Advanced Journal of Microbiology Research ISSN 2736-1756 Vol.17 (4), pp.001-002, December, 2023. Available online at www.internationalscholarsjournals.com © International Scholars Journals

Author(s) retain the copyright of this article.

Commentary

International Scholars Journals

Microbiological perspectives on malaria parasites and public health Katarina Glowka*

Department of Microbiology, University of Lodz, Lodz, Poland.

Received: 28-Nov-2023, Manuscript No. AJMR-23-123612; Editor assigned: 30-Nov-2023, PreQC No. AJMR-23-123612 (PQ); Reviewed: 15-Dec-2023, QC No. AJMR-23-123612; Revised: 22-Dec-2023, Manuscript No. AJMR-23-123612 (R); Published: 29-Dec-2023

DESCRIPTION

Malaria, a life-threatening infectious disease, is caused by various species of the Plasmodium parasite. This microscopic organism belongs to the genus Plasmodium and is transmitted to humans through the bites of infected female Anopheles mosquitoes (Akujobi et al., 2008). In the field of microbiology, the study of the malaria parasite is pivotal for understanding its intricate life cycle, host interactions, and the development of effective prevention and treatment strategies (Berri et al., 2015).

The deadliest species of the malaria parasite is Plasmodium falciparum, responsible for the majority of severe malaria cases and fatalities globally (Brooks et al., 2005). Other species that infect humans include *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, and *Plasmodium knowlesi*. Each species exhibits unique characteristics, influencing the severity and clinical manifestations of the disease (CASFM, 2017).

The life cycle of the malaria parasite involves both human and mosquito hosts, each playing a crucial role in the transmission and perpetuation of the disease. The cycle begins when an infected mosquito injects sporozoites into the human bloodstream during a blood meal (Corrégé, 2013). These sporozoites travel to the liver, where they infect hepatocytes and undergo a phase of rapid multiplication, resulting in the formation of merozoites.

Upon release from the liver cells, the merozoites invade red blood cells, initiating the symptomatic phase of malaria (Dadié et al., 2000). This cyclical invasion of red blood cells leads to the characteristic symptoms of the disease, including fever, chills, and anemia. Some merozoites develop into sexual forms known as gametocytes, which can be ingested by a mosquito during a subsequent blood meal, completing the parasite's life cycle (Dadié A et al., 2010).

The malaria parasite's ability to evade the human immune system is a testament to its evolutionary adaptability. One of the key mechanisms employed is antigenic variation, where the parasite alters the surface proteins it presents to the host's immune system. This constant modification of surface proteins hinders the immune system's ability to recognize and mount an effective response against the parasite, allowing it to persist and cause repeated infections (Fairbrother et al., 2006).

In addition to antigenic variation, the malaria parasite has evolved strategies to evade immune detection during its various life cycle stages. During the liver stage, the parasite resides within hepatocytes, where it is shielded from direct immune attack. Once the parasite moves into the bloodstream and infects red blood cells, it further manipulates host cell machinery to avoid detection, contributing to its ability to cause recurrent infections.

The severity of malaria is influenced by factors such as the species of Plasmodium involved, the individual's immune status, and access to healthcare. *P. falciparum* is known for its virulence, and infections with this species can lead to severe complications, including cerebral malaria, a life-threatening condition associated with neurological symptoms and high mortality rates (Fleury, 2015).

Microbiological research on the malaria parasite has played a crucial role in the development of diagnostic tools, therapeutic interventions, and preventive measures. Rapid diagnostic tests, which detect parasite antigens in blood samples, have become essential for quick and accurate malaria diagnosis, especially in resource-limited settings. Antimalarial drugs, such as artemisinin-based combination therapies, are effective in treating the symptomatic phase of the disease, although the emergence of drug-resistant strains is a growing concern.

Preventive strategies have proven instrumental in malaria control efforts. The use of insecticide-treated bed nets, indoor residual spraying, and intermittent preventive treatment for vulnerable populations, such as pregnant women, has contributed to a reduction in malaria-related morbidity and mortality. Ongoing efforts to develop a malaria vaccine have

^{*}Corresponding author. Katarina Glowka, E-mail: glowka@polsl.pl

shown promise, with the RTS,S/AS01 vaccine demonstrating efficacy in certain populations.

In conclusion, the study of the malaria parasite in the field of microbiology is essential for unraveling the complexities of the disease and devising effective control measures. The parasite's sophisticated life cycle, immune evasion mechanisms, and the impact of different Plasmodium species on disease severity provide valuable insights that guide ongoing research and public health initiatives. Continued collaboration between microbiologists, immunologists, and healthcare professionals is crucial for advancing our understanding of malaria and implementing innovative strategies to combat this persistent global health threat.

REFERENCES

- Akujobi CO, Ogbulie JN, Umeh SI, Abanno NU (2008). Antibiotic-resistant *Escherichia coli* in a government piggery farm in Owerri, Nigeria. Int J Biol Chem Sci. 2:363-367.
- Berri M, Slugocki M, Olivier M, Holbert S, Helloin E, Jacques I, Salmon CPN, et al (2015). L'activité antibactérienne et immuno modulatrice d'un extrait d'algue verte riche en polysaccharides sulfatés. Journ Rech Porc. 47:309-310.
- Brooks JT, Sowers EG, Wells JG, Greene KD, Griffin PM, Hoekstra RM, Strockbine NA (2005). Non-O157 Shiga toxin-producing *Escherichia coli* infections in the United States 1983-2002. J Infect Dis. 192:1422-1429.

- CASFM (2017). Comité de l'Antibiogramme de la Société Française de Microbiologie_EUCAST (European Committee on Antimicrobial Susceptibility Testing). Recommendations, 127 pages.
- Corrégé I (2013). Immunité des porcelets: Importance du colostrum. Tech Porc. 9:41-43.
- Dadié A, Karou TG, Faye-Kette HY (2000). Isolement d'agents pathogènes entériques en Côte d'Ivoire: *Escherichia coli* O157:H7 et E. coli entéro-aggrégant. Bull. Soc Pathol Exot. 93:95-96.
- Dadié A, Kouassi N, Dako E, Dje M, Dosso M (2014). Virulence, serotype and phylogenetic groups of diarrhoeagenic *Escherichia coli* isolated during digestive infections in Abidjan, Côte d'Ivoire. Afr J Biotechnol. 13:998-1008.
- Dadié A, Nzebo D, Guessennd N, Dako E, Dosso M (2010). Prevalence of enteropathogenic *Escherichia coli* in unpasteurized milk produced in Abidjan, Côte d'Ivoire. J Biol Chem Sci. 4:11-18.
- Fairbrother JM, Gyles CL (2006). *Escherichia coli* infections. Diseases of Swine. Iowa state University. 9:639-674.
- Fleury M (2015). Impact of antibiotic treatments on the digestive flora of piglets: *In vivo* study and development of an approach in *in vitro* fermentation system. Médecine humaine et pathologie, thèse Université Rennes. 1-237.