

OPEN ACCESS

ARTICLE INFO

Date Received: August 24, 2022 Date Revised: November 01 2022 Date Published Online December 25, 2022

*CORRESPONDENCE

Muhammad Subhan Nazar Department of Public Health and Nutrition The University of Haripur, Khyber Pakhtunkhwa, Pakistan

E-mail: drsubhannazar@gmail.com Phone: +92-304-6767297

JOURNAL OF BASHIR INSTITUTE OF HEALTH SCIENCES

RESEARCH ARTICLE

Prevalence of malaria in pre and post covid-19 era in district Mardan, Khyber Pakhtunkhwa, Pakistan: A cross sectional study

^aShehzad Usman, ^aUsman Ayub, ^aHamza Rafiq, ^aSuliman khan, ^aHassan Zubaid, ^{b*}Muhammad Subhan Nazar

^aDepartment of Medical Laboratory Technology, The University of Haripur, Khyber Pakhtunkhwa, Pakistan

^bDepartment of Public Health and Nutrition, The University of Haripur, Khyber Pakhtunkhwa, Pakistan

ABSTRACT

Background: There are large populations of people who are affected by malaria. In 2004, it has been reported that there were 350–500 million cases of the illness worldwide. More than two billion people, or more than 40% of the world's population, are at risk of developing malaria, and there are an estimated 1.1-1.3 million deaths from malaria globally each year, according to the WHO report. The objectives of the current study is to find out the prevalence of malaria in age and gender wise as well as determined the preand post effect of covid-19 on malaria. Method: A Cross-Sectional Study was designed by Bala Ghari hospital, Mardan, Khyber Pakhtunkhwa, Pakistan. A total number of 1146 patients' data were taken from the laboratory sections of Bala Ghari hospital, Mardan from 2017 till 2021. Out of 1146 samples, 657(57.32%) were males, while 350 (30.54%) were females and 139 (12.12%) were transgender. The ethical approval was obtained from The University of Haripur, Research and Ethic committee (approval number: MLT/0018). Variables for data were calculated by percentages and ratios. Results: The results showed that the prevalence of malaria was minimum in group A (3-10 years of age), which was 0.17 % of the total collected samples. While the prevalence of malaria was maximum, 23.56 % of the collected samples in group C (18-25 year of age). Furthermore, our results indicate that the prevalence of malaria in the precovid-19 era is 39.3 %, while in the post-covid-19 era is 41.9 %. The prevalence of malaria increased by 2.6 % in the post-covid-19 era. **Conclusion:** Major finding of our study is that malarial infection is higher in the post-covid-19 era as compared to the pre-covid-19 era because of the lack of access to healthcare facilities.

Keywords: Malaria, COVID-19, Prevalence, Plasmodium falciparum, Plasmodium vivax

INTRODUCTION

The word Malaria is derived from the Italian "mal aria", which means "poor air". Therefore it was linked to marshy environments. Dr. Ronald Ross, a British medical officer in Hyderabad, India, and Charles Louis Alphonse Laveran, a French army surgeon, both observed parasites in a patient's blood near the end of the 19th century, and discovered that mosquitoes spread malaria [1]. Giovanni Battista Grassi, an Italian scientist, later demonstrated that only Anopheles mosquitoes could transmit human malaria [2]. There are many nations that are affected by malaria, and it has been estimated that there were 350 million to 500 million cases of the illness worldwide in 2004 [3]. More than two billion people, or more than 40% of the world's population, are at risk of developing malaria, and there are an estimated 1.1-1.3 million deaths from malaria globally each year, according to the WHO report [4].

Human Plasmodium falciparum infection is caused by a complicated interaction of parasite-induced RBC changes and

microcirculatory abnormalities followed by local and systemic immunological responses, leading to a variety of clinical manifestations of varying severity [5]. Their adhesion to endothelial cells, blood cells, platelets, and uninfected RBCs causes sequestration of mature forms [6]. Numerous host receptors identified by parasite adhesins facilitate these interactions [7]. The primary cause of malaria outside of Africa and the second most common cause overall is Plasmodium vivax. Even though infections are rarely lethal, clinical illness can be crippling and has a huge negative impact on the population's health and economy [8]. The enhanced flexibility of infected reticulocytes that is shown as the parasites proliferate, in contrast to the increased stiffness that happens for P. falciparum-infected erythrocytes, is considered to be what allows P. vivax to remain in circulation [9]. To occasionally squeeze through the splenic cords and avoid removal from circulation, greater deformability is required [10].

