HUMAN VACCINES & IMMUNOTHERAPEUTICS
2025, VOL. 21, NO. 1, 2485840
https://doi.org/10.1080/21645515.2025.2485840

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REVIEW

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From Wuhan to Omicron K.P2 strain: A comprehensive review of SARS-CoV-2 phylogeny and public health implications of the latest booster vaccine

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ABSTRACT

The SARS-CoV-2 virus continues to evolve, with the Omicron KP.2 variant, a descendant of BA.2.86, emerging as a public health concern due to its rapid spread and resistance to existing immunity. This review examines the phylogenetic evolution of SARS-CoV-2, focusing on KP.2 and its key mutations (R346T, F456L, V1104L), alongside its epidemiological implications. It also discusses the development and approval of the KP.2-adapted booster vaccine, shown in clinical trials to significantly enhance immune responses and protect against symptomatic and severe disease, particularly in vulnerable groups. Despite vaccine advancements, challenges in global distribution and inequity persist, especially in low- and middle-income countries, increasing the risk of vaccine-resistant variants. The manuscript underscores the importance of equitable access to the KP.2-adapted booster to control the pandemic and prevent future outbreaks, while highlighting the need for continuous surveillance and broader-spectrum vaccine research as the virus evolves.

ARTICLE HISTORY
Received 20 November 2024
Revised 13 March 2025
Accepted 26 March 2025

KEYWORDS
Omicron KP.2; SARS-CoV-2 variants; COVID-19 booster vaccine; immune evasion; vaccine equity; viral mutations

Introduction

The SARS-CoV-2 virus primarily spreads through respiratory droplets but may also be transmitted through the air and contact with contaminated surfaces. Symptoms of COVID-19 range from asymptomatic to breathing difficulties and severe complications such as pneumonia, acute respiratory distress syndrome (ARDS), multi-organ failure, and death. As of 2023, the number of individuals infected globally has exceeded 760 million with more than 6.9 million deaths.[1] The pattern of COVID-19 has been characterized by periodic waves of infection driven by new variants of the virus emerging over time. The WHO classifies these variants based on their genetic mutations and potential impacts on transmissibility, disease severity, and its ability to evade immune responses. The Alpha variant (B.1.1.7) was the first to be designated as a Variant of Concern (VOC), followed by other variants such as Beta (B.1.351), Gamma (P.1), and Delta (B.1.617.2), each presenting new challenges.[1] Among the most significant variants is the Omicron variant (B.1.1.529), the most mutated SARS-CoV-2 variant. Omicron was notable for its high number of mutations, particularly in the spike protein, which is the primary target of most COVID-19 vaccines. This allowed Omicron to spread rapidly, evading immunity from previous infections and vaccinations. While Omicron generally caused milder disease than earlier variants, its high transmissibility significantly increased cases. Several sub-variants have emerged within the omicron lineage, each with distinct genetic profiles. One such subvariant is KP.2 (JN.1.11.1.2), which has recently gained attention due to its potential to evade existing immune defenses and its rapid spread in certain regions. Considered to be a descendant of the omicron sub-variant, BA.2.86, nicknamed "Pirola," and the JN.1, it was first detected on January 2, 2024, in India and has been included between variants under monitoring (VuMs).[1–3]

Efforts to mitigate the COVID-19 pandemic has been primarily focussed on vaccination, with vaccines from Pfizer-BioNTech, Moderna, AstraZeneca, and Johnson & Johnson developing at an unprecedented pace. As of 2023, there are approximately 200 vaccine candidates in preclinical and clinical stages of development, while 12 vaccines have been granted Emergency Use Listing (EUL) by the World Health Organization, including COMIRNATY, JCOVDEN and VAXZEVRIA.[4] However, there are about 50 distinct COVID-19 vaccines that have been licensed for use in at least one country. This broader count includes vaccines developed and approved in different regions (for example, those approved in China, Russia, Cuba, India, and elsewhere) that might not all appear on the WHO EUL list]. These vaccines

