data collection, analysis, and discussion. The literature was carefully examined and chosen following the PRISMA guidelines.

### Statistical Analysis

The data were collected and analyzed by using the SPSS 26.0 statistical software (IBM Corp., Armonk, NY, USA). The frequencies and percentages were calculated and presented in tabular and figure formats. The cases for each continent were entered as the dependent variable, with the continent itself serving as the grouping (independent) variable. A *p*-value of less than 0.05 was considered statistically significant.

## Results

The global prevalence of SARS-CoV-2, variant BA.2.86, is presented in Table I, Figures 1 and 2. The new variant crossed the international borders of 5 continents and 89 countries and infected 19,532 people worldwide from August 14, 2023, to February 28, 2024 (Table I, Figure 1, 2).

In Europe, 32 countries are affected and involved 12,667 people (64.85%), North and South America 18 countries with 3,515 cases (17.99%), Asia 27 countries with 2,063 people (10.56%), Oceania 2 countries with 689 cases (3.52%), and Africa 10 countries with 598 (3.06%) cases (Figure 2). The Omicron BA.2.86 effected the people mainly in the United Kingdom 3,228 (16.52%), Sweden 2,380 (12.18%), USA 1,929 (9.87%), Denmark 1,621 (8.29%), Canada 1,516 (7.67%), France 833 (4.26%), Japan 810 (4.14%), Netherlands 725 (3.71%), Germany 681 (3.48%), Spain 665 (3.40%), South Korea 556 (2.84%), Australia 512 (2.62%), South Africa 489 (2.50%), Belgium 344 (1.76%), Greece 255 (1.30%), Switzerland 230 (1.17%), Israel 225 (1.15%), Poland 214 (1.09%), Italy 196 (1.00%), Austria 191 (0.97%), Ireland 182 (0.93%), New Zealand 177 (0.90%), Slovakia 155 (0.79%), Lithuania 141 (0.72%), Finland 114 (0.58%), Luxembourg 105 (0.53%), Thailand 103 (0.52%), Singapore 100 (0.51%), Malaysia 81

**Table I.** The global prevalence of SARS CoV-2 sublineage BA.2.86 cases, and cases during the past 4 weeks<sup>11</sup>.

Country involved	Total cases of BA.2.86 (%)	Number of cases in the past 4 weeks	The difference in the number of cases during the last 4 weeks
United Kingdom	3,228 (16.52%)	86	3,142
Sweden	2,380 (12.18%)	7	2,373
USA	1,929 (9.87%)	58	1,871
Denmark	1,621 (8.29%)	3	1,618
Canada	1,516 (7.67%)	110	1,406
France	833 (4.26%)	4	829
Japan	810 (4.14%)	31	779
The Netherlands	725 (3.71%)	3	722
Germany	681 (3.48%)	4	677
Spain	665 (3.40%)	0	665
South Korea	556 (2.84%)	1	555
Australia	512 (2.62%)	8	504
South Africa	489 (2.50%)	0	489
Belgium	344 (1.76%)	1	343
Greece	255 (1.30%)	0	255
Switzerland	230 (1.17%)	4	226
Israel	225 (1.15%)	3	222
Poland	214 (1.09%)	13	201
Italy	196 (1.00%)	9	187
Austria	191 (0.97%)	0	191
Ireland	182 (0.93%)	4	178
New Zealand	177 (0.90%)	6	171
Slovakia	155 (0.79%)	0	155
Lithuania	141 (0.72%)	0	141
Finland	114 (0.58%)	3	111
Luxembourg	105 (0.53%)	0	105
Thailand	103 (0.52%)	0	103
Singapore	100 (0.51%)	0	100
Malaysia	81 (0.41%)	0	81
Slovenia	76 (0.38%)	0	76
Norway	67 (0.34%)	0	67
Croatia	62 (0.31%)	0	62
Turkey	57 (0.29%)	0	57
<b>Total Cases</b>	<b>19,020</b>	<b>358</b>	<b>18,662</b>

