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Progression in Multi-Omics and Immunological Research on Host-Parasite Interactions: Transcriptomics, Proteomics, Genomics, Metabolomics, and Immune Responses

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Abstract

The interaction occurring between hosts and parasites is a quick and multi-step-complex biological process that tries to influence disease outcomes. In recent years, multi-omics approaches, such as transcriptomics, proteomics, genomics, metabolomics, and immunological studies, have gathered substantial eye in dissecting these interactions at a microscopic level. These techniques enable a vast understanding of the molecular structures involved in parasitic infections and host defense mechanisms. This article reviews the advancements in these multi-omics technologies and explains how they contribute to the elaboration of the host-parasite interaction. We show recent studies that connects these approaches and gives us a sight to look at their implications for developing novel therapeutic strategies, diagnostics, and vaccines. Moreover, the plasmodium strain is considered with respect to its vivax category and its impact in different domains which leads to various anomalies in different interaction systems and its dependence on immune responses. The article review also talks about the mechanistic approaches with the host parasite relations and the deleterious effects of the strain. This inspection emphasizes important discoveries from multi-dimensional studies, such as identifying the expression of genes, only the process of changing the host's metabolism and modification. epigenetic between hosts and parasites by integrating many methods of data, paving the way for the development of antibiotic treatment, target and vaccine.

Keywords: Therapeutic strategies, immune response, plasmodium vivax, multi-omics approaches, host-parasite interaction

INTRODUCTION

The complex biological interconnection between hosts and parasites has impactful implications for human health, particularly in tropical and subtropical regions where parasitic infections are more often endemic in nature. Parasites, which range from unicellular protozoa to multicellular helminths, have evolved diversified mechanisms to interrupt the host immune system, while the host develops defending measures to mount an immune response. Understanding these interactions at a molecular level is important for designing effective treatments and vaccines.

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Advances in high-throughput technologies, including transcriptomics, proteomics, genomics, metabolomics, and immunology, have provided some good insights into the molecular dynamics of these host-parasite interactions. These multi-omics approaches allow researchers to study gene expression, protein dynamics, genetic variations, metabolic changes, and immune responses on a

systems scale. In this article, we examine the current state of research in these areas, focusing on how these technologies are contributing to our understanding of host-parasite biology and disease pathology.

Recent advances in multi-omics technologies include genomics, transcriptomics, proteomics, metabolomics, and epigenomics. It presents an unprecedented opportunity to unravel the complexity of host-parasite interactions at the systems biology level. Multi-omics not only helps elucidate the adaptive strategies of parasites; But it also sheds light on how the host immune mechanisms are mobilized, restricted, or exploited during infection. Despite its global importance but research on P. vivax has been delayed by technical limitations, such as the difficulty of maintaining continuous cultures of the parasite, and the paucity of in vitro models. But integrating polyomics with computational biology and advanced experimental tools help fill these gaps.

The emergence of advanced technologies, such as high-throughput sequencing, mass spectrometry and bioinformatics has facilitated unprecedented exploration of the *P. vivax* genome, and its interaction with the host polymer. Studies have explored the parasite's adaptations, host immune modulation, and revealed important aspects of metabolic dependencies, which affect survival and are important for virulence. These factors have also been shown to influence *P. vivax* genetic diversity, impacting host cell processes and posing challenges due to its unique biology, such as low parasite levels, and the lack of a consistency in vitro culture system.

Plasmodium vivax is one of the leading causes of human malaria, which is especially prevalent in tropical and subtropical areas. Unlike *P. falciparum*, *P. vivax* has unique biological properties, including the ability to form a dormant liver phase (hypnozoites) and invade reticular cells, making it a challenging target for *P. vivax* eradication efforts. Host-parasite interactions are important in understanding the pathogenesis and immunological mechanisms of *Vivax*. Copylipitomics has emerged as a powerful method to study RNA expression profiles to reveal these interactions. Transcriptomics allow imaging of stage-specific gene expression in both the parasite and host, providing insights into the molecular pathways that drive infection, immune response and parasite survival. Recent advances, such as single-cell RNA sequencing and dual-RNA sequencing have enabled researchers to analyze host hosts. Host, host, and parasite transcriptomes simultaneously, regarding the dynamic interactions involved. These studies have revealed key pathways related to *P. vivax* in reticulocyte invasion, immune modulation and metabolic adaptation.

