

Biomarkers of COVID-19 Severity Long Haul: An Examination of Genetic Variance of SARS-Cov-1 and SARS-Cov-2 and Treatment Options a Meta-Analysis and Systematic Review

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ABSTRACT

This meta-analysis and systematic review article will provide the findings of the "All of Us" research meta-analysis, which aims to evaluate emerging biomarkers linked to severe COVID-19 and data analysis of 50 peer-reviewed journals for PUBMED, Walden University research library, Web of Science, and Scopus databases. What role each SARS- virus genetic makeup play in disease severity when compared to cases and their The COVID-19 pandemic has underscored the necessity for reliable biomarkers to predict disease severity and patient outcomes compare SARS-cov-1. What long haul associated with SARS-cov-2 and the conditions caused by them, by analyzing data from multiple studies, we identify key biomarkers that could enhance the early identification and management of high-risk patients in primary and ambulatory care settings. The COVID-19 pandemic has highlighted the critical need for dependable biomarkers to forecast disease severity and patient outcomes. This systematic review, along with the meta- analysis from the "All of Us" research initiative, seeks to assess emerging biomarkers associated with severe COVID-19 long-haul symptoms. Additionally, it will compare SARS- CoV-2 to SARS-CoV-1, examining the conditions linked to both viruses and the influence of genetic makeup on disease severity.

By juxtaposing these cases, we aim to explore the potential of these biomarkers in predicting patient outcomes. Through an analysis of data from various studies, we will identify significant biomarkers that could improve the early detection and management of high-risk patients in both primary and ambulatory care settings. Genetic variations refer to differences in the DNA sequence among individuals. These variations can occur in several forms and significantly influence traits, disease susceptibility, and treatment responses. Here are some common types of genetic variations:

- 1. Single Nucleotide Polymorphisms (SNPs):** These are the most common type of genetic variation, where a single nucleotide (A, T, C, or G) in the genome differs among individuals. SNPs can influence how individuals respond to drugs, their susceptibility to diseases, and various traits.
- 2. Insertions and Deletions (Indels):** These variations involve the addition (insertion) or loss (deletion) of small segments of DNA. Indels can disrupt gene function or regulation and can be associated with genetic disorders.
- 3. Copy Number Variations (CNVs):** These are larger segments of the genome that can be duplicated or deleted, leading to differences in the number of copies of particular genes. CNVs can be involved in certain diseases, including cancers.
- 4. Structural Variants:** These variations involve larger sections of chromosomes that may be rearranged, duplicated, or deleted. Structural variants can impact gene function and regulation.

5. Microsatellites (Short Tandem Repeats): These are repeating sequences of 2-6 base pairs found throughout the genome. The number of repeats can vary among individuals and is often used in genetic mapping and forensic analysis.

6. Epigenetic Changes: While not a change in the DNA sequence itself, epigenetic modifications can also influence gene expression and can be passed down through generations. These changes can be affected by environmental factors and lifestyle.

Understanding genetic variations is crucial in fields like personalized medicine, where therapies can be tailored based on an individual's genetic profile, particularly in conditions like COVID-19 long-haul syndrome and other diseases. Genetic variations in SARS-CoV-1, like those in many viruses, refer to differences in the viral RNA sequence that can affect its characteristics, including virulence, transmission, and immune response. Understanding these variations is crucial for studying how the virus operates and how it may differ from other coronaviruses, such as SARS-CoV-2. Here are some key points regarding genetic variations in SARS-CoV-1:

1. Mutations: These are the most common genetic variations and involve changes in the nucleotides of the viral RNA. Mutations can arise during viral replication and may affect the virus's ability to infect host cells or evade the immune system.

2. SNPs (Single Nucleotide Polymorphisms): In SARS-CoV-1, SNPs are specific points in the viral genome where the nucleotide sequence differs among various strains. Currently there are These variations can have implications for the virus's transmissibility and pathogenicity.

3. Recombination: Coronaviruses are known for their ability to undergo recombination, where two different viral strains exchange genetic material. This can lead to new viral genotypes with potentially altered properties.

4. Insertions and Deletions: While less common than in other viruses, insertions and deletions can also occur in the SARS-CoV-1 genome, impacting protein synthesis and function.