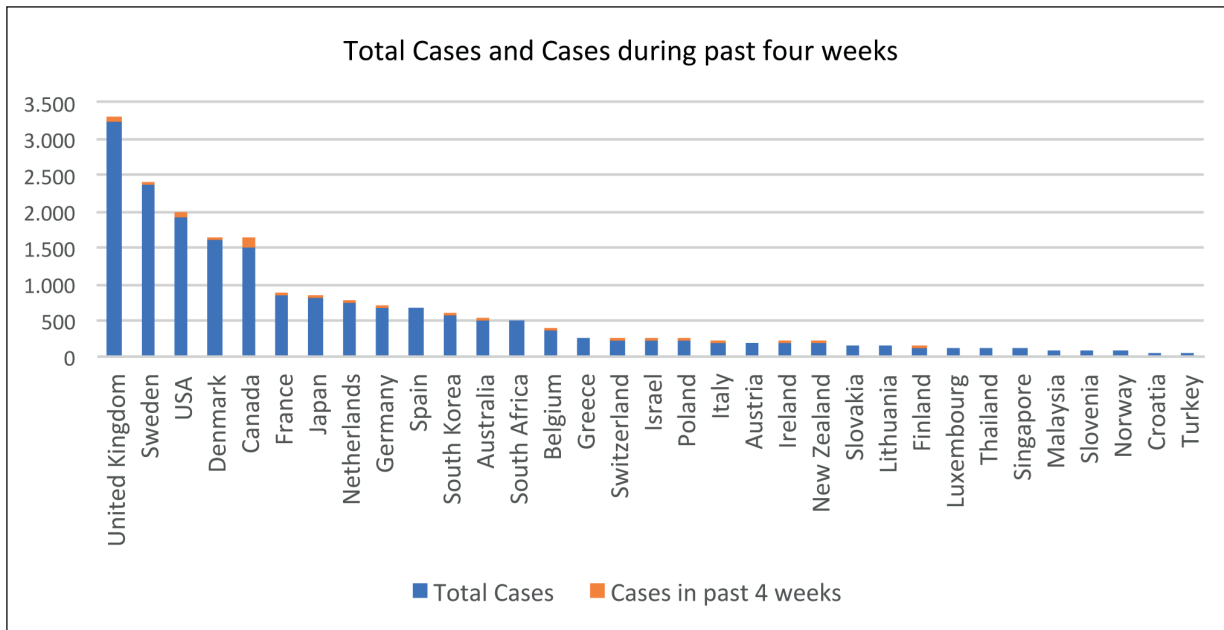
Countries with the number of cases less than 50 were not included in this table (total countries 89, total cases 19,532; 56 countries with a number of cases 512 were not included). Data were recorded from August 14, 2023 to February 28, 2024.

(0.41%), Slovenia 76 (0.38%), Norway 67 (0.34%), Croatia 62 (0.31%), and Turkey 57 (0.29%) (Table I, Figure 2).

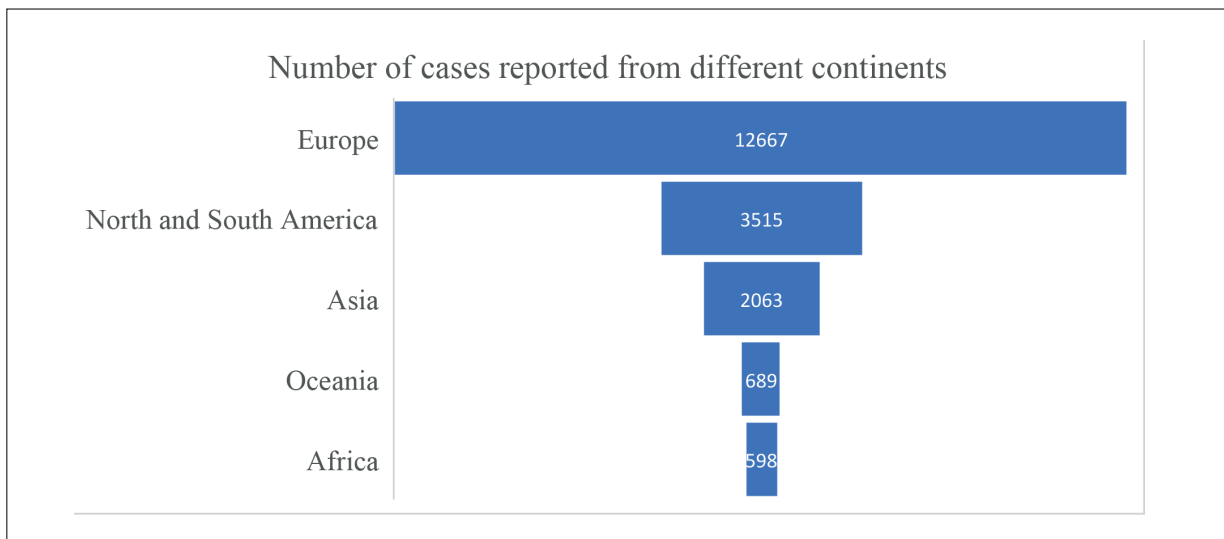
The virus also spread in other 56 countries in which the virus infected less than 50 people per country, including Mauritius (49), Mozambique (46), China (43), Czech Republic (42), Russia (33), Portugal (30), India (25), Indonesia (23), Brazil (22), Puerto Rico (20), Ukraine (20), Iceland (19), Bahrain (11), Kosovo (9), Chile (9), Hungary (8), Laos (8), Romania (7), Taiwan (6), Bulgaria (6), Hong Kong (5), Vietnam (5), Cambodia (5), Oman (4), Tunisia (4), Philippines (4), Guatemala (3), Nigeria (3), Sint Maarten (3), Ecuador (3), Montenegro (3), Myanmar (3), Zambia (2), Nepal (2), Pakistan (2), Sri Lanka (2), Kenya (2), Brunei

