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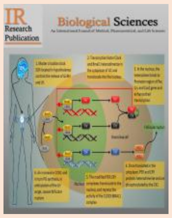

XEC: The Next Frontier in COVID-19 Evolution and Biotechnological Interventions

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ABSTRACT

The XEC strain of SARS-CoV-2, a recombinant variant, presents significant challenges due to its mutations that enhance immune escape potential and potentially alter transmission dynamics. As the world continues to confront the evolving nature of COVID-19, biotechnological innovations, including genomic surveillance, CRISPR-based diagnostics, and mRNA vaccine platforms, have been essential in responding to emerging variants. However, the XEC variant's ability to evade immunity requires ongoing adaptation of these technologies, including precision diagnostics and updated vaccines. Despite progress, substantial gaps remain in understanding the pathophysiology of new variants like XEC, their impacts on vulnerable populations, and the efficacy of current therapeutics. Future research should prioritize investigating the molecular mechanisms driving XEC's pathogenicity, long-term vaccine effectiveness, the development of novel therapeutics, and the integration of biotechnology into public health policies. Furthermore, enhanced international collaboration and data sharing are critical for improving global surveillance and preparedness. Addressing these research gaps through multidisciplinary efforts will be crucial in mitigating the impact of future viral threats and safeguarding global health.

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Introduction

The XEC strain is a recombinant variant of SARS-CoV-2 that combines genetic material from previous lineages, notably Omicron (BA.2) and Delta. Recombinant variants arise when a host is co-infected with multiple viral strains, enabling genetic exchange during replication (1). This mechanism gives XEC distinct mutations, particularly in the spike protein, which influence its biological behavior. One significant feature of XEC is its enhanced ability to bind to ACE2 receptors due to mutations in the receptor-binding domain (RBD), potentially increasing transmissibility (2). Moreover, the strain exhibits mutations in the N-terminal domain (NTD), which may reduce recognition by neutralizing antibodies from prior infections or vaccinations (3). Epidemiological reports suggest that XEC is associated with higher secondary attack rates and increased immune evasion, raising concerns about its potential to cause new waves of infection. Studying variants such as XEC is crucial for understanding the dynamic interplay between viral evolution, host immunity, and public health interventions. Emerging variants often challenge existing vaccines and therapeutics by harboring mutations that alter viral fitness and immune recognition (4). For instance, the XEC strain's RBD mutations may compromise the efficacy of monoclonal antibody treatments and existing mRNA vaccines. In addition to public health implications, emerging variants provide valuable insights into viral evolution. Recombinant strains like XEC offer a natural model for studying the processes of genetic exchange and adaptation. These insights can inform predictive models for variant emergence and guide the design of updated vaccines and therapeutics (5). However, real-time monitoring of emerging variants enhances pandemic preparedness. Genomic surveillance and biotechnological tools such as CRISPR-based diagnostics allow for early detection and rapid response, minimizing the risk of widespread outbreaks (6). By studying XEC and similar variants, researchers can refine these tools and strategies, ensuring robust responses to future pandemics.

Biological and Epidemiological Characteristics of the XEC Strain

The XEC strain of SARS-CoV-2 has emerged as a recombinant variant that combines genetic material from previous lineages, most notably Omicron (BA.2) and Delta. This genetic recombination has given rise to significant mutations, potentially altering the strain's biological characteristics and epidemiological behavior. Understanding these changes is essential for assessing their impact on public health and developing effective intervention strategies.

Genetic mutations and evolutionary insights

The XEC strain is distinguished by a combination of mutations in its spike protein, which is critical for viral entry into host cells. Key mutations in the receptor-binding domain (RBD) increase the virus's affinity for the ACE2 receptor, facilitating more efficient host cell infection (7). These mutations are similar to those observed in highly transmissible variants like Omicron but are further enhanced by features inherited from Delta, such as increased replication efficiency. Recombination is the primary mechanism driving XEC's evolution, arising when a host is co-infected with multiple SARS-CoV-2 variants. During replication, genetic material from these variants is exchanged, resulting in a strain with novel properties (8). This evolutionary process underscores the adaptability of SARS-CoV-2 and its ability to overcome environmental and immunological pressures. Moreover, the XEC strain exhibits mutations in the N-terminal domain (NTD) of the spike protein, which contribute to immune evasion by reducing recognition by neutralizing antibodies (9). These changes may render current vaccines and monoclonal antibody treatments less effective, necessitating updates to immunization strategies.