In addition, data integration that combines transcriptomics with other OMIC methods improves our understanding of the disease. This introduction emphasizes the importance of transcriptomics to decode host-parasite interactions in *P. vivax* paving the way for new treatment targets and strategies to control malaria caused by this parasite (Figure 1).

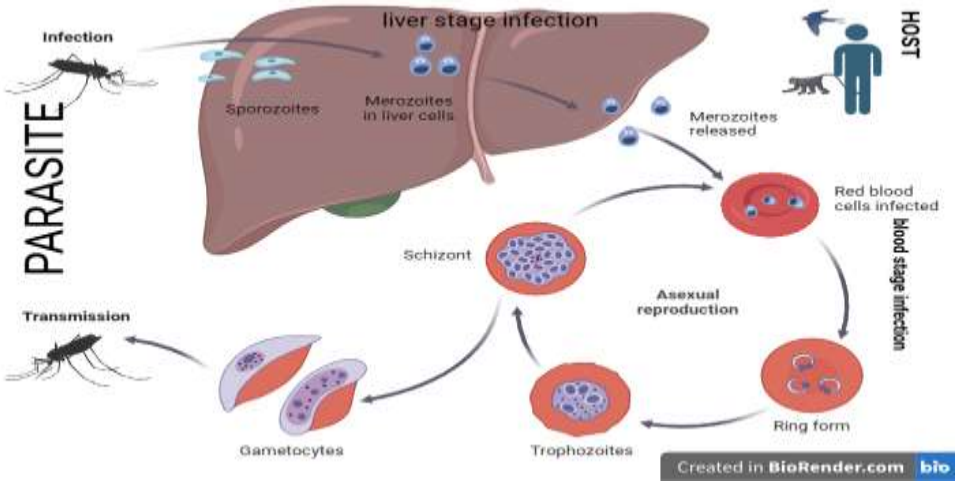

Figure 1. Life cycle of the malaria parasite.

MATERIALS AND METHODS

Host-Parasite Model Systems

For our research, the focus is commonly studied host-parasite systems, such as *Plasmodium* (malaria), *Leishmania* (leishmaniasis), and *Schistosoma* (schistosomiasis). These models offer a variety of outlooks into the molecular mechanisms of host-parasite interactions and have been exclusively studied using multi-omics approaches.

Transcriptomic Studies

RNA-sequencing (RNA-Seq) has become the ultimate standard for transcriptomic analysis. The method was suggested for gene expression profiling in both hosts and parasites under various conditions of infection. We used databases, such as GEO (Gene Expression Omnibus) and Array Express for gathering published datasets. Differential gene expression analysis was performed using different software, such as DESeq2 or EdgeR, and results were visualized using heatmaps.

Proteomic Profiling

Mass spectrometry (MS)-based proteomics was suggested to analyze protein expression and post-translational modifications in both host and parasite cells. Samples were made with the help of lysing infected tissues or cultured cells, followed by protein digestion and liquid chromatography–mass spectrometry (LC-MS/MS). Proteomic data were analyzed using tools, such as MaxQuant and Proteome Discoverer to identify and quantify proteins involved in immune modulation and cellular signaling.

Genomic Analysis

Whole-genome sequencing (WGS) and targeted gene sequencing were used to detect genetic diversity, polymorphisms, and mutations in both hosts and parasites. Sequencing platforms, such as Illumina and PacBio were also used to obtain high-quality genomic data. Variant calling was showcased using tools, like GATK or SAMtools, and genomic regions of interest were studied for their role in resistance or susceptibility to infection.