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have played an essential role in slowing the spread of the virus, lessening the severity of illness, and preventing deaths, especially among vulnerable groups such as the elderly and those with underlying medical conditions. These vaccination efforts have significantly changed the trajectory of the pandemic. Booster vaccinations are now a part of the COVID-19 vaccination strategy, as immunity tends to wane several months after the initial vaccination doses are given. Booster doses are intended to strengthen the immunity provided by the initial vaccines, particularly against new variants that could partially evade immune responses. On August 22, 2024, a COVID-19 booster vaccine known as the "Omicron KP.2-adapted 2024–2025 Formula," which targets the KP.2 strain and other related sub-variants, was authorized by the Food and Drug Administration and is recommended for all individuals aged 6 months and older.[5] The emergence of KP.2 has highlighted the ongoing challenges in controlling the COVID-19 pandemic, emphasizing the importance of continued vigilance and adjusting public health strategies accordingly.

This review aims to explore the emergence of the KP.2 variant, detailing its genetic characteristics, epidemiological impact, and public health concerns. It also investigates the development process of the KP.2 booster vaccine, discussing the need to create a variant-specific booster and its action and safety data. The review also explores the public health implications of the KP.2 booster, including its impact on COVID-19 control, vaccine distribution, and equity, as well as challenges related to public perception and ensuring access, notably in low- and middle-income countries. Finally, it examines the evolutionary trajectory of SARS-CoV-2, the implications for future vaccine research, and the potential for developing broader spectrum vaccines to manage COVID-19.

The evolution of SARS-CoV-2 and its variants

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the etiological agent for COVID-19. It is a betacoronavirus closely related to the human SARS-CoV virus, which caused the 2002–2004 SARS outbreak. Since the pandemic, the SARS-CoV-2 virus has recorded the highest amount of genomic data for a single pathogen that has served to understand the biology of the virus.[6] Evolutionary events that could only be previously inferred indirectly, such as the emergence of variants with distinct phenotypes like immune evasion, severity, and transmissibility, were observed in SARS-CoV-2.[7] Coronaviruses are RNA viruses and, thus, have a rapid rate of observable and measurable evolution occurring on timescales of months or years. This viral evolution is driven by the rate at which mutations arise and are spread through populations. Natural selection acts to correct advantageous mutations, such as the D614G mutation, which is responsible for the higher transmissibility of the virus.[7]

Early phylogeny of SARS-CoV-2

The first full genomic sequence of SARS-CoV-2 and its structural organization was reported by the Yongzhen Zhang team in China following the COVID-19 outbreak in Wuhan in the Hubei Province.[8] The SARS-CoV-2 genome is arranged as 50-untranslated region (UTR)-replicate complex (orf1ab)-structural proteins Spike(S)-Envelope(E)-Membrane(M)-Nucleocapsid(N))- 30-UTR. This sequence (NC_045512) was deposited in the National Center for Biotechnology Information (NCBI) GenBank in January 2020.[8] Since 2019, several studies have conducted phylogenetic analyses on SARS-CoV-2 based on various genomic sequences.[9–13] Phylogenetic analysis of 160 SARS-CoV-2 genomes revealed three central variants distinguished by random amino acid variations.[14] A four-genome phylogeny conducted in Chile reported two viral variants from Europe and Asia.[15] The characterization and phylogenetic analysis of the first three genomes from Italy revealed a single amino acid variation in the surface glycoprotein.[16] A European phylogenetic analysis report on two SARS-CoV-2 genomes revealed novel variants that pointed to the initial stages of viral evolution.[17] Yellapu et al.[9] analyzed 540 complete genome sequences from 20 countries using the reference genome (NC_045512). They found that 246 out of 540 genomes showed amino acid variations in at least one of four structural genes [surface glycoprotein (S), envelope protein (E), membrane glycoprotein (M), and nucleocapsid (N)] with the S-protein recording the highest rate of amino acid variations. Up to 202 genomes showed 34 types of amino acid variations in the S proteins such as L5F, A27V, Y28N, T29I, H49Y, S50L, L54F, N74K, E96D, D111N, F157L, G181V, S221W, T240I, S248R, A344S, A348T, R408I, G476S, V483A, H519Q, A520S, A570V, D614G, H655Y, Q675H, F797C, A930V, D936Y, S940F, A1078V, D1168H, N1178D, and D1259H. The D614G variation was observed in 160 genomes, indicating its conservation across these genomes. The N-protein recorded the second-highest number of amino acid variations. 65 genomes showed 25 types of variations such as D3Y, N4D, P6T, P13L, P14L, S23T, A35T, P46S, D128Y, R185C, S194L, S197L, S202N, R203K, G204R, T205I, A207G, G215S, S232T, G238C, T271I, Q289H, S327L, D343V, and P344S. The R203K variation was observed in 21 genomes, G204R in 19 genomes, and S197L in 15 genomes. Only three genomes showed two types of amino acid variations, such as L37R and P71L, in the E protein. Six genomes showing A2S, V70I, and T175M amino acid variations were observed in the M protein.In December 2020, a novel SARS-CoV-2 lineage bearing many mutations in the spike region was discovered to spread in the United Kingdom.[18] This lineage was named by the World Health Organization (WHO) as a Variant of Concern (VOC) Alpha and was later pango classified as B.1.1.7.[19,20] Two additional rapidly growing lineages were reported in the following weeks in South Africa and Brazil – VOCs Beta (Pango lineage B.1.351) and Gamma (Pango lineage P.1), respectively.[21,22] Although Alpha was the first VOC discovered, phylogenetic analyses indicate that Beta likely emerged in June 2020 before it was later reported.[7] Each of these lineages was characterized by many genetic differences concerning the background viral population, with some carrying signatures of enhanced transmissibility (Alpha) or immune evasion properties (Beta).[7] In May 2021, the Delta lineage (B.1.617.2), identified as circulating in India, quickly replaced all three previous VOCs, resulting in a drastic surge in reported cases worldwide.[23,24] Omicron (B.1.1.529) Pango lineages BA.1–BA.5, reported in South Africa and Botstudies