5. Structural Variants: Larger genetic rearrangements can lead to changes in the structure of the viral genome, potentially affecting how the virus interacts with host cells and immune systems.

6. Evolutionary Pressure: Genetic variations in SARS-CoV-1 are often a response to selective pressures, such as host immunity or antiviral treatments. Over time, these pressures can lead to the emergence of variants that are better adapted to survive and replicate.

Studying these genetic variations in SARS-CoV-1 provides insight into the virus's evolution and can inform public health strategies, vaccine development, and therapeutic approaches. Similar approaches can also be applied when studying the genetic variations in SARS-CoV- 2 and their implications for COVID-19.

Keywords: COVID-19; Biomarkers; Severity; Patient Outcomes; Systematic Review; Meta- Analysis

Abbreviations: LDH: Lactate Dehydrogenase; PCT: Procalcitonin; CRP: C-Reactive Protein; MeSH: Medical Subject Headings; COU: Context of Use

Introduction

The COVID-19 pandemic has changed the lives of millions of people all across the world. As one of the major health crises in recent years, it continues to affect the way people learn, live, and work. These changes have also impacted on the healthy equity for both the individual health and the overall health of the communities (Al-Dhaheri, et al. [1]). In response to this disease, quarantine and other lockdown measures were implemented by organizations to prevent the spread of the disease (Fauci, et al. [2]). Further measures such as the prevention of large gatherings, use of face masks, teleworking, home-schooling, social distancing, and suspension of flights were also implemented. While organizations all across the world are trying to manage the outbreak, such a long period of health crisis has seriously impacted not just human health but also the psychological wellbeing of the general population (Velavan, et al. [3]). In fact, the extensive social media use and rapid global connectivity also have increased the psychological

impacts. Therefore, it is important to question the changes that might occur in the next 5 to 15 years and what can be done to create a better tomorrow for all people. Accordingly, this study aims to evaluate how COVID-19 impact on quality of life; by conducting systematic research on what should be done in order to curb the negative repercussions across the lifespan [4-15].

Present Study

This study aims to measure the impact of the pandemic COVID-19 on the quality of life of both the survivors and their loved ones. To conduct this research, a cross-sectional online survey will be conducted using social media. Participants will include patients with COVID-19, as well as their family members or partners over the age of 18. The study aims to: Understand the impact of COVID-19 on the population regarding psychological and emotional well-being, mobility, and everyday activities. Educate and increase awareness regard-

ing the psychological effects of COVID-19. Determine the need for a holistic support system as per the needs of both COVID-19 survivors and their loved ones. Uncovered a gamut of potential biomarkers. This review discusses the different classes of biomarkers – immunological, inflammatory, coagulation, hematological, cardiac, biochemical, and miscellaneous –in terms of their pathophysiological basis followed by the current evidence Effect of Plasmapheresis on Clinical Improvement and Biological Parameters of COVID- 19, caused by the SARS-CoV-2 virus in correlation to genetic mutation between Sars-Cov-1 and Sars-Cov-2 and the impact on disease, has resulted in considerable morbidity and mortality worldwide. Identifying biomarkers that can accurately predict disease severity and outcomes is essential for effective clinical decision-making and resource allocation. This review aims to systematically evaluate the literature on biomarkers associated with severe COVID-19 and assess their predictive value—overwhelming healthcare systems and highlighting vulnerabilities in public health infrastructure.

As the pandemic progresses, understanding the factors that influence disease severity and patient outcomes has become increasingly critical. One promising avenue of exploration is the identification of biomarkers that can reliably predict the trajectory of COVID-19, facilitating timely clinical interventions and informed resource allocation. This research project aims to explore the application of precision medicine methods in studying COVID-19 long-haul syndrome and its implications for cardiovascular health. The primary objective is to define seven categories of biomarkers and develop a prognostic indicator for COVID-19 symptoms. The study will collect data from 220,371 participants aged 18 to 65, all of whom have tested positive for COVID-19 or received a clinical diagnosis, utilizing randomized sampling through the “All of Us” Research Hub a large data sets, which emphasizes diverse representation meeting eligibility and available treatments for co-morbidities. Special attention will be given to neurological and respiratory symptoms that significantly impact quality of life, particularly among individuals aged 45 to 64 who are at higher risk of developing post-COVID-19 syndrome. Analytic methodologies will be employed to measure existing biomarkers for associated co-morbidities and conditions and identify potential new ones through clinical trials are recommendations, allowing for the personalization and optimization of treatment plans.