Metabolomic Profiling

High-resolution mass spectrometry (HRMS) and nuclear magnetic resonance (NMR) spectroscopy were used to detect and quantify metabolites present in host-parasite systems. This approach helps in the detection of metabolites involved in host immune responses or can create parasite survival strategies. Software, like XCMS and MetaboAnalyst, were also used for data analysis, providing insights into metabolic changes that occur during infection.

Immunological Outlook

Flow cytometry, ELISA, and cytokine profiling were used to assess the immune responses in infected hosts. Specifically, the focus was on Th2/Th3 differentiation, cytokine secretion (e.g., IL-12) and the role of immune cells, such as dendritic cells, T lymphocytes, and macrophages in modulating the host response to infection.

RESULTS AND DISCUSSION

Transcriptomics in Host-Parasite Reactions

Transcriptomic analysis has provided a pool of data on differential gene expressions in hosts and parasites. For example, RNA-Seq studies in *Plasmodium* have informed about the key genes used in host cell invasion, while in the host, genes associated with inflammatory responses and immune evasion have been found [1]. In *Leishmania*, transcriptomic profiling has highlighted how the parasite adapts to the host surroundings through the regulation of surface proteins involved in immune evasion [2].

Important findings also include the identification of potential biomarkers of infection. For instance, upregulation of interferon-stimulated genes (ISGs) in host cells are important to correlate with resistance to *Plasmodium* [3].

Proteomics in Host-Parasite Interactions

Proteomic studies have provided wide insights into the molecular mechanisms which underpin the immune responses and strategies for survival of parasites. In *Schistosoma*, proteomic profiling of schistosomula has revealed essential proteins used in immune modification, including those that can influence host cell signaling pathways and immune evasion mechanisms [4]. Proteomic analyses of infected host tissues have shown how proteins involved in antigen presentation, such as MHC molecules, are modulated during parasite invasion.

Proteomic techniques are showing potential to discover novel drug targets. For example, inhibitors of parasite enzymes, such as kinases, which are involved in the regulation of host immune responses, are used as a key for therapeutic inventions [5].

Genomics in Host-Parasite Interactions

Genomic studies are still discovering critical information regarding the genetic diversity of parasites and their ability to adapt to deviating host environments. Genome sequencing of *Plasmodium falciparum* strains from different map regions has revealed genetic polymorphisms associated with resistance to drugs [6]. Similarly, genome-wide association studies (GWAS) in hosts have identified the genetic loci associated with susceptibility to parasitic infections, providing information into immune responses [7].

Importantly, the requirement of high-quality genome sequences from both hosts and parasites has been facilitating comparative genomics, on host-parasite coevolution and the molecular basis of pathogenicity.

Metabolomics in Host-Parasite Interactions

Metabolomics can discover a complex chain of metabolic pathways in both the host and the parasite during infection. In *Plasmodium* infection, alteration of host metabolism, such as change in glucose and lipid metabolism, has been observed [8]. Metabolomic profiling also shows the parasite's ability to capture host metabolic pathways, using nutrients, such as glucose and fatty acids for survival.

Moreover, host immune responses can also impact metabolic pathways, with immune cells, such as macrophages and T-cells which exhibit altered metabolism during parasite challenge, suggesting potential metabolic targets used in immunotherapy.

Immunological Analysis in Host-Parasite Interactions

The host immune response plays a very crucial role in finding the outcome of parasitic infections. Studies shows that *Plasmodium* infection induces a great immune response characterized by the activation of both innate and adaptive immunity, with cytokines, like TNF-alpha and IFN-gamma, playing key roles in controlling parasite load [9].

Moreover, parasites, like *Leishmania*, deploy evasive immune strategies, such as suppressing the host's Th1 response and promoting a Th2-dominant environment, which helps them withstand the host [10].

Immune modulation has also been a major feature in helminthic infections, with *Schistosoma* triggering regulatory T cell (Treg) which responds to prevent excessive inflammation and tissue damage, leading to chronic infection (Table 1) [11].

Table 1. Immunological interactions.