have increasingly shownswana in November 2021, started new global waves of infection.[25] The first three lineages of Omicron (BA.1, BA.2, and BA.3) emerged independently around the same time in October 2021, followed by BA.4 in mid-December 2021 and BA.5 in January 2022.[26] The emergence of the BA.3 lineage has been suggested to result from an ancestral recombination event between BA.1 and BA.2. In contrast, the emergence of BA.4 and BA.5 lineages was possibly through a previous inter-lineage recombination event.[25] Although these VOCs emerged in different parts of the world, they all had a significantly higher growth advantage than predecessor variants. They shared sets of mutations such as ΔH69/V70, N501Y, and E484K, which suggests probable convergent evolution.[26,27] Following the emergence of JN.1 SARS-CoV-2 in December 2023, the omicron variant KP.2 (JN.1.11.1.2) was discovered in early January 2024. It rapidly became the dominant variant in India, spreading to other parts of the world. The KP.2 SARS-CoV-2 variant carries three defining mutations in the S protein, namely F456L, R346T, and V1104L, contributing to its increased viral fitness. The origin of Omicron remains uncertain. Phylogenetic analyses of global SARS-CoV-2 sequences have not identified any closely related intermediary sequences between Omicron and its nearest variants. This makes the pathway leading to Omicron emergence a critical area for further research. Additionally, evolutionary analyses have not discovered any distinctive mutational profile or frameshift event that could suggest that Omicron directly evolved from the Alpha, Beta, Delta, or Gamma variants.[28,29] Figure 1 below summarizes the different strains, years and country of origin.

The omicron K.P2 variant

Nextstrain illustrated JN.1 lineage and showed that complex recombination, antigenic drift, and convergent evolution caused immune-escape mutations, such as independently acquired mutations such as R346T, L455F/S, F456L, and T572I, by many lineages. JN.1 subvariants, including KP.2 (JN.1.11.1.2) and KP.3 (JN.1.11.1.3), are members of a "FLiRT" group of variants.[30] The origin of the KP.2 (JN.1.11.1.2) variant, as a direct descendant of the Omicron JN.1 lineage, can be traced to December 2023 in the United States.[31] Alterations in the spike protein, amongst the other unsettling characteristics of the FLiRT variant, are responsible for the virus pathogenicity.[32] The distinctive identifiers for FLiRT are the two spike protein mutations: F to L at position 456 and R to T at position 346. However, KP.2 has a higher viral fitness due to its reproduction number, which is 1.22 times greater than JN.1.[31] The increased heterogeneity in KP.2, as well as JN.1 and KP.3 RBD variants, as proposed by AF2-predicted conformational ensembles, may cause these variants to influence a more mobile RBD structure to regulate and evade antibody neutralization.[30]