Transmission dynamics and immune escape potential

The XEC strain has demonstrated enhanced transmissibility, attributed to its mutations in the spike protein. Epidemiological data suggest that the variant is associated with higher secondary attack rates and faster spread within populations compared to earlier strains (10). This increased transmissibility may result from the strain's improved ability to bind ACE2 receptors and infect host cells efficiently. Immune escape is another critical feature of the XEC strain. Studies have shown that its spike protein mutations reduce the neutralizing capacity of antibodies elicited by previous infections or vaccinations (11). This immune evasion potential raises concerns about breakthrough infections, particularly in populations with waning immunity or limited vaccine coverage. Moreover, the XEC strain's ability to evade T-cell responses has been observed, further compromising immune defense mechanisms (12). This could lead to more severe infections in vulnerable individuals and necessitates a reassessment of current therapeutic and prophylactic measures. The convergence of high transmissibility and immune escape underscores the need for continuous genomic surveillance and rapid updates to biotechnological tools, such as vaccines and diagnostic assays. Understanding these dynamics is crucial for mitigating the public health impact of XEC and similar variants. Figure 1 below illustrates the key characteristics of the XEC strain, focusing on its genetic mutations, enhanced transmissibility, and immune evasion capabilities. It highlights how mutations in the spike protein, particularly in the receptor-binding domain (RBD), increase its binding affinity to ACE2 receptors, leading to faster spread.

Biotechnological Approaches in Tackling the XEC Variant

As emerging variants like XEC continue to challenge existing interventions, biotechnology provides powerful tools for monitoring, detecting, and mitigating their impact. Advances in genomic surveillance, CRISPR-based diagnostics, and vaccine technologies have proven instrumental in addressing the evolving threats posed by SARS-CoV-2 variants.