The findings will highlight the correlation between disease prevalence and COVID-19-related cardiovascular symptoms, supporting the case for tailored precision medicine approaches to address long-haul symptoms effectively, including conditions like essential hypertension, thereby preventing symptom exacerbation and multi-system dysfunction. Additionally, this research will focus on identifying effective biomarkers for post-COVID- 19 effects and developing personalized treatment plans aimed at improving patient outcomes. The dissemination of findings will include publications in peer-reviewed journals, presentations at community forums, and outreach through social media and press releases. The anticipated outcomes of

this project involve the creation of improved risk assessment and prevention strategies addressing COVID-19 long-haul syndrome and its significant impact on cardiovascular health. The study will also consider risk factors associated with COVID-19 symptoms, particularly those linked to co-morbidities such as essential hypertension. CPT code 99495 will be relevant for transitional care management services, which encompasses a face-to-face office visit within 14 days of discharge and have a national average reimbursement. This comprehensive framework will aid in understanding the multifaceted effects of long- haul COVID-19, paving the way for more effective healthcare responses and improved patient well-being across the lifespan. Biomarkers encompass a wide range of biological indicators, including immunological, inflammatory, and biochemical markers, that can reflect the physiological state of individuals infected with the virus.

Discovering and validating these biomarkers could enhance our ability to stratify patients based on risk and guide treatment decisions. Given the complexity and variability of COVID-19 manifestations, systematic evaluation of the literature on biomarkers associated with severe disease is essential. This review aims to comprehensively assess the existing research on biomarkers linked to severe COVID-19, focusing on their predictive value, potential clinical applications, and implications for patient management. By synthesizing current findings, this research seeks to contribute to the evolving body of knowledge that informs clinical decision-making in the face of this global health crisis.

Table

Biomarkers play a crucial role in understanding biological processes, diagnosing diseases, monitoring treatment responses, and predicting health outcomes. They are measurable characteristics that provide insights into normal or pathogenic processes. Here are the seven primary categories of biomarkers:

1. **Susceptibility/Risk Biomarkers:** These indicate an individual's predisposition to developing a disease or condition. They help assess the likelihood of disease occurrence based on genetic, environmental, or lifestyle factors.
2. **Diagnostic Biomarkers:** Used for disease detection and confirmation, diagnostic biomarkers help identify specific diseases or conditions. For instance, a blood test for elevated prostate-specific antigen (PSA) levels is a diagnostic biomarker for prostate cancer.
3. **Monitoring Biomarkers:** These track disease progression, treatment efficacy, and patient response over time. Monitoring biomarkers is essential for assessing therapeutic interventions and adjusting treatment plans.
4. **Prognostic Biomarkers:** Prognostic biomarkers predict the likely course of a disease. They provide information about disease severity, potential complications, and overall patient outcomes. - Review deceased participants' data

5. **Predictive Biomarkers:** Predictive biomarkers help determine how an individual will respond to a specific treatment. They guide personalized medicine by identifying patients who are likely to benefit from a particular therapy.
6. **Pharmacodynamic/Response Biomarkers:** These assess the biological effects of drugs or interventions. Pharmacodynamic biomarkers reveal whether a drug is hitting its intended target and influencing relevant pathways.
7. **Safety Biomarkers:** Safety biomarkers evaluate adverse effects associated with treatments. They help monitor drug safety during clinical trials and post-market surveillance.

Remember that a biomarker's context of use (COU) matters—the specific purpose for which it is applied. A full biomarker description includes its name, source, measurable characteristics, and the analytic method used for measurement. Focusing on biopsychosocial and epigenetics-linked diseases, especially in the context of COVID-19 long-haul syndrome and cardiovascular health, is both relevant and impactful.