Except for sub-Saharan Africa, P. vivax is the most common human malaria parasite. It is present in many tropical and subtropical climates [11]. More than 200 million clinical instances of P. vivax infection occur each year, with over 3.2 billion individuals worldwide at risk [12]. In the WHO South-East Asia Region in 2010, 2.4 million confirmed malaria cases were recorded [13]. India is the source of 66% of confirmed cases, despite a 28% drop in infections between 2000 and 2010 [14]. Eight nations in the area recorded 2.426 fatalities due to malaria in 2010, with India reporting the majority of these deaths [15]. While P. falciparum infection often demonstrates a higher mean parasitemia index in infected people, P. vivax infection typically displays a low parasitemia index because it prefers to invade reticulocytes rather than erythrocytes [16]. It is therefore difficult to identify P. vivax in infected asymptomatic persons and mixed-species infections by standard light microscopy, necessitating the use of a more sensitive diagnostic instrument to determine the level of P. vivax parasitemia burden [17].

The progress of eradication in various nations provides evidence that malaria might be eradicated with the available instruments [18]. The emergence of pesticide resistance among the vectors and the increase of ACT failures suggest that the current methods for eradicating malaria may not be sufficient [19]. Two GYPB-A hybrid genes that encode the Dantu blood group antigen are added by a complicated structural rearrangement in the glycophorin gene cluster in the second newly reported novel malaria resistance gene [20].

The objective of the current study is to find the prevalence of malaria in pre and post COVID-19 era in District Mardan, KPK Pakistan. Furthermore to find the prevalence of malaria age and gender-wise.



Figure 1. The approximate areas of the world where malaria transmission occurs are depicted on this map. (Source, Adopted from: CDC).

MATERIALS AND METHODS

Study design, setting, and participants

The Cross-Sectional Study was designed at the department of Medical Lab Technology, The University of Haripur, KPK Pakistan with the collaboration of Bala Ghari Hospital, Mardan, KPK, Pakistan. The secondary data were collected from the Bala Ghari Hospital Mardan, during the period of (2017-2021). We had included patients (both male and female) with having age of

3–67-year-old. The malaria presentations in the pre-Covid-19 and post COVID-19 ere were diagnosed in Bala Ghari Hospital Mardan. The pre COVID-19 era was considered from August 2017 till November 2019 and post COVID-19 ere from 2020 till 2021. Malarial symptoms of all registered patients' data were collected from the Bala Ghari Hospital. The variables include, gender, age wise, yearly, positive, negative malaria test, Plasmodium vivax, and Plasmodium Falciparum were analyzed pre and post COVID-19 era.

Inclusion and exclusion criteria

Only Patients who have symptoms of fever, chills, sweats, headaches, vomiting, nausea, aches in the body, and a feeling of dread were included. Data of malarial register patients collected before 2017 and after 2021 were excluded from this study. The malaria and COVID-19 co-infection cases were also excluded from this study.

Statistical analysis

Discrete Variables including (gender, age wise, yearly, positive, negative malaria test, Plasmodium vivax, and Plasmodium Falciparum) were analyzed in terms of frequencies and percentages by Microsoft excel.

RESULTS

Age-wise frequency of malaria among the collected samples

Descriptive analysis was performed on the collected samples. (Table 1) shows the age-wise distribution of the respondents. The results showed that the prevalence of malaria was low 0.17 % of the total collected samples in group A. while the maximum prevalance 23.56 % of the collected samples was observed in Group C.

Gender-wise frequency of malaria among the collected samples

Gender-wise frequency of the malaria among the collected samples was also observed. Out of 1146 samples, 657 were males while 350 were females and 139 were transgender (Table 2). (Figure 2) and (figure 3) shows the graphical representation of the percentage of the malaria among male, female and transgender in the collected samples. The results were verified among males, females, and transgender. The majority of the respondents were males.

| S. NO | AGE | FREQUENCY | PERCENT |
|---------|-------|-----------|---------|
| Group A | 3-10 | 2 | 0.17% |
| Group B | 10-18 | 124 | 10.82% |
| Group C | 18-25 | 270 | 23.56% |
| Group D | 25-33 | 262 | 22.86% |
| Group E | 33-41 | 224 | 19.54% |
| Group F | 41-48 | 181 | 15.79 |
| Group G | 48-59 | 76 | 6.63% |
| Group H | 59-67 | 7 | 0.61% |

 Table 1. Descriptive analysis of the collected samples.

Frequency of malarial cases among the collected samples

The serological test was performed to diagnose the malaria frequency among the collected samples. Out of 1146 samples, 1106 cases were observed positive, while 40 were observed negative. (Figure 2) depicts the graphical representation of the malaria frequency among the collected samples in which positive cases are 96 % and negative are 4 %.

Frequency of plasmodium species among collected samples

Plasmodium species were also differentiated among the collected samples. Out of 1146 total cases, 113 cases were identified as Plasmodium falciparum, while 1033 cases were found as Plasmodium vivax (Table 2). (Figure 3) shows the graphical representation of different species of plasmodium among the collected positive samples.

| Gender | Total tests | Positive | Negative | Discarded |
|-------------|-------------|----------|----------|-----------|
| Male | 657 | 640 | 15 | 2 |
| Females | 350 | 336 | 13 | 1 |
| Transgender | 139 | 130 | 9 | 0 |

 Table 2. Descriptive analysis of total collected samples.