Advances in genomic surveillance and diagnostics

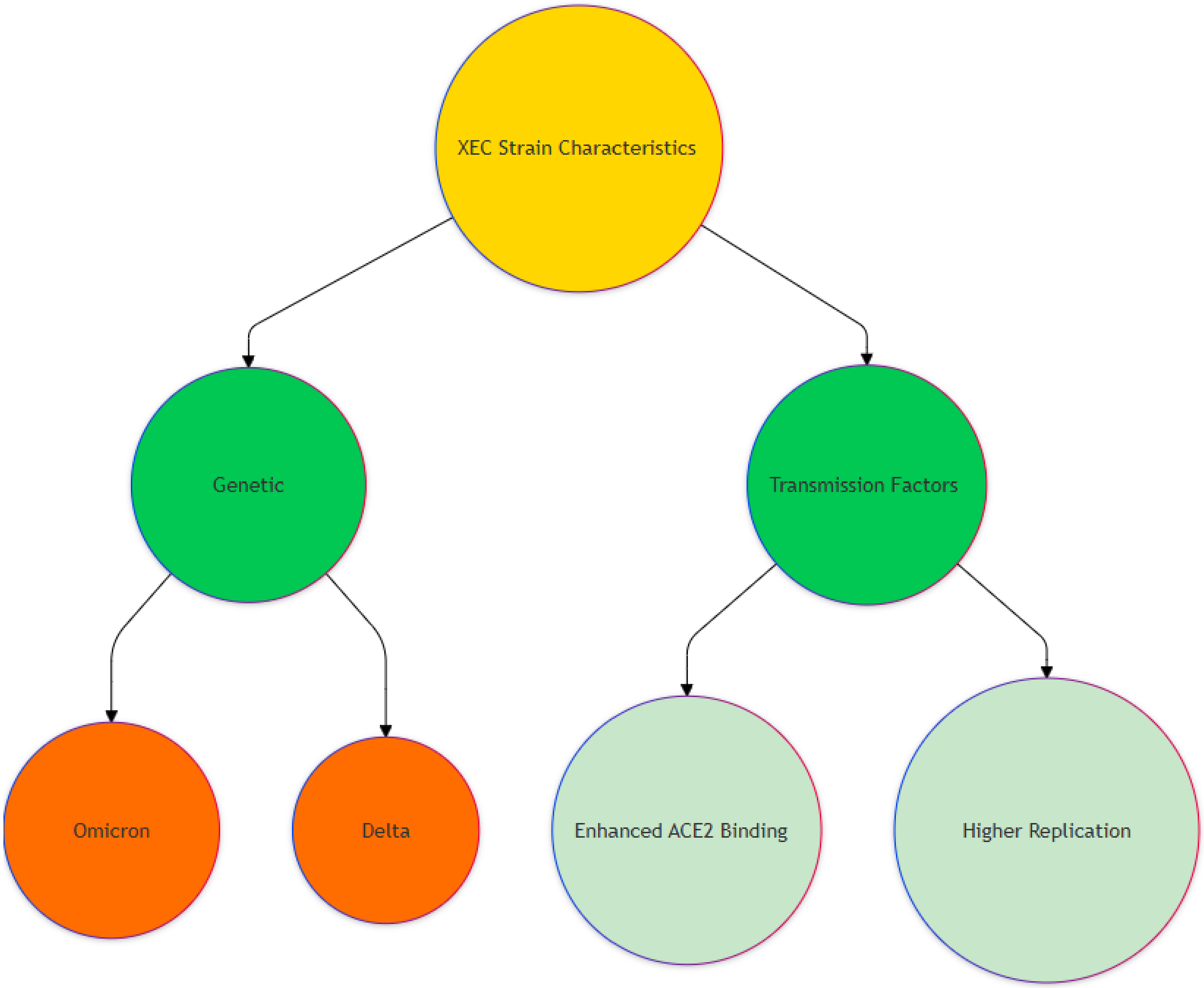

Figure 1. Key features of the XEC strain: a visual insight

Genomic surveillance has been a cornerstone in tracking the evolution of SARS-CoV-2 and its variants. The emergence of the XEC strain underscores the importance of high-throughput sequencing platforms, such as Illumina and Oxford Nanopore technologies, which enable rapid and accurate sequencing of viral genomes. These platforms have identified XEC's recombinant origin, revealing its combination of Omicron and Delta mutations (13). Bioinformatics tools like Nextstrain and GISAID are pivotal in analyzing and visualizing the spread of variants globally, providing real-time insights into XEC's epidemiological dynamics (14). Such tools help public health officials prioritize resources and inform intervention strategies. Diagnostics have also evolved to address the challenges of identifying recombinant strains. Multiplex PCR assays, capable of targeting unique mutations in XEC's spike protein, have been developed to distinguish it from other variants (15). These innovations enable early detection and improved outbreak management.

Role of CRISPR technology in variant detection

CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) technology has revolutionized viral detection, offering precise and rapid identification of SARS-CoV-2 variants, including XEC. CRISPR-based diagnostic platforms, such as SHERLOCK and DETECTR, utilize guide RNAs specific to variant-defining mutations, enabling real-time and portable testing (16). The CRISPR-Cas12 and Cas13 systems have been adapted to identify the mutations unique to XEC, including those in the receptor-binding domain. These systems amplify target sequences and produce fluorescent or colorimetric signals upon detection, providing a cost-effective alternative to traditional PCR (17). Moreover, CRISPR offers potential beyond diagnostics. It can be used for functional studies of XEC's mutations, helping researchers understand how these changes affect transmissibility, immune escape, and pathogenesis (18). The scalability and adaptability of CRISPR make it an invaluable tool in addressing emerging variants.

Innovations in vaccine development and mRNA platforms

The XEC variant's ability to evade immunity highlights the need for updated vaccines tailored to its unique genetic profile. mRNA vaccine platforms, pioneered by Pfizer-BioNTech and Moderna, are particularly suited to this challenge due to their rapid adaptability and scalability (19). These platforms allow for the swift incorporation of XEC's mutations into vaccine candidates, providing timely responses to new variants. Advances in nanoparticle-based delivery systems have further improved the stability and immunogenicity of mRNA vaccines. Lipid nanoparticles, for instance, enhance the delivery of mRNA to target cells, ensuring robust immune responses against XEC (20). Moreover, next-generation vaccines, such as multivalent or pan-coronavirus vaccines, are being developed to provide broader protection against recombinant variants like XEC and potential future strains (21). Adjuvant technologies are also evolving to boost vaccine efficacy. Novel adjuvants, such as AS03 and Matrix-M, have been shown to enhance immune responses, particularly in populations with waning immunity (22). These innovations will be critical in combating XEC and mitigating its impact on public health. Figure 2 below outlines key biotechnological strategies employed to combat the emerging XEC variant of SARS-CoV-2. These approaches include genomic surveillance using high-throughput sequencing and bioinformatics tools, CRISPR-based diagnostic platforms like SHERLOCK and DETECTR, and the development of mRNA vaccines with modular design and nanoparticle delivery systems.