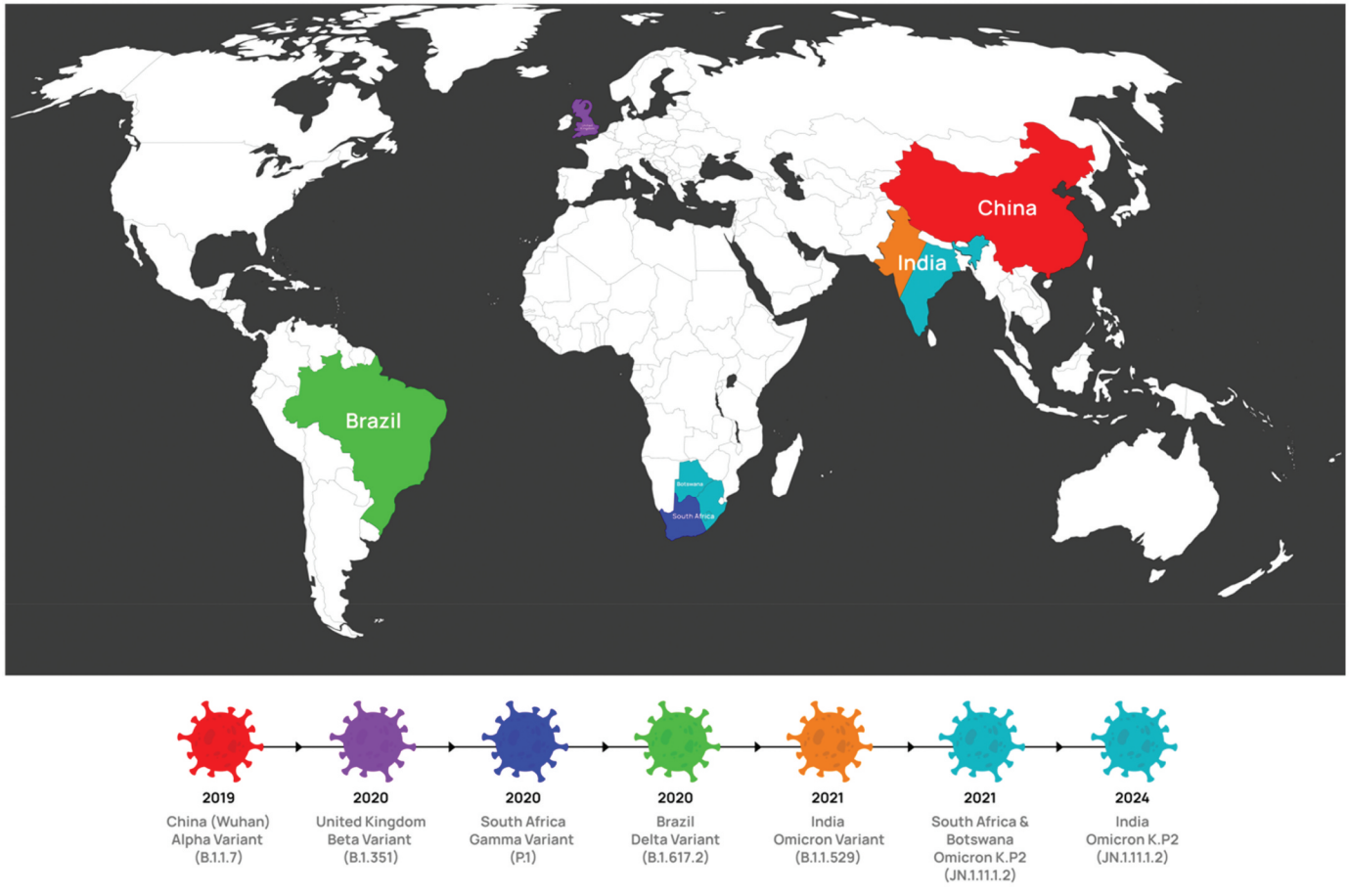

Figure 1. Illustration of the evolution of COVID-19 variants from the Wuhan strain to the current omicron K.P2 strain, originating countries and respective years.