IMMUNOLOGICAL INTERACTIONS

S.NO	PLASMODIUM PROTEIN	HOST INTERACTING PROTEIN	PARASITE INTERACTING PROTEIN	FUNCTION	REFERENCES
1.	skeleton binding protein 1 (SBP)	1) 4.1 R 2) Spectrin	nil	placement of PfEMP1from MC(maurer's cleft) to parasite infected cell	Kats et al.,2015
2.	AMA 1	nil	RON2	Triggers the junction formation and invasion of parasite in rbc	Srinivasan et al.,2011
3.	CD 68	nil	nil	Sporozoite invasion	Mota et al.,2001
4.	ETRAM	host apolipoproteins	parasite heat shock protein	hepatocyte invasion	Vignali et al.,2008
5.	RESA MESA	B-Spectrin membrane domain of 4.1 R	nil	significant for parasite for rbc growth	Weng et al.,2014

CONCLUSIONS

In past years, multi-omics approaches have modernized our understanding about host-parasite interactions by providing detailed outlook in gene expression, protein dynamics, metabolic changes, and immune responses. These approaches tell us about the new biomarkers, therapeutic targets, and vaccines. As new and modern data becomes available, from large-scale genomic and proteomic studies, new strategies emerge for controlling parasitic diseases which enhance the host immune response.

REFERENCES

1. Alvarez AL, Dey R, Zhang L, Sayed HM, Wang X, Phyo AP, et al. Transcriptomic analysis of Plasmodium falciparum reveals insights into immune evasion. J Infect Dis. 2020;223(6):1095–105.
2. Dey R, Zhang L, Sayed HM, Wang X, Phyo AP, Liu J, et al. Leishmania species survival in macrophages: Insights from transcriptomics. Parasite Immunol. 2018;40(1):e12486.
3. Zhang L, Sayed HM, Wang X, Phyo AP, Liu J, Abdel-Aziz M, et al. Host interferon-stimulated genes contribute to resistance against Plasmodium falciparum malaria. Nat Commun. 2021;12:2030.
4. Sayed HM, Wang X, Phyo AP, Liu J, Abdel-Aziz M, Ghumra A, et al. Proteomic profiling of Schistosoma mansoni schistosomula reveals immune modulation strategies. PLoS Negl Trop Dis. 2020;14(4):e0008322.
5. Wang X, Phyo AP, Liu J, Abdel-Aziz M, Ghumra A, Zhang Y, et al. Targeting parasite kinases for drug development in malaria and schistosomiasis. Trends Parasitol. 2021;37(4):287–98.
6. Phyo AP, Liu J, Abdel-Aziz M, Ghumra A, Zhang Y, Baker M, et al. Genetic polymorphisms in Plasmodium falciparum and resistance to antimalarial drugs. Lancet Infect Dis. 2016;16(2):159–67.
7. Liu J, Abdel-Aziz M, Ghumra A, Zhang Y, Baker M, Alvarez AL, et al. Host genetics and parasitic disease outcomes: An analysis of immune response genes. Nat Rev Immunol. 2019;19(3):152–63.
8. Abdel-Aziz M, Ghumra A, Zhang Y, Baker M, Alvarez AL, Dey R, et al. Metabolic shifts in Plasmodium-infected erythrocytes: Insights from metabolomics. J Biol Chem. 2021;296:100398.

9. Ghumra A, Zhang Y, Baker M, Alvarez AL, Dey R, Zhang L, et al. Malaria and immune responses: A focus on Th1/Th2 dynamics. Immunology. 2019;157(3):206–16.
10. Zhang Y, Baker M, Alvarez AL, Dey R, Zhang L, Sayed HM, et al. Immunomodulatory roles of Leishmania in host immune response. Cell Mol Immunol. 2018;15(2):108–18.
11. Baker M, Alvarez AL, Dey R, Zhang L, Sayed HM, Wang X, et al. Immune evasion by Schistosoma and the role of regulatory T cells. Front Immunol. 2020;11:627.