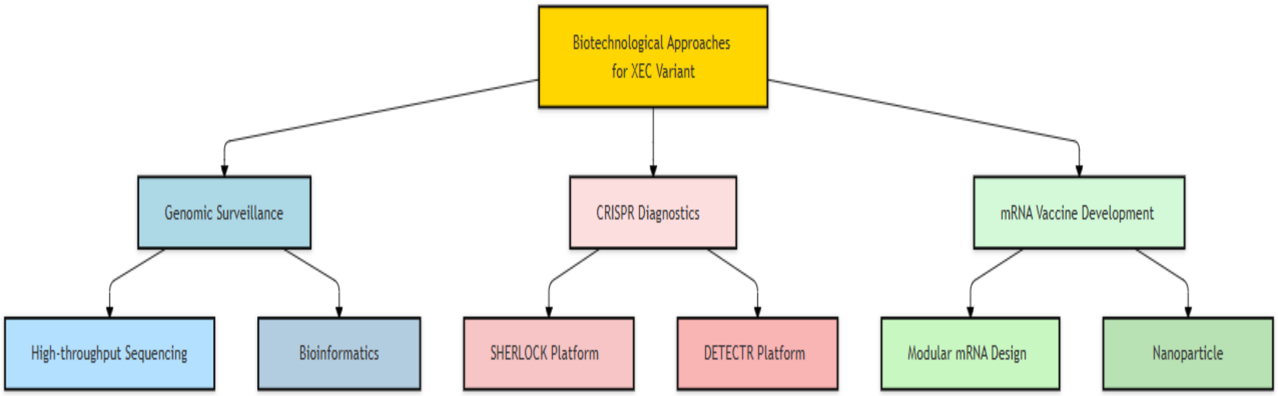

Figure 2. Biotechnological approaches in tackling the XEC variant: genomic surveillance, CRISPR diagnostics, and mRNA vaccines.

Research Gaps and Challenges

Despite advancements in understanding SARS-CoV-2 variants, the XEC strain presents several unresolved questions. Its recombinant nature, immune evasion capabilities, and unique pathophysiological attributes pose challenges requiring focused research.

Understanding XEC pathophysiology

One critical research gap involves the need for comprehensive insights into the pathophysiology of the XEC strain. Although initial studies highlight its enhanced receptor-binding affinity and immune escape mechanisms, little is known about how these features translate into disease severity or clinical outcomes. Specifically, the role of XEC mutations in influencing viral replication, tissue tropism, and immune response modulation remains underexplored (23). Moreover, emerging evidence suggests that recombination may impact the virus's ability to trigger hyperinflammatory responses, such as cytokine storms, which have been linked to severe COVID-19 cases (24). However, the extent to which XEC drives such responses compared to earlier variants is unclear. Understanding these mechanisms is crucial for predicting clinical severity and tailoring therapeutic interventions.

Impacts on co-morbid conditions and vulnerable populations

The potential exacerbation of co-morbidities by the XEC strain is another significant area of uncertainty.

SARS-CoV-2 variants have been shown to disproportionately affect individuals with underlying conditions, such as diabetes, cardiovascular disease, and chronic respiratory disorders (25). However, there is limited data on how XEC interacts with these conditions and whether it poses a heightened risk. Furthermore, the impact of XEC on immunocompromised individuals, pregnant women, and the elderly—groups already vulnerable to severe COVID-19 outcomes—requires urgent investigation. For instance, reduced vaccine efficacy and delayed viral clearance in these populations could lead to prolonged infections, increasing the risk of further viral evolution (26). Another challenge involves understanding the socioeconomic and demographic disparities in XEC's impact. Early epidemiological data suggest that healthcare accessibility and pre-existing health inequalities may exacerbate the burden of this variant in low-income populations, but more studies are needed to confirm these trends.

Limitations in current therapeutics

Current therapeutics for COVID-19 face significant limitations when addressing the XEC strain, primarily due to its immune escape capabilities. Monoclonal antibody therapies, such as Sotrovimab and Evusheld, have shown reduced efficacy against emerging recombinant variants, including XEC (27). The mutations in XEC's spike protein hinder antibody binding, rendering these treatments less effective. Antiviral drugs like Remdesivir and Molnupiravir remain valuable tools, but their effectiveness against XEC-specific mutations has yet to be fully evaluated. Preliminary findings suggest that XEC's replication dynamics might influence antiviral efficacy, necessitating further clinical studies (28). Vaccination strategies also face challenges, as existing vaccines were designed to target earlier variants. The reduced neutralization capacity of vaccine-induced antibodies against XEC highlights the need for updated vaccines and booster doses (29). Moreover, the global inequity in vaccine distribution poses a challenge in achieving widespread immunity, allowing the XEC variant to continue circulating and evolving. Innovative therapeutic approaches, such as multi-epitope vaccines and broad-spectrum antivirals, are promising but remain in the early development stages. Bridging these gaps requires concerted efforts in research, funding, and international collaboration to ensure timely and effective responses to the XEC variant.