As of April 2024, the KP.2 three novel mutations, R346T, F456L, and V1104L, appeared to have a growth advantage, becoming more dominant in multiple regions.[30] These mutations differentiated the mutation profile of KP.2 spike protein from the JN.1 variant. Convergent Omicron mutations can advance high transmissibility and antigenicity by controlling the interaction between the binding to the host receptor and robust immune evasion profile. This may be a constant strategy of Omicron variant evolution, which would cause combinatorial exploration of the mutations to evade antibody neutralization with maintained ACE2 binding affinity.[30] According to the Center for Disease Control and Prevention (CDC) data, the KP.2 variant of the FLiRT family accounted for about 25% of newly sequenced cases during the 2 weeks concluding on April 27. However, it is responsible for over 40% of recent infections in combination with the KP.3 variant of the SARS-CoV-2.[32] For example, The Infectious Disease Society of America (IDSA) has raised concerns about a recent COVID-19 wave due to a surge in COVID-19 cases in the UK, South Korea, and New Zealand. As of May 2024, 238 Omicron KP.2 sub-variant cases were recognized by The Indian SARS-CoV-2 Genomics Consortium (INSACOG). Of these, 36 and 146 cases were in Bengal and Maharashtra, respectively, surpassing the previously prevalent JN.1 variant.[32] KP.2 is quite resistant to the sera of persons vaccinated with the recent XBB.1.5 monovalent vaccine despite its lower infectivity than JN.1.[31] Although there is some degree of antibody cross-neutralization in recipients of the XBB.1.5 monovalent booster or in recipients who developed XBB.1.5 BTI, the immune escape of KP.2 and KP.3 may require vaccine adaptation. Reports of reduced vaccine efficacy should prompt this. There is limited documentation of the current vaccines' effectiveness against the symptomatic and severe illnesses caused by the two sub-variants. With the FDA's yearly anticipation of the vaccine formulation, the next monovalent vaccine may be based on JN.1 or KP.2 and available in Fall 2024.[33]

The new booster vaccine targeting omicron K.P2

The COMIRNATY (2024–2025 formula) and SPIKEVAX are updated COVID-19 booster vaccines developed by Pfizer and Moderna, respectively, based on the FDA recommendation from the VRBPAC in June 2024 to focus on targeting the Omicron KP.2 variant of SARS-CoV-2 following a significant rise in Omicron KP.2 variants.[34,35] The emergence of the Omicron K.P2 variant prompted the development of a booster vaccine targeting this specific lineage. Due to the prevalence of the KP.2 strain, the composition of the monovalent vaccine is directed at the KP.2 variant. However, it generates immune responses from other sub-lineages of JN.1, such as KP.3. The new booster vaccine delivers nucleoside-modified mRNA into host cells using a lipid medium as the vehicle. The mRNA codes for the expression of the spike (s) antigen in the host, a glycoprotein specific to the KP.2 variant of SARS-CoV-2.[36] An immune response is mediated by the host immunity system when this antigen is recognized, thus producing antibodies to mount a defense against the offending antigen, which recognizes and destroys the KP.2 variant.[36] The mRNA is transported efficiently into the cells through the lipid vehicle for translation into spike protein.

The clinical trials and observational studies showed good safety margins and efficacy of the new booster vaccine. COMIRNATY significantly increased neutralizing antibody titers following administration, with geometric mean concentrations (GMCs) rising threefold compared to primary vaccination.[36] The 100% sero-response rates corresponded to improved immune response and more robust defense against the KP.2 variant. While maintaining a safety profile consistent with previous formulations, it showed 95% efficacy against confirmed COVID-19 cases. A similar clinical trial conducted on the SPIKEVAX booster vaccine demonstrated significant improvement in immune response in participants aged 18 and older when compared to the primary series, indicating effectiveness, especially in older adults.[37] The new booster shows improved immunity against specific mutations of the omicron variants compared to previous versions. The earlier versions targeted the alpha and delta variants of COVID-19. In contrast, the new booster targeted the JN.1 sub-lineage, including KP.2. The adverse effects were comparable to previous formulations and maintained a safety profile.[36,37]