(2), Timor-Leste (2). Moreover, one case each was reported from Peru, Argentina, Honduras, Guadeloupe, Qatar, Dominican Republic, Mexico, Botswana, Algeria, Bolivia, Lebanon, Cameroon, Grenada, Colombia, North Macedonia, Costa Rica, and Kuwait.

While analyzing the data per million population in each continent, the result revealed that there is a higher number of cases in Europe 12,667 (64.85%), North and South America 3,515 (17.99%), Asia 2,063 (10.56%), compared to Oceania 689 (3.52%), and Africa 598 (3.06%) (Figure 2). However, there was no significant difference in the per million case rate of SARS CoV-2 sublineage BA.2.86 between the continents ( $p=0.406$ ).



**Figure 1.** The global prevalence of SARS-CoV-2 sublineage BA.2.86 cases, and cases during the past 4 weeks.



**Figure 2.** The transmission trends of SARS-CoV-2 sublineage BA.2.86 in different continents.

## Discussion

The global population has been significantly affected by the COVID-19 pandemic. As of October 27, 2023, the pandemic has caused over 771.40 million cases and 6.97 million deaths<sup>1</sup>. More recently, a new variant, SARS-CoV-2, BA.2.86, has been identified in many countries across the globe, and the disease is transmitted by changing its transmission trends with various

sub-lineages. This study was conducted as the continuation of an earlier study<sup>5</sup> for a better understanding of global transmission trends with the latest epidemiological updates of the new variant BA.2.86. The SARS-CoV-2, novel variant BA.2.86, spread over six continents and 89 countries and affected 19,532 people worldwide. The disease is more prevalent in the United Kingdom, the United States of America, and European countries (Table I, Figures 1 and 2).

Since the initiation of the COVID-19 pandemic in December 2019, the SARS-CoV-2 virus has undergone numerous mutations; over 3,370 lineages have been identified with emerging variant BA.2.86<sup>12,13</sup>. BA.2.86 extends from the BA.2 lineage, a subvariant of Omicron, which dominated COVID-19 cases and has mutated into distinct subvariants. BA.2.86 is now replaced by the fastest-growing variant JN.1, which accounts for 15%-29% of circulating variants in the US. JN.1 is comparable to BA.2.86; however, it has an additional mutation (L455S) in the spike protein<sup>14</sup>. It is essential to understand the linkage of SARS-CoV-2 variants, BA.2.86, with weather conditions and seasonal variations. Landier et al<sup>15</sup> reported that weather conditions can contribute to the intensification of the wave of COVID-19 in the northwest hemisphere states, particularly during the transition from summer to winter.

Reeve et al 2023<sup>16</sup> investigated an outbreak of the BA.2.86 variant in the East of England. The authors found 45 (33 residents, 12 staff), cases of variant BA.2.86. The occurrence rate among the residents was 87%, 19 (42.22%) were symptomatic, and one was hospitalized. Among the 33 resident cases, 29 (87.87%) had been vaccinated four months earlier. In our previous study<sup>5</sup>, we concluded that the new Omicron variant BA.2.86 has affected 264 people in 23 countries in four weeks. The authors found that the disease spreads swiftly and is transmitted more rapidly. The Omicron new variant BA.2.86, raised more concern as the level of neutralization of the vaccine immune serum against the previous earlier variants, including Alpha, Beta, Gamma, and Delta, decreased less than four times<sup>17</sup>. Once the neutralizing antibody in the population decreases to a certain level, the immune responses may be unable to protect the circulating strains. This might lead to a new infection wave and cause the spread of this new variant in many countries<sup>18,19</sup>.