Multidisciplinary Strategies for Future Preparedness

As the world faces emerging infectious diseases like COVID-19 and its evolving variants, such as XEC, it is critical to develop comprehensive and multidisciplinary strategies to ensure future preparedness. These strategies must integrate biotechnology, public health policies, and international collaboration to respond effectively to future pandemics.

Integrating biotechnological tools and public health policies

The integration of biotechnological tools with public health policies is essential for enhancing pandemic preparedness and response. Advances in biotechnology, particularly in genomics, diagnostics, and vaccine development, have significantly contributed to the swift identification and containment of SARS-CoV-2 variants, including XEC. However, to maximize their impact, these tools must be supported by robust public health frameworks that prioritize early detection, rapid diagnostics, and equitable vaccine distribution. Genomic surveillance, which employs next-generation sequencing technologies, enables the real-time tracking of viral mutations. Incorporating this surveillance into public health policies allows for targeted interventions, such as adjusting vaccination strategies based on emerging variants like XEC (30). Furthermore, CRISPR-based diagnostic platforms can provide rapid, point-of-care testing, aiding in the early identification of new variants and supporting public health decisions (31).

Public health policies should also focus on the equitable distribution of biotechnological interventions, ensuring that vulnerable populations in both high- and low-income regions are protected. This includes the timely deployment of vaccines, therapeutics, and diagnostic tools, particularly to underserved and high-risk communities (32). Moreover, public health systems must prioritize adaptive regulatory frameworks that can quickly approve novel biotechnologies for emergency use, such as mRNA vaccines, which have proven to be highly effective in responding to the rapid mutation of SARS-CoV-2 (33). By bridging the gap between biotechnology and policy, future pandemic responses can be more agile and effective in minimizing both the health and socio-economic impacts of emerging variants like XEC.

Global collaboration and data sharing

Global collaboration and data sharing are essential components of pandemic preparedness, particularly in the face of rapidly evolving pathogens such as SARS-CoV-2. The COVID-19 pandemic highlighted both the importance and the challenges of global scientific cooperation in tracking viral mutations, sharing genomic data, and coordinating research efforts. Moving forward, fostering international partnerships and ensuring the equitable sharing of data will be crucial in preventing and managing future pandemics. Initiatives such as the Global Initiative on Sharing All Influenza Data (GISAID) have shown the value of open-source data sharing in tracking the spread of variants like XEC. The real-time submission of genomic data by countries and research institutions allows for the swift identification of emerging mutations, helping to guide public health decisions (34). The XEC variant’s unique recombination underscores the need for continued global surveillance networks that can monitor such variants across geographic regions.

International collaborations between governments, scientific communities, and private industries are also necessary to accelerate vaccine and therapeutic development. For instance, the rapid development of mRNA vaccines for COVID-19 was made possible by partnerships between pharmaceutical companies, public health organizations, and funding bodies such as the Coalition for Epidemic Preparedness Innovations (CEPI) and the U.S. Operation Warp Speed (35). These collaborations must continue post-pandemic to address emerging viral strains like XEC and prepare for future global health threats. Moreover, data sharing should not only be limited to genomic information but also encompass epidemiological, clinical, and demographic data to better understand the global distribution of variants and their impacts on different populations. Cross-border research collaborations, facilitated by international organizations like the World Health Organization (WHO), can help ensure a coordinated response to future outbreaks. This will enable scientists and public health officials to make data-driven decisions, optimizing resources and reducing the spread of new variants globally.

Conclusion

The XEC strain of SARS-CoV-2 presents unique challenges due to its recombinant nature, mutations that enhance its immune escape potential, and possible changes in transmission dynamics. Although much is still to be understood about this variant, it is clear that it carries significant implications for both public health and biotechnology. The recombinant characteristics of the XEC strain, coupled with mutations that enable it to partially evade immune responses, make it a formidable challenge in the fight against COVID-19. This strain's ability to potentially bypass immunity from prior infection or vaccination underscores the need for ongoing research to better understand its behavior and impact. Biotechnological innovations, such as genomic surveillance, CRISPR-based diagnostic tools, and mRNA vaccine platforms, have been critical in the rapid detection and response to SARS-CoV-2 variants. The ability to monitor viral evolution in real time has allowed for swift public health interventions and the continuous adaptation of diagnostic methods and therapeutic strategies. However, the XEC variant's ability to partially evade immunity necessitates a continuous adaptation of these technologies. Early intervention, precision diagnostics, and updated vaccine formulations are crucial to controlling the spread of this variant and preparing for future threats.