Beyond monovalent booster vaccines, studies have increasingly shown the benefits of heterologous boosting – using different vaccine platforms for the primary series and booster doses – to enhance immunogenicity and breadth of immune protection. Clinical trials and real-world data indicate that heterologous boosters, including adenoviral vector vaccines (e.g., AstraZeneca, Sputnik V, Johnson & Johnson) followed by mRNA boosters, elicit stronger and broader immune responses than homologous regimens. A study by Das et al. (2023) demonstrated that heterologous boosting with mRNA vaccines after an initial adenovirus-based regimen resulted in a significantly higher increase in neutralizing antibodies and T-cell responses compared to homologous schedules.[38] Similar findings were observed in a study by Maher et al. (2024), where individuals primed with AstraZeneca and boosted with Pfizer exhibited an increase in neutralizing titers against SARS-CoV-2 variants, surpassing homologous mRNA regimens.[39]

Heterologous boosters also confer superior protection against emerging variants. Studies conducted in the UK and Germany has shown that mixing vector-based and mRNA vaccines not only enhances immune responses but also improves protection against severe disease outcomes, particularly among high-risk groups. Data from the COV-BOOST trial indicated that heterologous booster schedules resulted in higher antibody titers and broader immune responses, making them a crucial strategy in combating evolving SARS-CoV-2 variants.[40] The new booster vaccines targeting Omicron KP.2 benefit from these immunogenicity insights, emphasizing their role in sustaining high levels of protection against SARS-CoV-2 variants. The incorporation of heterologous booster strategies alongside monovalent KP.2-targeting vaccines could further optimize global vaccination efforts, particularly in populations with prior heterologous exposures. While more research is required to further evaluate the durability of immune responses elicited by KP.2 boosters and their effectiveness against potential new SARS-CoV-2 mutations, the COMIRNATY and

SPIKEVAX KP.2-targeting boosters demonstrate strong efficacy and immunogenicity. Additionally, global evidence underscores the importance of heterologous boosting in enhancing immune responses. Ongoing surveillance and clinical trials will be critical in assessing the long-term benefits of these updated booster vaccines in the evolving landscape of SARS-CoV-2.

Public health implications

The Omicron variant of SARS-CoV-2 emerged in late 2021 and caused a rapid increase in COVID-19 cases in several countries with substantial COVID-19 vaccination coverage and infection-induced immunity levels.[38] In the United States, boosters have become highly recommended and continues to hold a critical component of the US Centers for Disease Control (CDC) public health response to reduce adverse outcomes from COVID-19.[39] In recent studies have reported waning immunity in effectiveness of booster vaccine against the Omicron variant of the original monovalent COVID-19 vaccines. Still, protection against severe illness was more stable and long-lasting.[40] Initial real-world efficacy data from the US suggests that the bivalent booster, designed to protect against Omicron, enhances protection relative to no booster vaccination. The emergence of the Omicron variant has emphasized the importance of COVID-19 booster shots.[40,41] The USA and the UK have already initiated booster dose vaccination among their citizens to control the spread of the Omicron variant. Fully vaccinated residents who received a booster dose had a ten times lower risk of contracting COVID-19 than residents who had received the primary vaccination series or were unvaccinated.[42] The WHO, US FDA, and EU have approved several vaccines for emergency use with 65–95% efficacy, and most countries, including the USA, UK, India, and EU, have been rigorously vaccinating their citizens. Although vaccination was initiated worldwide, the unequal distribution among developed and developing nations may become a reason for further viral spread.[43] The vaccination process was severely affected by the hesitancy shown by people throughout the world.

