

Transcriptomic Analysis of Host Pathogen Interactions in Infectious Diseases

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DESCRIPTION

Transcriptomic analysis of host pathogen interactions in infectious diseases has become one of the most powerful approaches for understanding the molecular mechanisms underlying infection, immune response, and disease progression. Infectious diseases are dynamic biological processes involving continuous interaction between invading pathogens and host defense systems. These interactions are mediated by complex changes in gene expression within both the host and the pathogen. Transcriptomics provides a comprehensive view of these changes, enabling researchers to capture global Ribonucleic Acid (RNA) expression patterns that reveal how pathogens adapt to host environments and how host cells respond to infection. At the core of host pathogen transcriptomic studies is RNA sequencing, which allows simultaneous profiling of thousands of genes in both host and pathogen. This dual RNA sequencing approach provides a unique opportunity to study infection biology in a holistic manner. Unlike traditional methods that focus on either the host or the pathogen separately, dual transcriptomics captures the dynamic interplay between the two systems. This enables identification of virulence factors, immune response genes, and regulatory pathways that determine infection outcomes. They must evade immune detection, acquire nutrients, and establish a niche for survival and replication. Transcriptomic analysis reveals that pathogens often activate stress response genes, metabolic adaptation pathways, and virulence-associated genes when exposed to host immune pressures. Bacterial pathogens may upregulate genes involved in iron acquisition, as iron is tightly sequestered by host proteins during infection. Similarly, viral pathogens reprogram host cellular machinery to favor viral replication while suppressing antiviral responses.

On the host side, infection triggers a highly coordinated immune response involving innate and adaptive immune systems. Transcriptomic profiling of infected host cells reveals rapid induction of inflammatory cytokines, chemokines, and interferon-stimulated genes. These gene expression changes are essential for recruiting immune cells to the site of infection and activating antimicrobial defenses. However, excessive or dysregulated immune responses can also contribute to tissue

damage and disease severity. Transcriptomic data helps identify pathways associated with both protective immunity and immunopathology. One of the most important applications of transcriptomic analysis in infectious diseases is the identification of host biomarkers for disease diagnosis and prognosis. Gene expression signatures can distinguish between different types of infections, such as bacterial versus viral infections, or identify stages of disease progression. These transcriptomic biomarkers can be used to develop diagnostic tools that are faster and more accurate than traditional microbiological methods. They also enable early detection of severe disease cases, allowing timely intervention. Pathogen transcriptomics provides valuable insights into virulence mechanisms and drug resistance. By analyzing gene expression profiles of pathogens under different conditions, researchers can identify genes that contribute to pathogenicity and survival. Antibiotic-resistant bacteria often exhibit altered expression of genes involved in efflux pumps, cell wall synthesis, and stress response pathways.

Host transcriptomic responses are highly context-dependent and vary based on pathogen type, infection stage, and host genetic background. Single-cell RNA sequencing has revealed that immune responses are not uniform across all cells but instead consist of diverse cell populations with distinct transcriptional states. Some immune cells exhibit strong pro-inflammatory responses, while others adopt regulatory or suppressive roles. This cellular heterogeneity plays a crucial role in determining infection outcomes and disease severity. Spatial transcriptomics has further advanced the understanding of host pathogen interactions by preserving the spatial context of gene expression within infected tissues. This approach reveals how immune cells are organized around infection sites and how pathogens spread within tissue environments. Spatial mapping has shown that immune responses are often localized, with distinct microenvironments forming within infected tissues. These spatial patterns are critical for understanding disease progression and tissue damage. Computational analysis plays a central role in interpreting host pathogen transcriptomic data. Bioinformatics pipelines are used to separate host and pathogen reads, quantify gene expression, and identify differentially expressed genes. Machine learning approaches are increasingly used to classify infection types, predict disease severity, and identify key

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Received: 01-Dec-2025, Manuscript No. TOA-25-41971; **Editor assigned:** 03-Dec-2025, PreQC No. TOA-25-41971 (PQ); **Reviewed:** 16-Dec-2025, QC No. TOA-25-41971; **Revised:** 23-Dec-2025, Manuscript No. TOA-25-41971 (R); **Published:** 30-Dec-2025, DOI: 10.35248/2329-8936.25.11.228.

Citation: Ibe C (2025). Transcriptomic Analysis of Host Pathogen Interactions in Infectious Diseases. Transcriptomics. 11:228.

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regulatory genes. Multi-omics integration enhances transcriptomic analysis by combining gene expression data with genomic, proteomic, and metabolomic information. This

integrated approach provides a more comprehensive understanding of infection biology.