The integration of biotechnology with public health policies, alongside global collaboration and data sharing, has been instrumental in the pandemic response. These efforts have facilitated a more coordinated global response, enabling faster mobilization of resources and interventions. However, significant gaps remain in our understanding of the pathophysiology of new variants like XEC. More research is needed to understand how these variants interact with the immune system and affect vulnerable populations, such as the elderly and those with co-morbid conditions. However, current therapeutics, including monoclonal antibodies and antiviral drugs, are facing challenges against the evolving XEC strain. This highlights the need for more effective treatments that can specifically target the XEC variant and other emerging strains. As the virus continues to mutate, it is essential to develop more versatile therapies and ensure their global accessibility, especially in low- and middle-income countries, where healthcare resources are limited. Future research must focus on several critical areas to enhance our ability to manage future viral variants and pandemics. Understanding the pathophysiology of XEC and other emerging variants is essential, particularly the specific mutations that affect replication, tissue tropism, and immune modulation, as well as their impact on disease severity in vulnerable populations. Long-term vaccine efficacy against variants like XEC needs to be thoroughly studied, with a focus on immune response differences and strategies for booster vaccinations. Moreover, developing new antiviral drugs and monoclonal antibodies that can overcome immune escape mechanisms is crucial, including antiviral cocktails and small molecules targeting various stages of the viral lifecycle. Integrating biotechnology into public health policies is vital for swift pandemic responses, necessitating adaptive regulatory frameworks and equitable distribution of resources, especially in low- and middle-income countries. Enhancing global epidemiological monitoring and data sharing will also be pivotal, enabling real-time detection of new variants and coordinated responses. Addressing these gaps through interdisciplinary collaboration will ensure better preparedness and more effective management of emerging viral threats, ultimately safeguarding public health.

Contribution of authors

- Mustapha Abdulsalam conceptualized the study, focusing on the evolution of the XEC strain of SARS-CoV-2, its genetic mutations, and the biotechnological approaches needed to address this emerging threat. He contributed to drafting and revising the sections on the strain's biological characteristics, transmission dynamics, immune escape, and advancements in diagnostic and therapeutic interventions.
- Musa Ojeba Innocent contributed to the analysis of the epidemiological aspects of the XEC strain, including its transmission patterns, immune evasion mechanisms, and the potential impact on public health. He also provided critical input on the global response to the XEC variant and strategies for early detection.
- Miracle Uwa Livinus explored the role of biotechnological tools, such as CRISPR technology, in detecting and analyzing the XEC strain. Her contributions were crucial in outlining how genomic surveillance and diagnostic technologies can aid in rapid identification and monitoring of the virus.
- Fatimoh Abdulsalam Danjuma reviewed the implications of the XEC strain on vaccine development, specifically focusing on mRNA platforms. She provided valuable insights into the challenges of creating effective vaccines that address the new mutations and immune escape capabilities of the XEC variant.
- Idowu Afeez Temitope contributed to understanding the interactions between the XEC strain and co-morbid conditions. He examined how individuals with underlying health conditions may be more susceptible to severe outcomes and how current therapeutics may need to be adapted.
- Ishola Jonathan Adekunle provided a key analysis of the limitations of existing therapeutics and the importance of continued research into novel antiviral treatments. His contributions helped identify critical gaps in knowledge regarding the long-term effectiveness of current strategies against the XEC strain.

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Conflict of Interest

The authors declared no conflict of interest.

