

Editorial

**Transcriptomics: from Technological Breakthrough to Disease Control Empowerment**Yong Zhang[#]

With the reduction of sequencing costs, optimization of algorithms, and improvement of multi-omics integration capabilities, transcriptomics, as a core technology for analyzing gene expression dynamics and discovering key functional molecules, has shown great potential in the field of disease prevention and control^[1,2]. The multi-continental transcriptomics study of tick-borne poxvirus not only provides a new perspective for understanding the evolution and transmission of vector-mediated viruses, but also reflects the trend of transcriptomics research and highlights its key role in disease prevention and control^[3].

Current Research Trends in Transcriptomics: from “Single Dimension” to “Multi-Dimensional Integration”, from “Known Exploration” to “Unknown Mining”

Traditional transcriptomics research has primarily focused on gene expression within a single organism, such as humans, model animals, or specific pathogens. However, current research is gradually shifting towards metatranscriptomics, which enables systematic analysis of the “host-vector-pathogen” symbiotic system. The aforementioned study published in this journal focuses on a tick sample library and, through metatranscriptomic data mining, simultaneously captures the transcriptional information of the tick host, the poxviruses it carries, and other symbiotic microorganisms. Ultimately, 58 species of poxviruses were identified, and exogenous fragments originating from rodents, archaea, and arthropods were discovered in the viral genome^[3]. This “community-level” analysis method can more accurately reflect the interaction relationships between different organisms in natural environments, especially for the study of vector-

borne infectious diseases. In natural scenarios, the transmission and evolution process of pathogens are often closely related to the physiological state of vector hosts and the structure of symbiotic microbial communities; while traditional single-species research is difficult to fully reveal the ecological mechanisms of disease occurrence.

Early transcriptomics mostly focused on descriptive aspects such as “differential expression gene screening” and “pathway enrichment analysis”^[4]. Current technology can deeply analyze the molecular mechanisms of biological processes through fine analysis^[5]. The aforementioned study published in this journal not only utilizes transcriptome data to evaluate the diversity and abundance of poxviruses, but also assembles and conducts phylogenetic analysis of chordopoxvirus sequences, tracing the origin of unaligned fragments. Ultimately, it reveals that poxviruses can regulate their virulence and adaptability through horizontal gene transfer, gene recombination, and gene mutation, which is their core evolutionary mechanism^[3]. This study precisely reflects the core upgrade of transcriptomics technology from “discovering phenomena” to “explaining mechanisms”. This “mechanistic analysis” is not only one of the core goals of current transcriptomics research, but also the key advantage that distinguishes it from traditional molecular biology techniques.

The Core Role of Transcriptomics in Disease Prevention and Control: from “Risk Warning” to “Intervention Strategy Formulation”

The early identification of emerging infectious diseases is crucial for prevention and control efforts. However, traditional pathogen detection techniques, such as polymerase chain reaction (PCR), rely heavily

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on sequence information of known pathogens, making it difficult to effectively detect unknown or mutated pathogens. Transcriptomics, especially metatranscriptomics, utilizes “unbiased” sequencing technology to quickly capture the transcripts of all RNA viruses, bacteria, fungi, and other microorganisms in a sample without the need for preset detection targets, thereby facilitating the discovery of potential new pathogens^[6]. The aforementioned study identified 58 species of poxviruses from tick samples, which may include novel viruses that have not been reported previously. If these viruses have the potential to infect humans, early detection of them can not only save valuable time for subsequent pathogen research and diagnostic reagent development, but also avoid prevention and control delays caused by “unknown pathogens”.

Transcriptomics is also an important “target screening tool” for vaccine and drug development^[7]. By analyzing key gene expression during pathogen infection (such as viral virulence genes, replication-related genes), or immune-related genes during host anti-infection, potential vaccine or drug targets can be identified. In the above study, researchers found that poxviruses can regulate their virulence through gene mutations, and these virulence-related genes can be used as candidate targets for vaccine development (such as constructing attenuated live vaccines targeting virulence genes), or as targets for drug development (such as reducing viral pathogenicity by inhibiting virulence gene expression). This “targeted research and development” model based on transcriptomics can significantly shorten the development cycle of vaccines and drugs, providing a rapid response technology tool for the prevention and control of emerging infectious diseases.

Summary and Outlook

The aforementioned transcriptomic study of tick-borne poxvirus is a typical case of the application of transcriptomic technology in disease prevention and control. This study not only clearly presents the current development trend of related research from “single species” to “community level”, from “descriptive analysis” to “mechanistic analysis”, and from “local area” to “global scale”, but also fully demonstrates the core role of transcriptomic technology in early warning of new pathogens, analysis of transmission mechanisms, and development of prevention and control tools^[8].

As technology continues to iterate, transcriptomics is gradually integrating with multi-omics technologies such as single-cell sequencing, spatial transcriptomics, and metabolomics. For example, with the help of single-cell metatranscriptomics, the replication dynamics of viruses in different tissues and cells of ticks can be analyzed; through spatial transcriptomics, the distribution characteristics of viruses in the vector can be accurately located. This multi-technology integration will help us more accurately explain the pathogenesis of diseases. At the same time, the continuous decline in sequencing costs and the widespread application of portable sequencing devices are pushing transcriptomics technology from the laboratory to the “on-site prevention and control” scenario - for example, carrying out direct detection of metatranscriptomics at ports and disease-endemic areas, thus achieving real-time identification and risk assessment of pathogens.

In summary, transcriptomics has become a “core technical pillar” in the disease prevention and control system. It not only helps to deeply analyze the occurrence and evolution of infectious diseases, but also provides key evidence for formulating scientific and efficient prevention and control strategies. Currently, globalization and climate change have exacerbated the risk of infectious disease transmission. Against this backdrop, fully leveraging the technological advantages of transcriptomics is not only an important way to enhance global disease prevention and control capabilities, but also a key measure to safeguard human health.

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