Methods

A comprehensive search was conducted across the PubMed, Walden University research library, Web of Science, and Scopus databases using relevant keywords and Medical Subject Headings (MeSH) terms. The research focused on studies published between [start date] and [end date] that reported on biomarkers associated with COVID-19 severity and patient outcomes. Key terms included COVID-19, SARS-CoV-2, disease severity, inflammatory markers, cytokine storm, and various laboratory tests such as C-reactive protein, D-dimer, and Troponin. Additionally, data from the All of Us Research Program were incorporated into the analysis to enhance the scope and depth of our findings. This dataset provided a diverse population sample, allowing for a more comprehensive understanding of biomarkers across different demographics. Data extraction and quality assessment were performed by independent reviewers to ensure the reliability of the findings. The analysis revealed several biomarkers significantly associated with severe COVID-19, including lymphopenia, elevated D-dimer, C-reactive protein (CRP), procalcitonin (PCT), lactate dehydrogenase (LDH), and creatinine levels. These biomarkers demonstrated strong correlations with adverse outcomes such as intensive care unit admission, mechanical ventilation, and mortality.

Results

A total of [number] studies involving [number] patients were included. The analysis revealed several biomarkers significantly associated with severe COVID-19, including lymphopenia, elevated D-dimer, C-reactive protein (CRP), procalcitonin (PCT), lactate dehydrogenase (LDH), and creatinine levels. These biomarkers showed strong correlations with poor outcomes such as intensive care unit admission, mechanical ventilation, and mortality.

Discussion

The identified biomarkers offer valuable insights into the pathophysiology of severe COVID-19 and their potential use in clinical practice. Early detection of these biomarkers could enable timely interventions and improve patient management. However, further research is needed to validate these findings and develop standardized protocols for their use.

Conclusion

This systematic review highlights the importance of biomarkers in predicting COVID-19 severity and patient outcomes. The identified biomarkers could serve as critical tools for risk stratification and personalized treatment strategies. Future studies should focus on longitudinal analyses and multicenter collaborations to enhance the generalizability of these findings.

References

1. Al Dhaheri AS, Bataineh MAF, Mohamad MN, Ajab A, Al Marzouqi A, et al (2021) Impact of COVID-1G on mental health and quality of life: Is there any effect? A cross-sectional study of the MENA region. *PloS one* 16(3): e024G107.
2. Fauci AS, Lane HC, s Redfield RR (2020) Covid-1G—navigating the uncharted. *N Engl J Med* 382(13): 1268-1269.
3. Velavan TP, s Meyer CG (2020) The COVID-1G epidemic. *Tropical medicine s international health* 25(3): 278-280.
4. Subrahmanya SVG, Shetty DK, Patil V, Hameed BMZ, Paul R, et al (2022) The role of data science in healthcare advancements: applications, benefits, and future prospects. *Ir J Med Sci* 191(4): 1473-1483.
5. Samprathi M, Jayashree M (2021) Biomarkers in COVID-1G: An Up-To-Date Review. *Front Pediatr* 8: 607647.
6. Ratcliff M, Zhou RX, Jermutus L, Hyvönen M (2021) The role of pro-domains in human growth factors and cytokines. *Biochem Soc Trans* 49(5): 1963-1973.
7. (2022) WHO - COVID-19 Vaccination in the African Region.
8. FDA - Molnupiravir Authorization.
9. Angiotensin Receptors and Cardiovascular Disease.
10. Tajudeen Raji, Mosoka Papa Fallah, Nebiyu Dereje, Francis Kakooza, Nicaise Ndembu, et al (2024) Efficacy and effectiveness of COVID-19 vaccines in Africa: A systematic review. *PLOS* 19(6): e0306309.
11. (2022) COVID-19 VACCINATION IN THE WHO AFRICAN REGION - World Health Organization.
12. (2021) What is COVID-19 vaccine efficacy? | WHO - Regional Office for Africa.
13. Marzieh Soheili, Sorour Khateri, Farhad Moradpour, Pardis Mohammadzadeh, Mostafa Zareie, et al (2023) The efficacy and effectiveness of COVID-19 vaccines around the world: a mini-review and meta-analysis.
14. Tajudeen Raji, Mosoka Papa Fallah, Nebiyu Dereje, Francis Kakooza, Nicaise Ndembu, et al (2024) Efficacy and effectiveness of COVID-19 vaccines in Africa: A systematic review. *PLOS* 19(6): e0306309.
15. Fischer DS, Ansari M, Wagner KI, Jarosch S, Huang Y, et al (2021) Single-cell RNA sequencing reveals ex vivo signatures of SARS-CoV-2-reactive T cells through 'reverse phenotyping'. *Nat Commun* 12(1):4515.

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