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Data Availability

Not applicable

References

1. Nájera, R.; Delgado, E.; Pérez-Alvarez, L.; Thomson, M.M. Genetic recombination and its role in the development of the HIV-1 pandemic. AIDS 2002, 16 (Suppl 1), S3–16.
2. Datta, P.K.; Liu, F.; Fischer, T.; Rappaport, J.; Qin, X. SARS-CoV-2 pandemic and research gaps: Understanding SARS-CoV-2 interaction with the ACE2 receptor and implications for therapy. Theranostics 2020, 10 (16), 7448–64.
3. Cromer, D.; Stein, M.; Reynaldi, A.; Schlub, T.E.; Wheatley, A.K.; Juno, J.A.; Davenport, M.P. Neutralizing antibody titers as predictors of protection against SARS-CoV-2 variants and the impact of boosting: a meta-analysis. Lancet Microbe 2022, 3 (1), e52–61.
4. Thakur, S.; Sasi, S.; Pillai, S.G.; Nag, A.; Shukla, D.; Singhal, R.; Velu, G.S.K. SARS-CoV-2 mutations and their impact on diagnostics, therapeutics, and vaccines. Front. Med. 2022, 9, 815389.
5. Abdulsalam, M.; Musa, I.O.; Livinus, M.U.; Elelu, S.A.; Ibrahim, G.O.; Salami, O.L.; Pal, S.K. Blue bioeconomy and biomedical innovation. In Marine Bioprospecting for Sustainable Blue-bioeconomy; Springer Nature Switzerland: Cham, Switzerland, 2024; pp. 143–57.
6. Thomas, S.; Abraham, A.; Baldwin, J.; Piplani, S.; Petrovsky, N. Artificial intelligence in vaccine and drug design. In Vaccine Design: Methods and Protocols, Volume 1: Vaccines for Human Diseases; 2022; pp. 131–46.
7. Ou, J.; Zhou, Z.; Dai, R.; Zhang, J.; Zhao, S.; Wu, X.; Zhang, Q. V367F mutation in SARS-CoV-2 spike RBD emerging during the early transmission phase enhances viral infectivity through increased human ACE2 receptor binding affinity. J. Virol. 2021, 95 (16), e01128–21.
8. Arnold, B.J.; Huang, I.T.; Hanage, W.P. Horizontal gene transfer and adaptive evolution in bacteria. Nat. Rev. Microbiol.

2022, 20 (4), 206–18.

9. Zabidi, N.Z.; Liew, H.L.; Farouk, I.A.; Puniyamurti, A.; Yip, A.J.W.; Wijesinghe, V.N.; Lal, S.K. Evolution of SARS-CoV-2 variants: implications on immune escape, vaccination, therapeutic and diagnostic strategies. Viruses 2023, 15 (4), 944.
10. Telenti, A.; Hodcroft, E.B.; Robertson, D.L. The evolution and biology of SARS-CoV-2 variants. Cold Spring Harb. Perspect. Med. 2022, 12 (5), a041390.
11. Abdulsalam, M.; Fatima, Z.Y.U.; Hasiya, U.A.; Ummulkhuthum, A.T.; Aisha, W.N.; Muhammad, F.Y. Deciphering the genetic code: mechanisms, evolution, and implications for biotechnology. World J. Adv. Res. Rev. 2024, 21 (1), 858–68.
12. Wang, L.; Nicols, A.; Turtle, L.; Richter, A.; Duncan, C.J.; Dunachie, S.J.; Payne, R.P. T cell immune memory after COVID-19 and vaccination. BMJ Med. 2023, 2 (1), 1–10.
13. Simon-Loriere, E.; Montagutelli, X.; Lemoine, F.; Donati, F.; Touret, F.; Bourret, J.; Paquin, A. Rapid characterization of a Delta–Omicron SARS-CoV-2 recombinant detected in Europe. 2022.
14. Saheed, Y.K.; Salau-Ibrahim, T.T.; Abdulsalam, M.; Adeniji, I.A.; Balogun, B.F. Modified bi-directional long short-term memory and hyperparameter tuning of supervised machine learning models for cardiovascular heart disease prediction in the mobile cloud environment. Biomed. Signal Process. Control 2024, 94, 106319.
15. Shah, M.; Woo, H.G. Omicron: a heavily mutated SARS-CoV-2 variant exhibits stronger binding to ACE2 and potently escapes approved COVID-19 therapeutic antibodies. Front. Immunol. 2022, 12, 830527.
16. Jones, T.C.; Biele, G.; Mühlemann, B.; Veith, T.; Schneider, J.; Beheim-Schwarzbach, J.; Drosten, C. Estimating infectiousness throughout SARS-CoV-2 infection course. Science 2021, 373 (6551), eabi5273.
17. Sande, M.G.; Rodrigues, J.L.; Ferreira, D.; Silva, C.J.; Rodrigues, L.R. Novel biorecognition elements against pathogens in the design of state-of-the-art diagnostics. Biosensors 2021, 11 (11), 418.
18. Triggle, C.R.; Bansal, D.; Ding, H.; Islam, M.M.; Farag, E.A.B.A.; Hadi, H.A.; Sultan, A.A. A comprehensive review of viral characteristics, transmission, pathophysiology, immune response, and management of SARS-CoV-2 and COVID-19 as a basis for controlling the pandemic. Front. Immunol. 2021, 12, 631139.
19. Rouf, N.Z.; Biswas, S.; Tarannum, N.; Oishee, L.M.; Muna, M.M. Demystifying mRNA vaccines: an emerging platform at the forefront of cryptic diseases. RNA Biol. 2022, 19 (1), 386–410.
20. Guevara, M.L.; Persano, F.; Persano, S. Advances in lipid nanoparticles for mRNA-based cancer immunotherapy. Front. Chem. 2020, 8, 589959.
21. Cankat, S.; Demael, M.U.; Swadling, L. In search of a pan-coronavirus vaccine: next-generation vaccine design and immune mechanisms. Cell Mol. Immunol. 2024, 21 (2), 103–18.
22. Levin, E.G.; Lustig, Y.; Cohen, C.; Fluss, R.; Indenbaum, V.; Amit, S.; Regev-Yochay, G. Waning immune humoral response to BNT162b2 Covid-19 vaccine over 6 months. N. Engl. J. Med. 2021, 385 (24), e84.
23. Ovsyannikova, I.G.; Haralambieva, I.H.; Crooke, S.N.; Poland, G.A.; Kennedy, R.B. The role of host genetics in the immune response to SARS-CoV-2 and COVID-19 susceptibility and severity. Immunol. Rev. 2020, 296 (1), 205–19.
24. Jiang, Y.; Rubin, L.; Peng, T.; Liu, L.; Xing, X.; Lazarovici, P.; Zheng, W. Cytokine storm in COVID-19: from viral infection to immune responses, diagnosis and therapy. Int. J. Biol. Sci. 2022, 18 (2), 459–70.
25. Carethers, J.M. Insights into disparities observed with COVID-19. J. Intern. Med. 2021, 289 (4), 463–73.
26. Tregoning, J.S.; Flight, K.E.; Higham, S.L.; Wang, Z.; Pierce, B.F. Progress of the COVID-19 vaccine effort: viruses, vaccines, and variants versus efficacy, effectiveness, and escape. Nat. Rev. Immunol. 2021, 21 (10), 626–36.
27. Tada, T.; Zhou, H.; Dcosta, B.M.; Samanovic, M.I.; Chivukula, V.; Herati, R.S.; Landau, N.R. Increased resistance of SARS-CoV-2 Omicron variant to neutralization by vaccine-elicited and therapeutic antibodies. EBioMedicine 2022, 78, 1–8.
28. Niklasch, M.; Zimmermann, P.; Nassal, M. The hepatitis B virus nucleocapsid—dynamic compartment for infectious virus production and new antiviral target. Biomedicines 2021, 9 (11), 1577.
29. Patel, N.; Trost, J.F.; Guebre-Xabier, M.; Zhou, H.; Norton, J.; Jiang, D.; Smith, G. XBB.1.5 spike protein COVID-19 vaccine induces broadly neutralizing and cellular immune responses against EG.5.1 and emerging XBB variants. Sci. Rep. 2023, 13 (1), 19176.
30. Fernandes, Q.; Inchakalody, V.P.; Merhi, M.; Mestiri, S.; Taib, N.; Abo El-Ella, D.M.; Dermime, S. Emerging COVID-19 variants and their impact on SARS-CoV-2 diagnosis, therapeutics and vaccines. Ann. Med. 2022, 54 (1), 524–40.
31. Kumaran, A.; Jude Serpes, N.; Gupta, T.;