The Omicron variant BA.2.86 has over 30 mutations, which raised the possibility that the virus may evade neutralizing antibodies (NAbs) induced by vaccination or infection<sup>20</sup>. The Omicron subvariant, BA.2.86 spread to many states globally, raising apprehension among the public as its spike protein contains 34 additional mutations<sup>21</sup>. It is worth mentioning that BA.2.86 is a highly mutated variant and has raised concerns about its potential to evade COVID-19 vaccination or prior SARS-CoV-2 infection-elicited immunity<sup>22</sup>.

The reports of newly emerged Omicron subvariants BA.2.86 have proven that the variants have continued to spread and infected people

in numerous states<sup>23</sup>. The transmission trends are increasing; thus, the virus infects the global population. The vaccination or natural infection against SARS-CoV-2 prevents severe disease and death. The global people assume that the pandemic has not ended but continues in different forms with various transmission trends. The regional and international communities must struggle to maintain their capacity to stand an emergency response in case of any further infection surges<sup>24</sup>. The Omicron variant has numerous mutations that make it highly transmissible, infectious, capable of immune evasion, and able to cause disease in vulnerable individuals, which results in rapid community spread<sup>25</sup>.

There are multiple factors, including genetic mutations, immune escape mechanisms, and population dynamics, which may be involved in the rising spread rate of this novel Omicron variant. The Omicron new variant BA.2.86 is characterized by a substantial number of genetic mutations, particularly within the spike protein. These mutations may confer an increased affinity for host cell receptors and may enhance entry and replication of the variant<sup>26</sup>.

Nonetheless, vaccines are highly effective in disease prevention even though over time, the efficacy of vaccine-induced immunity may decrease, particularly against new variants with significant genetic divergence from the original virus. This waning immunity may result in an increased susceptibility to infection, permitting the virus to spread easily within vaccinated populations. Additionally, the high population density, social interactions, and inadequate public health measures may facilitate the rapid transmission of the new Omicron variant<sup>27</sup>.

Individuals with previous exposure to SARS-CoV-2, mainly those infected with earlier variants, may have a decreased immunity against the new Omicron variant due to its genetic dissimilarity<sup>28,29</sup>. This may lead to an increased susceptibility to reinfection and contribute to the spread of the new variant. The enhanced transmissibility of the new variant of Omicron, BA.2.86, among people, including vaccinated individuals, can be attributed to a combination of genetic mutations, immune escape mechanisms, waning immunity, population dynamics, and variability in vaccine effectiveness. It is vital to understand these factors for optimizing public health strategies, including the implementation of booster vaccinations, improved surveillance, and continued adherence to preventive measures, to mitigate the spread of SARS-CoV-2.



### **Study Strengths and Limitations**

This is the comprehensive global data-based study added to the literature to demonstrate the global occurrence and transmission trends of the new Omicron variant BA.2.86. However, a limitation of this study is that only a few limited sources and documents are available, and this limited literature cannot support more definite conclusions. Based on the limited data, it is difficult to draw a conclusive conclusion that BA.2.86 is less or more transmissible in future. There is also a chance that the disease may spread widely, and we will just have to wait for more data to understand the transmission trends of this new SARS-CoV-2, sublineage BA.2.86.

### **Conclusions**

The SARS-CoV-2, sublineage BA.2.86, spread over six continents, involved 89 countries and affected 19,532 people around the world. The disease is more prevalent in the United Kingdom, Sweden, the USA, Denmark, Canada, France, Japan, Netherlands, Germany, Spain, South Korea, and Australia. The virus spreads in countries that have well-established healthcare systems, and the maximum number of people are vaccinated. The global health authorities need to rethink their policies and preventive measures and must implement strict strategies to stop the outbreak of such emerging and re-emerging variants across the globe to minimize the disease burden regionally and internationally as the worldwide, public has still not recovered from the shock of the COVID-19 pandemic.

### **Acknowledgements**

We thank the Researchers Supporting Project number (RSP-2024 R47), King Saud University, Riyadh, Saudi Arabia.