As we transition to endemicity, inequitable access to vaccines, particularly in low and middle-income countries (LMICs), still poses risks of unprecedented disruptions and the emergence of viral mutations, which potentially lead to notorious vaccine-resistant variants. These missteps learned from the previous responses to the human immunodeficiency virus (HIV) and influenza outbreak founded the hypothetical plan to ensure that vaccine accessibility to LMICs is not impeded. Inequalities in vaccination coverage, influenced by disparities in wealth, education, geographic access, and gender, lead to lower full immunization among disadvantaged groups – with rural and urban rates varying considerably by country – and wealth disparities predominantly driving booster vaccine access.[44] Many high-income countries directly negotiate large advance orders for the vaccine, leaving resource-limited countries scrambling for access. This poses a severe public health concern as the supply shortages and national procurement methods of some countries that bypassed the vaccine pillar hindered the optimal function of COVAX in delivering timely and adequate doses to participating countries.[45]

Accorsi et al.[46] reported findings from an observational study that estimated the association of receipt of three doses or two doses of mRNA vaccines (BNT162b2 or mRNA-1273), compared with each other and with no vaccination, with symptomatic SARS-CoV-2 infection, stratified by the Omicron and Delta variants among individuals in the US. This Centers for Disease Control and Prevention – led study used a test-negative, case-control analysis of 70 155 tests from symptomatic adults 18 years or older with COVID-like illness tested December 10, 2021, through January 1, 2022, by a national pharmacy-based testing program (4666 COVID-19 testing sites across 49 US states).

The study results demonstrated that the likelihood of vaccination with three mRNA vaccine doses (vs. unvaccinated) was significantly lower among both Omicron cases than

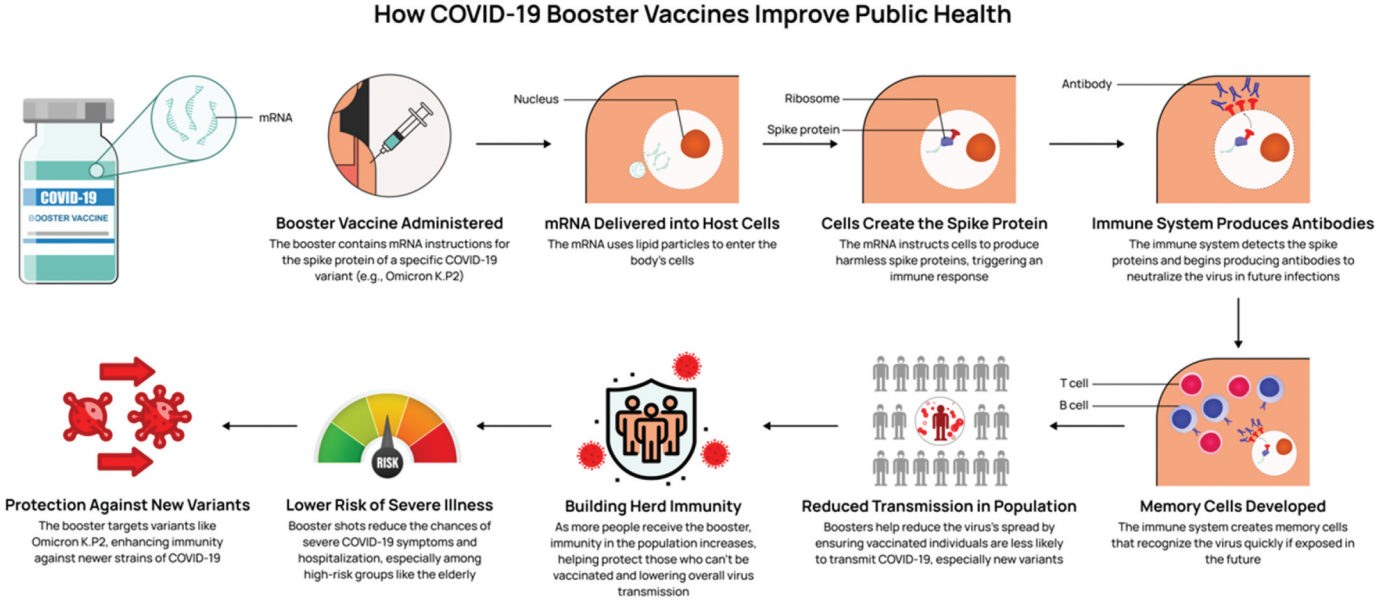

Figure 2. Image showing how the latest COVID-19 booster vaccine will improve public health.