Figure 2. Graphical representation of diagnosed samples of Plasmodium species.

 Table 3. Descriptive analysis of Plasmodium vivax and Plasmodium falciparum species.

| Gender | Total tests | P. Vivax | P. Falciparum |
|-------------|-------------|----------|---------------|
| Male | 657 | 593 | 64 |
| Females | 350 | 318 | 32 |
| Transgender | 139 | 122 | 17 |



Figure 3. Graphical representation of the frequency of Plasmodium vivax and Plasmodium falciparum among the collected positive samples including male, females and transgender.

DISCUSSION

The COVID-19 pandemic has caused millions of infections, hundreds of thousands of fatalities, and significant social damage, due to detentions and other limitations put in place to stop the spread of the illness [21]. The worldwide burden of malaria has decreased as a result of recent advances in malaria control and eradication, but these gains are fragile, and development has

halted during the past five years. Withdrawing effective therapies frequently causes a quick rebound of malaria, which particularly threatens pregnant women and fragile young children. COVID-19 has badly affected the malaria protections and treatment programs in our society [22]. For example, insecticide-treated nets must be replaced on a regular basis to prevent malaria, but distribution campaigns have been postponed or abandoned. People may cease visiting medical institutions for the diagnosis and treatment of malaria because they were afraid of contracting COVID-19 or because they cannot afford transportation, and medical personnel need greater resources to protect themselves from covid-19 [23]. Furthermore, there were interruptions in the supplies of drugs and diagnostics materials to malaria affected area. It is anticipated that these disruptions would cause a doubling of the number of young African children dying from malaria in the upcoming year and may have an influence on attempts to slow the spread of medication resistance [24].

We offer proposal to restart malaria control activities and continue elimination efforts in the context of the covid-19 pandemic, which is anticipated to be a long-term challenge. To avoid a comeback of malaria, all spheres of society including government sector, funders, the commercial sector, and civil society organizations have critical responsibilities to play. To create integrated health care systems that can continue control actions against covid-19, malaria, and other priority infectious illnesses, scarce resources must be allocated effectively [25].

In order to check, the negative impact of covid-19 on the prevalence of malaria, we had conducted this study. Result of our study showed that the prevalence of malaria in the pre-covid-19 era is 39.3 % and in the post-covid-19 era is 41.9 %. The prevalence of malaria increased by 2.6 % in the post-covid-19 era. These findings clearly indicate the negative impact of covid - 19 on the prevalence of malaria in our society. Furthermore, we found that males were more affected than females and the percentage of Plasmodium vivax infections were more than Plasmodium falciparum.

Developed nations in the world are already struggling to provide healthcare and deal with the covid-19 pandemic's secondary social and economic implications [26]. In nations where malaria is endemic, precautions must be taken to safeguard medical personnel while enduring malaria control efforts [27]. The world community cannot afford to stop funding well-established initiatives that have made a big contribution to the tremendous advancements made in the fight against malaria and other illnesses. Instead of going inwards at the cost of the most vulnerable people in the world, we must keep looking outside. The covid-19 outbreak has decimated effective malaria programs, and they must be restored as soon as possible to avoid an old virus getting a fresh start [28].

CONCLUSION

Our study concludes that malaria infection rates were greater in the post-covid-19 period as compared to pre-covid-19 era, because of the lack of access to healthcare facilities, hesitation for hospital visits. Therefore, we suggest that health care organization should also focus on eradication of malaria while treating covid-19 cases especially in vulnerable communities.

ACKNOWLEDGEMENT

We are obliged to Dr. Shagufta Naqvi, Senior Lecturer, Department of Community Health Sciences, Jinnah Medical and Dental College, Karachi, for reviewing our manuscript.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

AUTHOR CONTRIBUTION

S Usman, H Rafiq, S Khan, H Zubaid collected and interpreted the secondary data from hospital. MS Nazar prepared the draft and made changes according to checklist for the cross-sectional study. U Ayub revised the final draft of manuscript.

AVAILABILITY OF DATA AND MATERIALS

Data will be available on request.

CONSENT FOR PUBLICATION

All authors declare consent for publication.