James, A.; Sharma, A.; Kumar, D.; Pandey, S. Advancements in CRISPR-based biosensing for next-gen point of care diagnostic application. Biosensors 2023, 13 (2), 202.

32. Mohite, P.; Yadav, V.; Pandhare, R.; Maitra, S.; Saleh, F.M.; Saleem, R.M.; Uti, D.E. Revolutionizing cancer treatment: viral vaccines, monoclonal antibodies, and proteolysis-targeting chimeras in immunotherapy. ACS Omega 2024, 9 (7), 7277–95.
33. Abdulsalam, M.; Salihu, A.T.; Usman, H.Y.; Usman, M.Y. Protein biosynthesis in microorganisms: mechanisms, regulation, and biotechnological applications. World J. Adv. Res. Rev. 2024, 21 (1), 869–81.
34. Saheed, Y.K.; Balogun, B.F.; Odunayo, B.J.; Abdulsalam, M. Microarray gene expression data classification via Wilcoxon sign rank sum and Grey Wolf optimized ensemble learning models. IEEE/ACM Trans. Comput. Biol. Bioinform. 2023, 20 (6), 3575–87.
35. Kim, J.H.; Hotez, P.; Batista, C.; Ergonul, O.; Figueroa, J.P.; Gilbert, S.; Bottazzi, M.E. Operation Warp Speed: implications for global vaccine security. Lancet Glob. Health 2021, 9 (7), e1017–25.