among SARS-CoV-2–negative controls; a similar pattern was observed with three vs two doses of mRNA vaccines. The relatively higher odds ratios for the association with Omicron infection suggested less protection (i.e., corresponding with lower estimated vaccine effectiveness) for Omicron than for Delta, underscoring the ongoing need for a layered public health approach to preventing SARS-CoV-2.[46] This is important, as many countries continue to have an insufficient supply of vaccines. If a 3-dose schedule is more effective, it would be informative for these countries to know whether a 2-dose schedule may still provide considerable protection against severe disease when vaccine supplies are limited. Accorsi et al. provide the ORs for the 2-dose schedule for symptomatic SARS-CoV-2 infection by month since the second dose. These ORs indicate limited to no effectiveness of the 2-dose schedule against the symptomatic Omicron infection by 4–6 months after the second dose.[47] Moreover, in many countries, including the US, the pandemic continues to be substantially driven by unvaccinated individuals. While it is helpful to provide booster vaccinations, particularly to high-risk groups, only vaccinating those who are not yet vaccinated will result in sustainable control of COVID-19 and prevent additional morbidity and mortality.

COVID-19 vaccine inequity places the health of the global population at risk and exacerbates socio-economic repercussions, especially in low- and middle-income countries. Initiatives launched to combat vaccine inequity, such as the Fair Allocation Framework for the COVID-19 Vaccines (COVAX), have been unsuccessful as several governments, primarily from high-income countries, have scaled down their contributions to the initiative. Furthermore, COVAX has not seriously engaged with the Access to COVID-19 Tools (ACT) Health Systems Connector, as was initially intended, leading to crucial health systems components critical to vaccine delivery being overlooked. Several strategies can be employed to help achieve the desired global immunization goals, such as Intellectual Property waivers, increased donations, and activation of new COVID-19 vaccine manufacturing hubs. In addition, continued advocacy for vaccine equity by all involved and affected stakeholders, as well as critical amendments to existing or upcoming legislation and funding mechanisms, will help address the shortcomings of current inequitable vaccine distribution.[48] Figure 2 below summarizes how the booster vaccine improves public health.

Conclusion

In conclusion, this research has explored the evolutionary trajectory of SARS-CoV-2, with a specific focus on the Omicron KP.2 variant and the public health implications of the current booster vaccine. The findings bring to fore the dynamic nature of SARS-CoV-2 mutations, particularly in the spike protein, which has facilitated immune evasion and increased transmissibility. The emergence of the KP.2 variant, with its unique mutations (R346T, F456L, and V1104L), highlights the virus's capacity for rapid adaptation, posing new challenges in vaccine development and public health response.

The development of the KP.2-adapted booster vaccine represents a significant advancement in the ongoing fight against COVID-19. Clinical trials and observational studies have demonstrated its efficacy in increasing neutralizing antibodies and providing enhanced protection against symptomatic and severe disease, especially in vulnerable populations. The KP.2 booster is particularly crucial in mitigating the impact of current and future variants, given the variant's ability to partially evade immunity conferred by earlier vaccines. Additionally, this review highlights the persistent global challenge of vaccine inequity, which threatens to undermine the progress made in controlling the pandemic. Disparities in vaccine distribution, particularly in low- and middle-income countries, continue to pose significant risks for the emergence of new variants and the potential for prolonged outbreaks. Ensuring equitable access to vaccines, including variant-specific boosters, remains critical to achieving long-term control of COVID-19 on a global scale.

Disclosure statement

No potential conflict of interest was reported by the author(s).

Funding

The author(s) reported that there is no funding associated with the work featured in this article.

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Authors contribution statement

Adewunmi Akingbola conceptualized, edited the manuscript, wrote the Conclusion, Abiodun Adegbesan, Ademola Aiyenuro and Olajumoke Adewole edited the manuscript, Ayotomiwa Idris wrote the Introduction, Favour peters wrote the Evolution of SARS-COV-2 and its variants, Timilehin Adeleke wrote the Omicron K.P2 variant, Olusola Aremu wrote the Booster Vaccine, Tolani Odukoya wrote the Public Health Implications, Owolabi Abdullahi provided Figure 1 and 2. All authors agreed to the mauscript.

Data availability statement

Research study didn't generate any data.

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