FUNDING SOURCE

N/A

REFERENCES

- 1. Tuteja, R., Malaria an overview. The FEBS journal, 2007. 274(18): p. 4670-4679.
- 2. Cox, F.E., History of the discovery of the malaria parasites and their vectors. Parasit Vectors, 2010. 3(1): p. 5.
- 3. Korenromp, E., Malaria incidence estimates at country level for the year 2004. Proposed estimates and draft report. World Health Organization, Roll Back Malaria, MERG Task Force on Malaria Morbidity, 2005.
- 4. Sardar, S., et al., Artesunate-induced hemolysis in severe complicated malaria A diagnostic challenge: A case report and literature review of anemia in malaria. IDCases, 2021. 25: p. e01234.
- 5. Maier, A.G., et al., Malaria parasite proteins that remodel the host erythrocyte. Nature Reviews Microbiology, 2009. 7(5): p. 341-354.
- 6. Rowe, J.A., et al., Adhesion of Plasmodium falciparum-infected erythrocytes to human cells: molecular mechanisms and therapeutic implications. Expert Rev Mol Med, 2009. 11: p. e16.
- 7. Buffet, P.A., et al., The pathogenesis of Plasmodium falciparum malaria in humans: insights from splenic physiology. Blood, 2011. 117(2): p. 381-92.
- 8. Jason, L.A., et al., The economic impact of ME/CFS: individual and societal costs. Dynamic Medicine, 2008. 7(1): p. 1-8.
- 9. Hodder, A.N., et al., Analysis of structure and function of the giant protein Pf332 in Plasmodium falciparum. Molecular microbiology, 2009. 71(1): p. 48-65.
- 10. Adams, J.H. and I. Mueller, The Biology of Plasmodium vivax. Cold Spring Harb Perspect Med, 2017. 7(9).
- 11. Organization, W.H., Global malaria control and elimination: report of a technical review. 2008.
- 12. Dayanand, K.K., R.N. Achur, and D.C. Gowda, Epidemiology, drug resistance, and pathophysiology of Plasmodium vivax malaria. Journal of vector borne diseases, 2018. 55(1): p. 1.
- 13. de Silva, N. and R. Wickremasinghe, Counting malaria out--what progress? Indian Journal of Medical Research, 2010. 131(4): p. 475-478.
- 14. O'Meara, W.P., et al., Changes in the burden of malaria in sub-Saharan Africa. The Lancet infectious diseases, 2010. 10(8): p. 545-555.
- 15. Autino, B., et al., Epidemiology of malaria in endemic areas. Mediterranean journal of hematology and infectious diseases, 2012. 4(1).
- 16. Akala, H.M., et al., Plasmodium interspecies interactions during a period of increasing prevalence of Plasmodium ovale in symptomatic individuals seeking treatment: an observational study. The Lancet Microbe, 2021. 2(4): p. e141-e150.
- 17. Oyedeji, S.I., H.O. Awobode, and P.U. Bassi, Molecular investigation of sub-microscopic and mixed Plasmodium species infection in North-Central Nigeria. Asian Pac J Trop Dis, 2017. 7(4): p. 220-224.
- 18. Talapko, J., et al., Malaria: the past and the present. Microorganisms, 2019. 7(6): p. 179.
- 19. Burrows, J.N., et al., New developments in anti-malarial target candidate and product profiles. Malaria journal, 2017. 16(1): p. 1-29.
- 20. Leffler, E.M., et al., Resistance to malaria through structural variation of red blood cell invasion receptors. Science, 2017. 356(6343): p. eaam6393.
- 21. Rogerson, S.J., et al., Identifying and combating the impacts of COVID-19 on malaria. BMC medicine, 2020. 18(1): p. 1-7.
- 22. Fairhurst, R.M., et al., Artemisinin-resistant malaria: research challenges, opportunities, and public health implications. The American journal of tropical medicine and hygiene, 2012. 87(2): p. 231.
- 23. Liu, Q., et al., The experiences of health-care providers during the COVID-19 crisis in China: a qualitative study. The Lancet Global Health, 2020. 8(6): p. e790-e798.
- 24. Farooq, U. and R. Mahajan, Drug resistance in malaria. Journal of vector borne diseases, 2004. 41(3/4): p. 45.
- 25. Burrows, J.N., et al., Designing the next generation of medicines for malaria control and eradication. Malaria journal, 2013. 12(1): p. 1-20.
- 26. O'Connor, K., et al., Mental health impacts of COVID-19 in Ireland and the need for a secondary care mental health service response. Irish journal of psychological medicine, 2021. 38(2): p. 99-107.
- 27. Ajayi, I.O., O.O. Ajumobi, and C. Falade, Malaria and COVID-19: commonalities, intersections and implications for sustaining malaria control. The Pan African Medical Journal, 2020. 37(Suppl 1).
- 28. Moyes, D., D.J. Griffiths, and P.J. Venables, Insertional polymorphisms: a new lease of life for endogenous retroviruses in human disease. Trends in genetics, 2007. 23(7): p. 326-333.

Publisher's note: Bashir Institute of Health Sciences remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license and indicate if changes were made. The

images or other third-party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this license, visit http://creativecommons.org/licenses/by/4.0/.

© The Author(s) 2022.