### **Funding**

The study was supported by the Researchers Supporting Project number (RSP-2024 R47) at King Saud University, Riyadh, Saudi Arabia.

### **Conflicts of Interest**

The authors declare no conflict of interest.

### **Ethics Approval**

In this study, information was obtained from publicly available data sources; hence, ethical approval was not required.

### **Informed Consent**

Not applicable due to the design of the study.

### **Authors' Contributions**

SAM, study concept, manuscript writing, and editing. ASM, DMH, literature review, data collection, data entry and data analysis.

### **ORCID ID**

Sultan Ayoub Meo: 0000-0001-9820-1852  
Anusha Sultan Meo: 0000-0001-5213-3233  
Dost Muhammad Halepota: 0000-0001-7705-8348

### **References**

- 1) World Health Organization (WHO) WHO Coronavirus Dashboard. Available at: <https://covid19.who.int/> (Accessed on October 27, 2023).
- 2) Centres for Disease Control Prevention (CDC). The Risk Assessment Summary for SARS CoV-2 Sublineage BA.2.86. Available at: <https://www.cdc.gov/respiratory-viruses/whats-new/covid-19-variant.html> (Accessed on October 24, 2023).
- 3) Our World in Data. Coronavirus (COVID-19) Vaccinations. Available at: <https://ourworldindata.org/covid-vaccinations> (Cited date October 24, 2023).
- 4) Meo SA, Meo AS, Al-Jassir FF, Klonoff DC. Omicron SARS-CoV-2 new variant: global prevalence and biological and clinical characteristics. *Eur Rev Med Pharmacol Sci* 2021; 25: 8012-8018.
- 5) Meo SA, Meo AS, Klonof DC. Omicron new variant BA.2.86 (Pirola): Epidemiological, biological, and clinical characteristics - a global data-based analysis. *Eur Rev Med Pharmacol Sci* 2023; 27: 9470-9476.
- 6) Harvey WT, Carabelli AM, Jackson B. SARS-CoV-2 variants, spike mutations and immune escape. *Nat Rev Microbiol* 2021; 19: 409-424.
- 7) Ramesh S, Govindarajulu M, Parise RS, Neel L, Shankar T, Patel S, Lowery P, Smith F, Dhanasekaran M, Moore T. Emerging SARS-CoV-2 Variants: A Review of Its Mutations, Its Implications and Vaccine Efficacy. *Vaccines (Basel)* 2021; 9: 1195.
- 8) World Health Organization (WHO). Tracking SARS-CoV-2 variants. Available at: <https://www.who.int/activities/tracking-SARS-CoV-2-variants> (Accessed on October 22, 2023).
- 9) European Centre for Disease Prevention and Control. SARS-CoV-2 Variants of Concern as of Sept 7, 2023 Available at: <https://www.ecdc.europa.eu/en/covid-19/variants-concern>. (Accessed on September 20, 2023).
- 10) Wannigama DL, Amarasiri M, Phattharapornjaroen P, Hurst C, Modchang C, Chadsuthi S, Anupong S, Miyanaga K, Cui L, Fernandez S, Huang AT, Ounjai P, Tacharoenuang R, Ragupathi

- NKD, Sano D, Furukawa T, Sei K, Leelahavanichkul A, Kanjanabuch T, Higgins PG, Nanbo A, Kicic A, Singer AC, Chatsuwat T, Trowsdale S, Khatib A, Shibuya K, Abe S, Ishikawa H, Hongsing P; Pathogen Hunters Research Team. Pathogen Hunters Research Team. Tracing the new SARS-CoV-2 variant BA.2.86 in the community through wastewater surveillance in Bangkok, Thailand. *Lancet Infect Dis* 2023; 23: e464-e466.
- 11) GISAID- The Global Initiative on Sharing All Influenza Data. Available at: <https://gisaid.org/hcov19-variants/> (Accessed on October 27, 2023, and February 28, 2024).
  - 12) Harris E. CDC Assesses Risk From BA.2.86, Highly Mutated COVID-19 Variant. *JAMA* 2023; 330: 1029.
  - 13) Scarpa F, Ciccozzi M. On the SARS-CoV-2 BA.2.86 lineage: A mutation point of view. *J Med Virol* 2023; 95: e29079.
  - 14) Centre for Disease Control Prevention (CDC). CDC Continues to Track the Growth of JN.1. Available at: <https://www.cdc.gov/ncird/whats-new/JN.1-update-2023-12-22.html> (Accessed on Feb 27, 2024).
  - 15) Landier J, Paireau J, Rebaudet S. Cold, and dry winter conditions are associated with greater SARS-CoV-2 transmission at the regional level in western countries during the first epidemic wave. *Sci Rep* 2012; 11: 12756.
  - 16) Reeve L, Tessier E, Trindall A, Abdul Aziz NIB, Andrews N, Futschik M, Rayner J, Didier-Serre A, Hams R, Groves N, Gallagher E, Graham R, Kele B, Hoschler K, Fowler T, Blandford E, Mahgoub H, Hoffmann J, Ramsay M, Dabrera G, Chand M, Zambon M, Sharp A, Heinsbroek E, Lopez Bernal J. High attack rate in a large care home outbreak of SARS-CoV-2 BA.2.86, East of England, August 2023. *Euro Surveill* 2023; 28: 2300489.
  - 17) Li Q, Nie J, Wu J. SARS-CoV-2 501Y.V2 variants lack higher infectivity but do have immune escape. *Cell* 2021; 184: 2362-2371.e9.
  - 18) Wang K, Jia Z, Bao L. Memory B cell repertoire from triple vaccinees against diverse SARS-CoV-2 variants. *Nature* 2022; 603: 919-925.
  - 19) Liu S, Liang Z, Nie J, Gao WB, Li X, Zhang L, Yu Y, Wang Y, Huang W. Sera from Breakthrough Infections with SARS-CoV-2 BA.5 or BF.7 Showed Lower Neutralization Activity against XBB.1.5 and CH.1.1. *Emerg Microbes Infect* 2023; 12: 2225638.
  - 20) Lasrado N, Collier AY, Hachmann NP, Miller J, Rowe M, Schonberg ED, Rodrigues SL, LaPiana A, Patio RC, Anand T, Fisher J, Mazurek CR, Guan R, Wagh K, Theiler J, Korber BT, Barouch DH. Neutralization escape by SARS-CoV-2 Omicron subvariant BA.2.86. *Vaccine* 2023; 41: 6904-6909.
  - 21) Wang Q, Guo Y, Liu L, Schwanz LT, Li Z, Nair MS, Ho J, Zhang RM, Iketani S, Yu J, Huang Y, Qu Y, Valdez R, Luring AS, Huang Y, Gordon A, Wang HH, Liu L, Ho DD. Antigenicity and receptor affinity of SARS-CoV-2 BA.2.86 spike. *Nature* 2023; 624: 639-644.
  - 22) Hu Y, Zou J, Kurhade C, Deng X, Chang HC, Kim DK, Shi PY, Ren P, Xie X. Less neutralization evasion of SARS-CoV-2 BA.2.86 than XBB sublineages and CH.1.1. *Emerg Microbes Infect* 2023: 2271089.
  - 23) Dyer O. Covid-19: Infections climb globally as EG.5 variant gains ground. *BMJ* 2023; 382: 1900.
  - 24) Berkley S. Ending the COVID-19 pandemic means helping countries to catch up with vaccination, not giving up. *BMJ* 2022; 376: o786.
  - 25) Gupta S. Evolution of pathogen virulence: Studying the complex interplay of pathogen interactions, virulence and transmission helps us understand how they evolve and spread. *EMBO Rep* 2023; 24: e57611.
  - 26) Markov PV, Ghafari M, Beer M, Lythgoe K, Simmonds P, Stilianakis NI, Katzourakis A. The evolution of SARS-CoV-2. *Nat Rev Microbiol* 2023; 21: 361-379.
  - 27) Mongin D, Bürgisser N, Laurie G, Schimmel G, Vu DL, Cullati S; Covid-SMC Study Group; Courvoisier DS. Effect of SARS-CoV-2 prior infection and mRNA vaccination on contagiousness and susceptibility to infection. *Nat Commun* 2023; 14: 5452.
  - 28) Cohen D, Izak M, Stoyanov E, Mandelboim M, Perlman S, Amir Y. Predictors of reinfection with pre-Omicron and Omicron variants of concern among individuals who recovered from COVID-19 in the first year of the pandemic. *Int J Infect Dis* 2023; 132: 72-79.
  - 29) COVID-19 Forecasting Team. Past SARS-CoV-2 infection protection against re-infection: a systematic review and meta-analysis. *Lancet* 2023; 401: 833-842.